ACCELERATION OF COEVOLUTION DETECTION FOR PREDICTING PROTEIN INTERACTIONS

by

Alex Rodionov

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Graduate Department of Electrical and Computer Engineering
University of Toronto

Abstract

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Protein function is the ultimate expression of the genetic code of every organism, and determining which proteins interact helps reveal their functions. MatrixMatchMaker (MMM) is a computational method of predicting protein-protein interactions that works by detecting co-evolution between pairs of proteins. Although MMM has several advanced features compared to other co-evolution-based methods, these come at the cost of high computation, and so the goal of this research is to improve the performance of MMM. First we redefine the computational problem posed by the method, and then develop a new algorithm to solve it, achieving a total speedup of 570x over the existing MMM algorithm for a biologically meaningful data set. We also develop hardware which has not yet succeeded in further improving the performance of MMM, but could serve as a platform that could lead to further gains.

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Chapter 1

Introduction

Proteins are one of the basic building blocks of all living organisms. The genetic code encoded within DNA molecules in every cell is a blueprint for creating proteins, which serve specific functions within an organism, and through those functions are involved in virtually every biological process in nature. By studying the functions of proteins, we can gain insight into the workings of life.

Most proteins carry out their functions by interacting with other proteins [41], and these protein-protein interactions (PPIs) play a key role in regulating many important biological processes. These include signal transduction (communication within and outside the cell), DNA replication, and muscle contraction [52]. Many diseases are the result of a dysfunction or breakdown in the signaling pathways mediated by PPIs [32]. Consequently, building a map of interacting proteins helps provide information for developing treatments for those diseases.

Approaches to detecting PPI can be broadly classified into two categories [41]: experimental, and computational. Experimental methods are performed in the lab using real protein samples, and include techniques such as Yeast-two-Hybrid (Y2H) [53] and Tandem Affinity Purification with Mass Spectrometry (TAP-MS) [47]. They are costly, time-consuming, can only be applied to a subset of known proteins, and have high error rates [48]. Computational methods make use of *a priori* biological data about proteins, such as the DNA sequences that encode them, or the shape of their complete three-dimensional structures, in order to make predictions as to which proteins interact. They have their own drawbacks – being predictive in nature, computational approaches often fail to give a complete and accurate picture of PPIs. The two classes of approach complement each other, with computational methods making predictions that can then be studied in detail experimentally, and experimental data being used to refine the models upon which predictive computational methods are built.

No one class of methods is above the rest – the best ”gold standard” data sets on known protein-protein interactions come from predictions verified by multiple methods [8], and thus the development of new methods of PPI detection should provide additional perspectives upon which to discover new interactions and verify existing ones.

MatrixMatchMaker [44] (MMM) is a novel theoretical method of PPI detection that makes predictions based on the correlated evolutionary rates of families of similar proteins found across many species. MMM has numerous advantages compared to other similar evolution-based methods (discussed in Section 2.2), at the expense of being more computationally demanding, specifically, having an exponential worst-case runtime complexity (Section 2.3.7).

1.1 Origins of the Research Project

The work presented in this thesis is the result of an interdisciplinary collaboration with the Department of Medical Biophysics/Ontario Cancer Institute, with the aim of applying engineering expertise in algorithm, software, and hardware design to accelerate a computationally demanding scientific application that would benefit from such a speedup.

In May of 2009, my supervisor Jonathan Rose and I were approached by Dr. Elisabeth Tillier from the Department of Medical Biophysics at the University of Toronto.

She was on the thesis defense committee of another one of Jonathan's graduate students, William Lo, whose thesis [26] was about hardware acceleration of a medical application. She came to us describing a computationally demanding application of her own – Matrix-MatchMaker (MMM), a novel method of detecting protein-protein interactions – with the hope that we could assist in giving this application the same hardware acceleration treatment.

1.2 Goals

The goal of this research is to accelerate the MMM application, thus allowing larger data sets to become computationally tractable for analysis, potentially leading to new science. Originally, our goal on the Engineering side of this collaboration was strictly to accelerate the MMM algorithm using hardware, but that is not a prudent course of action until algorithm-level thinking and optimizations have been applied, which in turn cannot be done unless the underlying problem targeted by the algorithm has been well-defined and understood.

Given the above, we intend to achieve the goal of accelerating MMM by:

1. Understanding the computational problem presented by MMM and writing a formal problem definition, and redefining the problem if necessary to aid algorithm design.
2. Developing a faster software algorithm to solve the problem.
3. Implementing some subset of the new algorithm in hardware to further increase performance, if possible.

1.3 Overview

The work presented in this thesis begins with an attempt to understand the MMM [44] method of PPI detection from a mathematical and algorithmic point of view. Extracting a problem definition from the application source code and the Methods section of the original paper ([44]) reveals that the problem, and the algorithm used to solve it, do not exactly match the functional goal stated in the paper.

This prompted the creation of a new problem definition for MMM, which we call *strict*, to differentiate it from the original problem, which is referred to as *non-strict*. A new algorithm is then developed to solve the strict version of the problem via decomposition into many *maximum clique* graph sub-problems, and solving them using a modified version of an existing branch-and-bound maximum clique algorithm.

Finally, an attempt is made to accelerate part of the new algorithm by creating a digital system on a Field Programmable Gate Array (FPGA) that implements a parallel maximum clique solver. This is done with the assumption that since the maximum clique subproblems have exponential worst-case time complexity, then they would dominate the runtime of the new algorithm when given large enough inputs, and therefore comprise the ideal part of the overall algorithm to accelerate with hardware.

This thesis will begin by describing MMM and any relevent biological background in Chapter 2, including a problem definition for the original non-strict version of MMM. Also included will be a description of the maximum clique problem, the chosen algorithm that will be used to solve it, and a survey of previous work on hardware acceleration of max clique.

Chapter 3 contains the definition of the new, strict MMM problem and describes the algorithm that is developed to solve it, along with results showing the performance and accuracy of the new algorithm versus that of the original. Chapter 4 details the hardware design of an FPGA-based parallel maximum clique solver, while Chapter 5 concludes.

Chapter 2

Background

This chapter provides some necessary background for understanding the new work presented in Chapters 3 and 4. Section 2.1 provides background on protein-protein interactions along with methods used to detect and predict them, with Section 2.2 specifically covering coevolution-based methods. Section 2.3 describes MatrixMatchMaker as presented in [44], including the existing problem definition and algorithm. Section 2.4 describes graph-theoretical tools that will be used later on in developing an improved MMM algorithm. Section 2.5 lists previous work in building hardware engines to solve the maximum clique problem. Finally, Section 2.6 describes the data sets that will be used as inputs to gather results in Chapters 3 and 4.

2.1 Protein-Protein Interactions

In this section, we describe the ways in which proteins interact and provide an overview of some of the experimental and computational methods that are currently used to detect and predict interactions.

2.1.1 Types of Interactions

Proteins can either interact as pairs (binary interactions) or combine with more than one other protein to form a protein complex (co-complex interactions). Additionally, the interactions may form long-term stable structures, or they may be transient and short-lived. There is also a distinction between physical interaction and functional interaction – the latter does not necessarily imply the former. Functionally interacting proteins can, for example, be part of the same biochemical pathway which accomplishes some task without the two proteins ever being in physical contact.

Interaction can also be considered between protein domains, rather than entire proteins. Domains are subunits of proteins, encoded by subsections of the overall amino acid sequence, that can be independent structurally and functionally from each other. An interaction between two multi-domain proteins may take place at one or more of their domains and not necessarily involve the entire structure of the protein.

2.1.2 Experimental Methods

Several experimental methods exist to directly observe evidence of protein-protein interactions. The two most widely-used are Yeast Two-Hybrid (Y2H) and Tandem Affinity Purification combined with Mass Spectrometry (TAP-MS) [39].

In the Y2H method, a modified version of a transcriptional activator protein is synthesized and spliced into a yeast cell's genome. In its unmodified form, this activator protein would normally bind to DNA and causes a gene to become active and lead to the synthesis of some other protein. The modified version, however, is broken in half (into its two component domains) and to each half is attached the two proteins of interest that are desired to be tested for pairwise interaction. By being broken in half, this modified transcription protein can no longer perform its function. However, if the two proteins of interest do interact, then the two halves will connect and make the transcription protein whole again. It can then perform its function of binding to DNA and activating the expression of a gene, which synthesizes a protein. The presence of that protein then indicates whether the original interaction occurred.

Y2H is used to detect binary physical interactions, and since it is performed on living yeast cells it can detect both stable and transient interactions.

TAP-MS, on the other hand, is primarily used to study the composition of stable protein complexes that involve many proteins. With this method, a protein of interest is modified to include a tag structure, and is allowed to interact in a cellular environment and form complexes. One or two purification steps are performed to wash away everything except the structural tag, thus preserving the protein of interest and its interaction partners. After purification, only the protein complexes remain and mass spectrometry is performed to discover the identity of the other members of the complex.

There are numerous disadvantages of using experimental methods [41]. For one, they are not applicable to all proteins or protein interactions. For example, it is difficult to study transient complexes experimentally. They are also expensive and time-consuming, and often have low accuracy with inconsistent results between different methods [14].

2.1.3 Computational Methods

Complementing experimental methods, computational methods have been developed to predict the presence of interactions between proteins, of which some will be described here.

Gene neighbour methods [4] rely on the observation that interacting proteins tend to be encoded in neighbouring areas in an organism's genome. The presence of similar gene clusters in related organisms can be used to predict that the proteins encoded by those genes interact. This technique is not useful in eukaryotic organisms (organisms whose cells have a nucleus) because interacting proteins tend to no longer occur close together in their genomes.

The gene fusion method [27] relies on the observation that interacting proteins found in one genome have homologous variants of their amino acid sequences fused into a single gene in some other genome. It is thought that the fusion occurs to optimize the expression of these interacting proteins.

There also exist structural approaches to predicting PPIs, which examine the folded three-dimensional structures of proteins. Naturally, they are limited to proteins for which structures are known. One class of structural methods attempts to search for complementary shapes between proteins at which they may form interfaces and interact [23]. In addition to predicting which proteins interact, it is also possible with structural methods to determine the nature of an interaction.

Another way to predict protein-protein interactions is by detecting coevolution, and this class of methods will be discussed in the next section.

2.2 Coevolution

Proteins that interact are more likely to coevolve (evolve at the same rate) than those that do not [17]. Thus, by determining whether two proteins coevolved, one can predict whether or not they interact. This section will describe coevolution and how that relationship can be leveraged for this purpose.

2.2.1 Definition

A protein is a chain of amino acid molecules, and the specific sequence of amino acids that defines a protein is coded for within DNA — three sequential nucleotides (A, G, T, or C) within a DNA strand specify one of 64 possible combinations, 20 of which correspond to amino acids found in nature. Uncorrected errors can occur when DNA is copied, causing one amino acid to be substituted for another, changing the structure of the protein. If this change is beneficial, then the cell and organism in which the mutation took place is more likely to survive and propagate that change (and the converse is also true). This is the process of natural selection and evolution.

Assume two proteins do interact, as part of some biochemical pathway within an organism. Then if one of the proteins happens to mutate, its structure may be changed such that it can no longer interact with its partner, distrupting a potentially important function within the host organism and decreasing its survival odds. Thus, if evolution is to occur, natural selection demands that *both* partners must evolve at more or less the same rate in order for continued interaction to be feasible. This is why coevolution between two proteins is a good indicator of possible interaction [17].

Although coevolution can be applied to entire proteins, it is also possible to detect coevolution (and interaction) between protein domains as well.

2.2.2 Homologous Proteins

A protein may evolve into multiple distinct variants, and those in turn may evolve again into different forms, and so forth, creating a *phylogenetic tree* of shared ancestry. Protein variants which share a common evolutionary ancestor are called *homologous*. Homologous proteins can further be classified as *orthologous*, meaning they now exist in different species, or *paralogous*, meaning they exist within the same species.

Orthologous proteins (orthologs) are created when a new species branches off, carrying a copy of the gene that encodes a protein, that is then free to evolve along its own path. Paralogous proteins (paralogs) arise when a gene is duplicated within a species' genome, which is then free to slowly change in function over evolutionary time.

Homologous proteins form a protein family, which share similar structure and function [13]. Many algorithms exist [25] that cluster proteins together into homologous protein families, based on the similarity of their amino acid sequences.

2.2.3 Measuring Evolutionary History

The existence of a family of homologous proteins represents the result of a shared evolutionary history [9]. It is possible to detect coevolution between two proteins by comparing two such histories, thus requiring two families of homologous protein variants. The following describes how an implied history of a single protein family can be quantified.

Proteins are strings of amino acids. It is possible to calculate a number, a *phylogenetic distance*, that represents how different two such strings are. Depending on the exact method used, this distance often corresponds to the number of amino acid substitutions required to transform one protein into the other and thus can be used to quantify the amount of evolutionary divergence between them [30].

Multiple Sequence Alignment (MSA) [15] is an algorithm that operates on all the homologous proteins within a protein family. During the process, gaps are inserted in between the amino acids as a best guess as to where amino acids have been inserted/removed with respect to other proteins in the family, in order to minimize the apparent differences in corresponding amino acid positions across the family.

After MSA is performed, all pairwise distances between the homologous proteins can be calculated and placed into a *distance matrix*. A simple method to calculate each distance is to count the number of differences between the aligned amino acid sequences of two proteins and divide by the length of the aligned sequences. Figure 2.1 illustrates an example family of homologous proteins that are first aligned with MSA and then have all their pairwise distances calculated using this simple method and placed into the resulting distance matrix. Tools such as CLUSTALW [43] are available for both performing MSA and creating distance matrices.

The calculated distance between any two proteins in a family represents the amount of evolution that has occurred between them and their common ancestors, providing a degree of relatedness. A distance matrix contains the distances between all the family members, and thus provides a quantitative representation of their history.

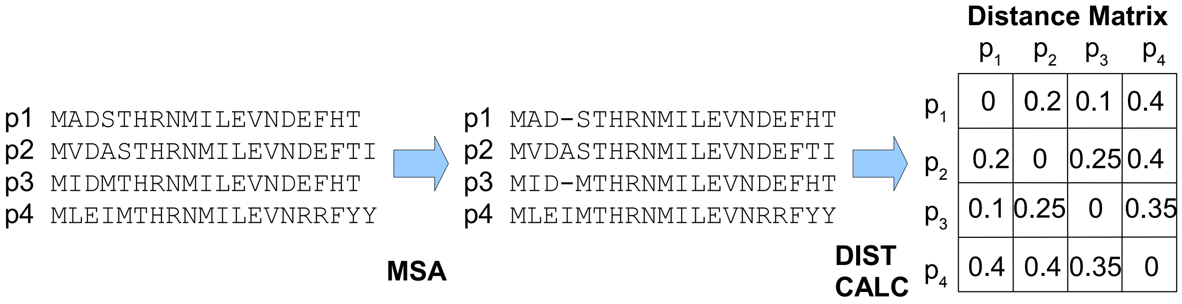

Figure 2.1: The process used to generate a distance matrix for a family of homologous proteins.

2.2.4 Existing Methods

There are a number of existing approaches for detecting PPI using coevolution. Mirror Tree [34, 36, 38, 33, 46] compares two distance matrices, representing the phylogenetic trees of two families of proteins. The algorithm calculates a correlation value for the pair of matrices which represents the likelihood that the two protein families interact. This method was used successfully in generating the *E. coli* protein interaction network [34].

Mirror Tree has some some disadvantages. Both matrices must contain distances between the same number of homologous proteins, from the same set of species. If more species exist in one family than the other, then the larger matrix must be trimmed. Similarly, if more than one protein exists from a species (a paralog), then one must be chosen, or iterated over in multiple calls of the algorithm.

Mirror Tree is a method of detecting *sequence coevolution*, meaning it relies on examining the amino acid sequences of pairs of proteins as a metric for coevolution. It is also possible to detect *expression coevolution* between proteins, which is based on the concept that in order for protein-protein interactions to occur properly, the amounts/concentrations of the interacting partners must be similar within an organism. The abundance of a protein is controlled by its amount of gene expression, which is in part governed by control mechanisms encoded in an organism's DNA. By correlating the amounts of expression between two proteins, it is possible to predict whether or not they interact.

Predictions arising from expression co-evolution have been found [17] to be largely independent from predictions due to sequence co-evolution, meaning that the two methods can complement each other.

An issue that arises with sequence coevolution methods is that natural selection within a protein can occur due to evolutionary pressures on the organism as a whole rather than in the service of preserving protein-protein interactions. Corrective post-processing measures can be employed to factor out this species-wide evolutionary signal in order to reduce false positive prediction of interactions [19].

Correlated Mutation Analysis (CMA) methods [40] search for finding mutations (or lack thereof), in the form of amino acid substitutions, in similar locations between two proteins. Amino acids have positive or negative electric charge, so a substitution can change the way a protein interaction physically happens, potentially disrupting it. Co-evolution must occur, and mutations must be correlated, for the interaction to continue. CMA can detect interaction between different locations of the same protein, and between proteins from the same homologous protein family.

2.3 MatrixMatchMaker

MMM is an application that predicts protein-protein interactions between two families of homologous proteins using coevolution. It does this by pairing up proteins from one family with proteins from the other which share common evolutionary histories.

These implicit evolutionary histories are provided, for each family, in the form of matrices containing all pairwise phylogenetic distances between the proteins in the family. These distances are values that represent the dissimilarity in the amino acid sequences of two proteins, and are used as a measure of the amount of evolution separating them from one or many common ancestors.

Consequently, two submatrices that are similar represent two subsets of proteins that share common evolutionary histories, and the MMM algorithm finds the largest such similar submatrix pairs (one submatrix from both protein families). A larger pair of similar submatrices corresponds to more species that exhibit the same pattern of change between their homologous versions of two proteins. Therefore, the size of the largest similar submatrix pair(s) represents the likelihood that the associated subsets of proteins coevolve, and therefore interact.

The MMM approach is similar to that of Mirror Tree, in that it looks for correlation between the distance matrices of two protein families. However, it goes further by correlating the sub-matrices as well, leading to the following advantages:

1. The two initial distance matrices may be of different sizes.
2. Coevolution can be considered over a subset of the homologous proteins, in addition to the entire families. Thus, coevolution can be inferred between the individual proteins of the two families.
3. As a corollary of 1, paralogs can be included in the protein families as well as orthologs, since multiple proteins from the same species are allowed.

2.3.1 Definitions

Let A and B be two families of homologous proteins, containing N proteins $\{a_1, a_2, \ \dots \ , a_N\}$ and M proteins $\{b_1, b_2, \ \dots \ , b_M\}$, respectively.

A distance matrix of size k is a $k \times k$ symmetric matrix with zeros in the main diagonal, and is synonymous with "$k \times k$ distance matrix".

Let $\hat{\text{A}}$ and $\hat{\text{B}}$ be phylogenetic distance matrices of size N and M, respectively. $\hat{\text{A}}$ contains all pairwise distances between members of A, and $\hat{\text{B}}$ contains all pairwise distances between members of B. The matrices are generated by performing a MSA on the proteins of each family and then calculating the pairwise distances between the aligned proteins.

$\hat{\mathrm{A}}_{ij}$ (or $\hat{\mathrm{B}}_{ij}$) refers to the distance between two proteins a_i and a_j (or b_i and b_j), and is independent of which rows and columns in the matrix each protein corresponds to.

A distance submatrix $\hat{\mathrm{C}}$ of size k is also a distance matrix, and it contains all pairwise distances between a subset of k proteins $\{a'_1, a'_2, \ldots, a'_k\}$ from A or $\{b'_1, b'_2, \ldots, b'_k\}$ from B. Again, $\hat{\mathrm{C}}_{ij}$ is the distance between two proteins a'_i and a'_j (or b'_i and b'_j), and is also independent of the row and column order of C. However, $\{a'_1, a'_2, \ldots, a'_k\}$ or $\{b'_1, b'_2, \ldots, b'_k\}$ can be arbitrarily chosen from A or B in any order.

2.3.2 Method Overview

MMM detects coevolution between the two protein families via the amount of shared evolutionary history between them. If $\hat{\mathrm{A}}$ and $\hat{\mathrm{B}}$ are thought to represent those histories, then their submatrices will represent sub-histories, over a subset of proteins.

A shared evolutionary history between families A and B then corresponds to a submatrix of $\hat{\mathrm{A}}$ and a submatrix of $\hat{\mathrm{B}}$ that are similar. The larger the size of these similar submatrices, the greater the amount of coevolution between the protein families.

MMM finds the largest such pairs of similar submatrices, with their size being the output, indicating the strength of the evidence for coevolution, and therefore interaction. A pair of similar submatrices also pairs up individual proteins from A and B, indicating that they coevolve. All submatrix pairs of the maximum size are found.

2.3.3 Similarity

At the core of MMM is the concept of similarity between two sub-matrices. The original definition, as given in [44], will be presented here.

The distances in matrix $\hat{\mathrm{A}}$ cannot be directly compared to distances in matrix $\hat{\mathrm{B}}$ because MSA was performed on each family separately, causing the distances in either matrix to represent only relative measures of evolution between members of the same

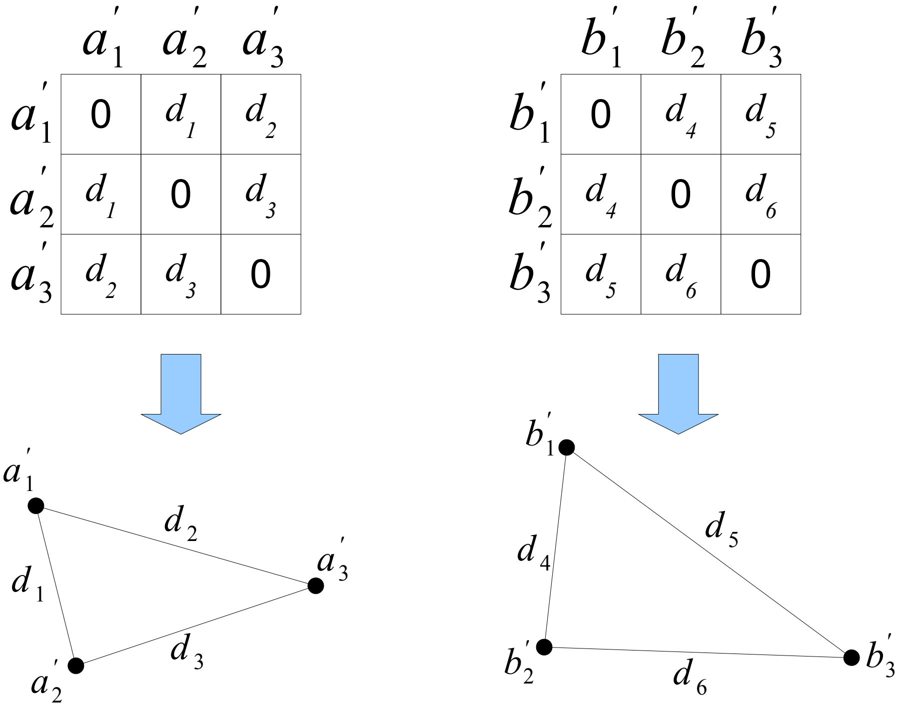

Figure 2.2: Two submatrices of size 3 for a triplet of proteins from each family

family. For this reason, MMM compares ratios of distances, rather than distances themselves, to infer a shared evolutionary history.

Submatrices of size 3

Consider two submatrices of size 3: $\hat{\text{A}}'$ containing distances between proteins $\{a'_1, a'_2, a'_3\} \subseteq$ A, and $\hat{\text{B}}'$ containing distances between proteins $\{b'_1, b'_2, b'_3\} \subseteq$ B. Each submatrix contains the three distances between all the proteins in each triplet, labeled in Figure 2.2 as d_1, d_2, d_3 in $\hat{\text{A}}'$ and d_4, d_5, d_6 in $\hat{\text{B}}'$.

$\hat{\text{A}}'$ and $\hat{\text{B}}'$ represent similar evolutionary histories, and therefore imply coevolution between a'_1 and b'_1, a'_2 and b'_2, and a'_3 and b'_3, if:

1. d_1 through d_6 are all nonzero, since zero distances imply no evolution, which can not be taken as evidence of coevolution.

2. $\frac{d_1}{d_4} \approxeq \frac{d_2}{d_5} \approxeq \frac{d_3}{d_6}$, which conceptually states that the two triangles formed by distances d_1, d_2, d_3 and d_4, d_5, d_6 are similar.

The definition in [44] expresses condition 3 as three separate relationships, each with an additional *tolerance* parameter α to control how exact the similarity must be:

$$\frac{|d_1 d_5 - d_2 d_4|}{d_1 d_5 + d_2 d_4} < \alpha \qquad \frac{|d_2 d_6 - d_3 d_5|}{d_2 d_6 + d_3 d_5} < \alpha \qquad \frac{|d_1 d_6 - d_3 d_4|}{d_1 d_6 + d_3 d_4} < \alpha \tag{2.1}$$

When α equals 0, $\hat{\mathrm{A}}'$ and $\hat{\mathrm{B}}'$ must be exactly similar, with the nonzero entries of one submatrix being equal to a common multiplicative constant times the matching entries in the other. When α equals 1, the three relationships will always hold true as long as none of the distances d_1 through d_6 are zero. This parameter α is an input to MMM along with the distance matrices $\hat{\mathrm{A}}$ and $\hat{\mathrm{B}}$. Also note that in general, phylogenetic distances do not obey the triangle inequality, thus the analogy of similar submatrices to that of similar triangles should be taken as a conceptual aid.

Submatrices of size $k \geq 3$

The definition of similarity will now be extended for submatrices of larger size. First, note that the minimum size for similar submatrices is 3, since a submatrix of size 1 contains only a single, zero distance between a protein and itself, and two submatrices of size 2 can be trivially made to equal each other with a choice of a single scaling factor.

Let $\hat{\mathrm{A}}'$ and $\hat{\mathrm{B}}'$ be $k \times k$ submatrices of $\hat{\mathrm{A}}$ and $\hat{\mathrm{B}}$ respectively. Each submatrix represents all pairwise distances between a subset $\{a'_1, a'_2, \ \ldots \ , a'_k\}$ of A and a subset $\{b'_1, b'_2, \ \ldots \ , b'_k\}$ of B. Finally, let the *tolerance* α be a value in $[0, 1]$.

$\hat{\mathrm{A}}'$ and $\hat{\mathrm{B}}'$ are said to be *similar* within tolerance α if for any choice of 3 distinct indices u, v, w between 1 and k, the submatrix of size 3 formed by the distances between a'_u, a'_v, and a'_w is similar to the submatrix of size 3 formed by the distances b'_u, b'_v, and b'_w.

2.3.4 Problem Definition

Define a *match* of size k to be a set of k protein pairs $\{(a'_1, b'_1), (a'_2, b'_2), \ldots, (a'_k, b'_k)\}$ such that $\mathrm{A}' = \{a'_1, a'_2, \ldots, a'_k\} \subseteq \mathrm{A}$, $\mathrm{B}' = \{b'_1, b'_2, \ldots, b'_k\} \subseteq \mathrm{B}$, and the two $k \times k$ submatrices formed by the distances between A' and B' are similar as defined in Section 2.3.3. Additionally, proteins a'_i and b'_i in each of the k pairs must come from the same species. Let M^k be the set of all matches of size k.

Given two families of proteins and their phylogenetic distance matrices $\hat{\mathrm{A}}$ and $\hat{\mathrm{B}}$ as in Section 2.3.1, and a tolerance parameter α as in Section 2.3.3, the MMM problem calls for finding the set M^{k^*}, where k^* is the largest possible value of k such that M^{k+1} is empty. If no such k exists, MMM returns the empty set.

The value k^* represents the amount of coevolution between the two protein families, and each match in M^{k^*} represents a set of coevolving protein pairs.

2.3.5 Tolerance Adjustment

The existing implementation of the MMM algorithm provides an optional feature to reduce the tolerance α as a function of phylogenetic distance. This allows a more stringent comparison to take place when the distances involved are very small or very large, thereby assigning a lesser biological significance to such extreme distances.

To implement the optional tolerance adjustment, each of the six distances involved in the comparison of two submatrices of size 3 is input into a piecewise linear function, shown in Figure 2.3. The function's shape is configured with three parameters: `stepLo`, `stepHi`, and `stepMax`. The output of each function evaluation is an adjusted value of the tolerance, α'. The minimum of the six resulting adjusted tolerances is then substituted for α in the similarity comparison of the submatrices.

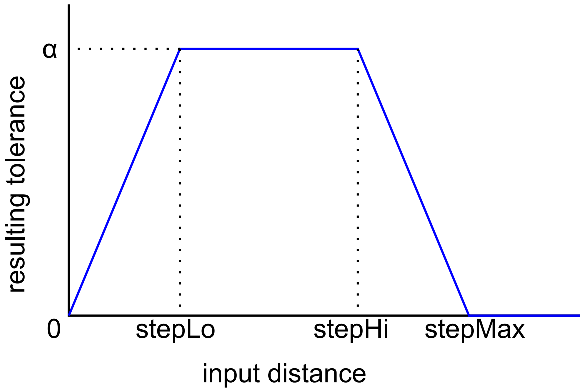

Figure 2.3: Piecewise-linear function for adjusting the tolerance based on distance

2.3.6 Algorithm

The existing MMM algorithm's outer loop (Procedure 1) iterates over all possible pairs of submatrices of size 3. For each pair that is similar, represented by the set of pairs Q, a recursive subroutine doRecursion (Procedure 2) is called to expand Q.

This is done by attempting to include another protein pair (i', j') in Q from a set of protein pairs that are not in Q. For each such attempt, every pair of submatrices of size 3 formed by (i', j') and all combinations of existing protein pairs in Q are tested for similarity.

Procedure 1 MMM ()

```
$M^{k^*} = \emptyset$
$k^* = 0$
for $i_1 = 0$ to $N$, $i_2 = i_1 + 1$ to $N$, $i_3 = i_2 + 1$ to $N$ do
  for $j_1 = 0$ to $M$, $j_2 = 0$ to $M$, $j_3 = 0$ to $M$ do
    if $(N - i_1) + 3 < k^*$ then
      return $M^{k^*}$
    end if
    $Q = \{(i_1, j_1), (i_2, j_2), (i_3, j_3)\}$
    if similarTriplets $(i_1, i_2, i_3, j_1, j_2, j_3)$ then
      doRecursion $(Q, i_1)$
    end if
  end for
end for
return $\{k^*, M^{k^*}\}$
```

Procedure 2 doRecursion (Q, i_1)

```
for $i' = i_1 + 1$ to $N$ do
  for $j' = 1$ to $M$ do
    $good$ = true
    for all $(i_x, j_x), (i_y, j_y) \in \mathrm{Q},\ x < y$ do
      if not similarTriplets $(i_x, i_y, i', j_x, j_y, j')$ then
        $good$ = false
      end if
    end for
    if $good$ then
      $\mathrm{Q}' = \mathrm{Q} \cup \{(i', j')\}$
      doRecursion $(\mathrm{Q}', i')$
    end if
  end for
end for
if $|\mathrm{Q}| \geq k^*$ then
  if $|\mathrm{Q}| > k^*$ then
    $\mathrm{M}^{k^*} = \emptyset$
    $k^* = |\mathrm{Q}|$
  end if
  $\mathrm{M}^{k^*} = \mathrm{M}^{k^*} \cup \{\mathrm{Q}\}$
end if
```

Procedure 3 similarTriplets $(i_1, i_2, i_3, j_1, j_2, j_3)$

```
$d_1 = \hat{\mathrm{A}}_{i_1 i_2}$;   $d_2 = \hat{\mathrm{A}}_{i_2 i_3}$;   $d_3 = \hat{\mathrm{A}}_{i_1 i_3}$
$d_4 = \hat{\mathrm{B}}_{j_1 j_2}$;   $d_5 = \hat{\mathrm{B}}_{j_2 j_3}$;   $d_6 = \hat{\mathrm{B}}_{j_1 j_3}$
if $d_1 = 0$ or $d_2 = 0$ or $d_3 = 0$ or $d_4 = 0$ or $d_5 = 0$ or $d_6 = 0$ then
  return false
end if
if not sameSpecies($a_{i_1}, b_{j_1}$) or not sameSpecies($a_{i_2}, b_{j_2}$) or not sameSpecies($a_{i_3}, b_{j_3}$) then
  return false
end if
$\alpha' = \min(\mathrm{PWLFunc}(d_i), 1 \leq i \leq 6)$ // optional, set $\alpha' = \alpha$ otherwise
$c_1 = |d_1 d_5 - d_2 d_4| \div (d_1 d_5 - d_2 d_4)$
$c_2 = |d_2 d_6 - d_3 d_5| \div (d_2 d_6 - d_3 d_5)$
$c_3 = |d_1 d_6 - d_3 d_4| \div (d_1 d_5 - d_3 d_4)$
if $c_1 < \alpha'$ and $c_2 < \alpha'$ and $c_3 < \alpha'$ then
  return true
else
  return false
end if
```

If all tests pass, (i', j') is included in Q, forming a larger match, and doRecursion is called recursively to continue to expand the match. Recursion terminates once ther are no more protein pairs that can be added. PWLFunc refers to an evaluation of the piecewise linear function described in Section 2.3.5.

At each stage of recursion, M^{k^*} and k^*, representing the largest matches and their size (respectively) are updated to reflect the largest matches found so far.

There is a single early exit condition in Procedure 1 that terminates the algorithm if the number of remaining protein pairs in the outer loop is less than k^*.

2.3.7 Algorithm Complexity

The worst-case runtime complexity of the algorithm presented in Section 2.3.6 is exponential. To see this, consider the case when the two input protein families A and B both contain N proteins from the same species, and the distances between any two proteins is the same nonzero value c. Since the two distance matrices $\hat{A}$ and $\hat{B}$ are identical, we know trivially that the largest pair of similar submatrices consists of $\hat{A}$ and $\hat{B}$ themselves, with the largest match size k^* being equal to its maximum value of N.

However, there are $N!$ valid matches that arise from pairing up $\hat{A}$ and $\hat{B}$, corresponding to all the possible permutations of pairing the N proteins of A with the N proteins of B. Since the algorithm must identify and list each one of these matches, we know that the complexity is at least $O(N!)$, which is equivalent to exponential time.

2.4 The Maximum Clique Problem

This section reviews an important graph problem that will become relevant in Section 3 as part of the new algorithm, which solves a redefined MMM problem in a graph-theoretical manner.

2.4.1 Problem Definition

The maximum clique problem ("max clique") problem is a well-known NP-hard problem [20]. Given an undirected graph $G = (V, E)$, a clique $Q \subseteq V$ is a subset of vertices such that $(u, v) \in E$ for all $u, v \in Q$ when $u \neq v$. A maximum clique is a clique Q such that no clique of size greater than $|Q|$ exists in G. The maximum clique problem calls for finding one or all of the maximum cliques of a graph.

2.4.2 Östergård's Algorithm

This is an algorithm [31] that provides an exact solution to the maximum clique problem. Procedure 4 lists pseudocode for a modified version of the algorithm which returns all the maximum cliques of a graph.

Östergård does not provide a complexity analysis for his algorithm, as seems to be common for maximum clique algorithms [45, 51, 22, 7]. The performance of these algorithms is very dependent on the structure of the input graph. The problem of finding a single maximum clique in an arbitrary graph is NP-hard, yielding a worst case exponential run time. Therefore, it stands to reason that finding all the maximum cliques in a graph must be at least as hard.

Procedure 4 Ostergard($G = (V, E)$)

```
$\omega \leftarrow 0$
$Q \leftarrow \emptyset$
for $i = |V|$ to $1$ do
    $U \leftarrow \emptyset$
    for $j = i + 1$ to $|V|$ do
        if $(v_i, v_j) \in E$ then
            $U \leftarrow U \cup \{v_j\}$
        end if
    end for
    OstergardRecursive($\{v_i\}$, U)
    MSPV($v_i$) $\leftarrow \omega$
end for
return $\{Q, \omega\}$
```

Procedure 5 OstergardRecursive(q, U)

```
if $U = \emptyset$ then
    if $|q| > \omega$ then
        $\omega \leftarrow |q|$
        $Q \leftarrow \{q\}$
    else if $|q| = \omega$ then
        $Q \leftarrow Q \cup \{q\}$
    end if
else
    while $U \neq \emptyset$ do
        if $|q| + |U| < \omega$ then
            return
        end if
        $i \leftarrow \min\{j : u_j \in U\}$
        if $|q| + \text{MSPV}(u_i) < \omega$ then
            return
        end if
        $U \leftarrow U \setminus \{u_i\}$
        $U' \leftarrow \{u' \in U : (u_i, u') \in E\}$
        OstergardRecursive($q \cup \{u_i\}$, $U'$)
    end while
end if
```

2.4.3 Graph Colouring

Related to maximum clique is the graph colouring problem. Given a graph $G = (V, E)$, a colouring of the graph assigns a label $c(v)$ to each $v \in V$ such that $c(v) \neq c(u)$ if $(u, v) \in E$ for all vertices $u, v \in V$.

An optimal vertex colouring uses the least possible number of colours, which is referred to as a graph's *chromatic number* $\chi(G)$. The chromatic number is equal to a graph's maximum clique size, and finding χ and an optimal vertex colouring is an NP-hard problem [20]. Approximate algorithms exist [3] which can provide a vertex colouring that may use more than χ colours, but can be done in polynomial time with respect to graph size. The number of colours used in such colourings is an upper bound for the maximum clique size of a graph.

2.5 Hardware Maximum Clique Solvers

This section overviews previous work in creating hardware implementations of maximum clique algorithms. Bertoni et al. [2] presented an FPGA-based implementation of an approximate maximum clique solver that used a series of neural networks to estimate the maximum clique size. Their algorithm produced the optimal maximum clique size in many cases.

Perez et al. [28] implemented an exact maximum clique solver based on a model of computation originally intended for biological, DNA-based computers. Their approach is highly parallel, and solves the maximum clique problem in polynomial time but exponential circuit size, which limits the maximum size of the input graph. Using four Xilinx Virtex 4 [12] FPGAs, they report solving maximum cliques on graphs with up to 64 vertices in comparable time to modern software implementations.

Wakabayashi et al. [49] present a rather unusual FPGA-based maxmimum clique solver. Their method generates an instance-specific circuit which is hardwired to solve exactly one maximum clique problem, effectively making the compilation of the circuit by the CAD tool part of the algorithm. For their test cases, which were graphs of up to 200 vertices, the compilation time for each ranged from 1-2 hours and the finding of the maximum clique by the hardware required up to a few seconds. Including the compilation time as part of their algorithm run time, they still achieved an over 8x speedup against a software algorithm.

2.6 Data Sets

This section describes the pairs of distance matrices that we will be using as our inputs to generate the results in Chapters 3 and 4. These sets were provided to us by our collaborators, and we will describe the process used to generate them.

The first data set consists of 1225 pairs of distance matrices, corresponding to all the pairwise combinations of 50 distance matrices. In order to generate the matrices, the Homologene[1] database was used. It is a repository of proteins from many species, grouped into clusters of homologous proteins.

First, clusters containing at least one human protein were selected. Then, all the human proteins from all of the clusters were taken as a whole and re-clustered using the CD-HIT package [24], with the settings configured at 60% identity and 70% coverage. In other words, each CD-HIT cluster consists only of human proteins from the original Homologene clusters. The original Homologene clusters were then merged based on which of their human representatives existed together in the CD-HIT clusters. These merged Homologene clusters were the final protein families used.

Each cluster was then aligned using MAFFT [21], a tool for performing Multiple Sequence Alignment. Finally, after alignment, a distance matrix was created for each cluster using Protdist[2]. 1469 matrices existed at this point, and the largest 50 by protein count were selected to create the data set, which will be referred to as BATCH50 from this point on. The largest two distance matrices in this set have 85 and 71 proteins.

The second data set was created from the OMA database [1], another repository of homologous protein clusters. It consists of one pair of matrices, corresponding to the tubulin alpha and tubulin beta subunits found in many species. These proteins interact to create the microtubules found in cells, forming the cell's cytoskeleton. The proteins from the OMA database included in each matrix are listed in Appendix A. Each matrix was created by aligning the proteins of the two clusters using MAFFT and then calculating distances with Protdist, using the PMB setting for distance calculation. These two matrices, representing one MMM problem, will be referred to as the TUBULIN_AB dataset. The tubulin alpha and tubulin beta matrices contain 516 and 485 proteins, repsectively.

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[1] `http://www.ncbi.nlm.nih.gov/homologene/`

[2] http://evolution.genetics.washington.edu/phylip/progs.data.prot.html

Chapter 3

New Algorithm

This chapter represents the start of the new work presented in this thesis. First, the existing MMM problem, which we refer to as the non-strict problem is analyzed, and found to be inconsistent with the intent of the original MMM paper. Next, a new, strict MMM problem is defined that addresses this issue. Then, a new algorithm is described in detail that solves the strict MMM problem. Finally, the performance and correctness of this new algorithm is compared to that of the existing one.

3.1 Non-strict Problem Analysis

The original definition of the MMM problem defines two submatrices to be similar if their corresponding submatrices of size 3 are similar. In our search to find more efficient algorithms to solve the same problem, we have found that the use of submatrices of size 3 (as described in Section 2.3.3) is not conducive to finding similar evolutionary histories between two protein families.

Given four proteins, $a_i, a_j \in$ A and $b_x, b_y \in$ B, define a *ratio of paired distances* (RPD) as the following function of two protein pairs:

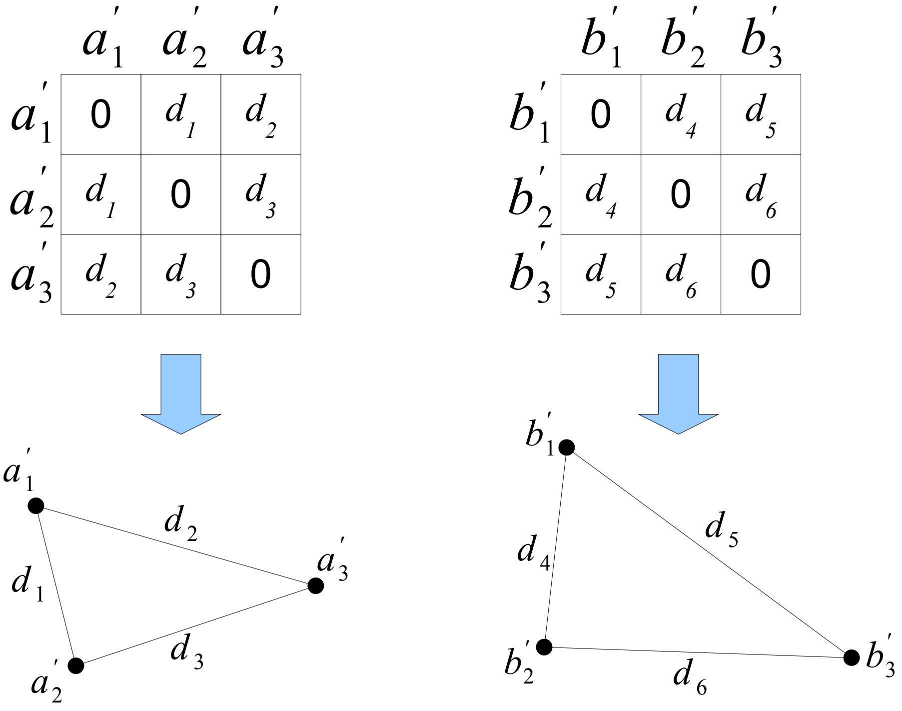


Figure 3.1: Two submatrices of size 3 for a triplet of proteins from each family.

$$R(a_i, b_x)(a_j, b_y) = \frac{\hat{\mathrm{A}}_{ij}}{\hat{\mathrm{B}}_{xy}} \quad \text{with } i \neq j \text{ and } x \neq y \tag{3.1}$$

For two submatrices of size 3 $\hat{\mathrm{A}}'$ and $\hat{\mathrm{B}}'$ (Figure 2.2, reproduced in Figure 3.1), the three relationships in Equation 2.1 define constraints on the distances in the submatrices, which can be rewritten as:

$$\frac{1}{\delta} \cdot \frac{d_2}{d_5} < \frac{d_1}{d_4} < \delta \cdot \frac{d_2}{d_5} \qquad \frac{1}{\delta} \cdot \frac{d_3}{d_6} < \frac{d_2}{d_5} < \delta \cdot \frac{d_3}{d_6} \qquad \frac{1}{\delta} \cdot \frac{d_1}{d_4} < \frac{d_3}{d_6} < \delta \cdot \frac{d_1}{d_4}$$
$$\text{with } \delta = \frac{1+\alpha}{1-\alpha} \tag{3.2}$$

Once rewritten in this form, it becomes more clear that each relationship constrains the ratio of two RPDs to be within δ, which is just a function of the tolerance, *alpha*.

The three RPDs that appear in Equation 3.1 are:

$$\begin{aligned} R(a'_1, b'_1)(a'_2, b'_2) &= \frac{d_1}{d_4} \\ R(a'_2, b'_2)(a'_3, b'_3) &= \frac{d_3}{d_6} \\ R(a'_3, b'_3)(a'_1, b'_1) &= \frac{d_2}{d_5} \end{aligned}$$

and each *similarity relationship* has the form:

$$\frac{1}{\delta} \cdot R_2 < R_1 < \delta \cdot R_2 \qquad \text{with } \delta = \frac{1+\alpha}{1-\alpha} \tag{3.3}$$

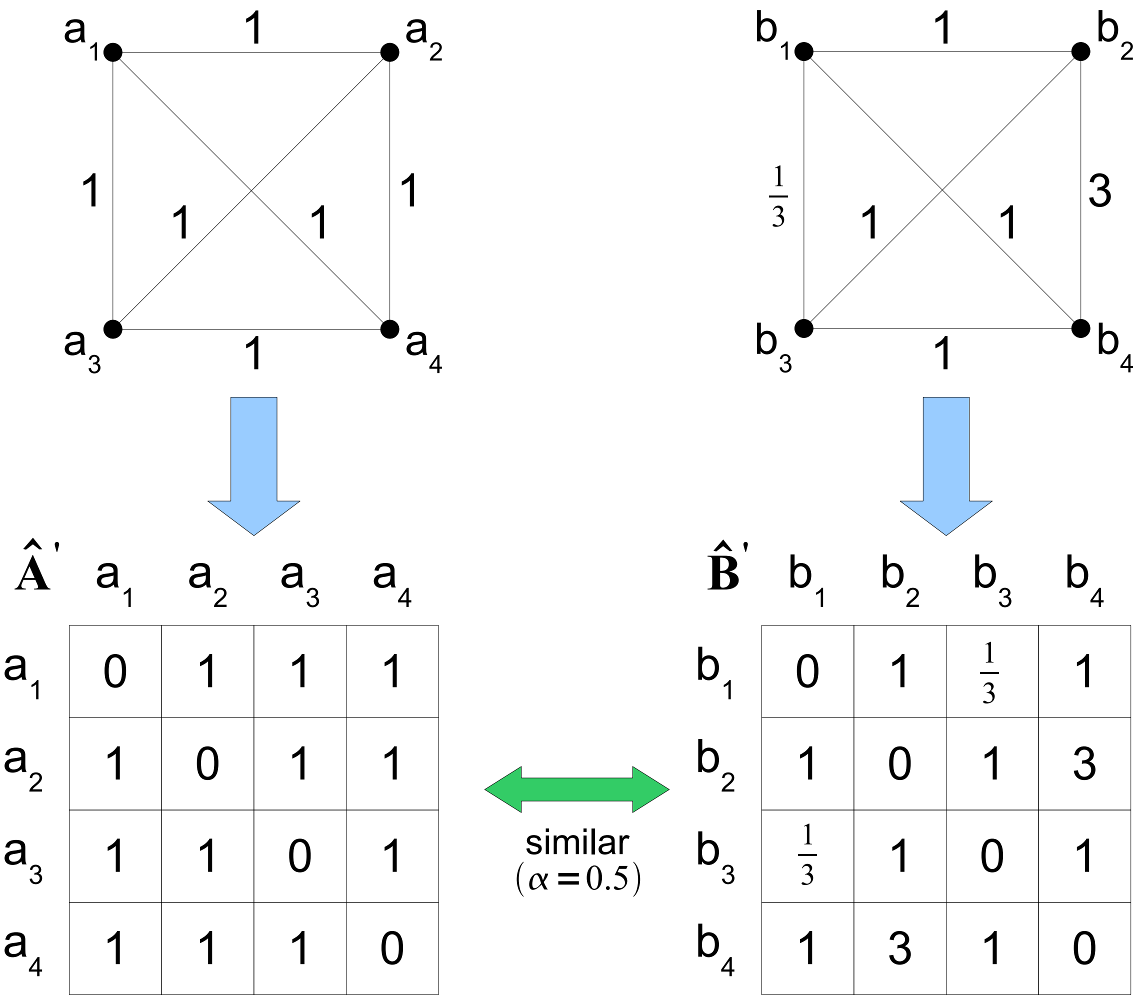
Thus, $\hat{\mathrm{A}}'$ and $\hat{\mathrm{B}}'$ together define three protein pairs (a'_i, b'_i) for $i = 1, 2, 3$, and for the two submatrices to be similar, it is necessary for every pair of RPDs between these three protein pairs to satisfy the similarity relationship given in Equation 3.3. This ensures that the two submatrices represent similar evolutionary histories, and that each (a'_i, b'_i) represents a coevolving pair of proteins.

MMM uses the similarity of pairs of submatrices of size 3 to define the similarity of pairs of submatrices of size greater than 3. However, this does NOT guarantee that every pair of RPDs between paired proteins will obey Equation 3.3. Consider the two submatrices $\hat{\mathrm{A}}'$ and $\hat{\mathrm{B}}'$ of size 4 as illustrated in Figure 3.2, and let $\alpha = 0.5$.

The similarity of $\hat{\mathrm{A}}'$ and $\hat{\mathrm{B}}'$ hinges on the similarity of four pairs of submatrices of size 3, representing all four possible ways to choose distinct, matching triplets of protein pairs from the set $\{(a'_i, b'_i) \colon i \in [1, 4]\}$, which are the protein pairings defined by the act of comparing $\hat{\mathrm{A}}'$ and $\hat{\mathrm{B}}'$.

Thus, the submatrix containing distances between the proteins $\left\{a'_x, a'_y, a'_z\right\}$ must be similar to the submatrix containing distances between the proteins $\left\{b'_x, b'_y, b'_z\right\}$ for $(x, y, z) \in \{(1, 2, 3), (1, 2, 4), (1, 3, 4), (2, 3, 4)\}$.

For the given submatrices, this is satisfied, meaning that under the existing MMM



$\hat{\mathbf{A}}'$	a_1	a_2	a_3	a_4
a_1	0	1	1	1
a_2	1	0	1	1
a_3	1	1	0	1
a_4	1	1	1	0

$\hat{\mathbf{B}}'$	b_1	b_2	b_3	b_4
b_1	0	1	$\frac{1}{3}$	1
b_2	1	0	1	3
b_3	$\frac{1}{3}$	1	0	1
b_4	1	3	1	0

Figure 3.2: Top: Two sets of 4 proteins and their pairwise distances. Bottom: Their distance submatrices, which are similar under $\alpha = 0.5$

problem definition, they are similar. However, the ratio of the RPDs $R\left(a'_1, b'_1\right)\left(a'_3, b'_3\right)$ and $R\left(a'_2, b'_2\right)\left(a'_4, b'_4\right)$ is 9, which disobeys the similarity relationship. Those two RPDs are never compared since the comparison requires 4 protein pairs, which cannot be expressed by choosing paired submatrices of size 3 in the manner described.

This example shows that the original problem definition is inconsistent with the stated intent in the original MMM paper [44] to discover coevolution between sets of proteins via their distance matrices. There, it is stated that two evolutionary histories are similar if the associated distance matrices are similar, which means that one matrix should be a scalar multiple of the other, within a tolerance. The problem definition is congruent with this ideal for submatrices of size 3, but not for larger submatrices, as some pairs of RPDs are not subject to the same constraints as other pairs.

3.2 Problem Redefinition

Given the flaw of the original stated MMM problem definition as exposed in Section 3.1, we have adopted a new problem definition as the operative one for the purposes of this work. This new problem definition will be referred to as the *strict MMM problem*, and is presented in this section. It only differs from the original (*non-strict*) MMM problem by its definition of the similarity between two distance matrices, such that all pairs of RPDs between paired vertices must now obey the similarity relationship, for submatrices of all sizes.

As before, we are given two sets of homologous proteins $\mathrm{A} = \{a_1, a_2, \ \ldots \ , a_N\}$ and $\mathrm{B} = \{b_1, b_2, \ \ldots \ , b_M\}$, along with their associated distance matrices $\hat{\mathrm{A}}$ and $\hat{\mathrm{B}}$, and a tolerance $\alpha \in [0, 1]$.

Let $\hat{\mathrm{A}}'$ be a submatrix of $\hat{\mathrm{A}}$, and $\hat{\mathrm{B}}'$ be a submatrix of $\hat{\mathrm{B}}$, and both submatrices be of size k. Then $\hat{\mathrm{A}}'$ and $\hat{\mathrm{B}}'$ are considered similar if and only if:

1. $\hat{\mathrm{A}}'_{ij} \neq 0$ and $\hat{\mathrm{B}}'_{ij} \neq 0 \qquad \forall\ i \neq j$

2. The RPDs $R(a'_i, b'_i)(a'_j, b'_j) = \frac{\mathrm{A}'_{ij}}{\mathrm{B}'_{ij}}$ and $R(a'_x, b'_x)(a'_y, b'_y) = \frac{\mathrm{A}'_{xy}}{\mathrm{B}'_{xy}}$ satisfy the similarity relationship (Equation 3.3) for all $i \neq j$ and $x \neq y$ between 1 and k.

If $\hat{\mathrm{A}}'$ and $\hat{\mathrm{B}}'$ are similar, and if proteins a'_i and b'_i come from the same species (for every $i \in [1, k]$), then the set of protein pairs $\{(a'_1, b'_1), (a'_2, b'_2), \ \ldots \ , (a'_k, b'_k)\}$ is considered to be a match.

Let M^k be the set of all matches of size k. The problem calls for finding the number k^* and the set M^{k^*}, with k^* being the largest possible value such that M^{k^*+1} is empty. If no such k^* exists, then the empty set is returned.

It will be shown in Section 3.4.2 that the solution to the strict MMM problem retains the biological legitimacy of the original non-strict MMM problem.

3.3 Algorithm

In this section, we develop an algorithm for solving the strict MMM problem defined in Section 3.2.

3.3.1 Graph-based Representation

First, we recast the strict MMM problem in a graph-theoretical manner. This is a more elegant representation of the problem than one which refers only to the input distance matrices.

Let $\mathrm{G} = (\mathrm{V}, \mathrm{E})$ be the *compatibility graph*, which represents the space of all possible solutions to the problem. The vertex set V represents all valid protein pairs between the input protein families A and B. That is, a vertex with label $a_i b_j$ exists for every protein pair (a_i, b_j) for $i \in [1, N]$ and $j \in [1, M]$ that has a_i and b_i as a member of the same species. For a vertex $v \in \mathrm{V}$ with label $a_i b_j$, define $v.a = i$ and $v.b = j$, representing the A and B proteins that v pairs up. Figure 3.3 provides a visual aid for this representation.

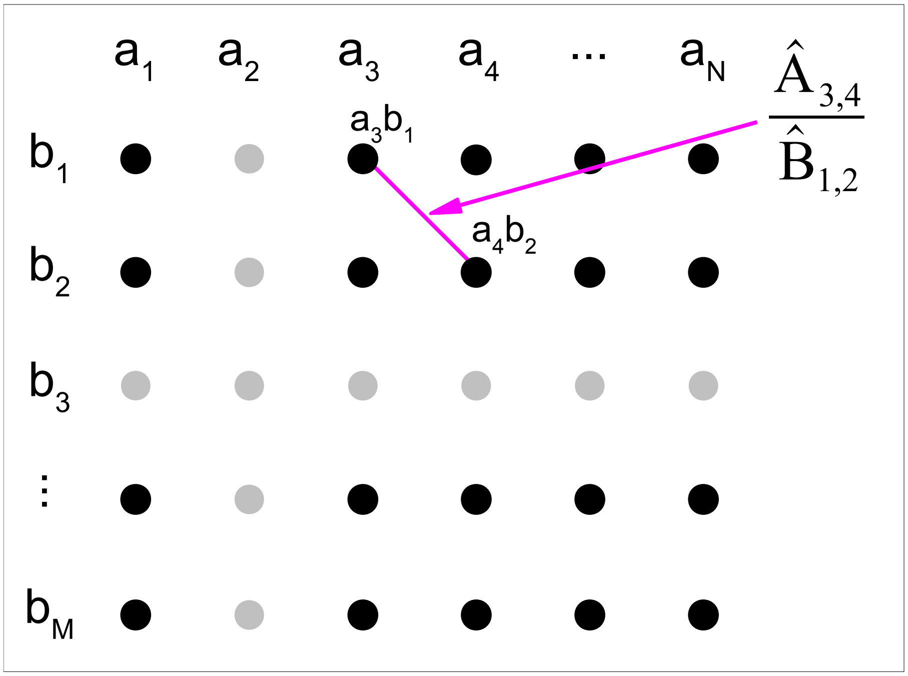


Figure 3.3: A sample graph G for two families of proteins. Dark circles are vertices representing all possible pairs of proteins from the same species, and greyed circles represent nonexistant vertices due to differing species labels. One edge is shown between vertices a_3b_1 and a_4b_2 along with its RPD label.

An edge $e \in \mathrm{E}$ exists between two vertices v and u in V if the RPD $R(u, v) = R(v.a, v.b)(u.a, u.b) = \hat{\mathrm{A}}_{v.a\,u.a} / \hat{\mathrm{B}}_{v.b\,u.b}$ exists and is nonzero. Each edge between two vertices u and v is labelled with its RPD $R(e) = R(u, v)$. Two RPDs are defined to be *compatible* if they obey Equation 3.3. Similarly, two edges e_1 and e_2 are compatible if their RPD labels $R(e_1)$ and $R(e_2)$ are compatible. Figure 3.4 shows this graphically, restating Equation 3.3 in the form of a number line. Finally, let $\Gamma(v)$ be the set of a vertex v's neighbours in G:

$$\Gamma(v) = \{u \in \mathrm{V} \colon (u, v) \in \mathrm{E}\}$$

We now show that within this graph-theoretical framework, a match can be represented by a subset of vertices from V that form a clique in which every pair of edges is compatible. First, a match is a set of protein pairs where each pair shares a species, and

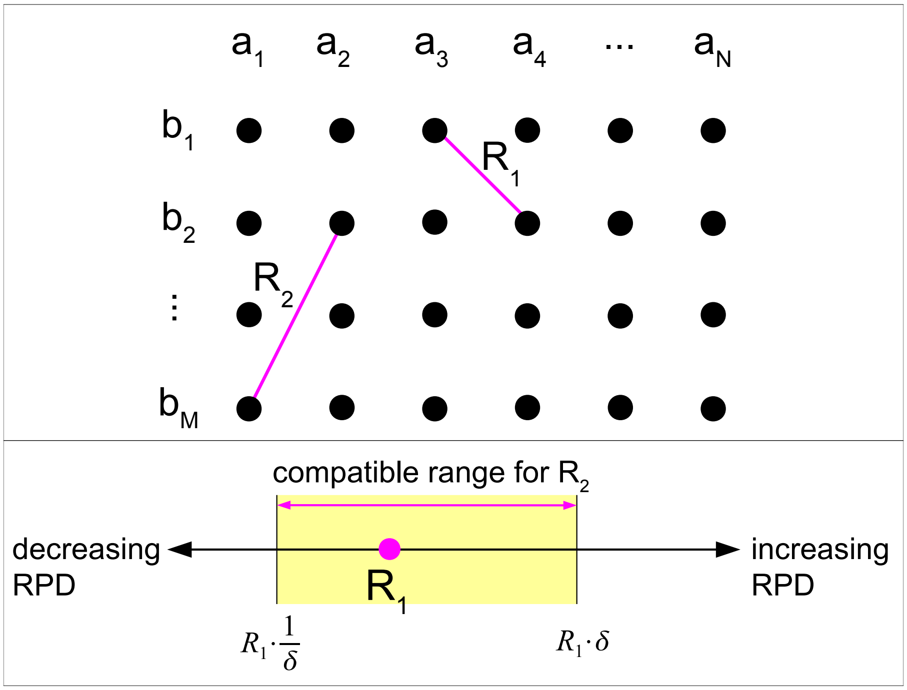


Figure 3.4: Top: Two edges with RPDs R_1 and R_2. Bottom: A graphical representation of the similarity relationship necessary for the two edges to be considered compatible.

this is satisfied by virtue of each vertex representing a pair of proteins from the same species. Next, the problem definition demands that in a match, the submatrices containing all the distances between the paired proteins must be similar. A clique implies that edges (and therefore RPDs) exist between every pair of proteins, which can only happen if none of the distances between the A or B proteins in the match are zero. This means that the associated distance submatrices for the protein subset will not contain zero entries outside the main diagonal – the first condition for submatrix similarity. Finally, the requirement that every pair of RPDs between protein pairs obey the similarity relationship is equivalent to the requirement that all edges be mutually compatible, according to the definition of edge compatibility. Figure 3.5 shows a match of size 4 as a clique containing 4 protein pairs.

Therefore, the problem definition, represented as a graph problem, calls for finding the set of *maximum compatible cliques* in G – the maximum cliques in G that contain only mutually compatible edges.

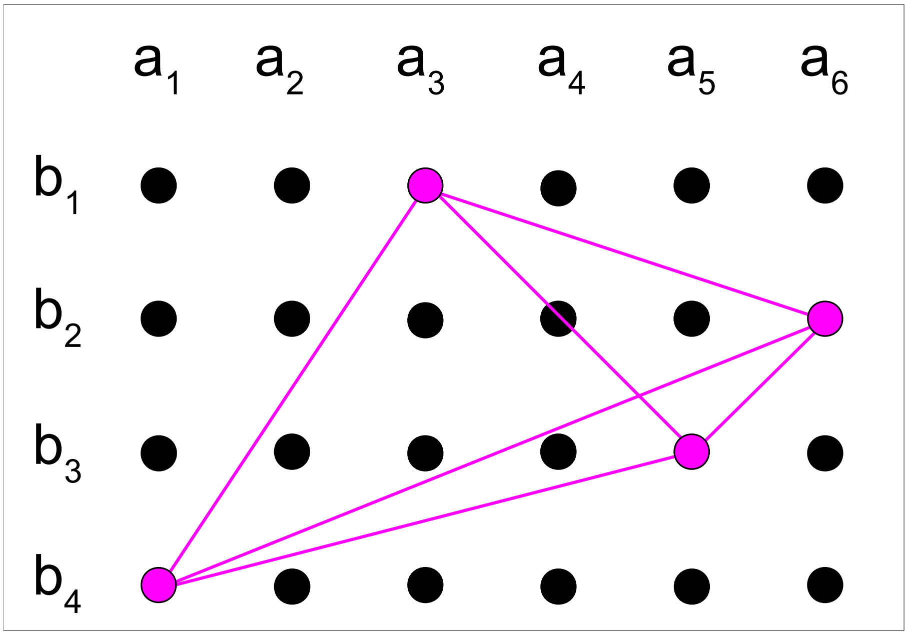


Figure 3.5: A clique representation of a match of size 4 containing protein pairs $\{(a_3, b_1), (a_6, b_2), (a_5, b_3), (a_1, b_4)\}$.

3.3.2 Method

Here, we outline the method used by the algorithm to solve the strict problem by finding the maximum compatible cliques of the compatibility graph G. The basic idea is to find maximum cliques on subgraphs of G which are constructed to contain only mutually compatible edges, and to choose these subgraphs such that all possible maximum compatible cliques are explored in the end. First, we will introduce a shortcut that will make it easier to find sets of mutually compatible edges.

Definition. An edge f is *forward-compatible* with edge e if $R(e) \leq R(f) < \delta R(e)$, with $\delta = (1 + \alpha)/(1 - \alpha)$.

Lemma 1. *Let* $\{r_1, r_2, \ldots, r_k\}$ *be a set of RPDs, and let* r_{min} *be an RPD from that set such that* $r_i \geq r_{min}$ *for all* i*. If all* r_i *are forward-compatible with* r_{min}*, then all* r_i *are compatible with each other.*

Proof. Suppose that all r_i are forward-compatible with r_{min} but there exist two RPDs r_i and r_j that are not compatible, and that without loss of generality, $r_j > r_i$. Since they are not compatible, $r_j > \delta r_i$, but this is impossible because $r_{min} \leq r_i < r_j < \delta r_{min}$ and $\delta \geq 1$. □

Lemma 2. *Let* $\{r_1, r_2, \ \dots \ , r_k\}$ *be a set of RPDs that are all compatible with each other, and let* r_{min} *be an RPD from that set such that* $r_i \geq r_{min}$ *for all* i. *Then, for all* $i \in [1, k]$, r_i *is forward-compatible with* r_{min}.

Proof. By the definition of r_{min}, $r_i \geq r_{min}$ for all i, so the left-hand side of the forward-compatibility relationship is trivially satisfied for all r_i. Now assume that all r_i are pairwise compatible and suppose that there exists an $r_i \geq \delta r_{min}$. But this is impossible, because then r_{min} and r_i would not be compatible. Thus, the right-hand side of the relationship is satisfied by contradiction. □

Theorem 3.1. *Let* $\{r_1, r_2, \ \dots \ , r_k\}$ *be a set of RPDs, and let* r_{min} *be an RPD from that set such that* $r_i \geq r_{min}$ *for all* i. *All* r_i *are compatible with each other if and only if every* r_i *is forward-compatible with* r_{min}.

Proof. True by Lemmas 1 and 2. □

Definition. The *forward-compatible neighbours* of some vertex v, with respect to an edge e, are:

$$\Gamma'(v, e) = \{u \in \Gamma(v) \colon \text{edge } (u, v) \text{ is forward-compatible with } e\}$$

A match is a clique, so given a graph that contains mutually compatible edges, any cliques found will be matches. Each of the matches of maximum size in G, which the problem (as defined in this chapter) calls for finding, is embedded in some subgraph H of G that consists of mutually compatible edges. Therefore, finding the maximum cliques of each H will yield these matches of maximum size in G.

Furthermore, each such subgraph H contains an *edge(s) of minimum RPD*, which have the smallest RPD amongst all edges in H. Theorem 3.1 tells us that H consisting of mutually compatible edges is synonymous with H consisting of edges that are forward-compatible with its edge(s) of minimum RPD.

Therefore, the strategy of our new algorithm is to iterate over each edge e_{min} in E, and assume that e_{min} is an edge of minimum RPD of a subgraph H that contains a subset of the maximum matches of G that we hope to find. For each e_{min}, we build a subgraph H which consists of edges of G that are forward-compatible with e_{min}. Then, the maximum cliques of H are found, each corresponding to a match of maximum size.

If our assumption about e_{min} was wrong, and H did not contain any matches of the maximum size k^*, then the matches returned through finding maximum cliques will be of smaller than k^* and can be ignored in the end. By keeping track of only the largest maximum cliques found over all iterations of e and generated subgraphs H, the solution to the problem is found.

Our algorithm operates such that each e_{min} is required to be part of every match found in its generated subgraph H. This makes each H smaller, because matches are forced to contain the two endpoint vertices of e_{min}, v_i and v_j, and the vertex set of H can be pruned accordingly. This results in a smaller maximum clique problem, and the two endpoints v_i and v_j to be implicitly included in every match found in H.

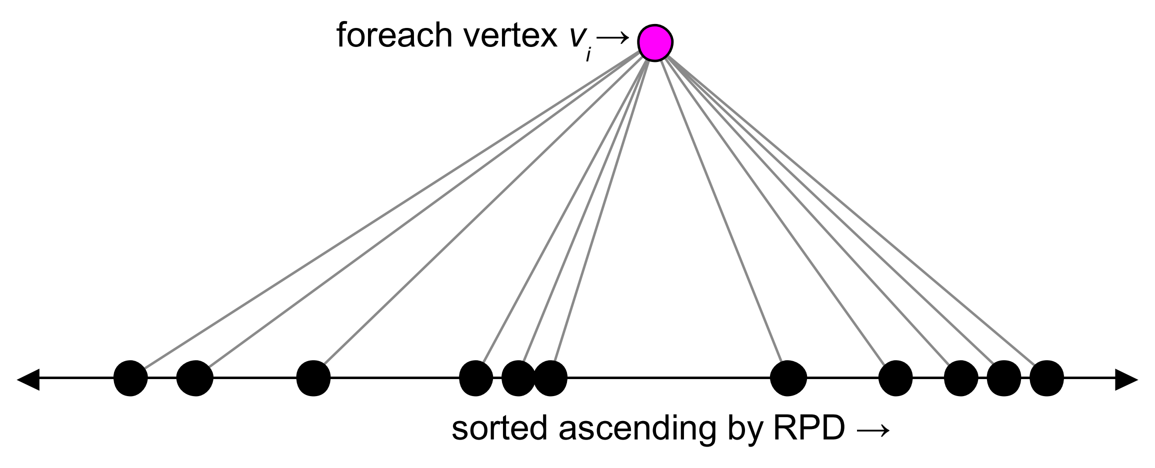


Figure 3.6: Step 1 of the new algorithm: A vertex v_i is chosen, and its neighbours sorted.

The following is a graphical summary of the algorithm. First, we iterate over all edges e_{min} in two steps. A vertex v_i is chosen by the outer loop (Figure 3.6), and its neighbours sorted by increasing RPD of the edge to v_i. Each neighbour v_j is then visited, and together with v_i, forms the current e_{min} (Figure 3.7).

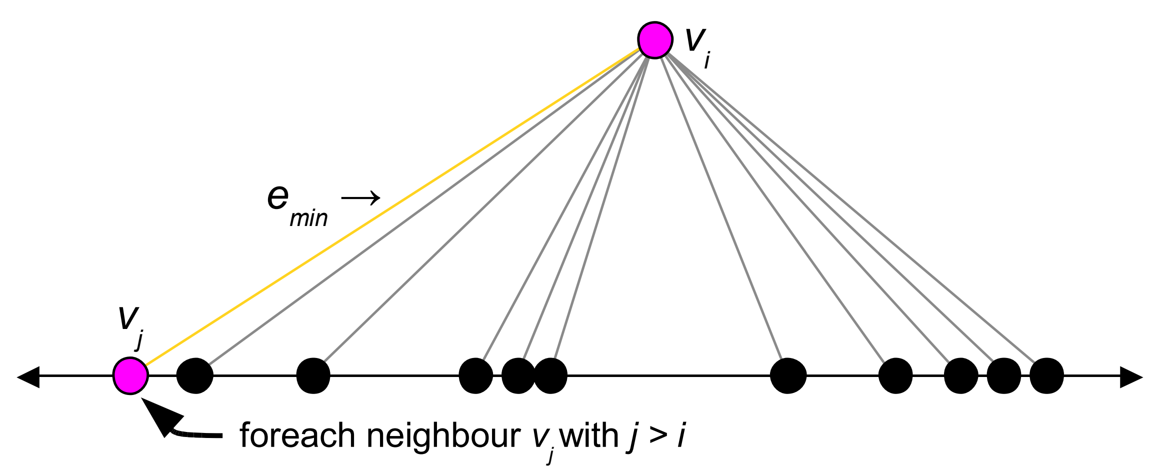


Figure 3.7: Step 2 of the new algorithm: A neighbour v_j of v_i is chosen from its sorted neighbour list, and together with v_i forms e_{min}.

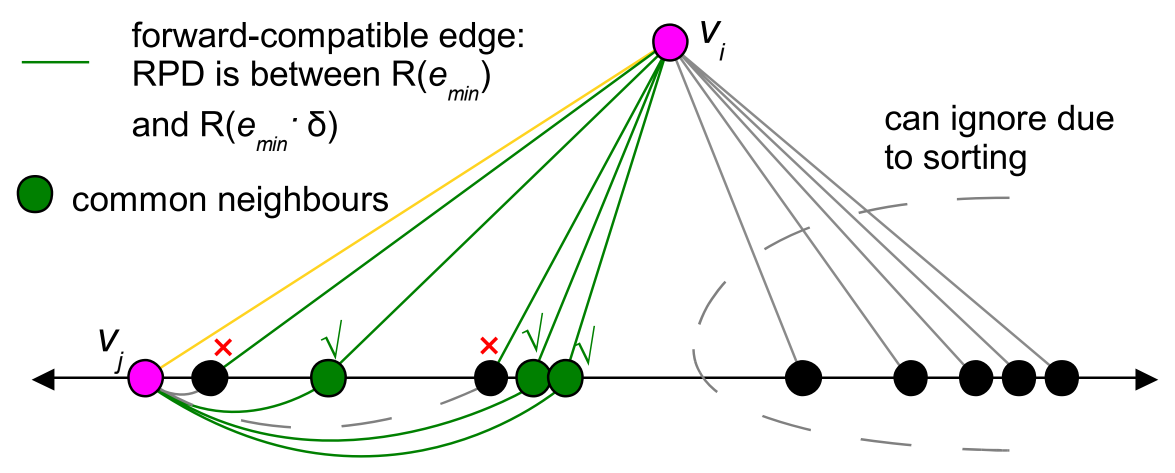


Figure 3.8: Step 3 of the new algorithm: The common forward-compatible neighbours of v_i and v_j form the vertex set of a subgraph H.

The subgraph H is constructed from the common neighbours of v_i and v_j that are forward-compatible with e_{min} (Figure 3.8). The sorting of v_i's neighbours speeds up this process. Then, with the edges of H pruned to edges from E that are forward-compatible with e_{min}, the maximum cliques of H are found and are each combined with v_i and v_j to create a match of maximum size (Figure 3.9). The largest matches found for all choices of e_{min} form the solution.

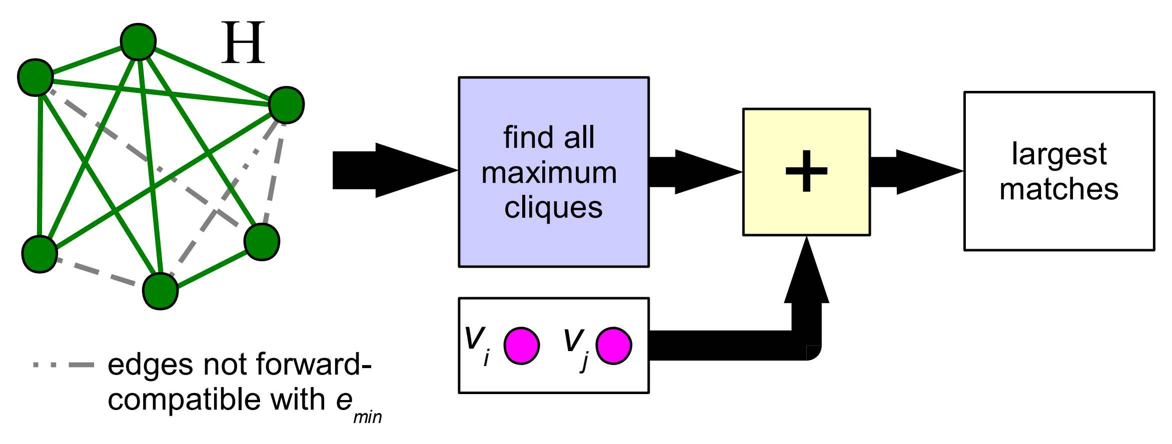


Figure 3.9: Step 4 of the new algorithm: Finding the maximum cliques of H, each of which is a match.

Note that unlike the existing algorithm, the new algorithm does not provide an optional feature to reduce the tolerance when comparing RPDs containing very small or very large distances (see Section 2.3.5). This is partly because the original implementation of tolerance reduction was defined only for submatrices of size 3. More importantly, if some pairs of RPDs are compared using a different tolerance than other pairs of RPDs, Theorem 3.1 no longer holds, and the method of solving an MMM problem described in this section would no longer be valid.

3.3.3 Algorithm Details

The algorithm is given in Procedure 6, and will now be described in detail. It assumes that the graph G has been constructed from A and B. At the beginning, M^{k^*} is initialized to the empty set, and during the course of the algorithm will hold the set of largest matches found so far. Similariy, k^* is initialized to zero, and will hold the largest thus far known match size.

Procedure 6 NewAlgorithm(G, α)

```
$M^{k^*} = \emptyset$
$k^* = 0$
for all $v_i \in V$ do
    $L = \{\gamma_x \colon \gamma_x \in \Gamma(v_i)$ and $R(v_i, \gamma_x) \leq R(v_i, \gamma_{x+1})\}$
    for $j' = 1$ to $|L|$ do
        $v_j = \gamma_{j'}$
        if $j \leq i$ then
            next $v_i$
        end if
        $e_{min} = (v_i, v_j)$
        $U = \text{BuildU}(v_i, v_j, L, j', e_{min})$
        if $|U| + 2 < k^*$ then
            next $v_j$
        end if
        $F = \text{BuildF}(U, i, e_{min})$
        $H = \{U, F\}$
        if not CheckSufficientDegrees(H) then
            next $v_j$
        end if
        $(\chi, \text{colour}) = \text{GreedyVertexColouring}(H)$
        if $\chi + 2 < k^*$ then
            next $v_j$
        end if
        $U' = \left\{u'_x \colon u'_x \in U \text{ and OrderUPredicate}(u'_x, u'_{x+1})\right\}$
        $\{Q, \omega\} = \text{Ostergard}((U', F), \max(0, k^* - 2))$
        UpdateMatches$(Q, \omega, v_i, v_j)$
    end for
end for
return $\left\{M^{k^*}, k^*\right\}$
```

Outer Loop

Together, the two outermost loops of the algorithm iterate over all edges in E. The first loop iterates over each vertex v_i in V. Its neighbours, $\Gamma(v_i)$, are sorted into an array L by increasing RPD of the edge between v_i to each neighbour. The second loop iterates over each neighbour vertex v_j in this array. All edges in E will eventually be spanned by the iterations of v_i and v_j. To ensure that each edge is visited only once, we only consider v_j for $j > i$, defined by some initial fixed and arbitrary ordering of vertices in V.

The edge between the current v_i and v_j is denoted e_{min}. The goal from this point on is to find the maximum cliques within the subgraph $\mathrm{H} = (\mathrm{U}, \mathrm{F})$ that contains all edges forward-compatible with e_{min}, and their adjacent vertices.

Building U

Procedure 7 BuildU($v_i, v_j, \mathrm{L}, j', e_{min}$)

```
$\mathrm{U} = \emptyset$
for $k' = j' + 1$ to $|\mathrm{L}|$ do
    $v_k = \gamma_{k'}$
    if not ForwardCompatible($(v_i, v_k), e_{min}$) then
        break
    else if ForwardCompatible($(v_j, v_k), e_{min}$) and DuplicateMinRPDCheck($e_{min}, i, v_j, v_k$) then
        $\mathrm{U} = \mathrm{U} \cup \{v_k\}$
    end if
end for
return U
```

The next step after choosing v_i, v_j, and $e_{min} = (v_i, v_j)$ is to build U, which is handled by Procedure 7. H will be constructed such that v_i and v_j will be implicitly part of every clique. This means:

- The vertex set U of the subgraph H only needs to contain $\Gamma'(v_i, e_{min}) \cap \Gamma'(v_j, e_{min})$, since only vertices adjacent to both v_i and v_j can be in cliques containing v_i and v_j. Also, because we are interested in the maximum compatible cliques, the edges from v_i to v_j to every member of U must be forward-compatible with e_{min}.
- U need not actually contain v_i and v_j, since they will be present in every clique found on H by construction, and can be appended later to all such returned cliques.

Building U is therefore done by calculating $\Gamma'(v_i) \cap \Gamma'(v_j)$, excluding v_i and v_j. Due to the sorting by ascending RPD performed earlier, finding $\Gamma'(v_i)$ is trivial. We iterate a vertex v_k over the sorted array L, starting from the vertex after v_j to the end of the array, and stopping early when (v_i, v_k) is no longer forward-compatible with e_{min}. At that point we know that subsequent vertices in L will continue to be greater than $\delta R(e_{min})$ by construction, and thus also not forward-compatible with e_{min}. Procedure 8 returns whether or not two edges are forward-compatible.

```
Procedure 8 ForwardCompatible($e, e_{min}$)
$\delta = (1+\alpha)/(1-\alpha)$
if $R(e_{min}) \leq R(e) < \delta R(e_{min})$ then
    return true
else
    return false
end if
```

As long as each v_k is found to belong to $\Gamma'(v_i, e_{min})$ during the iteration, it is also tested for membership in $\Gamma'(v_j, e_{min})$. If this test passes, then v_k is a member of both sets and can be added to U.

Handling Duplicate Minimum RPDs

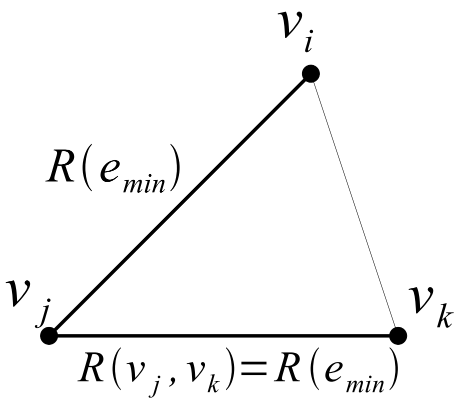


Figure 3.10: A situation where the RPD of edge (v_j, v_k) equals the RPD of e_{min}

A complication exists, however – the edge from v_j to v_k may have the same RPD as e_{min} (Figure 3.10). If this is the case, then during some future iteration of v_i, when it trades places with the current v_k, a duplicate visitation will occur. It is also possible for all three edges to have the same RPD. We arbitrate amongst these permutations by imposing an ordering such that v_k must follow both v_i and v_j. Procedure 9 implements this check, and is called before v_k is added to U.

Procedure 9 DuplicateMinRPDCheck(e_{min}, i, v_j, v_k)

```
if $R(e_{min}) = R(v_j, v_k)$ and $(j < i$ or $k < i)$ then
    return false
else
    return true
end if
```

Building F

F will contain all edges between members of U that are forward-compatible with e_{min}. This is done so that when maximum cliques are found in H, they will also be maximum compatible cliques. The edges between the members of U may have RPDs equal to that of e_{min} and face the same issue of possibly duplicating results in future iterations of v_i. Thus, Procedure 9 is called upon again to arbitrate amongst the possibilities.

Procedure 10 BuildF(U, i, e_{min})

```
F = $\emptyset$
for all $v_x \in$ U do
    for all $v_y > v_x \in$ U do
        if ForwardCompatible($(v_x, v_y), e_{min}$) and DuplicateMinRPDCheck($e_{min}, i, v_x, v_y$)
        then
            F = F $\cup$ $(v_x, v_y)$
        end if
    end for
end for
return F
```

Approximate Vertex Colouring

At this point, with H constructed, a maximum clique algorithm can be used to find the largest matches. However, before doing that, a greedy vertex colouring is performed on H in order to:

- Determine an upper bound on the chromatic number of H, which can be used to test whether H can yield matches of size k^* or higher or whether it should be ignored.
- Assign a colour class to each vertex in U to aid in determining a good heuristic ordering of vertices, which can decrease the time it takes to find the maximum cliques in H.

The algorithm to do vertex colouring, which was developed based on [3] as suggested in [31], is given in Procedure 11. Given the graph $\mathrm{H} = (\mathrm{U}, \mathrm{F})$, it assigns each vertex $u_i \in \mathrm{U}$ a colour, denoted colour(u_i), which is returned along with an approximate chromatic number χ which indicates the number of colours used. Pseudocode is given in Procedure 11.

Procedure 11 GreedyVertexColouring($\mathrm{H} = (\mathrm{U}, \mathrm{F})$)

```
$\chi = 0$
$\mathrm{O} = \{o_i \colon 1 \leq i \leq |\mathrm{U}| \text{ and } \deg(u_{o_i}) \leq \deg(u_{o_{i+1}})\}$
for $i = 1$ to $|\mathrm{U}|$ do
    found = false
    for $j = 1$ to $\chi$ do
        if $(u_{o_i}, u') \notin \mathrm{F}\ \forall u' \in \mathrm{C}_j$ then
            found = true
            colour($u_{o_i}$) = $j$
            $\mathrm{C}_j = \mathrm{C}_j \cup \{u_{o_i}\}$
            break
        end if
    end for
    if not found then
        $\chi = \chi + 1$
        colour($u_{o_i}$) = $\chi$
        $\mathrm{C}_\chi = \{u_{o_i}\}$
    end if
end for
return $\{\chi, \text{colour}()\}$
```

First, a traversal order O is created for the vertices in U that orders them by descending vertex degree. We find experimentally that this leads to a smaller number of colours being used, which is closer to the optimal colouring.

The vertices in U are traversed in the order specified by O. A colour class C_x exists for each colour x, such that a vertex u belongs to C_x if $\text{colour}(u) = x$. Each vertex u_{o_i} is placed into the lowest available colour class, which is defined as the smallest x for which u_{o_i} has no connection to any member of C_x. If no such color class can be found, a new one is created with u_{o_i} as its first member.

After all vertices have been coloured, Procedure 11 returns colour() along with χ.

Finding Maximum Cliques

Östergård's algorithm (as described in Section 2.4.2) is called to find maximum cliques in H. First, U is sorted by decreasing colour class, and by decreasing degree within a colour class. This is formalized in Procedure 12 as a boolean ordering predicate that must evaluate to true for any two vertices with adjacent indices in the sorted vertex set.

Procedure 12 OrderUPredicate(u'_i, u'_{i+1})

```
if $\text{colour}(u'_i) > \text{colour}(u'_{i+1})$ then
    return true
else if $\text{colour}(u'_i) = \text{colour}(u'_{i+1})$ then
    if $\deg(u'_i) > \deg(u'_{i+1})$ then
        return true
    else
        return false
    end if
else
    return false
end if
```

After finding maximum cliques, the set of maximum cliques is returned in Q, and their size in ω. Each returned clique combined with v_i and v_j is a match of size $\omega + 2$. Procedure 13 adds each match to M^{k^*}, and updates k^* if a new best match size has been found, clearing any previous matches in M^{k^*} first.

Procedure 13 UpdateMatches($\mathrm{Q}, \omega, v_i, v_j$)

```
if $\mathrm{Q} = \emptyset$ then
    return
else if $\omega + 2 > k^*$ then
    $k^* = \omega + 2$
    $\mathrm{M}^{k^*} = \emptyset$
end if
for all $q \in \mathrm{Q}$ do
    $\mathrm{M}^{k^*} = \mathrm{M}^{k^*} \cup (q \cup \{v_i, v_j\})$
end for
```

Early Exits

Throughout Procedure 6, several checks are done to verify that the subgraph H represents a worthy maximum clique problem – one that will yield matches of at least size k^*. Each check represents a tighter bound on the maximum clique size than the previous, as more information about H becomes available. If a check fails, then H is deemed unworthy and the next v_j is chosen. This increases the performance of the algorithm by skipping further steps that are guaranteed not to produce useful solutions.

The first check occurs after building U. The largest clique that can possibly be found would include all members of U plus v_i and v_j. Thus, if $|\mathrm{U}|+2$ is less than k^*, no matches of sufficient size can possibly be found.

Procedure 14 CheckSufficientDegrees($\mathrm{H} = (\mathrm{U}, \mathrm{F})$)

```
$sufDegreeVerts = 0$
for all $v \in \mathrm{U}$ do
    if $\deg(v) + 2 \geq k^* - 1$ then
        $sufDegreeVerts = sufDegreeVerts + 1$
    end if
end for
if $sufDegreeVerts + 2 >= k^*$ then
    return true
else
    return false
end if
```

The second check occurs after building F, when the degree of each vertex u in U is known. A clique of size k consists of k vertices, each having a degree of $k-1$. Therefore, in order for cliques of size k^* and above to exist in H, there must exist at least k^* vertices in U with degree of at least k^*-1, taking into account that each vertex in u also has implicit edges to v_i and v_j, effectively increasing each degree by 2. This check is implemented by Procedure 14.

The final check occurs after colours have been assigned to each vertex in U. The actual chromatic number of a graph, returned by an optimal vertex colouring (an NP-hard problem) equals the maximum clique size of the graph. However, the approximate greedy algorithm we use may return a greater number of colours than optimally necessary. This number χ is an upper bound on the maximum clique size of H, and therefore an upper bound on the size of matches that we can hope to find. Since each vertex has implicit edges to v_i and v_j, those two vertices each require their own colours, effectively increasing χ by 2. Therefore, $\chi + 2$ must be at least k^* to proceed.

3.3.4 Algorithm Complexity

We will now provide a worst-case analysis of the performance of the new algorithm described in Section 3.3.3. Similar to the worst-case analysis of the original algorithm (Section 2.3.7), the worst case occurs when both protein families A and B contain proteins from one species and have the same phylogenetic distance $c > 0$ between any two proteins. This results in $N!$ matches of size N, where $N = |\text{A}| = |\text{B}|$. Since the algorithm must list every one of these matches, its worst-case complexity must be at least $O(N!)$.

However, having such a large number of matches is improbable from a biological standpoint, as it would imply coevolution between every possible pair of proteins. In real problems, the proteins from the two input matrices come from a variety of species, which limits the number of valid pairs (pairs sharing a species) relative to the sizes of the input matrices. Furthermore, the distances in both matrices are not all identical, as in the worst case, and this creates variation in the RPDs within the problem. Due to this variation, and due to the tolerance α being kept low to avoid false positive results, mutually-compatible sets of edges are kept small, relative to the size of the total number of edges in the problem. For the same threshold, a more sparse distribution of RPDs (which are a function of the distances in the input matrices) would lead to a computationally simpler problem. The performance of the new algorithm in the average case is therefore highly data-dependent.

3.4 Results

In this section we compare the performance and accuracy of the new algorithm described in this chapter against that of the existing MMM algorithm described in Chapter 2.

3.4.1 Experimental Setup

We use the same software package as in [44] as the reference implementation for the existing MMM algorithm. A modified version of the existing software package implements the new MMM algorithm presented in this chapter. Both implementations are written in C++ and compiled for Linux-based operating systems. Experiments were run on a PC with an Intel Core i7-980X running at 4.215 GHz with 6 GB of DDR3 SDRAM running at 1.69 GHz. The software environment is a Linux-based operating system using kernel version 3.6.35-22.

The BATCH50 and TUBULIN_AB datasets were used as inputs for measuring performance, with a tolerance of 0.1 used throughout. BATCH50 contains 1,225 pairs of distance matrices, and TUBULIN_AB is a single pair of matrices, representing homologous variations of the Tubulin Alpha and Tubulin Beta proteins. The output data used to generate the results in this section is found in Appendix B.1.

3.4.2 Accuracy

By redefining the MMM problem in Section 3.2, we expect to change the outputs of the algorithm. Therefore, we must first give evidence that the output of the new algorithm is biologically correct. We will compare the outputs of the existing and new algorithms to show the nature of the change in output. Then we will refer to the work of our collaborators, who have since used the new algorithm in their work, to show that the new algorithm is still accurate despite these changes.

Over the 1225 problems in the BATCH50 data set, 249 problems yielded a maximum match size that is one protein smaller in the new algorithm than in the existing algorithm. An additional 7 problems had a maximum match size that was two proteins smaller. Of the remaining problems that yielded no change in maximum match size, the number of matches decreased by 620 on average. This difference in output between the existing and new algorithms is expected, since the new algorithm implements the "strict" version of the MMM problem, which yields a subset of the matches of the existing algorithm.

The TUBULIN_AB problem did not finish running (taking in excess of 4 days) under the existing algorithm, so the largest match size and count are unavailable.

Figure 3.11, reproduced from [37], is a Receiver Operating Characteristic (ROC) diagram that compares the accuracy of the new and existing algorithms when using different methods to prepare the input matrices. The datasets used in this comparison were neither BATCH50 nor TUBULIN_AB, but were generated from the same HomoloGene database as BATCH50. The ROC diagram plots the true positive rate (labeled as "sensitivity") against the false positive rate (labeled as "1 - specificity") of correctly predicting whether or not two families of proteins (two matrices) interact. The known interactions were obtained from the NCBI Gene [50], BioGRID [5], and HRPD [35, 29] protein interaction databases.

The data points on each curve in the ROC diagram were generated by varying the match size returned by MMM that was considered the threshold between "interacting"

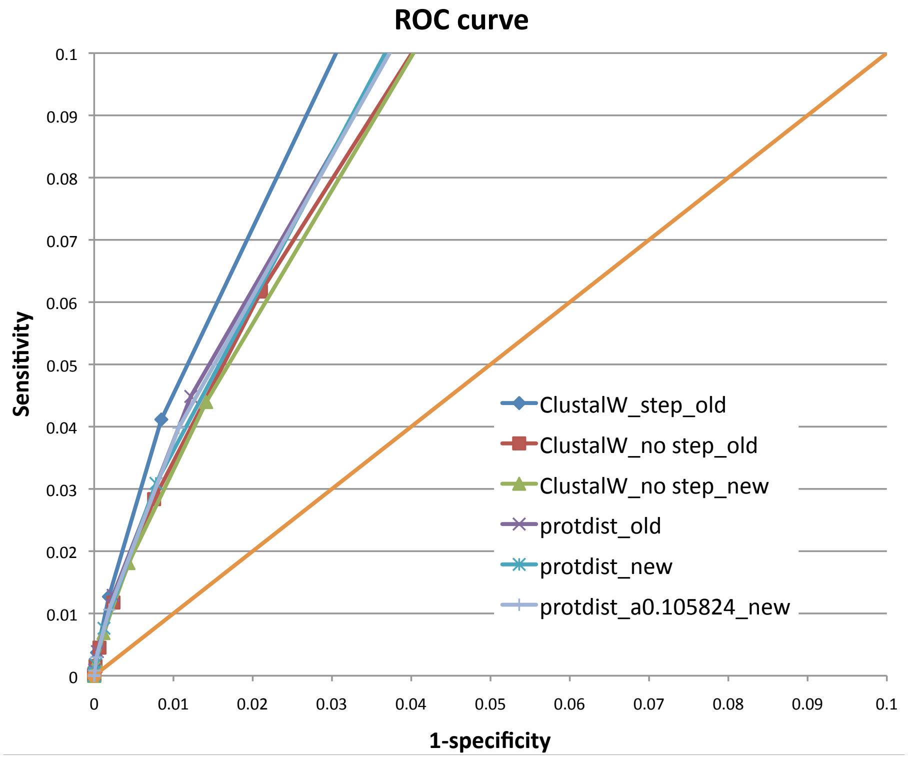


Figure 3.11: Receiver Operating Characteristic diagram comparing the accuracy of the new algorithm against that of the existing algorithm

and "non-interacting". The ideal point to be on an ROC diagram is in the upper-left-hand corner at x=0 (no false positives included) and y=1 (all true positives included). The line $y = x$ on the diagram represents zero predictive ability.

In Figure 3.11, "old" and "new" refer to the existing and new algorithms, respectively. "ClustalW" and "protdist" refer to the tools used to generate the distances in each matrix, and "step" and "no_step" refer to whether or not piecewise-linear threshold adjustment was enabled (applicable only to the existing algorithm, as described in Section 2.3.5). The piecewise-linear function parameters used were: `stepLo` $= 0.2$, `stepHi` $= 0.5$, and `stepMax` $= 0.9$. The tolerance was set to 0.1 in all cases except for the curve named `protdist_a0.105824_new` which used a tolerance of 0.105824.

The results presented in Figure 3.11 indicate that aside from the test case that uses ClustalW matrices and tolerance adjustment, the accuracy of the new algorithm is similar to that of the existing algorithm. The one curve with tolerance adjustment enabled (`ClustalW_step_old`) had the advantage of the three tolerance adjustment parameters `stepLo` `stepHi` and `stepMax` being chosen to maximize accuracy for this particular dataset.

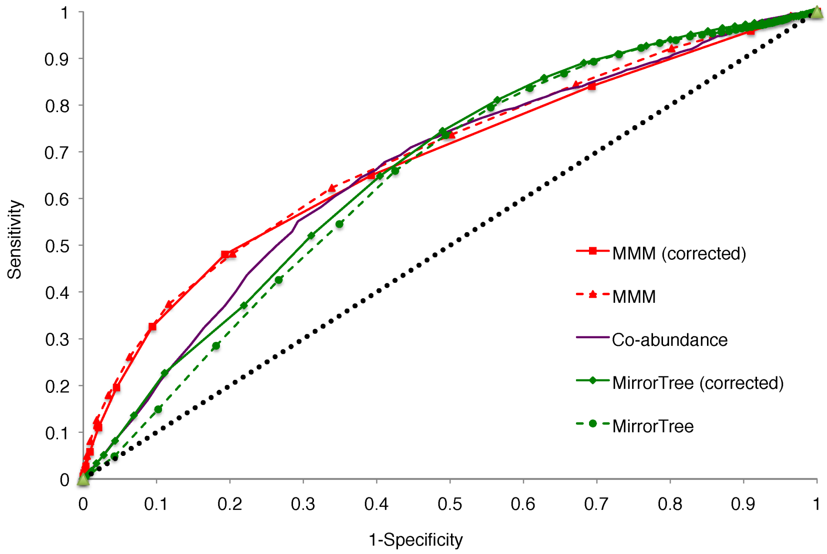


Figure 3.12: ROC diagram comparing the accuracy of the new MMM algorithm against that of other methods of coevolution detection

We now refer to another accuracy comparison, which compares our new algorithm against other methods of protein coevolution detection. Figure 3.12 is an ROC diagram reproduced from [8] which gives the results of this comparison, with the two curves labeled "MMM" representing our new algorithm. A curve that tends to the top-left of the diagram represents a coevolution detection method that is more accurate. The points on each curve were generated by varying the classification threshold for interacting versus non-interacting proteins. For our algorithm, this corresponds to the returned maximum match size for two matrices. The other two methods have their own concepts of such a threshold.

Figure 3.12 illustrates that our new algorithm compares favourably to the other methods. The data set used to generate these curves is neither BATCH50 or TUBULIN_AB, but a more comprehensive set of protein clusters from the OMA database [1]. The curves “MMM(corrected)” and “MirrorTree(corrected)” refer to a post-processing step performed after running the respective algorithms that improves the accuracy of coevolution detection. In the context of our new algorithm (“MMM(corrected)”), it involves solving an auxiliary coevolution problem between each input matrix and a specially-designed distance matrix. The details are external to our algorithm and outside the scope of this paper, beyond the fact that it involves a repeated use of the algorithm with specially-formatted inputs.

3.4.3 Performance

We now compare the performance of the new algorithm versus that of the existing algorithm. We run both algorithms using the BATCH50 and TUBULIN_AB datasets as inputs. Results for the 50 longest-running problems under the existing algorithm are shown in Table 3.1. The **Matrix 1** and **Matrix 2** columns identify, for each problem, the two distance matrices used as input, with **N** and **M** being their respective sizes in number of proteins. Numerical matrix names refer to filenames from the BATCH50 set. **CV** is the total number of compatibility graph vertices in each problem, which is equal to how many of the possible $\mathbf{N} \times \mathbf{M}$ protein pairs share the same species. **PV** refers to the total number of compatibility graph vertices processed during the course of the entire problem. It is equal to the sum, over all maximum clique sub-problems, of the input size (in vertices) of each maximum clique sub-problem. Finally, $\mathbf{T_{existing}(s)}$ and $\mathbf{T_{new}(s)}$ refer to the running times, in seconds, of the existing and new algorithms respectively. Results for the remainder of the 1,225 total problems in the BATCH50 set can be found in Appendix B.

Figure 3.13 is a graph showing the ratio of run times of the new algorithm over the existing algorithm for each of the 1,225 MMM problems in the BATCH50 set. The speedup ratios are sorted in ascending order, with the average speedup being 80x. Comparing the sum of the run times under the new and existing algorithms over the entire set yields a speedup of 570x.

The TUBULIN_AB problem did not complete under the existing algorithm, so we only have a minimum running time of 354,780 seconds. This means that the minimum speedup for this problem is 890x.

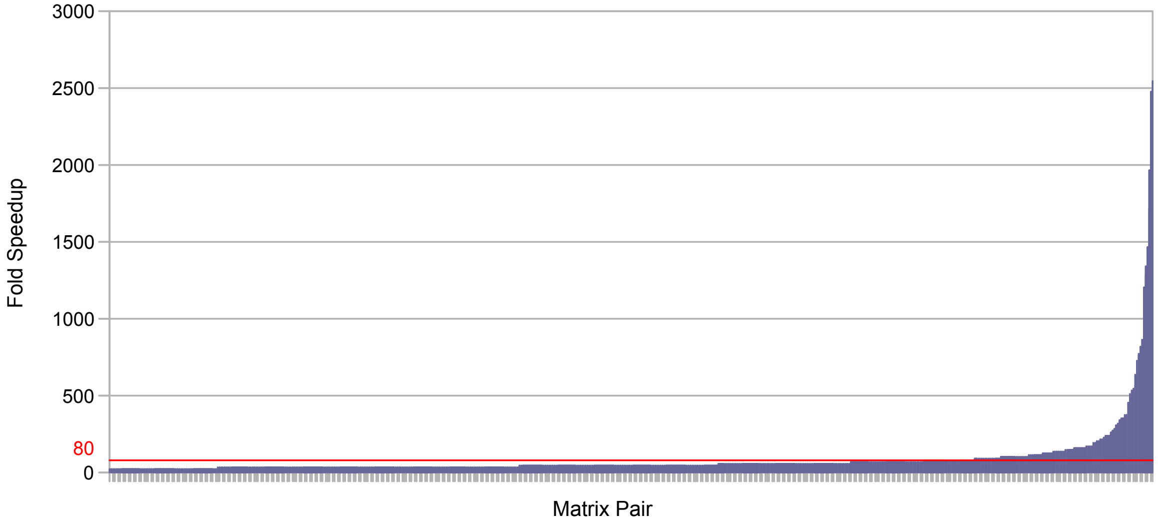


Figure 3.13: BATCH50 per-problem speedup of new algorithm versus existing algorithm. The red line indicates the average speedup, which is 80x

Figure 3.14 shows the relationship between each MMM problem's execution time and the sum of the sizes (in vertices) of all the problem's maximum clique sub-problems. Both the BATCH50 and TUBULIN_AB data sets are represented. The relationship is roughly linear, with the running time being proportional to the total processed vertices to the power of 1.14. Problems which took a very short execution times were ignored, since non-algorithm-related overhead within the executable would become a nontrivial component of the total execution time.

We will now present an approximate relationship between the input matrix sizes N and M and the execution time of the new algorithm. There are $O(NM)$ vertices in the compatibility graph. The outer loops iterate over every vertex pair (v_i, v_j), and there are $O((NM)^2)$ such pairs. Each pair represents a maximum clique problem, with the number of vertices being ideally some fraction of the NM compatibility graph vertices, which depends only the tolerance α in this ideal case. The total number of processed vertices is then $O((NM)^3)$, and the running time is therefore $O(((NM)^3)^{1.14}) = O((NM)^{3.42})$.

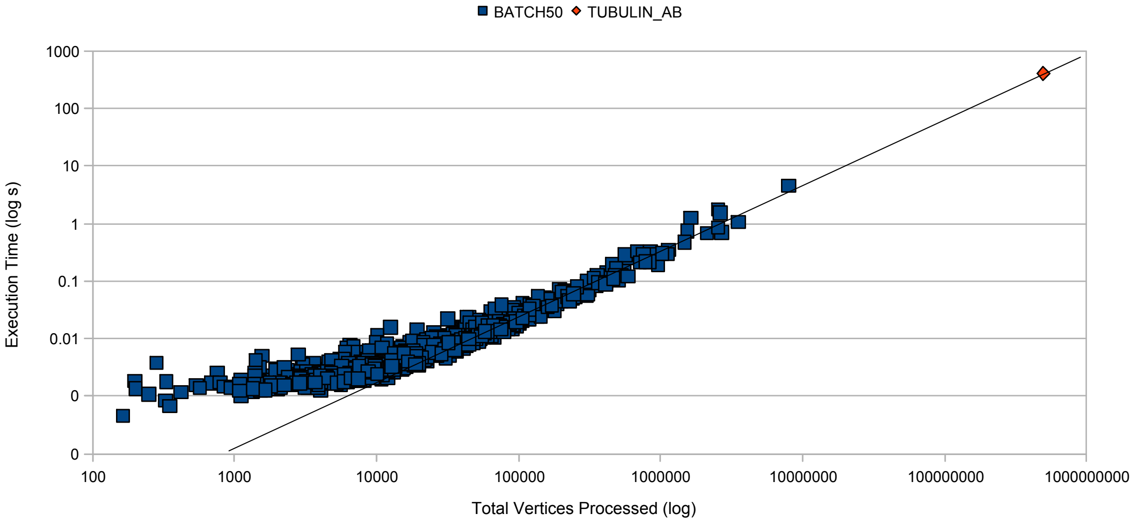


Figure 3.14: Total processed vertices versus time for problems in both data sets (log-log scale). The slope of the line of best fit is 1.14.

Matrix 1	**Matrix 2**	**N**	**M**	**CV**	**PV**	**$T_{existing}$(s)**	**T_{new}(s)**	**$T_{existing}/T_{new}$**
Tubulin A	Tubulin B	516	485	4157	494535578	$\geq$354780	401	$\geq$890
89932	104370	57	44	452	1628556	3030.99	1.2449	2435
88748	88482	69	47	629	7975550	2833.54	4.4713	634
105282	103789	55	45	421	2623821	2609.07	1.5184	1718
88748	87894	69	40	495	2533324	2313.67	1.7335	1335
106976	38064	57	42	287	678368	807.93	0.3262	2477
88748	38064	69	42	364	1539192	636.58	0.7377	863
88482	103789	47	45	385	1476697	573.78	0.4763	1205
88748	90856	69	50	328	845438	442.5	0.3285	1347
105282	88482	55	47	497	2531864	437.8	0.8628	507
105282	104370	55	44	305	757937	417.6	0.2847	1467
88482	38064	47	42	227	483420	217.42	0.1691	1286
88748	104370	69	44	495	2117585	147.38	0.6879	214
88748	105282	69	55	665	3505466	144.75	1.0509	138
88748	88589	69	41	444	1133472	127.94	0.3489	367
105282	88589	55	41	447	712540	113.84	0.2139	532
88748	103789	69	45	512	2686397	100.95	0.7063	143
88748	90389	69	44	425	563413	98.12	0.2872	342
106976	88482	57	47	346	866213	89.6	0.2949	304
88748	107220	69	38	415	1116276	78.84	0.2923	270
90856	88482	50	47	192	306729	77.23	0.1003	770
89932	105282	57	55	319	358703	67.12	0.1239	542
105282	87894	55	40	412	1022974	49.93	0.3051	164
105282	106838	55	47	291	559435	49.69	0.1518	327
90856	103998	50	46	122	31615	43.82	0.0222	1970
80191	100530	46	43	103	49570	41.08	0.0161	2550
107298	88589	56	41	486	840689	40.49	0.2159	188
2506	88748	85	69	587	776939	37.38	0.3089	121
88748	106976	69	57	364	600353	30.74	0.2510	122
106948	88748	71	69	633	961707	30.73	0.1907	161
88482	87894	47	40	386	783524	29.87	0.2161	138
90856	75001	50	38	159	75279	27.85	0.0387	719
103789	104370	45	44	273	479101	25.86	0.1264	205
105282	38064	55	42	286	525293	25.35	0.1293	196
106976	106838	57	47	273	455579	24.2	0.1936	125
90856	100530	50	43	107	42873	22.68	0.0237	958
105282	90856	55	50	248	350965	19.34	0.0831	233
88748	100934	69	46	237	75367	18.55	0.0329	564
88748	89932	69	57	471	532032	16.35	0.1260	130
106838	104370	47	44	245	360254	14.83	0.0929	160
103789	87894	45	40	306	464988	14.82	0.1122	132
90856	74548	50	47	182	190811	14.63	0.0465	315
90856	38064	50	42	178	135949	14.53	0.0539	269
90856	88589	50	41	124	44846	14.15	0.0186	762
105282	48010	55	43	249	315767	14.09	0.0913	154
88748	80191	69	46	273	119769	13.75	0.0401	343
106838	38064	47	42	240	409273	13.64	0.0885	154
74548	38064	47	42	185	169621	13.55	0.0477	284
106948	105282	71	55	453	408651	12.16	0.0979	124
2506	106948	85	71	465	302712	12.01	0.0653	184
104370	38064	44	42	234	219407	10.67	0.0532	200

Table 3.1: Results for the 50 longest-running problems

Chapter 4

Hardware Acceleration

The ultimate goal of this research is to increase the performance of the MatrixMatchMaker method for determining protein interactions. In Chapter 3, we accomplished this by creating a new algorithm, which provided a large speed increase in software. In this chapter, we present a hybrid hardware/software implementation of this algorithm, with the goal of increasing the performance even further.

We chose to implement Östergård's maximum clique algorithm in hardware, leaving the remainder of the algorithm implemented in software. This is despite profiling the new algorithm, which indicated that less than 10% of runtime was spent solving maximum cliques. This was done using the data sets available at the time as input to the algorithm, which all completed in less than a minute of computation time. We hypothesized, however, that for more demanding data sets consisting of larger distance matrices, the time spent finding maximum cliques would increase and approach 100% of total runtime.

Our thinking was that, because the maximum clique problem is NP-hard, and the steps taken to set up each maximum clique problem in the new algorithm have polynomial time complexity with respect to the input size, that the max clique solving would dominate larger problem sizes. Unfortunately, larger data sets obtained after the hardware implementation was completed still did not exhibit a significant amount of runtime spent finding maximum cliques. We discovered this too late in the process to re-direct our acceleration efforts. As such, the primary contribution of this chapter should be thought of as an the acceleration of the max-clique problem in isolation.

4.1 Design Methodology

With the decision made to implement the maximum clique algorithm in hardware, the next step is to choose a suitable hardware platform. In the new algorithm, presented in Chapter 3, there is an abundance of maximum clique problems to solve, potentially one for every edge of the compatibility graph. Thus, performance could be gained by exploiting parallelism and solving many maximum clique problems simultaneously. This requires a platform that allows many independent control flows, one for each max clique problem. This, combined with the lack of data parallelism available in each maximum clique problem, makes GPUs an unattractive platform for implementing a maximum clique algorithm.

However, a Field-Programmable Gate Array (FPGA) would allow the implementation of many independent cores, each able to solve a single problem. Furthermore, the input to a maximum clique problem, which is a graph, can be represented with a binary adjacency matrix, reducing the amount of data required for a problem and thus mitigating memory bandwidth issues. Implementing digital logic on a fine-grained level would then allow efficient manipulation of the single-bit quantities in each matrix. For these reasons, we have chosen an FPGA as our hardware acceleration platform for the maximum clique problem.

4.2 Hardware Design

This section describes the design of our FPGA-based maximum clique solver. It is given a set of maximum clique problems from a host system that implements the remainder of

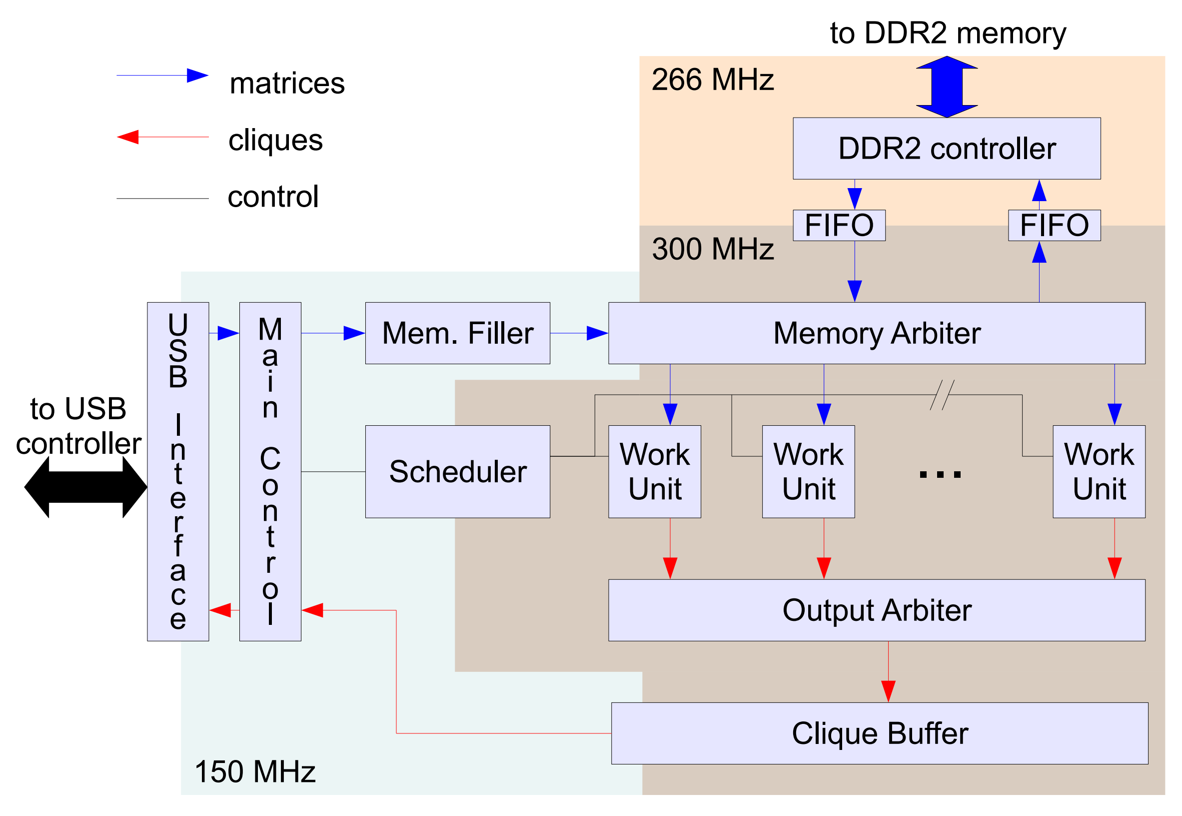


Figure 4.1: Block diagram of the parallel FPGA-based hardware maximum clique solver, indicating clock domains and signal paths.

the MMM algorithm in software. Each problem is a graph whose maximum cliques are to be found, and is represented as an adjacency matrix. After storing all the matrices in memory external to the FPGA, the system solves the set of problems using a series of work units, each capable of solving a single maximum clique problem at a time. Using multiple work units, many problems are solved in parallel. When all the problems in the set are solved, the largest cliques amongst all the problems are returned back to the host system.

A block diagram of the system is shown in Figure 4.1. There are two connections from the system to the outside world. The host communicates with the system using the Universal Serial Bus (USB) 2.0 protocol, providing matrices (maximum clique problems) as input, and receiving cliques as output. 1 GB of DDR2 SDRAM located outside the

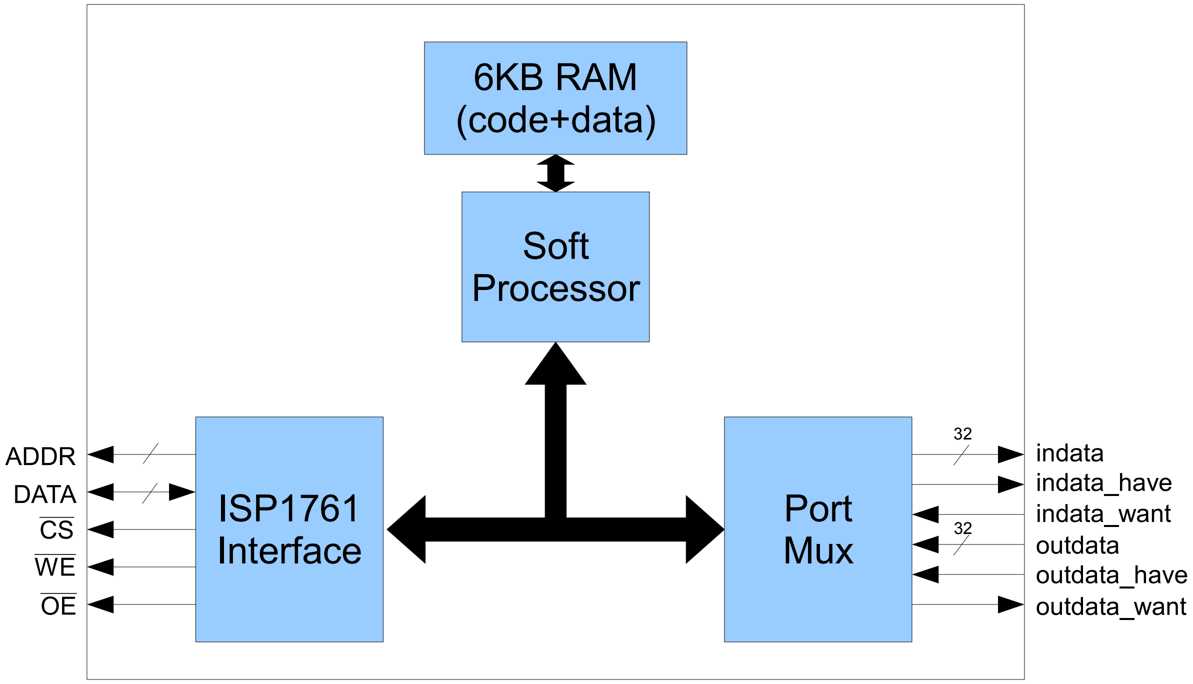


Figure 4.2: Block diagram of the USB Interface module

FPGA is used to hold incoming matrices for all the problems in a set. The modules implemented on the FPGA are described in the remainder of this section. The source code (in hardware description language) for our design is available in the supplementary files included with the electronic version of this document.

4.2.1 USB Interface

This module handles the details of communicating across the USB link with the host, providing a simple handshaked streaming interface to the rest of the system to receive adjacency matrices and return cliques. A block diagram is shown in Figure 4.2.

The physical USB connection exists outside of the FPGA and is handled by an NXP ISP1761 USB 2.0 controller chip [6], which the FPGA accesses via a memory-mapped register interface (shown on the left side of Figure 4.2). An Altera Nios II soft processor [10] communicates with the ISP1761, through the sub-module labeled “ISP1761 Interface” which simply maps the ISP1761’s bus into the processor’s address space.

The processor performs the steps necessary to initialize the ISP1761 and implements all protocol-specific formatting of packets sent and received on the USB link. When the physical USB connection is first made to the host, the processor performs the initial exchange of packets that properly enumerate and identify the hardware maximum clique solver as a USB slave device. Afterward, data payloads are exchanged with the host, and the processor acts as an intermediary between the USB link and the interface to the rest of the system through the "Port Mux" sub-module.

The Port Mux consists of a pair of 32-bit wide FIFOs memory-mapped into the processor's address space. One FIFO takes 32-bit data words from the processor and makes it available to the rest of the system through a 32-bit wide port called `indata`. The signals `indata_want` and `indata_have` implement flow control on this port. Similarly, the other FIFO receives 32-bit words from the rest of the system on the `outdata` port and makes it available to the processor for formatting and transmission across the USB link. Likewise, the signals `outdata_want` and `outdata_have` implement flow control on the `outdata` port.

4.2.2 Data Formats

This section describes the format of the data transmitted from and to the host on the `indata` and `outdata` ports for each problem set.

As shown in Figure 4.3, the stream of data on `indata` begins with a global header word that specifies settings global to the entire problem set. It contains the initial maximum clique size `init_maxsize`, and the `nocliques` bit. `init_maxsize` indicates the minimum size of cliques that should be considered. The `nocliques` bit specifies that only the maximum clique size should be returned, rather than the contents (vertices) of the maximum cliques.

Following the global header comes a series of one or more maximum clique problem definitions, each of which consists of a one-word problem header followed by an adjacency

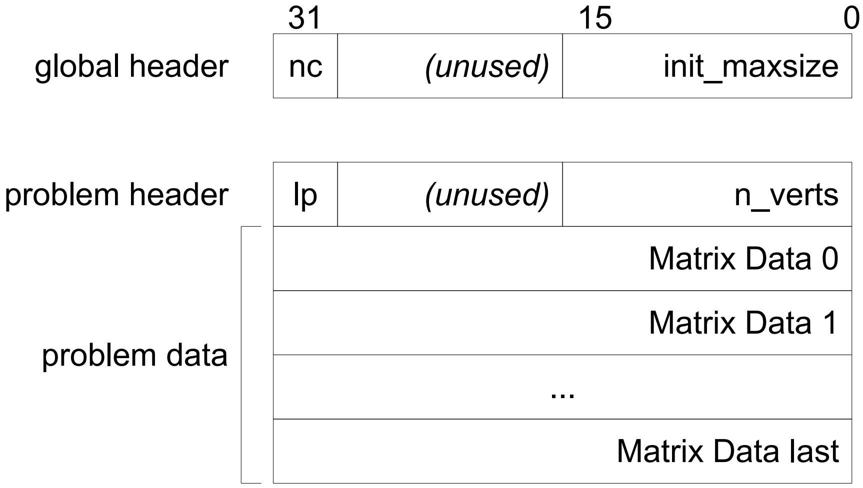


Figure 4.3: Format of incoming data on the `indata` port.

matrix representation of the graph on which to find maximum cliques. The header indicates the number of vertices in the graph, `n_verts`, as well as a `lastprob` bit which indicates that this is the last maximum clique problem in the set.

The adjacency matrix is represented as an array of bits, each indicating the presence of a connection between two vertices in the graph. The `n_verts` * `n_verts` bits in the matrix are packed into 32-bit words in row-major order and sent after the problem header. The last word is padded with zero bits at its most-significant end.

Figure 4.4 shows the format of the outgoing data stream on `outdata`. The initial header contains the maximum clique size and the number of maximum cliques, which is undefined if `nocliques` mode was specified in the input global header. If `nocliques` mode was not specified, the maximum cliques themselves follow. Each clique is represented by `max_clique_size+1` 16-bit words. The first word specifies the problem in the set in which this clique was found. The rest of the words specify the vertex indices, relative to that problem, which form the clique. The set of clique definitions are packed without gaps into 32-bit words, and padded with an empty 16-bit word at the end in the case of an odd number of 16-bit words.

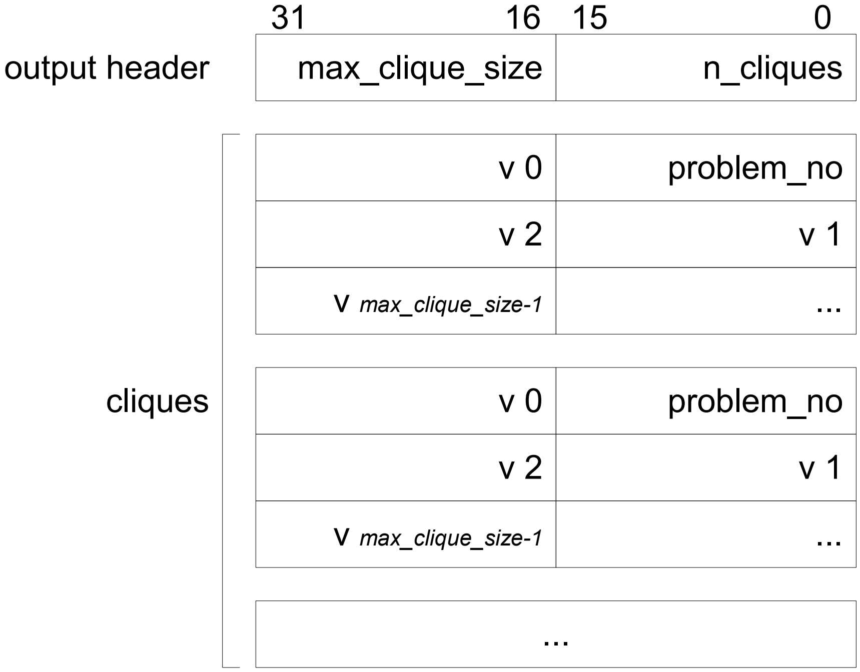


Figure 4.4: Format of outgoing data on the `outdata` port.

4.2.3 Main Control

This module contains a state machine which controls the high-level flow of execution of the solver. Solving a set of maximum clique problems occurs in three stages:

1. The *input phase*, when maximum clique problems in the form of adjacency matrices arrive from the USB interface, and are saved into off-chip memory.
2. The *processing phase*, when the maximum clique problems are solved.
3. The *output phase*, when the maximum cliques are returned back to the host via the USB interface.

The input and processing phases overlap to maximize performance. As each maximum clique problem arrives, it is immediately scheduled for solving as soon as its adjacency matrix is written into off-chip memory. Additional adjacency matrices continue to arrive simultaneous with the execution of already-downloaded and scheduled problems. The

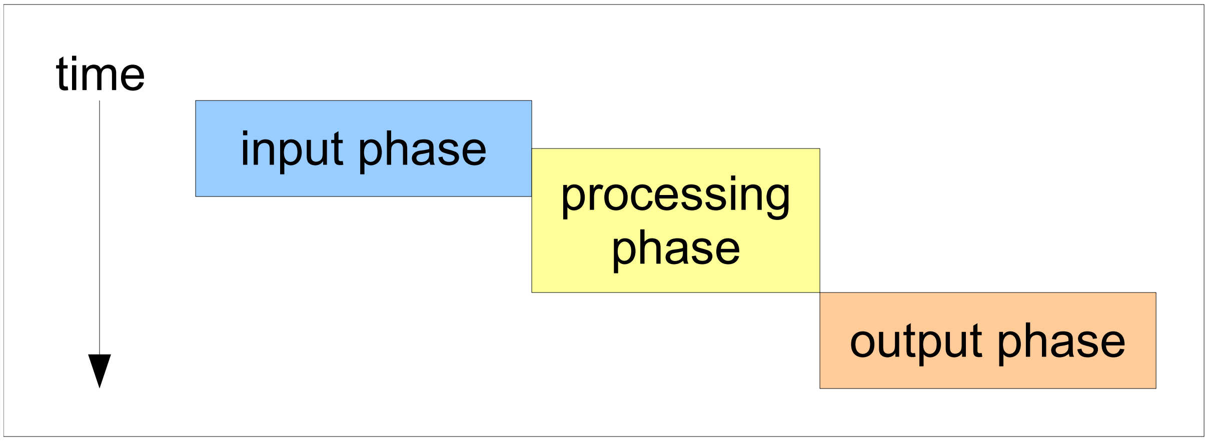


Figure 4.5: Main flow of execution

output phase must occur after the processing phase, because the set of maximum cliques is not guaranteed until the very last problem has finished being solved. For example, in the worst case, the very last problem in the set contains the largest cliques, invalidating the solutions of all previous problems. The relationship of the input, output, and processing phases is depicted in Figure 4.5.

The main control module implements this flow by performing the following steps:

1. Parse the global header from `indata` and reset the system.
2. Parse the problem header for a maximum clique problem, assign it a sequential problem number, and forward the matrix data, problem number, and number of vertices to the Memory Filler.
3. Once the Memory Filler reports the problem fully written into off-chip memory, inform the Scheduler of the problem number and number of vertices.
4. Repeat steps 2 to 3 until the last problem has been scheduled.
5. Wait until the Scheduler reports that all problems have been solved.
6. Tell the Clique Buffer to output its data stream, which is sent through `outdata` to the USB Interface and to the host.

4.2.4 Memory Organization

The following describes the layout of the off-chip DDR2 SDRAM memory, which is used to store the adjacency matrices for the maximum clique problems. The whole of the memory space is evenly partitioned into segments, each large enough to accommodate the largest possible matrix given the configured maximum number of vertices. Thus, an external memory address has two components. The highest-order bits specify the problem number, and the rest of the bits specify a 128-bit word of matrix data within that problem's adjacency matrix.

For example, a vertex limit of 4096 results in a maximum matrix size of 2 MB, allowing 512 matrices to be stored within 1 GB of DDR2 SDRAM. The upper 9 bits of the address then form the segment address specifying the problem ID, with the remaining 17 bits specifying a 128-bit word within that problem's matrix. In practice, problem sets contain more than 512 problems (up to 65536), so memory segments belonging to already-solved problems eventually become re-used by newer problems that await solving.

4.2.5 Memory Fill

The memory filler writes adjacency matrices into DDR2 SDRAM. An adjacency matrix is delivered as a stream of 32-bit-wide words from the Main Control module, which also provides the number of vertices and the problem's ID. The memory filler packs the incoming 32-bit words into the 128-bit words used by the DDR2 SDRAM and calculates the address to store each resultant word based on the given problem ID, respecting the memory layout presented in Section 4.2.4. The 128-bit-wide words and their addresses are then sent as write requests to the DDR2 Arbiter.

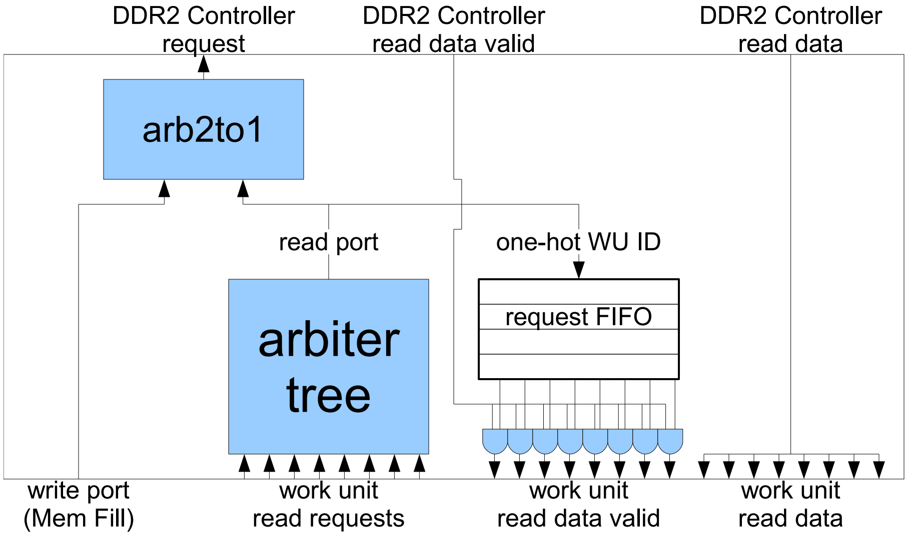


Figure 4.6: Memory Arbiter block diagram

4.2.6 Scheduler

The Scheduler assigns maximum clique problems to work units and monitors their completion. Problem descriptions, consisting of a problem ID and the number of vertices, arrive from the Main Control module and are placed into a queue. A problem at the head of the queue is then assigned to the first available work unit that isn't busy solving another problem.

4.2.7 Memory Arbiter

The Memory Arbiter allows the memory filler and work units to share access to the DDR2 SDRAM controller's single read/write port (Figure 4.6). At the highest level, this single read/write port is split into a read port and a write port by an `arb2to1` module. The write side is used by the memory filler to write matrices, and the read side is used by the work units to read them.

An `arb2to1` resolves simultaneous requests on its two ports by giving priority to the port opposite to the one that was last granted access. This ensures fair access to the memory. The write requests from the memory filler are accompanied with the write

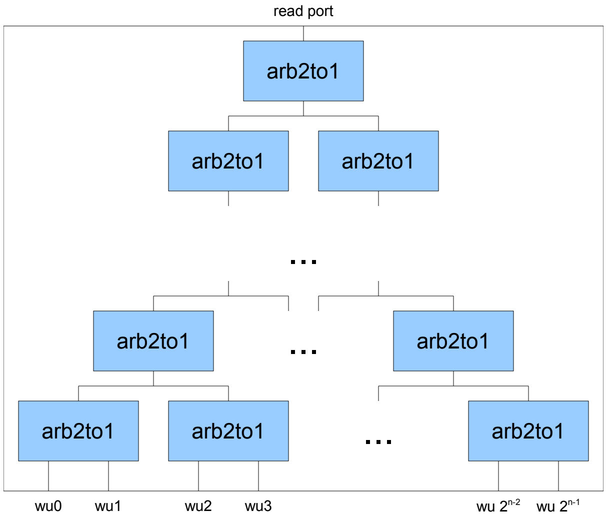


Figure 4.7: Tree Arbiter for Work Unit read requests

address and data, without any need for a further reply from the DDR2 controller. The read side is shared by all the work units, and each read request is followed, some time later, by a reply of valid data from the controller.

The single read port provided by the top-level `arb2to1` is shared by a power-of-2 number of work units through a tree of `arb2to1` stages, shown in Figure 4.7. The output of each arbiter stage is registered, which increases latency but allows the arbiter to scale to a large number of work units.

As each read request is successfully submitted to the read port of the top-level `arb2to1`, the ID of the work unit associated with the read request is simultaneously placed into a request FIFO. When valid read data arrives from the DDR2 controller, it is broadcast to all work units, and the request FIFO allows the arbiter to identify the work unit to send the "data valid" signal to. This scheme allows read and write requests to continue to be issued to the DDR2 controller even while waiting for outstanding read transactions to complete, thus improving performance.

4.2.8 Work Unit

Each work unit is a hardware implementation of Östergård's maximum clique algorithm. We will first describe our hardware-oriented version of the algorithm. The central data structure used in the algorithm is the *vspan*, or vertex span, and is just an array of vertices (represented by indices) that is sorted in ascending order by index. A vspan represents a set of candidate vertices that are under consideration for being added to the current clique being constructed. The entire vertex set for the maximum clique problem is a vspan.

The main operation performed on a vspan is *add-and-intersect*, *isect* for short. An isect operation on a vspan with k vertices $(u_0, u_1, \ \dots \ , u_k)$ generates its *child vspan*, which contains only the vertices u_i, $1 < i \leq k$ which are neighbours of the first vertex u_0. This operation represents the growth of a clique by the addition of the first vertex u_0 to the clique, and the intersection of the candidate vertex set (represented by the vspan) with the neighbour set of u_0. This ensures that the new candidate list, represented by the child vspan, only contains vertices that are neighbours of every vertex currently in the clique, which is an invariant of the algorithm. A vspan's child is unique, and it may be empty, resulting from none of the vertices u_1 through u_k being neighbours of the first vertex u_0.

A *sibling vspan* of a vspan $(u_0, u_1, \ \dots \ , u_k)$ is a contiguous subset of vertices $(u_i, u_{i+1}, \ \dots \ , u_k)$, $i > 0$ taken from an arbitrary vertex within the vspan to the end. A vspan with k vertices has $k - 1$ siblings. Recall that a vspan is a list of candidate vertices for inclusion in a clique, and that an isect operation on a vspan represents the inclusion of the first vertex only. An isect operation on a vspan's sibling then represents an alternate choice of vertex to include, with an isect on all siblings representing every possible choice. Finally, a *stub vspan* refers to a vspan with only one vertex. Its child is guaranteed to be empty.

Now we briefly describe the algorithm. Let the vertices in the maximum clique problem be labeled $(v_0, v_1, \ \dots \ , v_n)$. This vspan and its siblings are called the *top-level* *vspans*. The outermost loop of Östergård is realized by visiting the top-level vspans in reverse order, from the stub containing just v_n to the largest vspan containing v_0 through v_n.

A depth-first recursion is invoked on each visited top-level vspan via repeated isect operations (an isect of the top-level vspan, then the isect of its child, and so forth). Each isect adds a vertex to the *current clique*, and generates a child vspan along with a list of which of the child's siblings should be processed later. This is an implementation of Östergård's branch and bound conditions, and excludes siblings which will yield recursion paths that can't match or exceed the current maximum clique size. Recursion terminates when an empty vspan is encountered, at which point the current clique is recorded if it is as least as large as the current maximum size.

Then, with no more possible children to generate, recursion resumes from the previous level, and the latest vertex in the current clique is removed. Recursion resumes from a sibling vspan of the previous child. The sibling is chosen from the list of acceptable siblings which were returned by the isect operation that generated the child.

Eventually, there will be no more siblings to choose at a given level, and the recursion tree will be traversed upwards one level yet again (shrinking the current clique in the process), with a fresh set of siblings to choose from.

This process will eventually result in a return to the original top-level vspan at the top of the recursion tree. Assuming the top-level vspan contains $(v_i, v_i + 1, \ \dots \ , v_k)$, the current maximum clique size is then stored in the *maximum size per vertex array* as $MSPV(i)$. The outer loop then continues to the next-larger top-level vspan. The purpose of MSPV is to implement one of the branch and bound conditions used during each isect operation. By visiting the top-level vspans in reverse order, it is guaranteed that $MSPV$ will be defined for every vertex being visited.

The work unit architecture is shown in Figure 4.8, and we will now describe each sub-module's function.

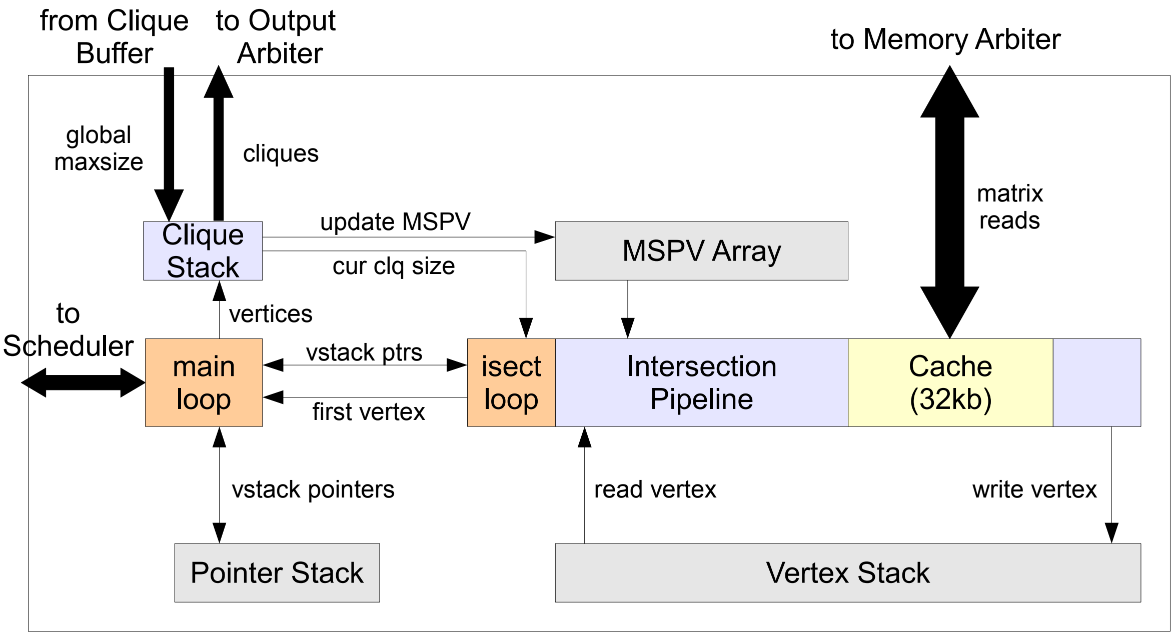


Figure 4.8: Work Unit block diagram

Main Loop

This block consists of a state machine and associated datapath that implement the iteration over the top-level vspans and all recursive processing. It is also the interface to the Scheduler, and is responsible for the highest-level execution and for maintaining the busy state of the work unit.

The Intersection Pipeline is called to perform all isect operations, which returns pointers into the Vertex Stack to represent the address of child vspans it generates. One of these pointers delineates the child's useful siblings from the rest. Each downward recursion performed by the main loop will save the set of pointers in the Pointer Stack so that when control returns to a given level, the state machine is able to resume processing for that level. The first vertex of the child is also returned by each isect, and is passed to the Clique Stack for maintaining the current clique set, before each downward recursion.

Clique Stack

This sub-module maintains the list of vertices in the current clique, and is controlled by the main loop, which can command it to add or remove a vertex fro the clique, and to report the clique to the outside world. Any combination of these requests can be made simultaneously in one cycle and are buffered in an internal FIFO to allow the main loop to continue processing while the Clique Stack carries the operations out at its own pace. Since the Clique Stack has knowledge of the current (and local to the work unit) clique size, it is also responsible for updating $MSPV$ under the command of the main loop.

Clique reporting is the process of sending the current clique to the Clique Buffer via the Output Arbiter. It only occurs if the clique is at least as large as the current global maximum within the entire solver, which is constantly updated by and broadcast to all work units. Note that perfect synchronization of the global maximum is not required, as a delayed update will only mean that an extra (sub-optimal) clique will be reported when it shouldn't have been. It will later be discarded by the Clique Buffer, which maintains the up-to-date version of the global maximum. However, attempting to not report smaller cliques earlier on is still useful, as it allows a work unit's Clique Stack to move on to other buffered add/remove/report commands from the main loop, and it saves clique reporting bandwidth to the Clique Buffer which is shared between all the work units.

Intersection Pipeline

The isect loop block, and Intersection Pipeline (which includes a pipelined cache), are responsible for efficiently carrying out an isect operation on a vspan. The main loop provides a pointer to a vspan, and is given back a pointer to the child vspan, along with the first vertex of the child vspan so that it may be added to the current clique. These pointers are addresses of locations in the Vertex Stack.

The exceptions to this are top-level vspans, which do not exist in the Vertex Stack, and instead of being specified by pointers are specified directly by their start and end indices. The indices of each vertex in between are contiguous and therefore implied, able to be generated by a counter rather than by a read from the Vertex Stack. An isect on a top-level vspan still generates a child vspan whose vertices will exist in the stack.

When the main loop asks the pipeline to perform an isect on the child vspan (and later, recursively, children of children) its vertices will be read sequentially from the Vertex Stack, from locations specified by a start and end pointer provided by the main loop. Sibling vspans are specified by simply advancing the pointer to the start of a vspan, skipping over vertices.

The pipeline, including the cache, is 8 clock cycles long. Vertices from the vspan are iterated by the “isect loop” block and fed into the start of the pipeline, one per cycle. The first stages read a vertex from the Vstack, and initiate both of the branch-and-bound tests in Östergård’s algorithm which continue in parallel with other pipeline stages. Next, the matrix lookup takes 5 cycles and is performed by the cache section of the pipeline. The matrix lookup determines whether the incoming vertex is a neighbour of the first vertex in the vspan, by reading the problem’s adjacency matrix. Finally, the last stage of the pipeline writes a vertex into the vertex stack if it was determined to be a neighbour of the input vspan’s first vertex, and if it passes the branch-and-bound tests initiated earlier in the pipeline.

The execution of the branch-and-bound tests is the most significant difference between the canonical pseudocode of Östergård’s algorithm presented in Section 2.4.2 and the hardware-oriented version in this chapter. A vspan is essentially a way of representing the candidate set U in Procedures 4 and 5, and each vertex in a vspan is a root of a recursion tree. However, the canonical version of the recursive step of the algorithm (Procedure 5) views the branch and bound conditions as “early exits” that cause a return to a higher level of recursion, while the hardware-specific algorithm performs these tests a level higher, as means of *preventing* the entering of an unfruitful lower level of recursion.

This is done by dividing the generated child vspan into a two parts, the first part representing sibling vspans that should be pursued as future roots of recursion, and the second part representing siblings which should not. This division is expressed by a single pointer, pointing to a vertex between the start and end pointers of the generated vspan, and is returned to the main loop to direct the traversal order of the algorithm.

Cache

This is a 32-kilobit direct-mapped cache organized as 32 1024-bit cache lines (each being 8 128-bit memory words). It is used to cache part of each maximum clique problem's adjacency matrix, which is stored off-chip in DDR2 SDRAM, with the intended goal of decreasing read latency and greatly improving performance. It is provided two vertices, and 5 cycles later (assuming a cache hit), it provides a single bit from the adjacency matrix indicating whether the two vertices are neighbours. A miss typically takes around 60 cycles to service.

The cache's pipeline first generates an address. It uses the indices of the two given vertices, the number of vertices in the problem, and the problem's ID assigned by the Main Control unit and provided by the Scheduler. Tags and data are then looked up in parallel, and then the data result, which is a multi-bit word due to the limitations of FPGA block RAM, is multiplexed to a single-bit result using the least-significant bits of the generated address. When a miss is serviced, the entire pipeline is halted, including the stages that feed the cache. Only the tag and data read stages need to be retried when the miss is finished being serviced.

When an isect operation is performed and the cache is queried, all neighbour queries are made between the first vertex of a vspan and the rest of the vertices in the vspan, meaning one of the indices provided to the cache will always stay the same during an isect operation. The adjacency matrix is symmetrical, so by forcing this constant index to indicate a row rather than a column, a very spatially-coherent row-major access pattern is generated.

Each work unit only reads external memory, simplifying the cache design and negating any need for a cache coherency scheme between the work units. The Memory Filler is guaranteed to finish writing a matrix before a work unit is scheduled to use it. All 32 cache lines are invalidated in parallel when a work unit is brought online with a new problem, allowing re-use of an area of external memory over time for different maximum clique problems with different matrix data.

Finally, the geometry of the cache was chosen based on two constraints, with no further experimentation performed to determine alternate configurations. First, the DDR2 Controller's minimum burst size is 8 128-bit words, so it would be inefficient for cache lines to be smaller than that. Second, the cache was chosen to be small enough such that enough memory blocks were available on the FPGA to facilitate the instantiation of multiple work units. In order to accept an entire 128-bit incoming word in one cycle when servicing a cache miss, four Altera M9K blocks had to be used, as each has a maximum power-of-2 width of 32 bits. Thus, the cache is the smallest it can be such that it can service misses in a single cycle, and with cache lines large enough to be a multiple of the memory burst size.

Cache Performance

Using the given cache configuration, we measured the cache hit rate for the BATCH50 and TUBULIN_AB datasets. This was done by emulating the hardware maximum clique solver within a software implementation of the new MMM algorithm, in order to emit the same addresses as the hardware. The cache hit rates for each problem are available in Appendix B.3. The average cache hit rate for the BATCH50 dataset is 98%. For the TUBULIN_AB problem, the hit rate is 93.5%.

Doubling the cache size to 64 kilobits (64 lines of 1024 bits) does not appreciably increase the hit rate for the BATCH50 problems, but increases the hit rate for TUBU-

LIN_AB to 98%.

4.2.9 Output Arbiter

The Output Arbiter allows all the work units to share access to the Clique Buffer, which stores maximum cliques. It uses a tree arbiter structure of `arb2to1` modules, similar to the one found in the Memory Arbiter. Data flow is only one way, and no replies are required back to the work units.

4.2.10 Clique Buffer

The Clique Buffer collects cliques from the work units and stores them into an on-chip buffer. During the output phase, it generates and formats the `outdata` output stream to be sent back to the host through the Main Control module. It also keeps track of the largest clique size seen so far, which is broadcast to the work units to prevent them from sending locally, but not globally, maximum cliques. As cliques arrive at the Clique Buffer, this check is made again, and cliques are only stored if they match or exceed the current global maximum. This is done again because an update in global maximum size does not reach the work units in a single cycle, meaning their concept of the current global maximum may be slightly out of date. If a new maximum is found, the buffer is cleared of its now-obsoleted solutions.

If `nocliques` mode is active, then the work units only transmit the size of the cliques they find and no vertices. The on-chip clique buffer remains empty, and the data transmitted back to the host on includes a header indicating the maximum clique size found.

4.3 Hardware/Software System

This section describes the complete experimental system we developed to accelerate MMM using hardware and software, which consists of:

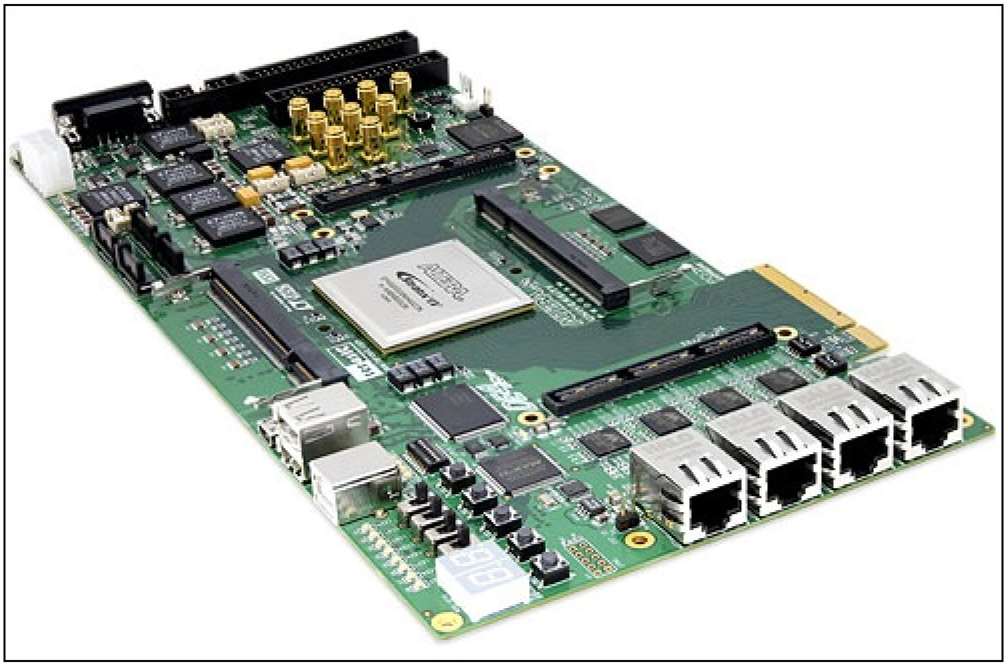


Figure 4.9: The Altera DE4 Development and Education Board (Terasic Technologies).

1. A host PC running an executable which implements, in software, all stages of the algorithm except the call to find the maximum cliques of each subgraph H. The software prepares all maximum clique problems for an entire iteration of the outer loop (for each v_i), and sends them in a batch to be solved by the hardware, collecting the cliques afterward.

2. A Terasic DE4 Board [42], shown in Figure 4.9, which implements the hardware design presented in Section 4.2. It contains an Altera Stratix IV FPGA [11] (part number EP4SGX530KH40C2), 1GB of DDR2 SDRAM, and an NXP ISP1761 USB controller which the FPGA uses to communicate with the host PC using the USB 2.0 protocol.

Figure 4.10 shows a block diagram of the system and indicates the flow of data. Maximum clique problems in the form of graphs are generated by the software-based portion of the MMM algorithm, and sent to the FPGA via the USB 2.0 link. The FPGA buffers the graphs in DDR2 SDRAM as they arrive from the PC, and reads them back

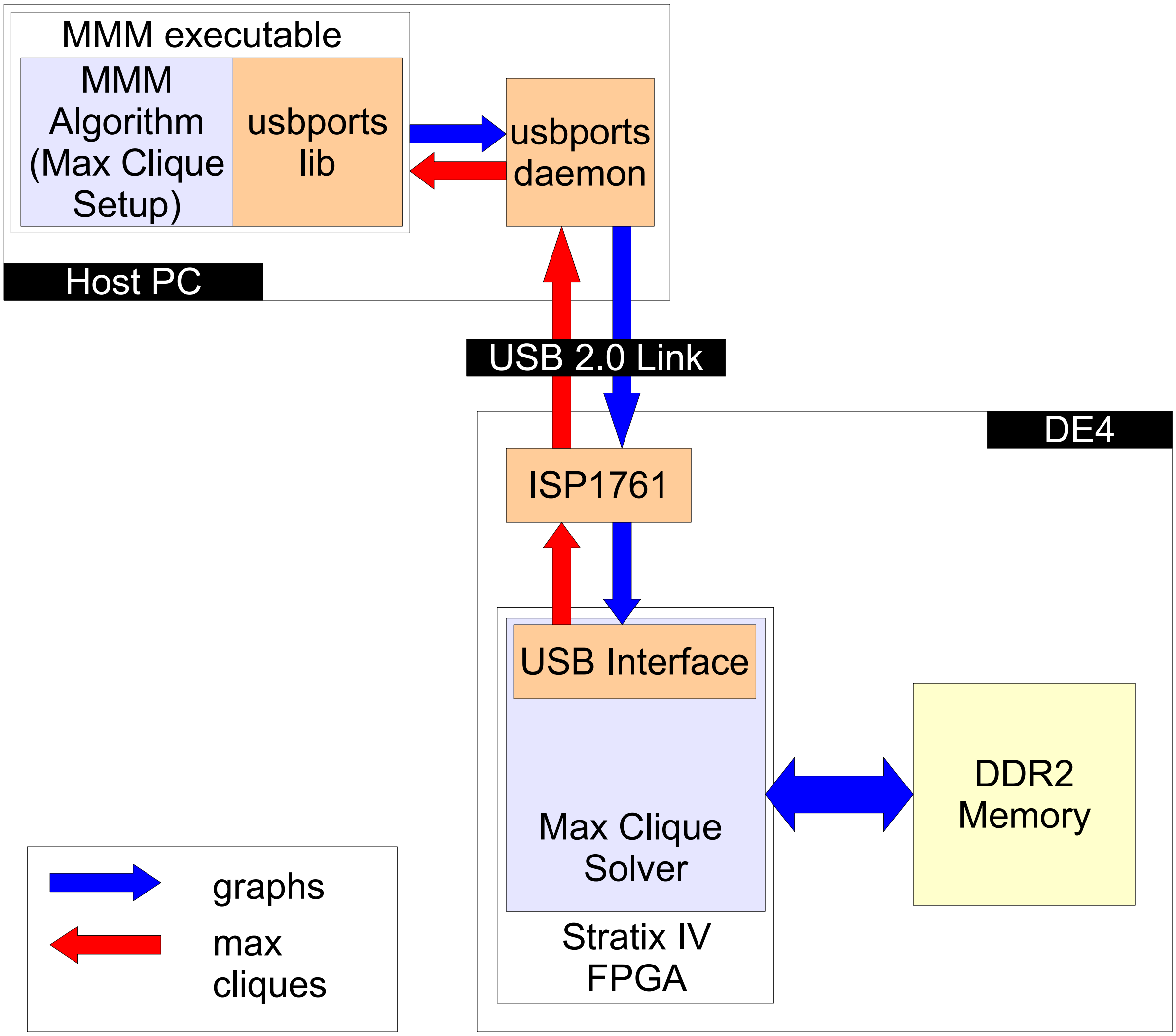


Figure 4.10: A top-level block diagram of the hardware/software system.

during the course of solving each maximum clique problem, as described above. The maximum cliques of the graphs are then sent back to the software through the USB 2.0 link.

4.3.1 USBPorts Package

Communication between the software portion of the algorithm and the maximum clique solver on the FPGA is handled by the USBPorts Package, shown as orange components in Figure 4.10.

USBPorts is a hardware and software library that abstracts communication between a C program running on a host computer and a hardware design implemented on an FPGA. It is a modification of the TM-4 Ports Package [18], redesigned as part of this present research to run over USB 2.0 rather than over a PCI link to the older generation Transmogrifier 4 hardware platform [16].

On the software side, the MMM executable links with a library that provides a UNIX file-like interface to the 32-bit `indata` and `outdata` signals on the FPGA, via `open`, `read`, `write`, and `close` calls. The library communicates through TCP/IP with a daemon that provides access to the host system's physical USB connection. This separation permits the executable to run on a physically different system than the PC hosting the USB link, but is a feature that we do not take advantage of for the sake of performance.

On the hardware side is a USB Interface module, which is the same one as previously described in Section 4.2.1. On one end, it communicates with the ISP1761 interface chip which handles the physical USB 2.0 connection. On the other end, it communicates via the remainder of the maximum clique solver via the 32-bit `indata` and `outdata` signals. In general, this module is auto-generated by a script, and allows connection to up to 128 user input/output signals of any bit width on the FPGA – `indata` and `outdata` are just the two signals we happened to choose for use in our hardware design.

4.3.2 Software Component

This section briefly describes the implementation of the software portion of the algorithm. The MMM executable that runs on the host PC takes two phylogenetic distance matrices and a tolerance parameter as inputs, and generates a set of maximum clique problems for the hardware, for each iteration of the v_i loop (review Sections 3.3.2 and 3.3.3 for more information). The maximum cliques are returned from the hardware back to the executable and the list of matches is updated. Essentially, the hardware acts as a drop-in replacement for the maximum clique finding portion of the new MMM algorithm.

The advantage of organizing maximum clique problems into sets, rather than sending them one at a time to the hardware, is that it allows the hardware to exploit parallelism by solving many problems at once. The disadvantage is that the software must wait for the results from the entire set to be returned before updating its knowledge of the current maximum clique size, possibly leading to less accurate pruning of problems based on the current maximum clique size.

4.3.3 Hardware Configuration

The hardware design presented in Section 4.2 is implemented on the Stratix IV FPGA located on the DE4 board. The design itself is parameterizable to scale to available FPGA resources, and we now describe the specific parametrization that was employed.

Our system has 16 work units, each capable of solving a maximum clique problem with up to 4096 vertices, yielding a maximum clique size of up to 31 vertices. These limits were chosen based on maximum clique problems found in typical MMM problems. Each work unit's vertex stack holds up to 16384 vertices. The 1GB of DDR2 SDRAM we use on the DE4 board runs at 266 MHz, with the work units running at 300 MHz and the rest of the system running at 150 MHz.

The Stratix IV EP4SGX530KH40C2 device contains 424,960 Adaptive Look-up Tables (ALUTs). Each ALUT contains a flipflop and a lookup table, and a pair of ALUTs is capable of implementing a logic function of up to 6 inputs (and certain 7-input functions as well). There are 1280 M9K memory blocks each containing 9,216 bits of RAM, and 64 M144K each containing 147,456 bits of RAM each. Half of the available ALUTs can be used as memory via their configuration bits, giving a total of 28,033,024 bits of on-chip memory.

The hardware design on the FPGA utilizes 16,266 ALUTs and 2,792,168 total bits of of on-chip memory. Although the total logic and on-chip memory usages are relatively low, 269 / 1280 of the M9K blocks are used, allowing for 32 and 64-unit solvers as the

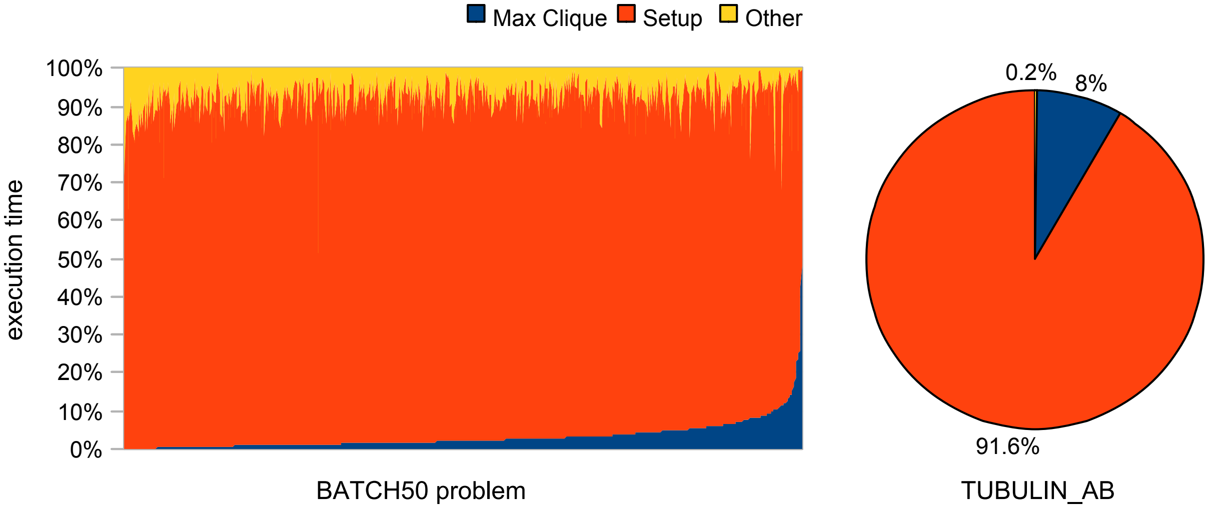


Figure 4.11: Percentage of total software execution time spent in solving maximum cliques and in the remainder of the MMM algorithm, for the 1,225 BATCH50 problems (left) and the TUBULIN_AB problem (right).

only larger power-of-two configuration. The 32-solver configuration was attempted, but would not meet timing requirements, failing setup time constraints by approximately 200 ps.

4.4 Results

This section compares the performance of the hybrid hardware/software system described in Section 4.3 and one that runs the MMM algorithm purely in software. The complete output data used to generate these results is available in Appendices B.2 and B.3.

In both systems, the hardware configuration of the host PC used to run the software is an Intel Core i7-980X running at 4.215 GHz with 6 GB of DDR3 SDRAM running at 1.69 GHz. The software environment is a Linux-based operating system using kernel version 3.6.35-22. Unless otherwise stated, the tolerance parameter α is set to 0.1.

Before providing any hardware results, we present a profile of the execution time of the software-only version of our new algorithm in Figure 4.11. It shows that on average, only 3% of the execution time is spent solving maximum cliques for BATCH50 problems,

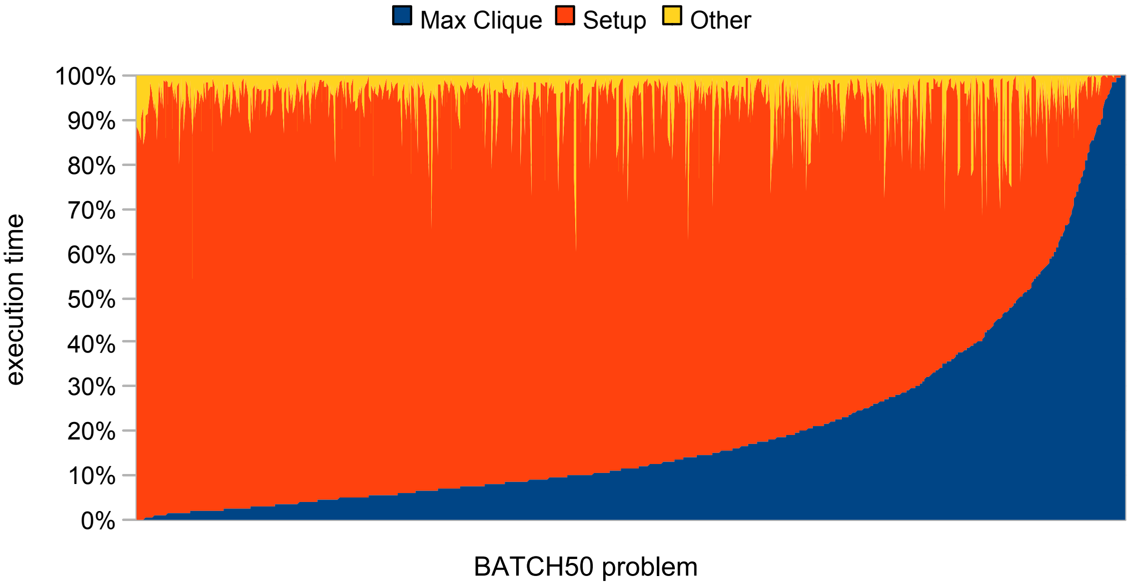


Figure 4.12: Percentage of total software execution time spent in solving maximum cliques and in the remainder of the MMM algorithm, for the 1,225 BATCH50 problems only, with $\alpha = 0.3$

and 8% for the TUBULIN_AB problem. Therefore, we cannot hope to gain a significant performance improvement in overall run time for these data sets by hardware accelerating the maximum clique portion of the algorithm. The portion labeled “Setup” refers to the rest of the time spent in our new algorithm, and dominates the run time.

However, by increasing the tolerance to 0.3, a similar profile run using only the BATCH50 problems (shown in Figure 4.12) demonstrates that the time spent solving maximum cliques increases to 20% of run time on average, and significantly more for some problems within the set. These results seem to indicate that the complexity of the maximum clique problems emitted by our new algorithm is dependent on the tolerance setting. We will continue to use a tolerance of 0.1 for the remainder of the results in this section, as higher tolerances are not biologically relevant and generate more false positive predictions.

Now we directly compare the total running times of the software-only and hardware-accelerated implementations of our new MMM algorithm. Figure 4.13 shows the results

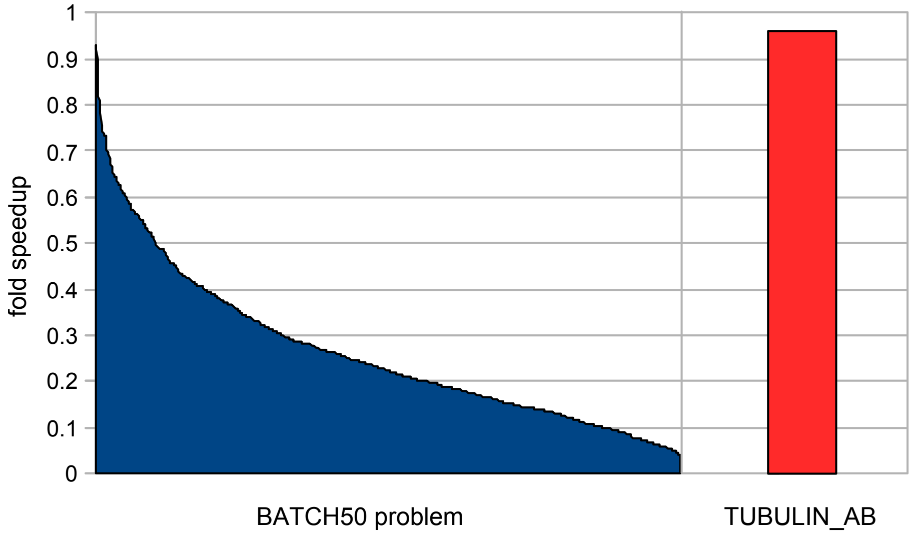


Figure 4.13: Fold speedup (software total time / hardware total time) for all 1,225 BATCH50 problems (in blue) and the TUBULIN_AB problem (in red)

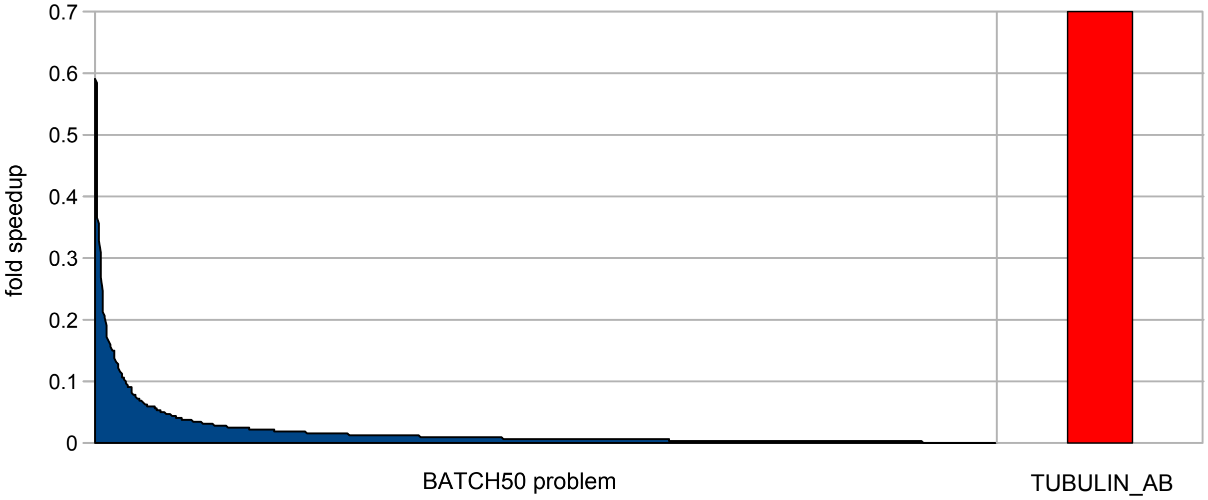


Figure 4.14: Fold speedup (software max clique time / hardware max clique time) for all 1,225 BATCH50 problems (in blue) and the TUBULIN_AB problem (in red)

Matrix 1	**Matrix 2**	$\mathbf{T_{swtotal}}$(s)	$\mathbf{T_{swmc}}$(s)	$\mathbf{T_{hwtotal}}$(s)	$\mathbf{T_{hwmc}}$(s)	$\mathbf{S_{total}}$	$\mathbf{S_{mc}}$
Tubulin A	Tubulin B	401	33	417	47	1.04	1.42
88748	88482	4.47	0.21	4.97	0.63	1.11	3.04
88748	87894	1.73	0.73	3.02	1.55	1.75	2.13
105282	103789	1.52	0.46	1.87	0.78	1.23	1.71
89932	104370	1.24	0.6	1.67	1.02	1.35	1.69
88748	105282	1.05	0.01	1.14	0.08	1.09	13.35
105282	88482	0.86	0.03	0.97	0.11	1.12	4.41
88748	38064	0.74	0.19	1.23	0.62	1.66	3.24
88748	103789	0.71	0.01	0.76	0.08	1.08	13.74
88748	104370	0.69	0.04	0.84	0.19	1.22	4.73

Table 4.1: Comparison of total and max-clique-only runtimes between the hardware and software implementations for the ten longest-running problems.

for both BATCH50 and TUBULIN_AB datasets. The hardware-accelerated version is on average 3.8x slower than the software-only implementation across the 1,225 problems of the BATCH50 dataset, with a respective slowdown of 1.04x for the TUBULIN_AB problem.

We repeat the comparison but now only compare the time spent solving maximum cliques. Figure 4.14 shows that the software-only maximum clique algorithm run time is on average 0.018 times that of the hardware implementation for the BATCH50 problems – a slowdown of 54.27x. The slowdown is only 1.42x for the TUBULIN_AB problem.

Table 4.1 lists the total and maximum clique solving times for the software ($\mathbf{T_{swtotal}}$, $\mathbf{T_{swmc}}$) and hardware ($\mathbf{T_{hwtotal}}$, $\mathbf{T_{hwmc}}$) implementations of the algorithm, for the ten longest-running problems under the software implementation. The remaining two columns provide, for each problem, the slowdown of the hardware implementation with respect to the software implementation, in terms of total runtime ($\mathbf{S_{total}}$) and maximum clique solving time ($\mathbf{S_{mc}}$).

In order to examine this slowdown further, we instrument the hardware with cycle counters to track the time spent performing various stages of execution on the FPGA. The results for both datasets are shown in Figure 4.15, and indicate the percentage of time spent of each call by the software to solve a maximum clique problem using the FPGA-based accelerator.

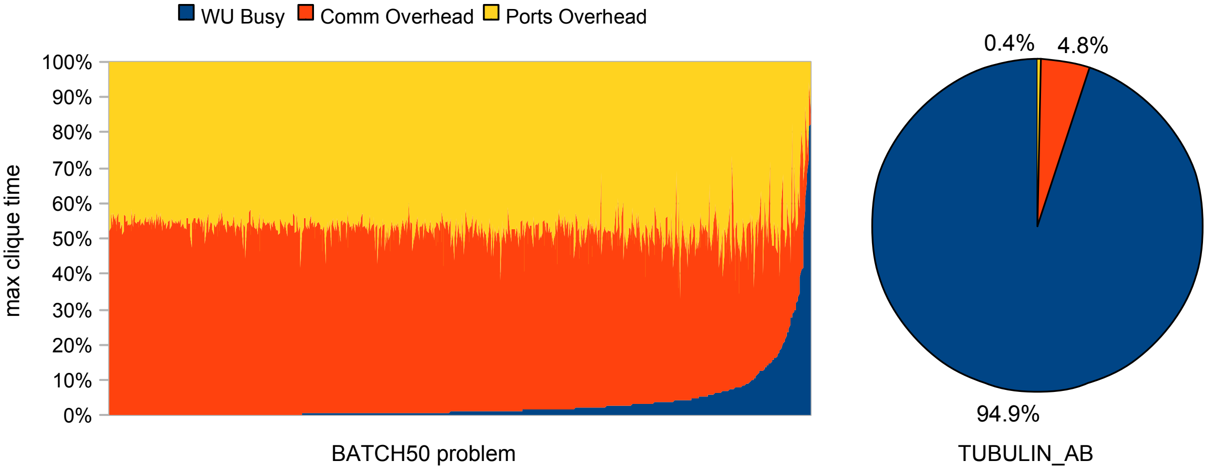


Figure 4.15: Execution time profile for solving maximum cliques in hardware

The portion of the graph marked "Ports Overhead" refers to the time that the actual hardware is idle, meaning that it indicates time spent by the operating system and the Ports package establishing a connection to the hardware, and sending/receiving data through TCP/IP from the USB daemon. It is 46% on average for the BATCH50 problems and 0.4% for the TUBULIN_AB problem.

The portion marked "Comm overhead" is time during which the hardware reported it was active, but all work units were idle, meaning that it refers to time spent exclusively downloading adjacency matrix data or uploading maximum cliques back to the host. It is 50% on average for the BATCH50 problems and 4.8% for the TUBULIN_AB problem.

Finally, the blue portion marked "WU Busy" refers to the fraction of the time in which at least one of the 16 work units was reported busy. It is 3.8% on average for the BATCH50 problems and 94.9% for the TUBULIN_AB problem. Furthermore, Figure 4.16 breaks down this time even further and indicates, on average, how many work units were being used to solve the sets of maximum clique problems provided to the hardware by the software. For the BATCH50 problems, an average of 8% (1.27/16) work units were utilized, while for the TUBULIN_AB problem, 63% (10.08/16) work units were utilized.

These results indicate that the limited USB 2.0 bandwidth is the main reason for the poor performance of the hardware. For the BATCH50 set, which consists of smaller

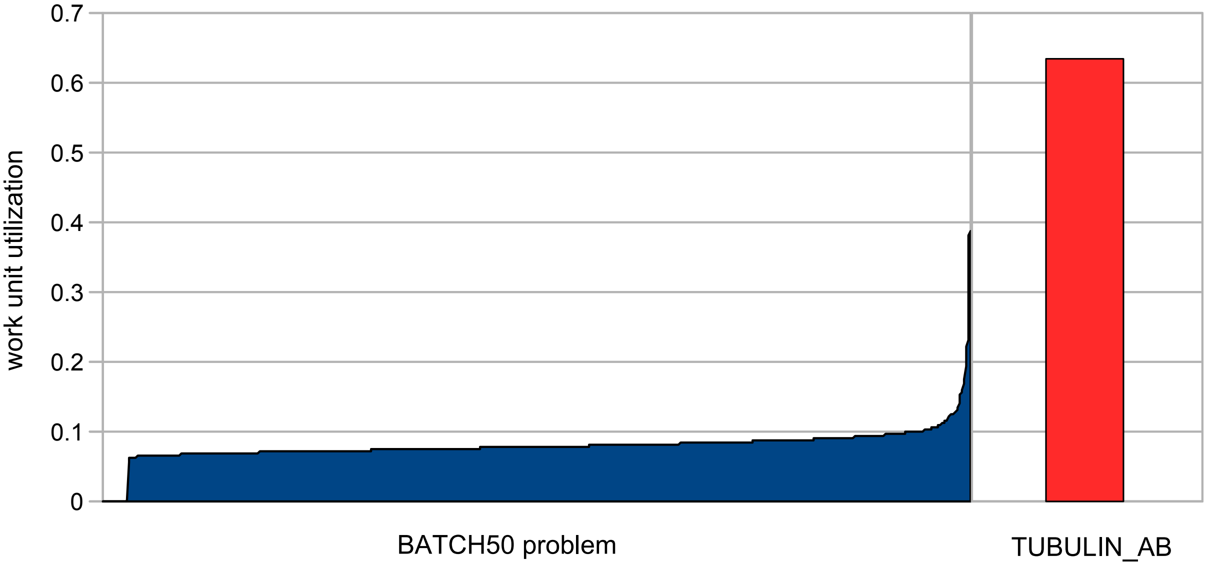


Figure 4.16: Average fraction of work units utilized

problems, the overhead of the Ports Package is a significant fraction of the run time, but becomes almost negligible for the longer-running TUBULIN_AB problem. Since the work units can operate in parallel with the uploading of maximum clique problems to the FPGA, the uploading time is absorbed well when running the TUBULIN_AB problem, with only 4.8% of the time spent idling. Despite that, there is still a lack of bandwidth to be able to utilize all 16 work units when not idling.

Another consideration is the cache hit rate. In Section 4.2.8, we showed that the hit rate is 98% for the BATCH50 problems and 93.5% for the TUBULIN_AB problem. A cache hit takes only one cycle, but a cache miss takes at least 60 cycles depending on contention for the memory controller. Therefore, even at a 98% hit rate, one in every fifty accesses is a miss, meaning more than half the time is spent servicing misses. Due to our DDR2 memory layout, the first access of every maximum clique problem in a set, no matter how small the problem, yields a miss. However, the level 2 and level 3 caches present in the Intel processor may be more efficient at holding the matrix data for many problems at once, yielding a lower miss rate in an already considerably faster memory hierarchy than the one we implemented on the FPGA.

Chapter 5

Conclusions

The prediction of protein-protein interactions assists in the discovery and study of protein function, which furthers our understanding of the function and dysfunction of biological processes in many different species, including humans. There exists an ecosystem of experimental methods and algorithms to predict protein-protein interactions, and they are often used in concert with one another to provide consensus from multiple points of view, owing to their individual strengths and weaknesses.

MatrixMatchMaker (MMM) is one such new algorithm, its strengths including more accurate predictions for certain types of interactions, and its chief weakness being its high computational demand. In this respect, our research advances the state of the art by:

1. Redefining the computational problem posed by the MMM method of protein-protein interaction detection, bringing it more in line with the method's original stated goal of predicting interactions via detecting co-evolution of proteins within multiple species.

2. Developing an algorithm to solve the newly-redefined MMM problem, which is significantly faster than the existing algorithm given the inputs we have tested with, while returning a subset of the existing interaction predictions due to the

new algorithm's more stringent prediction criteria. Given a set of 1225 coevolution detection problems, our new algorithm solves the entire set 566 times faster than the existing MMM algorithm, with an average per-problem speedup of 80 x. With our new algorithm, a more challenging coevolution problem from a different data set, previously intractable under the existing algorithm, is solved in 400 seconds on the same machine.

3. Measuring the practical time complexity of solving MMM coevolution problems using our new algorithm. For both of our data sets, the running time is nearly linearly dependent on the number of vertices processed in the creation of the maximum clique subproblems, which is related to the size of the inputs of the MMM problem in a very data-dependent manner. We also discover that for both data sets, the time spent in the theoretically NP-hard maximum clique portion of the algorithm is negligible when the tolerance parameter is set to 0.1, but becomes significant and even dominates for some of the problems when the tolerance is increased.

Additionally, we made a somewhat misguided (given our third contribution above) attempt to further increase the performance of our new algorithm by implementing the maximum clique solving portion of the algorithm with reconfigurable hardware on an FPGA. Due to the bandwidth limitations of our hardware platform, the hardware we implemented was not able to reach its full performance potential. However, given enough bandwidth and with changes in cache architecture, our hardware design potentially shows promise as a stand-alone system for solving maximum clique problems for a variety of other, non-MMM-related applications.

5.1 Future Work

In addition to improving the bandwidth-starved parallel hardware maximum clique solver, we envision two possible avenues for further research, with the aim of increasing the performance of coevolution detection using MatrixMatchMaker.

First, we found that the majority of run time in our new algorithm is spent preparing the maximum clique problems to be solved. In our implementation, this involves the creation of adjacency matrices representing the input graphs of these maximum clique problems. The creation of the matrices is a highly data-parallel task, and therefore suitable for acceleration on a general-purpose programmable graphics processing unit (GPU). Given that over 90% of the execution time in our algorithm was spent preparing matrices, up to a 10 x speedup of the total execution time is possible using GPU acceleration.

Second, we believe it may be possible to further improve the efficiency of our new algorithm by removing redundant work performed in its second outer-most loop. After a vertex v_j and the resulting edge $e_{min} = (v_i, v_j)$ is chosen, and the resulting maximum clique problem constructed and solved, the next choice of v_j from v_i's sorted list of neighbours will yield a new maximum clique problem that potentially shares many vertices with the first maximum clique problem. An intelligent scheme to identify identical (and therefore possibly redundant) sub-graphs between two such concurrent maximum clique problems could yield smaller maximum clique problems (reducing matrix construction time) and/or a faster traversal of v_i's neighbour list, and merits further investigation.

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Appendix A

TUBULIN_AB Dataset

This appendix describes which proteins are included in the two distance matrices that comprise the TUBULIN_AB dataset. The proteins are obtained from the OMA database at `http://www.omabrowser.org`. Sections A.1 and A.2 list numerical group identifiers (e.g 101892) as well as individual proteins (e.g ARATH|ARATH05173).

The component proteins for either matrix are obtained by first querying all the numerical group IDs in the database (search by "Group"), each of which will return a list of proteins. Combining all the proteins from all such lists, plus the individual proteins that follow the group IDs in Sections A.1 and A.2, yields the proteins for one matrix.

Each of the resulting proteins (both individuals and those belonging to a group) can be queried using the "Entry" search mode to provide the amino acid sequence for that protein. Performing a multiple sequence alignment on all of these amino acid sequences, followed by a phylogenetic distance calculation, yields a distance matrix.

A.1 Tubulin Alpha

101892 103614 106535 134820 49508 49828 49843 49852 49998 50076
50089 50097 50587 50638 50854 50931 51072 51102 51488 51501
51528 51737 51796 51829 51937 52373 52428 52629 52763 52860
53111 53204 53350 53494 53742 53951 54142 54508 54742 55075

55148 55237 55384 55702 56466 56974 57412 57658 57772 57927
59259 59339 59383 60638 61773 63028 63481 64351 65628 66120
66535 70303 70958 70979 71248 75063 81086 83185 85117 86137
88346 88452 90828 90896 92341 93505 96005 96826 97371 98346

ARATH|ARATH05173 BOVIN|BOVIN04940 BOVIN|BOVIN19717
BRAFL|BRAFL00141 BRAFL|BRAFL00209 BRAFL|BRAFL00527
CANFA|CANFA04262 CANFA|CANFA06674 CANFA|CANFA08254
CANFA|CANFA16382 CAVPO|CAVPO03083 CHICK|CHICK13712
CHOHO|CHOHO04565 CHOHO|CHOHO09487 CIOSA|CIOSA03625
CIOSA|CIOSA03626 CIOSA|CIOSA10455 DASNO|DASNO01737
ECHTE|ECHTE01592 ECHTE|ECHTE06277 ECHTE|ECHTE10503
ERIEU|ERIEU00088 ERIEU|ERIEU00115 ERIEU|ERIEU00393
ERIEU|ERIEU00848 ERIEU|ERIEU14448 GASAC|GASAC11197
GASAC|GASAC12885 HELRO|HELRO20539 HUMAN|HUMAN26820
IXOSC|IXOSC04123 LOTGI|LOTGI08142 LOTGI|LOTGI10522
LOTGI|LOTGI17633 LOTGI|LOTGI17635 LOTGI|LOTGI17741
LOTGI|LOTGI17954 LOTGI|LOTGI18761 LOTGI|LOTGI19330
LOTGI|LOTGI19751 LOTGI|LOTGI20753 LOTGI|LOTGI22706
LOTGI|LOTGI23231 MACEU|MACEU09430 MACMU|MACMU09170
MYOLU|MYOLU16074 NEMVE|NEMVE06149 NEMVE|NEMVE14716
NEMVE|NEMVE14717 NEMVE|NEMVE15968 NEMVE|NEMVE21816
NEMVE|NEMVE22353 NEMVE|NEMVE24201 OCHPR|OCHPR00581
OCHPR|OCHPR00604 ORYLA|ORYLA03584 ORYLA|ORYLA09587
PANTR|PANTR08391 PONAB|PONAB08209 POPTR|POPTR16654
PRIPA|PRIPA00215 RABIT|RABIT13490 RABIT|RABIT14366
RATNO|RATNO12096 SORAR|SORAR00213 SORAR|SORAR12428
TETNG|TETNG05398 TETNG|TETNG05399 TETNG|TETNG07043
TETNG|TETNG08855 XENTR|XENTR16320 XENTR|XENTR17136

A.2 Tubulin Beta

101639 113286 118154 120352 131996 44342 50121 50139 50166 50176
50198 50249 50413 50452 50469 50519 50709 51051 51238 51446
51702 51726 51787 51842 51948 52376 52495 53335 53405 53624
53758 54444 54753 55469 56254 56298 56710 56746 57891 59235
59879 62849 66261 68106 68587 68877 74402 77804 79920 82612
83890 84255 86966 91109 92169 99984

AEDAE|AEDAE14025
APIME|APIME03070
BOVIN|BOVIN12460
BOVIN|BOVIN12461
BOVIN|BOVIN17234
CAEBR|CAEBR14519
CANFA|CANFA18297
DIPOR|DIPOR00901
DIPOR|DIPOR01029
DIPOR|DIPOR12803
DIPOR|DIPOR12804
DIPOR|DIPOR12805
DIPOR|DIPOR12808
DIPOR|DIPOR12809
DIPOR|DIPOR14352
DIPOR|DIPOR14977
DIPOR|DIPOR15082
ECHTE|ECHTE13271
HELRO|HELRO00511
HELRO|HELRO11690
HUMAN|HUMAN04501
HUMAN|HUMAN12704
IXOSC|IXOSC05272
LOTGI|LOTGI16861
LOTGI|LOTGI17051
LOTGI|LOTGI17219
LOTGI|LOTGI17498
LOTGI|LOTGI17797
LOTGI|LOTGI17944
LOTGI|LOTGI17976
LOTGI|LOTGI17979
LOTGI|LOTGI18113
LOTGI|LOTGI18154
LOTGI|LOTGI18224
LOTGI|LOTGI18290
LOTGI|LOTGI18737
LOTGI|LOTGI18745
LOTGI|LOTGI19138
LOTGI|LOTGI19419
LOTGI|LOTGI20172
LOTGI|LOTGI20756
LOTGI|LOTGI21656
LOTGI|LOTGI23260
LOTGI|LOTGI23420
LOTGI|LOTGI23482
MACMU|MACMU01749
MACMU|MACMU15292
MACMU|MACMU17536
MONDO|MONDO01760
MONDO|MONDO09413
MONDO|MONDO09414
NEMVE|NEMVE21838
OTOGA|OTOGA07524
PANTR|PANTR21811
PONAB|PONAB12014
PONAB|PONAB17079
SORAR|SORAR12620

Appendix B

Output

B.1 New vs. Existing Algorithm

This section contains the full results used in comparing the new and existing algorithms in Section 3.4. Each row in Tables B.2 and B.3 lists the output for one MMM coevolution problem.

Table B.1: Column Legend

Column Name	**Description**
Name1	First matrix unique filename prefix
Name2	Second matrix unique filename prefix
N	Number of proteins in first matrix
M	Number of proteins in second matrix
CV	Number of vertices in the compatibility graph
TV	Total number of vertices in all maximum clique problems
OS	Largest match size (existing algorithm)
OC	Number of largest matches (existing algorithm)
OT	Running time in seconds (existing algorithm)
NS	Largest match size (new algorithm)
NC	Number of largest matches (new algorithm)
NT	Running time in seconds (new algorithm)
S	Speedup (OT / NT)

Table B.2: Output data for the BATCH50 dataset

Name1	Name2	N	M	CV	TV	OS	OC	OT	NS	NC	NT	S
2506	106948	85	71	465	302712	7	977	12.0094	7	533	0.0653	183.87
2506	88748	85	69	587	776939	7	11011	37.3833	7	4609	0.3089	121.03
2506	106976	85	57	449	417940	7	825	8.8800	7	276	0.1386	64.05
2506	89932	85	57	360	117606	7	211	3.9757	7	129	0.0331	120.09
2506	107298	85	56	303	37678	5	106	0.4128	5	43	0.0160	25.87
2506	105282	85	55	482	193060	6	291	4.5325	6	151	0.0712	63.64
2506	90856	85	50	289	109333	7	130	2.1856	7	10	0.0236	92.7
2506	105323	85	49	328	89561	7	138	2.1415	7	57	0.0266	80.57
2506	107601	85	48	302	66117	6	1166	2.0125	6	636	0.0174	115.68
2506	37889	85	48	239	49080	7	320	1.5967	7	196	0.0131	122.17
2506	74548	85	47	327	131507	6	2412	2.1485	6	1625	0.0318	67.55
2506	103997	85	47	344	88924	8	1	2.7323	8	1	0.0249	109.55
2506	88482	85	47	434	153238	6	18	3.3490	5	3153	0.0509	65.8
2506	106838	85	47	386	120174	5	1470	1.6000	5	874	0.0324	49.35
2506	103998	85	46	219	53901	8	16	1.3573	7	518	0.0135	100.89
2506	105677	85	46	352	91312	7	1	1.5837	7	1	0.0272	58.17
2506	81915	85	46	285	121395	9	22	6.9544	8	182	0.0293	237.29
2506	80191	85	46	269	141429	8	3	8.0045	7	3703	0.0362	221.09
2506	100934	85	46	269	97553	7	495	2.3115	7	126	0.0250	92.55
2506	103789	85	45	373	63221	5	1301	1.3671	5	868	0.0292	46.77
2506	90389	85	44	297	70758	7	158	1.8273	7	3	0.0195	93.89
2506	104370	85	44	351	44875	6	9	0.7957	6	4	0.0233	34.17
2506	100530	85	43	212	70709	8	20	2.6440	7	994	0.0165	160.5
2506	55705	85	43	266	77910	8	136	2.6880	8	18	0.0214	125.61
2506	101685	85	43	306	104291	8	81	2.4217	8	10	0.0302	80.25
2506	48010	85	43	312	114298	7	108	2.6500	7	22	0.0277	95.63
2506	107009	85	42	266	40471	6	24	0.8396	6	24	0.0121	69.37
2506	107429	85	42	254	57880	8	4	2.2220	7	56	0.0146	152.1
2506	38064	85	42	322	100731	7	198	1.5747	7	14	0.0283	55.63
2506	99789	85	41	226	44430	7	14	0.8220	6	324	0.0132	62.5
2506	88589	85	41	374	81449	5	130	1.4081	5	90	0.0219	64.29
2506	74414	85	40	223	53527	7	54	1.2208	7	5	0.0132	92.83
2506	87894	85	40	348	80172	6	584	1.9467	6	339	0.0247	78.83
2506	100937	85	40	222	56138	9	55	2.6363	9	4	0.0146	180.94
2506	100652	85	40	236	49677	7	12	1.1655	7	20	0.0121	96.35
2506	74812	85	40	269	48803	7	16	0.9183	6	83	0.0134	68.46
2506	55634	85	40	303	135647	7	350	2.8681	7	46	0.0330	86.99
2506	100610	85	40	221	54553	7	290	1.4023	7	89	0.0140	99.99
2506	62617	85	40	294	44569	8	1	0.8391	8	1	0.0165	50.8
2506	56150	85	39	207	57801	7	265	1.5957	7	161	0.0142	112.62
2506	104099	85	39	243	31901	6	102	0.5966	6	82	0.0114	52.37
2506	90603	85	39	274	91328	6	623	1.5645	6	235	0.0205	76.48
2506	106996	85	38	263	51115	7	66	1.4794	7	27	0.0150	98.48
2506	107220	85	38	288	48696	6	14	0.6888	6	6	0.0148	46.45
2506	107623	85	38	208	32314	7	65	1.2653	7	15	0.0096	132.33
2506	75001	85	38	280	40508	7	38	0.7498	7	30	0.0151	49.81
2506	88336	85	38	228	55829	8	2	1.2071	7	45	0.0153	78.8
2506	37353	85	38	267	63733	7	93	1.1428	7	38	0.0174	65.51
2506	105654	85	38	239	57325	8	2	2.1114	7	669	0.0163	129.69
106948	88748	71	69	633	961707	7	2266	30.7254	7	687	0.1907	161.08
106948	106976	71	57	230	25676	6	150	0.4982	6	102	0.0098	50.72
106948	89932	71	57	415	135131	9	88	4.5830	8	323	0.0397	115.34
106948	107298	71	56	394	71434	6	23	1.4358	6	6	0.0260	55.28
106948	105282	71	55	453	408651	9	18	12.1589	9	1	0.0979	124.24
106948	90856	71	50	271	84362	8	65	1.8775	8	11	0.0217	86.66
106948	105323	71	49	277	35188	6	194	0.7720	6	40	0.0128	60.12
106948	107601	71	48	316	99937	10	136	6.7101	10	32	0.0281	238.61
106948	37889	71	48	202	21987	5	561	0.3704	5	304	0.0072	51.19
106948	74548	71	47	262	76002	8	8	1.4114	7	228	0.0174	81.27
106948	103997	71	47	306	105851	8	84	4.0439	8	12	0.0279	144.77
106948	88482	71	47	423	220346	7	6	4.0618	6	1326	0.0488	83.24
106948	106838	71	47	258	84466	7	86	1.2346	7	28	0.0176	69.95
106948	103998	71	46	177	24600	7	12	0.6007	6	204	0.0087	69
106948	105677	71	46	299	53384	6	3	0.8791	6	2	0.0167	52.65

Name1	**Name2**	**N**	**M**	**CV**	**TV**	**OS**	**OC**	**OT**	**NS**	**NC**	**NT**	**S**
106948	81915	71	46	234	60602	8	196	2.3823	8	115	0.0179	132.94
106948	80191	71	46	241	72122	7	2	1.4947	6	159	0.0192	77.87
106948	100934	71	46	222	29582	7	26	0.6762	7	4	0.0109	62.27
106948	103789	71	45	385	205169	8	12	4.5215	8	2	0.0473	95.63
106948	90389	71	44	348	87804	7	607	2.3765	7	526	0.0244	97.6
106948	104370	71	44	431	159577	6	1945	2.8316	6	504	0.0457	62
106948	100530	71	43	158	30652	8	68	0.8632	7	133	0.0084	102.34
106948	55705	71	43	213	30876	8	16	0.9062	7	246	0.0102	88.86
106948	101685	71	43	290	56166	6	56	1.0513	6	21	0.0166	63.28
106948	48010	71	43	269	44562	7	44	0.8022	7	20	0.0145	55.2
106948	107009	71	42	268	74301	10	65	4.1010	9	4	0.0181	226.4
106948	107429	71	42	240	71409	9	8	1.7496	8	40	0.0165	106.01
106948	38064	71	42	287	105956	7	156	1.7617	7	42	0.0235	74.87
106948	99789	71	41	201	31842	8	27	0.9763	7	342	0.0104	93.95
106948	88589	71	41	317	60071	4	10186	1.0381	4	10067	0.0162	64.03
106948	74414	71	40	190	23162	7	28	0.4789	7	10	0.0078	61.6
106948	87894	71	40	345	139399	7	9	2.3373	6	1001	0.0331	70.68
106948	100937	71	40	202	34181	8	1377	1.6044	8	512	0.0123	130.94
106948	100652	71	40	200	30531	6	109	0.4978	6	80	0.0095	52.65
106948	74812	71	40	283	58679	9	92	1.6986	9	11	0.0168	100.95
106948	55634	71	40	249	21272	5	63	0.3989	5	62	0.0083	47.99
106948	100610	71	40	179	19182	7	104	0.4510	7	70	0.0081	55.65
106948	62617	71	40	254	41439	6	7	0.6094	6	2	0.0123	49.72
106948	56150	71	39	167	35584	7	701	0.7216	7	19	0.0097	74.71
106948	104099	71	39	224	19294	8	41	0.7006	8	4	0.0103	67.83
106948	90603	71	39	256	46285	7	11	0.8681	6	447	0.0139	62.27
106948	106996	71	38	298	94317	8	1545	3.0367	8	312	0.0224	135.77
106948	107220	71	38	323	103217	7	53	1.7825	7	12	0.0250	71.2
106948	107623	71	38	202	74941	10	14	3.1509	9	4	0.0196	160.38
106948	75001	71	38	258	42336	6	216	0.6880	6	110	0.0127	54.24
106948	88336	71	38	214	27656	7	12	0.5038	6	121	0.0083	60.5
106948	37353	71	38	198	19735	6	12	0.3115	5	998	0.0074	42.06
106948	105654	71	38	213	27790	7	2	0.5387	6	158	0.0092	58.86
88748	106976	69	57	364	600353	8	72	30.7419	7	4964	0.2510	122.46
88748	89932	69	57	471	532032	8	157	16.3451	8	35	0.1260	129.76
88748	107298	69	56	215	105897	5	21998	2.2105	5	15874	0.0409	54.02
88748	105282	69	55	665	3505466	8	260	144.7520	8	40	1.0509	137.74
88748	90856	69	50	328	845438	10	5985	442.5020	10	1913	0.3285	1347.12
88748	105323	69	49	348	92237	5	9175	2.1914	5	7070	0.0350	62.66
88748	107601	69	48	381	52341	5	187	1.1011	5	18	0.0206	53.34
88748	37889	69	48	207	1557	3	1546	0.1681	3	0	0.0051	33.24
88748	74548	69	47	325	162696	6	840	2.3029	6	197	0.0323	71.32
88748	103997	69	47	450	374718	7	314	6.6168	7	8	0.0853	77.54
88748	88482	69	47	629	7975550	10	7100	2833.5400	10	1076	4.4713	633.72
88748	106838	69	47	324	509141	6	20309	9.4417	6	2646	0.1028	91.85
88748	103998	69	46	181	9898	3	9898	0.3963	3	0	0.0046	85.46
88748	105677	69	46	385	239254	6	16	5.9068	6	16	0.0632	93.54
88748	81915	69	46	263	61908	5	257	0.7377	5	152	0.0161	45.76
88748	80191	69	46	273	119769	4	62116	13.7498	4	50555	0.0401	343.18
88748	100934	69	46	237	75367	4	70532	18.5483	4	64329	0.0329	564.46
88748	103789	69	45	512	2686397	8	3	100.9460	7	1122	0.7063	142.93
88748	90389	69	44	425	563413	9	68	98.1200	9	24	0.2872	341.61
88748	104370	69	44	495	2117585	9	157	147.3820	9	17	0.6879	214.24
88748	100530	69	43	157	22691	5	1322	0.2955	5	617	0.0055	53.82
88748	55705	69	43	246	67168	5	37	0.6621	5	33	0.0137	48.17
88748	101685	69	43	357	310318	7	131	6.4628	6	1770	0.0712	90.83
88748	48010	69	43	318	236729	6	6225	4.9803	6	629	0.0493	101.01
88748	107009	69	42	306	61928	6	2	1.0275	5	6034	0.0202	50.97
88748	107429	69	42	268	49989	6	5	0.7101	5	215	0.0132	53.87
88748	38064	69	42	364	1539192	9	18016	636.5790	9	3386	0.7377	862.94
88748	99789	69	41	213	24351	5	72	0.3316	5	13	0.0081	40.93
88748	88589	69	41	444	1133472	7	95158	127.9390	7	37029	0.3489	366.69
88748	74414	69	40	217	64459	4	2345	0.5698	4	2007	0.0135	42.2
88748	87894	69	40	495	2533324	10	126	2313.6700	9	41833	1.7335	1334.7
88748	100937	69	40	218	19152	4	464	0.2616	4	377	0.0076	34.35
88748	100652	69	40	223	13885	4	79	0.2643	4	41	0.0065	40.88
88748	74812	69	40	349	76556	6	30	1.5936	6	9	0.0238	66.94

Name1	**Name2**	**N**	**M**	**CV**	**TV**	**OS**	**OC**	**OT**	**NS**	**NC**	**NT**	**S**
88748	55634	69	40	314	92880	5	4826	1.5099	5	3880	0.0277	54.6
88748	100610	69	40	192	34233	4	245	0.3147	4	219	0.0076	41.55
88748	62617	69	40	327	157587	5	5011	1.9634	5	4038	0.0329	59.59
88748	56150	69	39	177	18614	4	66	0.2220	4	40	0.0054	41.06
88748	104099	69	39	263	115391	5	595	1.1972	5	114	0.0277	43.3
88748	90603	69	39	307	56363	6	90	0.8992	6	61	0.0175	51.38
88748	106996	69	38	363	184640	6	2162	3.8782	6	721	0.0406	95.47
88748	107220	69	38	415	1116276	9	237	78.8389	9	75	0.2923	269.71
88748	107623	69	38	231	22575	5	1	0.3108	4	3038	0.0090	34.68
88748	75001	69	38	330	211179	5	46175	9.8958	5	33617	0.0668	148.15
88748	88336	69	38	249	115562	7	665	2.4459	7	240	0.0218	112.21
88748	37353	69	38	224	58101	6	2	0.7259	6	1	0.0137	53.1
88748	105654	69	38	248	84754	6	13	1.0728	6	8	0.0172	62.27
106976	89932	57	57	246	133834	7	44	1.6594	7	10	0.0274	60.64
106976	107298	57	56	81	248	3	248	0.0245	3	0	0.0011	22.5
106976	105282	57	55	313	304899	7	651	5.3216	7	146	0.0914	58.24
106976	90856	57	50	142	104598	8	99	3.8690	8	66	0.0253	152.86
106976	105323	57	49	239	25298	5	1660	0.4453	5	1076	0.0129	34.48
106976	107601	57	48	152	3585	4	297	0.0842	4	247	0.0030	28.41
106976	37889	57	48	142	755	3	755	0.0553	3	0	0.0025	22.06
106976	74548	57	47	238	228539	7	1642	9.0671	7	133	0.0627	144.72
106976	103997	57	47	102	8750	5	62	0.0712	5	40	0.0020	34.91
106976	88482	57	47	346	866213	8	39905	89.6043	8	12971	0.2949	303.85
106976	106838	57	47	273	455579	8	5	24.1971	7	9569	0.1936	124.95
106976	103998	57	46	135	2489	3	2489	0.0697	3	0	0.0022	31.59
106976	105677	57	46	276	103341	5	120	1.1159	5	80	0.0252	44.24
106976	81915	57	46	214	20533	4	2668	0.2375	4	2265	0.0082	29.09
106976	80191	57	46	169	13561	4	1455	0.1435	4	1198	0.0050	28.87
106976	100934	57	46	178	10552	4	448	0.1214	4	349	0.0050	24.17
106976	103789	57	45	258	233630	8	17	3.8841	7	234	0.0583	66.64
106976	90389	57	44	240	67005	7	4	1.1639	6	495	0.0197	59.11
106976	104370	57	44	224	311852	8	3848	9.1932	8	672	0.0698	131.76
106976	100530	57	43	149	2340	4	105	0.0604	4	103	0.0028	21.7
106976	55705	57	43	216	18783	5	21	0.2267	5	6	0.0078	29.15
106976	101685	57	43	200	51682	6	1	0.5235	6	1	0.0121	43.36
106976	48010	57	43	242	40884	7	5	0.4703	6	189	0.0141	33.24
106976	107009	57	42	179	2992	5	14	0.0809	5	4	0.0034	23.53
106976	107429	57	42	141	6925	5	69	0.0746	5	52	0.0032	23.44
106976	38064	57	42	287	678368	11	6097	807.9330	11	335	0.3262	2477.03
106976	99789	57	41	144	11069	4	132	0.0884	4	64	0.0030	29.17
106976	88589	57	41	339	130249	6	30	1.7791	5	3725	0.0270	65.84
106976	74414	57	40	137	7761	4	3733	0.1196	4	3340	0.0035	34.63
106976	87894	57	40	236	92393	7	134	1.3193	7	21	0.0230	57.25
106976	100937	57	40	135	3586	4	68	0.0523	4	63	0.0024	21.84
106976	100652	57	40	147	6547	4	199	0.0747	4	117	0.0027	27.54
106976	74812	57	40	189	15811	5	338	0.1895	5	162	0.0056	33.88
106976	55634	57	40	264	48573	5	5421	0.7676	5	3889	0.0158	48.7
106976	100610	57	40	136	2352	3	2352	0.0654	3	0	0.0024	27.54
106976	62617	57	40	249	64621	6	5995	1.3674	6	3029	0.0173	78.91
106976	56150	57	39	130	2068	3	2068	0.0575	3	0	0.0020	28.19
106976	104099	57	39	127	8250	4	4586	0.1332	4	3784	0.0038	34.72
106976	90603	57	39	191	19937	4	604	0.1739	4	451	0.0056	31.27
106976	106996	57	38	167	18380	6	11	0.1713	6	10	0.0051	33.68
106976	107220	57	38	110	5625	7	1	0.0521	7	1	0.0021	25.16
106976	107623	57	38	69	326	4	17	0.0176	4	9	0.0008	20.97
106976	75001	57	38	250	89470	5	770	0.7255	5	16	0.0171	42.5
106976	88336	57	38	193	29652	6	343	0.3470	6	156	0.0088	39.44
106976	37353	57	38	193	9366	4	1323	0.1308	4	1071	0.0061	21.54
106976	105654	57	38	179	10931	5	33	0.1317	5	21	0.0047	27.86
89932	107298	57	56	197	8844	4	501	0.1376	4	424	0.0048	28.63
89932	105282	57	55	319	358703	9	32	67.1177	8	4003	0.1239	541.85
89932	90856	57	50	184	45616	7	197	0.5627	7	49	0.0106	53.13
89932	105323	57	49	222	21997	7	14	0.3818	7	9	0.0086	44.3
89932	107601	57	48	234	54174	8	8	0.8168	7	216	0.0139	58.9
89932	37889	57	48	158	9302	6	5	0.1349	6	1	0.0041	32.97
89932	74548	57	47	214	51456	7	1	0.7681	7	1	0.0118	65.09
89932	103997	57	47	141	11336	7	118	0.1694	7	51	0.0037	45.42

Name1	Name2	N	M	CV	TV	OS	OC	OT	NS	NC	NT	S
89932	88482	57	47	370	299599	6	3560	5.4306	6	2612	0.0566	95.91
89932	106838	57	47	201	57906	5	1406	0.5908	5	847	0.0107	55.27
89932	103998	57	46	143	19599	7	290	0.2687	7	50	0.0053	50.75
89932	105677	57	46	227	50357	6	202	0.6376	6	23	0.0119	53.61
89932	81915	57	46	179	41399	7	105	0.5389	7	1	0.0098	55.02
89932	80191	57	46	180	63994	8	736	1.2144	8	454	0.0172	70.66
89932	100934	57	46	171	48187	8	11	0.5432	8	4	0.0100	54.33
89932	103789	57	45	287	250691	7	310	10.4431	7	146	0.0524	199.33
89932	90389	57	44	333	153746	9	9	4.3670	8	374	0.0389	112.23
89932	104370	57	44	452	1628556	11	3245	3030.9900	11	87	1.2449	2434.71
89932	100530	57	43	136	36359	8	90	0.5850	8	5	0.0084	69.55
89932	55705	57	43	159	45872	8	197	0.6686	8	62	0.0103	64.99
89932	101685	57	43	211	42769	6	508	0.5345	6	321	0.0112	47.65
89932	48010	57	43	202	62875	7	701	1.1365	7	163	0.0139	81.52
89932	107009	57	42	222	18028	7	2	0.3344	7	2	0.0069	48.52
89932	107429	57	42	207	34101	6	314	0.5354	6	30	0.0090	59.66
89932	38064	57	42	202	62624	6	897	1.0425	6	398	0.0139	75.18
89932	99789	57	41	149	24731	8	1	0.2450	7	7	0.0054	45.18
89932	88589	57	41	296	72363	4	21954	1.8044	4	21667	0.0191	94.63
89932	74414	57	40	134	24466	8	461	0.4301	8	157	0.0060	72.15
89932	87894	57	40	281	126832	7	4	2.1551	6	1442	0.0287	75.07
89932	100937	57	40	155	35341	8	160	0.4426	8	78	0.0081	54.45
89932	100652	57	40	157	13322	6	305	0.1611	6	81	0.0046	35.13
89932	74812	57	40	250	63998	8	298	1.5816	8	80	0.0159	99.41
89932	55634	57	40	187	5571	5	34	0.1469	5	9	0.0042	34.82
89932	100610	57	40	134	37588	8	20	0.6157	8	8	0.0077	79.58
89932	62617	57	40	190	36426	6	58	0.4757	6	31	0.0083	57.34
89932	56150	57	39	123	15251	8	143	0.1472	8	12	0.0041	36.22
89932	104099	57	39	169	55241	8	339	1.3598	8	18	0.0123	110.79
89932	90603	57	39	215	43962	6	369	0.4738	6	225	0.0105	45.32
89932	106996	57	38	279	66457	7	539	1.4605	7	7	0.0172	84.68
89932	107220	57	38	184	24619	5	890	0.2990	5	446	0.0067	44.81
89932	107623	57	38	141	11708	8	10	0.1352	8	2	0.0040	33.58
89932	75001	57	38	186	24426	7	78	0.3929	7	56	0.0067	58.64
89932	88336	57	38	184	45594	8	4	0.4901	7	5	0.0093	52.51
89932	37353	57	38	157	29214	7	10	0.4010	6	346	0.0069	57.82
89932	105654	57	38	157	44929	8	834	0.8542	8	572	0.0105	81.24
107298	105282	56	55	248	43232	5	311	0.3922	5	146	0.0117	33.61
107298	90856	56	50	174	15630	5	1939	0.1127	5	1032	0.0066	17.1
107298	105323	56	49	278	29399	5	2	0.3984	5	2	0.0101	39.29
107298	107601	56	48	228	10023	4	4815	0.1978	4	4132	0.0067	29.68
107298	37889	56	48	168	4549	3	4550	0.1092	3	0	0.0028	39.35
107298	74548	56	47	278	42212	5	1897	0.5353	5	1296	0.0138	38.78
107298	103997	56	47	132	2149	4	72	0.0270	4	71	0.0019	14.37
107298	88482	56	47	55	348	3	348	0.0143	3	0	0.0007	21.06
107298	106838	56	47	282	68338	5	4	0.4101	4	37944	0.0332	12.34
107298	103998	56	46	167	4192	3	4192	0.1050	3	0	0.0029	36.44
107298	105677	56	46	280	35915	5	534	0.5028	5	422	0.0123	41
107298	81915	56	46	223	19818	5	14	0.2619	5	13	0.0072	36.53
107298	80191	56	46	172	6245	5	242	0.0808	5	125	0.0036	22.5
107298	100934	56	46	220	19414	4	2537	0.2363	4	2087	0.0076	31.03
107298	103789	56	45	431	298925	6	879	4.9816	6	370	0.0666	74.8
107298	90389	56	44	136	3031	4	181	0.0457	4	181	0.0025	18.42
107298	104370	56	44	108	6617	4	2345	0.0753	4	2091	0.0030	24.87
107298	100530	56	43	167	6451	4	46	0.0783	4	31	0.0033	23.91
107298	55705	56	43	219	21588	4	2525	0.2364	4	2191	0.0075	31.57
107298	101685	56	43	324	72022	6	78	1.1152	6	36	0.0203	54.98
107298	48010	56	43	275	56127	5	2170	0.7222	5	1257	0.0158	45.82
107298	107009	56	42	226	15256	5	85	0.1834	5	48	0.0072	25.62
107298	107429	56	42	176	6589	4	590	0.0831	4	572	0.0035	23.73
107298	38064	56	42	227	29621	5	266	0.2367	5	211	0.0095	24.97
107298	99789	56	41	264	26228	5	885	0.3327	5	229	0.0091	36.4
107298	88589	56	41	486	840689	8	2930	40.4874	8	1518	0.2159	187.56
107298	74414	56	40	168	6957	4	1713	0.0753	4	1421	0.0036	20.98
107298	87894	56	40	142	11701	4	1216	0.0636	4	991	0.0035	17.93
107298	100937	56	40	169	5264	4	157	0.0682	4	153	0.0030	23
107298	100652	56	40	171	4089	4	83	0.0607	4	80	0.0028	21.54

Name1	**Name2**	**N**	**M**	**CV**	**TV**	**OS**	**OC**	**OT**	**NS**	**NC**	**NT**	**S**
107298	74812	56	40	131	687	4	3	0.0329	4	2	0.0017	19.56
107298	55634	56	40	225	10777	5	1	0.1471	4	421	0.0054	27.11
107298	100610	56	40	167	9311	4	2080	0.0921	4	1752	0.0038	24.47
107298	62617	56	40	224	17675	4	3918	0.2496	4	3242	0.0077	32.35
107298	56150	56	39	166	7530	3	7531	0.1996	3	0	0.0031	65.13
107298	104099	56	39	220	26270	4	6466	0.3521	4	5337	0.0093	37.8
107298	90603	56	39	178	5968	4	218	0.0812	4	213	0.0034	24.07
107298	106996	56	38	37	164	4	37	0.0089	4	37	0.0005	19.74
107298	107220	56	38	323	55433	6	2	0.7162	6	1	0.0179	40.12
107298	107623	56	38	120	1409	4	119	0.0237	4	117	0.0014	16.91
107298	75001	56	38	271	43793	5	2014	0.5244	5	1280	0.0133	39.55
107298	88336	56	38	123	1253	5	1	0.0288	4	47	0.0015	18.85
107298	37353	56	38	222	26282	4	6338	0.3523	4	5260	0.0094	37.36
107298	105654	56	38	219	28370	4	7102	0.3650	4	6209	0.0096	37.83
105282	90856	55	50	248	350965	9	46	19.3428	9	12	0.0831	232.71
105282	105323	55	49	288	12565	5	12	0.4208	5	11	0.0155	27.1
105282	107601	55	48	291	19234	6	3	0.4034	5	85	0.0142	28.33
105282	37889	55	48	165	282	3	281	0.0772	3	0	0.0037	20.6
105282	74548	55	47	264	120345	8	13	3.4383	8	3	0.0301	114.12
105282	103997	55	47	361	91305	6	2329	1.6116	6	45	0.0308	52.34
105282	88482	55	47	497	2531864	9	3554	437.7960	9	681	0.8628	507.39
105282	106838	55	47	291	559435	9	3836	49.6936	9	1170	0.1518	327.28
105282	103998	55	46	151	1495	3	1495	0.0759	3	0	0.0032	23.7
105282	105677	55	46	312	125800	6	3	1.5591	6	1	0.0336	46.42
105282	81915	55	46	206	73341	6	31	0.8256	6	8	0.0152	54.16
105282	80191	55	46	214	137194	6	449	1.3683	6	214	0.0237	57.85
105282	100934	55	46	191	76884	5	564	0.5785	5	417	0.0147	39.43
105282	103789	55	45	421	2623821	12	12	2609.0700	11	1081	1.5184	1718.27
105282	90389	55	44	258	127267	6	9	1.4162	5	3213	0.0355	39.86
105282	104370	55	44	305	757937	12	138	417.6030	12	8	0.2847	1466.6
105282	100530	55	43	129	21160	5	36	0.1493	5	20	0.0043	34.38
105282	55705	55	43	210	100330	5	1607	0.8929	5	1230	0.0187	47.76
105282	101685	55	43	292	304332	8	26	4.4738	8	6	0.0577	77.53
105282	48010	55	43	249	315767	8	173	14.0858	8	17	0.0913	154.21
105282	107009	55	42	229	29463	8	12	0.5600	7	40	0.0102	54.86
105282	107429	55	42	198	28284	6	560	0.4618	6	185	0.0088	52.61
105282	38064	55	42	286	525293	9	4	25.3479	9	1	0.1293	195.98
105282	99789	55	41	173	9022	7	2	0.1906	7	2	0.0054	35.04
105282	88589	55	41	447	712540	5	152863	113.8390	5	100890	0.2139	532.25
105282	74414	55	40	180	89810	6	49	0.7524	6	37	0.0149	50.37
105282	87894	55	40	412	1022974	8	574	49.9276	8	50	0.3051	163.63
105282	100937	55	40	169	6082	4	182	0.1107	4	155	0.0045	24.41
105282	100652	55	40	177	9111	4	2766	0.1586	4	2563	0.0058	27.27
105282	74812	55	40	268	41905	8	13	1.0306	8	4	0.0159	64.98
105282	55634	55	40	252	10030	5	2	0.2652	5	2	0.0116	22.8
105282	100610	55	40	160	67240	4	1993	0.3840	4	1796	0.0103	37.35
105282	62617	55	40	265	156026	7	4	1.7770	6	307	0.0306	58.01
105282	56150	55	39	154	40173	5	18	0.2545	5	4	0.0070	36.47
105282	104099	55	39	206	172685	6	359	2.5334	6	191	0.0357	70.96
105282	90603	55	39	226	29827	5	334	0.3611	5	132	0.0098	36.8
105282	106996	55	38	250	46917	7	30	0.8132	7	6	0.0138	58.83
105282	107220	55	38	316	117923	7	2	1.4478	6	199	0.0313	46.24
105282	107623	55	38	182	6437	6	1	0.1416	5	71	0.0047	29.98
105282	75001	55	38	267	133737	6	75	1.4863	6	20	0.0340	43.76
105282	88336	55	38	180	78801	7	1	0.8278	6	315	0.0142	58.11
105282	37353	55	38	180	109570	5	19324	2.3972	5	9650	0.0277	86.5
105282	105654	55	38	199	135132	7	1	1.8247	6	502	0.0275	66.34
90856	105323	50	49	181	21981	5	12	0.3047	5	11	0.0070	43.44
90856	107601	50	48	166	16670	6	595	0.2586	6	169	0.0062	41.53
90856	37889	50	48	133	4744	4	172	0.0738	4	149	0.0026	28.39
90856	74548	50	47	182	190811	10	69	14.6302	9	1341	0.0465	314.95
90856	103997	50	47	268	64331	7	650	1.7677	7	318	0.0165	106.82
90856	88482	50	47	192	306729	9	27220	77.2272	9	4652	0.1003	769.63
90856	106838	50	47	154	101739	7	146	2.4202	6	2078	0.0210	115.44
90856	103998	50	46	122	31615	6	100158	43.8198	6	47057	0.0222	1970.14
90856	105677	50	46	184	30877	5	596	0.3456	5	442	0.0075	45.86
90856	81915	50	46	149	51371	7	96	1.0239	7	72	0.0113	90.9

Name1	**Name2**	**N**	**M**	**CV**	**TV**	**OS**	**OC**	**OT**	**NS**	**NC**	**NT**	**S**
90856	80191	50	46	143	51012	8	20	2.0154	7	16192	0.0178	113.37
90856	100934	50	46	152	42108	6	169	0.5030	6	75	0.0089	56.66
90856	103789	50	45	181	160454	8	552	5.6297	8	102	0.0374	150.41
90856	90389	50	44	143	21002	7	80	0.2855	6	681	0.0060	47.94
90856	104370	50	44	173	94481	9	81	2.7013	9	12	0.0179	150.61
90856	100530	50	43	107	42873	8	70930	22.6809	8	24354	0.0237	958.17
90856	55705	50	43	141	27415	7	16	0.3398	7	1	0.0052	65.12
90856	101685	50	43	171	49306	6	379	0.5524	6	176	0.0092	60.3
90856	48010	50	43	160	98872	9	3363	8.6348	9	1912	0.0281	307.67
90856	107009	50	42	147	22392	6	442	0.2999	6	362	0.0065	46.19
90856	107429	50	42	133	22616	8	165	0.5751	8	20	0.0060	95.89
90856	38064	50	42	178	135949	8	88	14.5286	8	3	0.0539	269.45
90856	99789	50	41	131	31371	8	5	0.5162	7	71	0.0069	74.66
90856	88589	50	41	124	44846	4	70665	14.1466	4	45381	0.0186	761.72
90856	74414	50	40	124	39270	8	520	1.3809	8	90	0.0084	163.56
90856	87894	50	40	182	101660	7	1533	2.2389	7	774	0.0219	102.09
90856	100937	50	40	127	30029	7	26	0.3882	6	1574	0.0079	49.44
90856	100652	50	40	126	13461	6	76	0.1450	6	50	0.0033	43.33
90856	74812	50	40	145	30090	7	2078	0.6654	7	898	0.0083	80.4
90856	55634	50	40	158	10851	4	997	0.1227	4	841	0.0043	28.86
90856	100610	50	40	124	49615	7	5384	1.4168	7	1835	0.0112	126.9
90856	62617	50	40	162	39079	8	541	0.8750	8	287	0.0079	110.19
90856	56150	50	39	115	34613	7	37	0.5946	7	18	0.0068	87.98
90856	104099	50	39	133	40445	6	4715	0.5506	6	470	0.0069	80.34
90856	90603	50	39	149	72354	8	309	1.9292	8	75	0.0136	141.79
90856	106996	50	38	128	12958	8	1	0.2048	7	38	0.0037	54.83
90856	107220	50	38	212	63123	8	32	1.7854	8	12	0.0162	110.14
90856	107623	50	38	138	16091	7	75	0.2299	6	583	0.0055	41.73
90856	75001	50	38	159	75279	6	81667	27.8523	6	53985	0.0387	718.86
90856	88336	50	38	122	23493	7	327	0.5197	7	205	0.0053	97.54
90856	37353	50	38	141	75616	8	23	1.7640	7	3571	0.0167	105.91
90856	105654	50	38	125	27496	8	2478	1.0528	8	1870	0.0066	160.63
105323	107601	49	48	173	6238	5	149	0.1164	5	95	0.0034	33.75
105323	37889	49	48	133	4925	6	2	0.0774	6	2	0.0025	30.36
105323	74548	49	47	202	17549	5	616	0.1723	5	470	0.0063	27.39
105323	103997	49	47	210	23969	5	5363	0.4056	5	3576	0.0083	48.96
105323	88482	49	47	250	9925	5	104	0.2435	5	104	0.0088	27.66
105323	106838	49	47	227	12229	4	685	0.1946	4	567	0.0066	29.58
105323	103998	49	46	127	12209	8	1053	0.2477	8	30	0.0047	52.39
105323	105677	49	46	216	18409	7	11	0.2896	7	1	0.0076	38.33
105323	81915	49	46	162	7683	6	6	0.1292	6	6	0.0041	31.81
105323	80191	49	46	145	8673	6	6	0.1209	5	381	0.0038	31.68
105323	100934	49	46	153	17981	7	296	0.3531	7	128	0.0059	59.62
105323	103789	49	45	230	6453	5	106	0.1911	5	83	0.0078	24.64
105323	90389	49	44	171	7551	6	2	0.1284	6	2	0.0039	32.96
105323	104370	49	44	222	6174	4	191	0.1551	4	171	0.0068	22.7
105323	100530	49	43	127	9720	6	108	0.1123	6	51	0.0034	32.95
105323	55705	49	43	157	16812	6	100	0.2019	6	23	0.0051	39.23
105323	101685	49	43	194	16502	6	25	0.2425	6	7	0.0064	37.66
105323	48010	49	43	179	5562	6	6	0.1232	6	6	0.0044	28.06
105323	107009	49	42	158	5998	6	42	0.0924	5	344	0.0030	30.52
105323	107429	49	42	146	5941	5	249	0.0855	5	152	0.0029	29.83
105323	38064	49	42	196	8221	4	228	0.1289	4	186	0.0050	26.03
105323	99789	49	41	137	13890	6	32	0.1471	6	8	0.0037	39.51
105323	88589	49	41	237	19380	4	4139	0.2579	4	3840	0.0078	33.26
105323	74414	49	40	128	4549	6	10	0.0683	6	4	0.0027	25.4
105323	87894	49	40	214	7546	5	22	0.1662	5	11	0.0058	28.59
105323	100937	49	40	127	7177	7	6	0.1193	6	470	0.0031	37.89
105323	100652	49	40	131	3084	6	12	0.0670	6	2	0.0022	29.82
105323	74812	49	40	163	7515	6	5	0.1035	6	3	0.0035	29.96
105323	55634	49	40	184	14282	6	136	0.1786	6	102	0.0054	33.26
105323	100610	49	40	122	4040	6	20	0.0610	6	1	0.0024	25.42
105323	62617	49	40	181	9556	5	217	0.1444	5	179	0.0049	29.27
105323	56150	49	39	113	4020	8	214	0.1362	8	106	0.0022	62.85
105323	104099	49	39	153	4599	7	18	0.1072	7	6	0.0034	31.18
105323	90603	49	39	153	4665	6	21	0.0786	6	20	0.0029	27.55
105323	106996	49	38	147	4583	5	33	0.0719	5	17	0.0025	28.59

Name1	Name2	N	M	CV	TV	OS	OC	OT	NS	NC	NT	S
105323	107220	49	38	189	7858	5	3	0.1294	5	3	0.0044	29.4
105323	107623	49	38	117	3255	6	31	0.0490	6	6	0.0019	25.94
105323	75001	49	38	174	8583	5	95	0.1097	5	50	0.0041	26.73
105323	88336	49	38	127	7099	6	13	0.0972	6	2	0.0027	35.8
105323	37353	49	38	161	8419	6	10	0.0994	5	127	0.0041	24.29
105323	105654	49	38	141	3018	6	1	0.0740	6	1	0.0027	27.16
107601	37889	48	48	134	5608	5	134	0.0614	5	116	0.0025	24.46
107601	74548	48	47	163	7623	6	54	0.1498	6	29	0.0037	41.01
107601	103997	48	47	198	18010	6	72	0.2141	6	72	0.0049	43.67
107601	88482	48	47	261	17172	4	1356	0.4116	4	970	0.0088	46.55
107601	106838	48	47	168	1983	5	10	0.0958	5	10	0.0031	31.24
107601	103998	48	46	121	10516	6	4	0.0683	5	614	0.0031	22.29
107601	105677	48	46	184	3599	5	42	0.1343	5	34	0.0038	35.62
107601	81915	48	46	150	18356	7	10	0.1856	6	513	0.0061	30.53
107601	80191	48	46	156	35447	6	447	0.2656	6	146	0.0085	31.23
107601	100934	48	46	140	10708	6	129	0.1073	6	50	0.0034	31.23
107601	103789	48	45	238	11831	5	219	0.3744	5	98	0.0082	45.7
107601	90389	48	44	196	22223	6	206	0.2697	6	40	0.0066	40.7
107601	104370	48	44	224	6896	4	238	0.2269	4	179	0.0072	31.53
107601	100530	48	43	106	18393	7	24	0.1323	6	157	0.0040	33.47
107601	55705	48	43	137	8654	6	24	0.0837	5	1431	0.0037	22.59
107601	101685	48	43	178	4807	5	113	0.1285	5	50	0.0038	34.22
107601	48010	48	43	166	13098	6	133	0.1631	6	95	0.0042	38.62
107601	107009	48	42	161	13976	7	14	0.1697	6	962	0.0043	39.63
107601	107429	48	42	146	14282	7	4	0.1468	7	4	0.0036	41.29
107601	38064	48	42	173	3035	5	4	0.1029	5	2	0.0035	29.61
107601	99789	48	41	127	7730	7	2	0.0685	7	2	0.0027	25.18
107601	88589	48	41	209	1400	3	1399	0.0988	3	0	0.0042	23.26
107601	74414	48	40	128	11465	6	72	0.0878	6	38	0.0030	29.18
107601	87894	48	40	213	6795	5	147	0.2281	5	62	0.0057	39.99
107601	100937	48	40	130	13831	6	116	0.1047	6	40	0.0047	22.2
107601	100652	48	40	129	10397	6	99	0.0794	6	1	0.0029	27.65
107601	74812	48	40	170	14077	8	4	0.2568	7	179	0.0045	56.58
107601	55634	48	40	152	1848	4	150	0.0608	4	128	0.0022	27.04
107601	100610	48	40	119	12887	6	299	0.0813	6	5	0.0029	27.87
107601	62617	48	40	157	2074	5	15	0.0876	5	10	0.0028	30.98
107601	56150	48	39	116	18043	6	167	0.1090	6	34	0.0037	29.29
107601	104099	48	39	138	5176	6	3	0.0615	5	218	0.0028	22.07
107601	90603	48	39	156	14710	6	16	0.1325	5	297	0.0038	35.23
107601	106996	48	38	174	16131	7	5	0.2256	7	2	0.0050	45.12
107601	107220	48	38	191	4631	5	24	0.1452	5	18	0.0040	36.21
107601	107623	48	38	129	14851	6	205	0.1200	6	118	0.0040	29.97
107601	75001	48	38	157	1383	6	1	0.0839	6	1	0.0026	32.51
107601	88336	48	38	133	8291	6	68	0.0816	5	552	0.0032	25.17
107601	37353	48	38	122	2710	6	2	0.0467	5	111	0.0020	23.6
107601	105654	48	38	136	11807	6	6	0.0945	6	6	0.0037	25.3
37889	74548	48	47	130	3828	5	6	0.0821	5	4	0.0023	36.31
37889	103997	48	47	136	5115	5	4	0.0801	5	4	0.0024	32.96
37889	88482	48	47	141	1721	3	1721	0.0601	3	0	0.0019	31.17
37889	106838	48	47	137	2564	4	46	0.0655	4	26	0.0020	32.33
37889	103998	48	46	117	13755	7	64	0.2151	7	41	0.0032	67.78
37889	105677	48	46	131	2344	5	3	0.0614	4	156	0.0020	30.48
37889	81915	48	46	126	5076	7	3	0.1176	7	2	0.0025	47.18
37889	80191	48	46	125	5324	6	33	0.1118	6	11	0.0024	46.23
37889	100934	48	46	124	6964	6	159	0.1181	6	54	0.0026	45.43
37889	103789	48	45	135	199	3	199	0.0440	3	0	0.0018	23.93
37889	90389	48	44	123	3152	6	1	0.0561	5	68	0.0018	30.45
37889	104370	48	44	131	789	3	789	0.0469	3	0	0.0017	27.28
37889	100530	48	43	109	4698	5	270	0.0694	5	213	0.0020	33.88
37889	55705	48	43	116	2733	5	43	0.0543	5	32	0.0019	28.92
37889	101685	48	43	122	1486	6	2	0.0583	5	175	0.0018	32.33
37889	48010	48	43	123	2269	6	1	0.0692	5	30	0.0019	35.7
37889	107009	48	42	116	6851	6	390	0.1345	6	226	0.0022	61.46
37889	107429	48	42	114	7681	6	197	0.1551	6	105	0.0023	68.75
37889	38064	48	42	120	537	3	537	0.0402	3	0	0.0015	26.28
37889	99789	48	41	107	3951	5	485	0.0533	5	264	0.0019	28.24
37889	88589	48	41	123	1116	3	1116	0.0332	3	0	0.0013	26.26

Name1	**Name2**	**N**	**M**	**CV**	**TV**	**OS**	**OC**	**OT**	**NS**	**NC**	**NT**	**S**
37889	74414	48	40	107	4302	6	1	0.0639	6	1	0.0018	36.44
37889	87894	48	40	119	565	3	565	0.0355	3	0	0.0014	25.47
37889	100937	48	40	106	3918	5	219	0.0600	5	154	0.0017	34.88
37889	100652	48	40	107	4612	7	20	0.1024	7	12	0.0019	54.04
37889	74812	48	40	113	3260	5	4	0.0596	5	4	0.0017	34.82
37889	55634	48	40	113	1044	4	93	0.0385	4	85	0.0014	26.86
37889	100610	48	40	105	3072	5	73	0.0504	5	29	0.0017	29.44
37889	62617	48	40	112	843	5	12	0.0449	5	5	0.0015	30.94
37889	56150	48	39	103	3768	5	109	0.0575	5	52	0.0016	35.27
37889	104099	48	39	105	1433	5	24	0.0375	5	20	0.0014	26.23
37889	90603	48	39	111	1852	4	178	0.0431	4	155	0.0015	28.66
37889	106996	48	38	107	4008	5	475	0.0715	5	327	0.0017	42.13
37889	107220	48	38	113	418	4	2	0.0283	3	0	0.0012	23.81
37889	107623	48	38	102	7285	6	259	0.1150	6	122	0.0020	56.95
37889	75001	48	38	107	1887	6	16	0.0569	6	6	0.0014	40.04
37889	88336	48	38	103	4113	6	28	0.0564	6	19	0.0017	33.8
37889	37353	48	38	106	1816	5	3	0.0436	5	3	0.0015	29.42
37889	105654	48	38	105	2082	6	2	0.0461	5	30	0.0015	30.79
74548	103997	47	47	189	26714	7	8	0.4163	7	8	0.0072	58.15
74548	88482	47	47	238	41700	5	230	0.3374	5	105	0.0113	29.94
74548	106838	47	47	230	179422	7	45	2.2977	7	22	0.0307	74.8
74548	103998	47	46	122	10453	5	2863	0.1377	5	1981	0.0040	34.23
74548	105677	47	46	212	41393	5	219	0.3723	5	130	0.0098	37.82
74548	81915	47	46	161	50527	7	2	0.7823	6	2137	0.0126	62.06
74548	80191	47	46	140	24829	8	54	0.6464	8	8	0.0058	112.16
74548	100934	47	46	154	21188	7	127	0.3125	7	117	0.0057	54.97
74548	103789	47	45	218	61365	7	150	0.6159	7	96	0.0139	44.46
74548	90389	47	44	175	19017	6	4	0.2076	5	472	0.0059	35.41
74548	104370	47	44	218	108417	8	87	2.4817	8	57	0.0252	98.44
74548	100530	47	43	119	25273	7	482	0.5057	7	367	0.0058	86.66
74548	55705	47	43	149	17420	7	24	0.2546	7	4	0.0050	51.19
74548	101685	47	43	185	43182	7	97	0.4651	6	427	0.0095	49.11
74548	48010	47	43	178	48675	8	24	0.9439	7	70	0.0107	87.97
74548	107009	47	42	154	17131	7	28	0.2407	6	329	0.0051	46.93
74548	107429	47	42	144	17742	7	25	0.2228	7	5	0.0057	39.26
74548	38064	47	42	185	169621	9	759	13.5502	9	30	0.0477	283.97
74548	99789	47	41	137	22328	8	6	0.3595	7	364	0.0053	68.34
74548	88589	47	41	223	18144	4	1228	0.1575	4	573	0.0061	25.95
74548	74414	47	40	122	26069	7	287	0.6110	7	24	0.0057	107.65
74548	87894	47	40	193	33555	5	1121	0.2454	5	738	0.0080	30.5
74548	100937	47	40	127	20185	7	45	0.2589	7	8	0.0053	48.65
74548	100652	47	40	130	8374	5	35	0.0920	5	22	0.0030	30.94
74548	74812	47	40	157	22501	7	6	0.2212	7	3	0.0056	39.17
74548	55634	47	40	178	9722	5	51	0.1250	5	32	0.0047	26.88
74548	100610	47	40	120	19096	7	103	0.3466	7	5	0.0046	74.68
74548	62617	47	40	174	43350	8	5	0.7167	7	323	0.0095	75.14
74548	56150	47	39	112	22194	7	7	0.2617	7	3	0.0046	57.11
74548	104099	47	39	147	41537	7	455	0.6734	7	62	0.0079	85.5
74548	90603	47	39	155	47017	8	215	1.5075	8	39	0.0112	134.26
74548	106996	47	38	145	15649	6	80	0.1582	6	31	0.0044	35.59
74548	107220	47	38	169	14360	7	1	0.1448	6	78	0.0048	29.96
74548	107623	47	38	111	9891	6	1942	0.1992	6	677	0.0044	45.08
74548	75001	47	38	165	36192	7	55	0.4321	7	4	0.0079	54.92
74548	88336	47	38	125	14377	8	5	0.1747	8	2	0.0035	49.24
74548	37353	47	38	163	68167	8	41	1.4475	8	3	0.0143	100.96
74548	105654	47	38	136	22079	7	36	0.3836	7	12	0.0055	69.2
103997	88482	47	47	235	61566	5	1188	1.3574	5	592	0.0110	123.33
103997	106838	47	47	172	21493	6	9	0.3410	6	9	0.0048	70.42
103997	103998	47	46	127	11661	8	40	0.1482	8	21	0.0032	45.61
103997	105677	47	46	220	15748	5	327	0.2479	5	184	0.0061	40.5
103997	81915	47	46	165	13365	7	173	0.1736	7	4	0.0055	31.75
103997	80191	47	46	161	15716	7	6	0.1514	6	194	0.0050	30.25
103997	100934	47	46	158	27675	9	47	0.3814	8	547	0.0073	51.96
103997	103789	47	45	214	31020	5	506	0.5306	5	184	0.0082	64.68
103997	90389	47	44	101	2406	6	6	0.0363	5	436	0.0017	22.02
103997	104370	47	44	131	3731	4	444	0.0706	4	343	0.0022	31.43
103997	100530	47	43	119	12698	8	4	0.1306	6	937	0.0037	35.74

Name1	**Name2**	**N**	**M**	**CV**	**TV**	**OS**	**OC**	**OT**	**NS**	**NC**	**NT**	**S**
103997	55705	47	43	159	17471	9	22	0.2269	7	275	0.0048	47.62
103997	101685	47	43	195	14177	7	2	0.2120	6	18	0.0055	38.67
103997	48010	47	43	173	11094	6	45	0.1313	6	34	0.0042	31.33
103997	107009	47	42	158	14001	8	52	0.3278	7	262	0.0045	72.61
103997	107429	47	42	147	9645	7	2	0.1017	6	58	0.0032	31.56
103997	38064	47	42	235	55729	6	28	0.8082	5	2206	0.0122	66.03
103997	99789	47	41	131	12814	8	12	0.1787	7	122	0.0033	54.43
103997	88589	47	41	119	3299	3	3299	0.0782	3	0	0.0014	56.38
103997	74414	47	40	152	13374	8	262	0.2373	8	66	0.0044	54.53
103997	87894	47	40	253	30171	6	3	0.5383	5	147	0.0100	54.01
103997	100937	47	40	132	10065	8	2	0.1258	7	348	0.0032	38.87
103997	100652	47	40	146	5304	6	160	0.0780	6	147	0.0027	28.5
103997	74812	47	40	143	8353	6	81	0.1212	5	327	0.0030	40.19
103997	55634	47	40	187	10438	4	741	0.1283	4	629	0.0039	33.29
103997	100610	47	40	128	10639	8	89	0.1451	8	18	0.0034	42.11
103997	62617	47	40	187	10696	6	238	0.1709	6	122	0.0046	36.79
103997	56150	47	39	125	7801	7	33	0.0844	7	5	0.0029	29.18
103997	104099	47	39	154	8322	6	42	0.1078	6	39	0.0032	33.64
103997	90603	47	39	155	11201	7	42	0.1479	6	671	0.0039	37.91
103997	106996	47	38	116	4555	6	56	0.0572	6	24	0.0019	30.55
103997	107220	47	38	344	93868	8	194	3.6155	8	36	0.0228	158.5
103997	107623	47	38	182	27906	8	2196	0.5988	8	1080	0.0086	69.25
103997	75001	47	38	184	13478	5	656	0.1743	5	407	0.0046	37.6
103997	88336	47	38	125	10991	7	22	0.0922	7	2	0.0029	31.81
103997	37353	47	38	154	7495	5	1272	0.1026	5	1147	0.0034	29.88
103997	105654	47	38	153	9858	8	6	0.1092	7	32	0.0035	30.77
88482	106838	47	47	237	198615	8	45	3.3395	7	1719	0.0459	72.77
88482	103998	47	46	127	1109	3	1109	0.0440	3	0	0.0019	23.2
88482	105677	47	46	268	88771	5	2535	0.8701	5	1442	0.0178	48.83
88482	81915	47	46	173	26343	5	42	0.1830	5	30	0.0057	32.17
88482	80191	47	46	188	43957	5	311	0.2849	5	260	0.0086	33.33
88482	100934	47	46	159	22545	4	972	0.1471	4	747	0.0052	28.19
88482	103789	47	45	385	1476697	12	29216	573.7760	12	6244	0.4763	1204.73
88482	90389	47	44	331	203437	8	635	4.6923	8	307	0.0650	72.14
88482	104370	47	44	378	336633	8	248	8.2844	8	62	0.1151	72
88482	100530	47	43	108	10344	4	910	0.0660	4	818	0.0027	24.65
88482	55705	47	43	168	42050	5	3837	0.3820	5	2905	0.0083	46.24
88482	101685	47	43	241	102228	6	190	0.7875	6	17	0.0197	39.99
88482	48010	47	43	214	105642	7	111	1.2503	7	52	0.0201	62.19
88482	107009	47	42	215	14992	5	76	0.2119	4	3355	0.0070	30.16
88482	107429	47	42	195	28688	5	3848	0.3332	5	2264	0.0077	43.36
88482	38064	47	42	227	483420	9	3442	217.4150	9	1082	0.1691	1285.51
88482	99789	47	41	141	10250	5	32	0.0878	5	3	0.0029	30.25
88482	88589	47	41	432	257792	7	24	4.0098	7	8	0.0801	50.05
88482	74414	47	40	141	32523	6	1	0.1540	5	54	0.0050	31.01
88482	87894	47	40	386	783524	8	893	29.8743	8	38	0.2161	138.23
88482	100937	47	40	142	7474	4	2193	0.0938	4	1914	0.0032	28.87
88482	100652	47	40	155	3819	4	50	0.0659	4	36	0.0027	24.09
88482	74812	47	40	267	26456	5	32	0.3358	5	22	0.0109	30.84
88482	55634	47	40	210	8942	5	16	0.1519	5	16	0.0060	25.16
88482	100610	47	40	131	19757	4	143	0.1459	4	100	0.0035	41.58
88482	62617	47	40	225	72068	6	1779	0.9094	6	64	0.0143	63.66
88482	56150	47	39	121	11250	4	99	0.0723	4	75	0.0026	28.18
88482	104099	47	39	173	53785	5	804	0.3785	5	435	0.0098	38.64
88482	90603	47	39	224	33703	5	230	0.3194	5	179	0.0081	39.66
88482	106996	47	38	284	71353	5	768	0.6048	5	722	0.0151	40.18
88482	107220	47	38	221	80268	6	639	0.7976	6	258	0.0174	45.83
88482	107623	47	38	146	2366	4	100	0.0568	4	27	0.0024	23.5
88482	75001	47	38	225	63308	5	381	0.6042	5	32	0.0146	41.37
88482	88336	47	38	181	40383	5	746	0.2896	5	585	0.0080	36.33
88482	37353	47	38	144	31127	5	2204	0.2085	5	1673	0.0067	31.12
88482	105654	47	38	163	52259	6	1274	0.5541	6	473	0.0096	57.93
106838	103998	47	46	128	6949	4	365	0.0632	4	317	0.0026	24.78
106838	105677	47	46	260	97073	6	16	0.7393	6	6	0.0161	45.81
106838	81915	47	46	195	53975	5	2038	0.4450	5	1107	0.0108	41.27
106838	80191	47	46	147	13756	5	18	0.1034	4	1227	0.0043	24.18
106838	100934	47	46	168	20029	5	3	0.1298	5	2	0.0052	25

Name1	**Name2**	**N**	**M**	**CV**	**TV**	**OS**	**OC**	**OT**	**NS**	**NC**	**NT**	**S**
106838	103789	47	45	229	227563	8	4	3.7363	7	956	0.0452	82.69
106838	90389	47	44	143	22955	6	864	0.2368	5	5592	0.0066	35.73
106838	104370	47	44	245	360254	7	27372	14.8264	7	9312	0.0929	159.58
106838	100530	47	43	147	11576	4	1154	0.0924	4	834	0.0037	24.71
106838	55705	47	43	182	44164	5	1180	0.3940	5	916	0.0090	43.97
106838	101685	47	43	222	42946	6	1207	0.4341	6	305	0.0103	42.12
106838	48010	47	43	221	85186	6	1338	0.7277	6	424	0.0151	48.32
106838	107009	47	42	157	17148	5	2086	0.1922	5	1542	0.0047	41.31
106838	107429	47	42	145	7133	5	38	0.0827	5	5	0.0030	27.51
106838	38064	47	42	240	409273	7	2643	13.6369	7	388	0.0885	154.13
106838	99789	47	41	147	20587	6	369	0.1473	6	360	0.0046	32.35
106838	88589	47	41	239	118675	6	120	0.7847	6	24	0.0218	35.97
106838	74414	47	40	143	14738	4	3808	0.1279	4	3290	0.0046	27.85
106838	87894	47	40	195	92311	6	914	0.8323	6	350	0.0173	48.11
106838	100937	47	40	141	8119	4	200	0.0776	4	161	0.0027	29.17
106838	100652	47	40	139	1395	4	141	0.0428	4	122	0.0022	19.1
106838	74812	47	40	156	8905	5	198	0.0974	5	154	0.0035	27.47
106838	55634	47	40	234	10882	5	21	0.1783	5	1	0.0070	25.33
106838	100610	47	40	134	9174	4	170	0.0665	4	122	0.0029	22.93
106838	62617	47	40	209	63218	7	151	0.8571	7	6	0.0117	73.42
106838	56150	47	39	117	6363	4	119	0.0469	4	95	0.0022	21.12
106838	104099	47	39	183	26113	5	199	0.1666	5	115	0.0071	23.45
106838	90603	47	39	151	19897	5	344	0.1407	5	104	0.0052	27.32
106838	106996	47	38	140	7032	5	9	0.0678	5	7	0.0029	23.6
106838	107220	47	38	173	23545	6	201	0.1942	6	49	0.0061	31.61
106838	107623	47	38	100	3754	5	127	0.0371	5	96	0.0016	23.59
106838	75001	47	38	186	64715	6	4	0.4960	5	845	0.0109	45.32
106838	88336	47	38	118	12924	6	84	0.0878	6	20	0.0030	29.74
106838	37353	47	38	221	47403	4	15028	0.8312	4	10445	0.0144	57.84
106838	105654	47	38	160	24548	5	807	0.1617	5	513	0.0056	28.66
103998	105677	46	46	121	3375	6	84	0.0488	6	62	0.0021	23.26
103998	81915	46	46	116	19171	6	584	0.1962	6	429	0.0042	46.23
103998	80191	46	46	114	18384	6	18	0.1638	6	8	0.0034	48.45
103998	100934	46	46	114	22078	8	47	0.3685	8	20	0.0051	72.68
103998	103789	46	45	122	328	3	328	0.0333	3	0	0.0018	18.47
103998	90389	46	44	106	5194	7	22	0.0634	7	10	0.0019	33.68
103998	104370	46	44	116	3275	4	1121	0.0420	4	942	0.0022	19.53
103998	100530	46	43	106	22618	7	336	0.2288	7	38	0.0041	56.33
103998	55705	46	43	108	10533	7	14	0.0895	6	455	0.0029	30.97
103998	101685	46	43	112	4787	5	59	0.0491	5	33	0.0019	25.33
103998	48010	46	43	111	6691	6	96	0.0619	6	59	0.0023	27.32
103998	107009	46	42	106	9634	7	14	0.0822	6	174	0.0023	35.08
103998	107429	46	42	106	13598	8	156	0.1714	8	80	0.0032	53.84
103998	38064	46	42	109	3856	4	18	0.0573	3	0	0.0016	35.76
103998	99789	46	41	100	12257	7	34	0.1159	7	26	0.0027	42.54
103998	88589	46	41	123	200	3	200	0.0273	3	0	0.0014	20.02
103998	74414	46	40	100	13918	8	46	0.1328	8	12	0.0032	42.14
103998	87894	46	40	111	935	3	935	0.0290	3	0	0.0014	20.75
103998	100937	46	40	98	13560	8	209	0.1575	8	8	0.0029	54.6
103998	100652	46	40	100	9760	7	61	0.1025	7	6	0.0025	41.67
103998	74812	46	40	102	6719	6	160	0.0693	6	34	0.0021	32.56
103998	55634	46	40	104	5757	7	8	0.0641	6	58	0.0019	34.02
103998	100610	46	40	98	14984	8	492	0.2087	8	50	0.0033	63.8
103998	62617	46	40	103	1811	5	49	0.0302	5	42	0.0015	20.2
103998	56150	46	39	97	17649	7	7	0.2328	7	4	0.0034	69.18
103998	104099	46	39	98	6095	6	105	0.0475	5	880	0.0024	20.18
103998	90603	46	39	100	5534	6	149	0.0431	6	99	0.0018	23.46
103998	106996	46	38	95	5877	6	59	0.0458	6	6	0.0019	24.62
103998	107220	46	38	102	1338	3	1334	0.0271	3	0	0.0012	23.01
103998	107623	46	38	94	12978	7	469	0.1182	7	171	0.0029	40.51
103998	75001	46	38	98	2021	6	6	0.0277	6	6	0.0013	20.67
103998	88336	46	38	94	7823	8	9	0.0808	8	3	0.0020	40.77
103998	37353	46	38	99	6372	6	93	0.0476	6	49	0.0019	25.22
103998	105654	46	38	97	5134	7	2	0.0492	6	54	0.0018	27.74
105677	81915	46	46	175	21712	6	205	0.2356	6	90	0.0058	40.5
105677	80191	46	46	150	10791	7	2	0.1398	6	12	0.0039	35.64
105677	100934	46	46	158	16864	7	4	0.2378	6	134	0.0050	47.75

Name1	**Name2**	**N**	**M**	**CV**	**TV**	**OS**	**OC**	**OT**	**NS**	**NC**	**NT**	**S**
105677	103789	46	45	249	78216	6	3	0.6457	5	158	0.0174	37.19
105677	90389	46	44	181	10622	5	140	0.1224	5	94	0.0042	28.88
105677	104370	46	44	246	79731	5	344	0.6430	5	114	0.0146	43.99
105677	100530	46	43	124	9355	6	8	0.0950	5	629	0.0030	31.56
105677	55705	46	43	166	24097	7	9	0.3427	7	2	0.0062	55.54
105677	101685	46	43	211	39538	8	22	0.5301	8	7	0.0099	53.29
105677	48010	46	43	201	34363	7	24	0.4061	7	18	0.0086	47.13
105677	107009	46	42	167	6437	4	1102	0.0866	4	927	0.0036	24.35
105677	107429	46	42	148	5097	5	134	0.0775	5	72	0.0029	26.7
105677	38064	46	42	225	53760	6	1	0.4304	5	1501	0.0114	37.76
105677	99789	46	41	141	16863	6	131	0.1857	6	40	0.0042	44.04
105677	88589	46	41	237	16069	4	802	0.1487	4	547	0.0063	23.69
105677	74414	46	40	134	6130	6	64	0.0832	6	56	0.0029	28.67
105677	87894	46	40	225	49476	6	226	0.4351	6	132	0.0118	36.99
105677	100937	46	40	134	9304	7	44	0.1130	6	209	0.0030	37.42
105677	100652	46	40	135	3300	5	18	0.0542	5	10	0.0023	23.94
105677	74812	46	40	171	9551	5	100	0.1132	5	67	0.0041	27.64
105677	55634	46	40	207	14684	5	53	0.1661	5	29	0.0057	29.11
105677	100610	46	40	125	6286	6	16	0.0802	6	2	0.0026	31.29
105677	62617	46	40	199	43581	7	25	0.5728	7	10	0.0095	60.18
105677	56150	46	39	113	4194	6	3	0.0466	5	104	0.0020	23.19
105677	104099	46	39	163	16346	6	1	0.1556	5	730	0.0050	31.42
105677	90603	46	39	163	10219	6	4	0.1119	6	4	0.0040	28.18
105677	106996	46	38	158	9013	6	2	0.0949	6	2	0.0034	27.6
105677	107220	46	38	209	30303	5	719	0.2639	5	422	0.0081	32.56
105677	107623	46	38	117	1793	4	222	0.0336	4	177	0.0017	19.69
105677	75001	46	38	191	31879	6	504	0.2923	6	306	0.0073	40.26
105677	88336	46	38	132	8302	5	25	0.0767	5	5	0.0030	25.62
105677	37353	46	38	178	19081	6	34	0.1993	6	4	0.0057	35
105677	105654	46	38	152	13881	5	610	0.1358	5	365	0.0042	32.17
81915	80191	46	46	135	36967	11	190	1.7581	10	229	0.0111	157.75
81915	100934	46	46	139	18977	7	82	0.2106	7	10	0.0049	42.86
81915	103789	46	45	169	42722	5	119	0.3792	5	85	0.0083	45.55
81915	90389	46	44	141	10589	8	29	0.1410	8	11	0.0037	37.77
81915	104370	46	44	182	66185	6	6	0.8561	5	3187	0.0136	62.96
81915	100530	46	43	116	38291	13	27	3.2937	11	720	0.0089	370.16
81915	55705	46	43	137	19726	9	11	0.3054	8	88	0.0048	64.3
81915	101685	46	43	156	20409	7	1	0.2624	6	229	0.0053	49.44
81915	48010	46	43	161	43305	9	42	0.8708	9	5	0.0099	87.81
81915	107009	46	42	136	7249	6	47	0.1036	6	33	0.0033	31.11
81915	107429	46	42	126	23763	7	522	0.2927	7	156	0.0058	50.84
81915	38064	46	42	170	32867	5	163	0.3444	5	34	0.0078	44.05
81915	99789	46	41	118	11509	7	23	0.1301	6	359	0.0033	39.48
81915	88589	46	41	146	12301	4	434	0.1289	4	433	0.0027	47.66
81915	74414	46	40	118	21492	10	24	0.3296	9	1	0.0046	71.07
81915	87894	46	40	147	18277	5	445	0.1808	5	208	0.0046	39.32
81915	100937	46	40	120	22448	11	33	1.0736	11	19	0.0071	151.81
81915	100652	46	40	120	17335	7	63	0.1432	7	44	0.0038	38.18
81915	74812	46	40	129	11164	7	15	0.1294	7	3	0.0034	37.96
81915	55634	46	40	156	7670	5	181	0.1330	5	127	0.0036	37.12
81915	100610	46	40	114	18194	9	10	0.2342	8	42	0.0050	46.45
81915	62617	46	40	147	18490	8	33	0.3112	7	150	0.0050	62.57
81915	56150	46	39	109	43118	9	1205	1.7517	9	118	0.0102	171.4
81915	104099	46	39	127	20392	8	52	0.2765	8	7	0.0044	62.44
81915	90603	46	39	133	30258	8	36	0.4228	8	24	0.0060	70.35
81915	106996	46	38	124	16278	7	659	0.1816	7	89	0.0046	39.7
81915	107220	46	38	152	8305	5	30	0.1122	5	10	0.0034	32.56
81915	107623	46	38	105	16237	9	14	0.3337	8	56	0.0059	56.24
81915	75001	46	38	140	13472	6	37	0.1607	6	16	0.0037	43.52
81915	88336	46	38	116	11644	8	2	0.1173	7	20	0.0031	37.52
81915	37353	46	38	143	39323	11	6	1.2692	11	4	0.0082	154.5
81915	105654	46	38	127	19861	11	8	0.5112	10	10	0.0052	97.64
80191	100934	46	46	131	24439	7	255	0.2893	7	122	0.0056	51.78
80191	103789	46	45	172	60110	5	330	0.3025	5	170	0.0109	27.77
80191	90389	46	44	147	43491	8	1320	2.0599	8	32	0.0086	240.08
80191	104370	46	44	161	40563	5	288	0.2153	5	223	0.0077	28.13
80191	100530	46	43	103	49570	13	108	41.0819	12	428	0.0161	2549.61

Name1	Name2	N	M	CV	TV	OS	OC	OT	NS	NC	NT	S
80191	55705	46	43	124	27471	9	80	0.5825	8	305	0.0055	105.26
80191	101685	46	43	141	19687	9	136	0.4851	9	22	0.0052	92.95
80191	48010	46	43	141	55734	9	81	2.0872	9	2	0.0134	155.89
80191	107009	46	42	130	6622	5	681	0.0937	5	532	0.0034	27.92
80191	107429	46	42	125	22037	7	96	0.3103	7	76	0.0052	59.71
80191	38064	46	42	142	17258	5	55	0.1867	5	10	0.0047	39.78
80191	99789	46	41	109	11694	7	12	0.1375	6	181	0.0033	41.4
80191	88589	46	41	155	12308	4	26	0.1640	4	22	0.0030	54.33
80191	74414	46	40	111	39323	10	277	2.7593	10	58	0.0091	303.72
80191	87894	46	40	155	17936	5	89	0.1231	5	47	0.0046	26.67
80191	100937	46	40	113	27886	11	4	1.7324	9	47	0.0081	214.91
80191	100652	46	40	116	23951	8	7	0.3898	7	361	0.0058	67.7
80191	74812	46	40	130	10008	6	41	0.1210	6	21	0.0031	38.53
80191	55634	46	40	128	4415	6	2	0.0638	5	53	0.0026	24.52
80191	100610	46	40	110	38730	11	326	7.6000	11	14	0.0093	819.76
80191	62617	46	40	128	8307	6	42	0.1014	6	16	0.0030	34.12
80191	56150	46	39	110	35744	11	16	7.4493	10	193	0.0115	648.72
80191	104099	46	39	112	28180	9	12	0.9782	8	463	0.0061	161.4
80191	90603	46	39	130	30870	6	761	0.2261	6	375	0.0072	31.22
80191	106996	46	38	132	18080	7	244	0.3228	7	174	0.0063	51.45
80191	107220	46	38	142	6338	4	458	0.0710	4	372	0.0030	24.03
80191	107623	46	38	111	22191	7	2768	0.5987	7	1196	0.0085	70.34
80191	75001	46	38	126	6061	6	82	0.0791	6	69	0.0028	28.09
80191	88336	46	38	115	16951	7	422	0.2163	7	158	0.0041	53.09
80191	37353	46	38	111	15319	6	49	0.1065	6	16	0.0033	31.93
80191	105654	46	38	116	39388	10	120	2.7674	10	14	0.0082	337.57
100934	103789	46	45	156	34092	5	285	0.1706	5	230	0.0061	27.8
100934	90389	46	44	128	10094	6	787	0.1292	6	453	0.0034	38.46
100934	104370	46	44	160	29767	4	13937	0.5637	4	11965	0.0082	68.54
100934	100530	46	43	109	20294	9	38	0.4157	8	99	0.0047	89.24
100934	55705	46	43	130	34179	8	11	0.4596	7	223	0.0070	65.7
100934	101685	46	43	143	15694	7	6	0.1532	6	42	0.0042	36.07
100934	48010	46	43	146	23731	6	367	0.1963	6	267	0.0056	34.86
100934	107009	46	42	129	10714	7	72	0.1416	6	1109	0.0038	36.87
100934	107429	46	42	123	12751	8	21	0.1951	8	7	0.0038	50.82
100934	38064	46	42	148	16223	4	8300	0.2468	4	7994	0.0055	44.48
100934	99789	46	41	116	15697	8	1	0.1789	7	27	0.0039	45.63
100934	88589	46	41	146	8335	4	5	0.0675	4	4	0.0024	28.39
100934	74414	46	40	109	13587	7	220	0.2148	7	155	0.0037	58.68
100934	87894	46	40	140	13377	5	58	0.0862	5	32	0.0035	24.28
100934	100937	46	40	113	18563	7	869	0.3219	7	386	0.0044	73.16
100934	100652	46	40	116	7939	6	2	0.0934	5	269	0.0032	29.24
100934	74812	46	40	123	4245	6	17	0.0650	6	5	0.0024	26.9
100934	55634	46	40	138	4241	5	7	0.0631	5	5	0.0027	23.62
100934	100610	46	40	112	22502	8	283	0.4052	8	70	0.0053	76.85
100934	62617	46	40	134	10655	7	11	0.1119	7	9	0.0033	33.69
100934	56150	46	39	107	14534	6	464	0.1637	6	336	0.0034	48.02
100934	104099	46	39	116	9976	7	20	0.1130	7	2	0.0029	38.96
100934	90603	46	39	128	14993	6	70	0.1381	6	6	0.0046	30.14
100934	106996	46	38	115	5019	5	639	0.0583	5	481	0.0027	21.92
100934	107220	46	38	139	6297	5	2	0.0613	5	2	0.0028	21.86
100934	107623	46	38	106	11581	6	245	0.1243	6	76	0.0031	40.3
100934	75001	46	38	128	7752	8	4	0.1054	7	22	0.0029	35.73
100934	88336	46	38	109	22471	8	58	0.3797	8	30	0.0045	84.54
100934	37353	46	38	130	16867	6	13	0.1194	5	1297	0.0042	28.14
100934	105654	46	38	115	12087	7	10	0.1203	6	158	0.0033	36.67
103789	90389	45	44	251	126769	5	15377	2.0214	5	11581	0.0371	54.49
103789	104370	45	44	273	479101	10	53	25.8592	10	4	0.1264	204.51
103789	100530	45	43	105	11261	6	6	0.0723	6	4	0.0025	29.11
103789	55705	45	43	166	49597	5	694	0.3606	5	343	0.0089	40.4
103789	101685	45	43	240	143486	7	98	1.5268	7	35	0.0240	63.67
103789	48010	45	43	209	159907	8	2	2.8965	7	835	0.0358	80.87
103789	107009	45	42	194	15019	5	540	0.1847	5	273	0.0057	32.41
103789	107429	45	42	166	14369	6	30	0.1719	6	17	0.0048	36.09
103789	38064	45	42	218	242323	9	177	8.0383	9	53	0.0535	150.37
103789	99789	45	41	151	10280	6	31	0.1126	6	10	0.0037	30.48
103789	88589	45	41	379	591320	5	32443	9.3408	5	22851	0.1216	76.82

Name1	**Name2**	**N**	**M**	**CV**	**TV**	**OS**	**OC**	**OT**	**NS**	**NC**	**NT**	**S**
103789	74414	45	40	139	36598	5	39	0.1772	5	28	0.0058	30.35
103789	87894	45	40	306	464988	8	76	14.8203	8	29	0.1122	132.07
103789	100937	45	40	138	6600	4	216	0.0675	4	153	0.0029	23.58
103789	100652	45	40	142	2915	4	331	0.0555	4	276	0.0027	20.48
103789	74812	45	40	217	26480	7	2	0.3422	6	185	0.0089	38.65
103789	55634	45	40	199	2808	4	106	0.1003	4	101	0.0053	19.01
103789	100610	45	40	128	30637	4	322	0.1401	4	296	0.0045	31.14
103789	62617	45	40	210	71747	7	53	0.7606	7	6	0.0139	54.67
103789	56150	45	39	121	17317	4	833	0.0970	4	573	0.0034	28.18
103789	104099	45	39	169	89584	5	3076	0.8619	5	1948	0.0176	48.87
103789	90603	45	39	190	16304	5	172	0.1708	5	141	0.0058	29.58
103789	106996	45	38	208	35923	6	117	0.4070	6	42	0.0091	44.52
103789	107220	45	38	234	86989	7	24	1.0191	6	353	0.0188	54.19
103789	107623	45	38	132	3256	5	6	0.0510	4	280	0.0024	21.32
103789	75001	45	38	218	73050	6	15	0.6726	6	10	0.0165	40.65
103789	88336	45	38	151	46795	8	31	0.5842	7	296	0.0088	66.29
103789	37353	45	38	145	53924	6	71	0.4484	6	27	0.0104	43.16
103789	105654	45	38	162	70187	6	32	0.6802	6	17	0.0129	52.83
90389	104370	44	44	354	55449	5	70	1.1267	5	22	0.0184	61.29
90389	100530	44	43	97	18934	9	248	0.3172	9	52	0.0046	69.61
90389	55705	44	43	115	10602	7	196	0.0739	7	46	0.0027	27.59
90389	101685	44	43	163	12313	7	4	0.1627	6	96	0.0042	39.15
90389	48010	44	43	164	28744	7	4	0.2390	6	351	0.0069	34.48
90389	107009	44	42	174	7644	6	247	0.1074	6	94	0.0039	27.44
90389	107429	44	42	165	9493	6	21	0.1207	6	9	0.0038	31.36
90389	38064	44	42	151	19419	6	399	0.2414	6	243	0.0047	51.88
90389	99789	44	41	116	5783	6	38	0.0486	5	614	0.0023	21.46
90389	88589	44	41	213	45965	6	4	0.5379	6	4	0.0098	54.67
90389	74414	44	40	100	16642	7	172	0.1054	7	35	0.0037	28.67
90389	87894	44	40	215	45833	7	66	0.7551	7	36	0.0114	66.26
90389	100937	44	40	117	14380	11	50	0.3586	10	12	0.0043	82.91
90389	100652	44	40	121	6399	7	4	0.0471	6	35	0.0023	20.18
90389	74812	44	40	194	13167	7	56	0.2142	7	3	0.0055	38.68
90389	55634	44	40	145	2665	4	316	0.0667	4	272	0.0023	29.31
90389	100610	44	40	100	19379	10	145	0.4286	10	18	0.0043	100.12
90389	62617	44	40	151	10138	6	1	0.1105	5	40	0.0034	32.98
90389	56150	44	39	87	8069	9	4	0.0532	8	30	0.0024	22.21
90389	104099	44	39	133	25397	8	179	0.2397	8	64	0.0056	42.86
90389	90603	44	39	182	23420	6	74	0.1931	6	9	0.0055	34.87
90389	106996	44	38	234	22514	7	28	0.3729	6	1564	0.0099	37.81
90389	107220	44	38	138	4276	5	7	0.0768	5	4	0.0023	33.76
90389	107623	44	38	102	7676	8	4	0.0630	7	115	0.0027	22.99
90389	75001	44	38	152	9736	5	21	0.1073	5	13	0.0034	31.4
90389	88336	44	38	156	11135	8	21	0.1467	8	21	0.0040	36.29
90389	37353	44	38	112	5649	6	44	0.0626	6	11	0.0020	30.71
90389	105654	44	38	121	21960	9	38	0.2106	8	312	0.0049	42.91
104370	100530	44	43	127	11949	4	416	0.0759	4	399	0.0032	23.35
104370	55705	44	43	150	32924	5	1514	0.2389	5	671	0.0062	38.27
104370	101685	44	43	220	75555	7	21	0.6868	7	10	0.0156	44.03
104370	48010	44	43	217	118002	6	4703	2.1224	6	2522	0.0254	83.44
104370	107009	44	42	230	23342	5	4	0.2410	4	1527	0.0081	29.7
104370	107429	44	42	211	46857	6	181	0.5771	6	17	0.0112	51.54
104370	38064	44	42	234	219407	9	170	10.6662	9	11	0.0532	200.32
104370	99789	44	41	133	10707	4	101	0.0802	4	80	0.0028	29.07
104370	88589	44	41	258	18016	4	474	0.1890	4	286	0.0090	20.91
104370	74414	44	40	122	19141	5	109	0.1051	5	79	0.0036	29.46
104370	87894	44	40	287	226848	7	67	2.9304	7	7	0.0454	64.48
104370	100937	44	40	152	8733	4	263	0.0843	4	232	0.0031	26.78
104370	100652	44	40	150	3198	4	199	0.0610	4	194	0.0027	22.6
104370	74812	44	40	259	60891	6	189	0.7858	6	79	0.0165	47.52
104370	55634	44	40	212	6003	4	98	0.1234	4	71	0.0058	21.17
104370	100610	44	40	118	12980	5	41	0.0774	5	27	0.0031	25.37
104370	62617	44	40	199	49115	6	2	0.3995	5	1588	0.0110	36.23
104370	56150	44	39	99	8589	4	1090	0.0539	4	973	0.0022	24.75
104370	104099	44	39	179	78556	6	324	0.7586	6	169	0.0132	57.28
104370	90603	44	39	221	29820	6	175	0.4320	6	89	0.0100	43.24
104370	106996	44	38	310	119235	8	13	3.2215	7	2419	0.0327	98.54

Name1	Name2	N	M	CV	TV	OS	OC	OT	NS	NC	NT	S
104370	107220	44	38	200	57272	6	139	0.5854	6	47	0.0123	47.75
104370	107623	44	38	128	6559	4	2601	0.0940	4	1926	0.0030	31.25
104370	75001	44	38	188	65986	6	10968	1.2804	6	4137	0.0172	74.49
104370	88336	44	38	181	52696	5	46	0.2991	5	36	0.0086	34.63
104370	37353	44	38	185	74862	5	312	0.6342	5	151	0.0147	43.21
104370	105654	44	38	156	42682	7	1	0.3479	7	1	0.0076	45.96
100530	55705	43	43	107	17515	9	26	0.3223	8	85	0.0037	87.68
100530	101685	43	43	109	9089	8	69	0.1363	8	11	0.0027	50.62
100530	48010	43	43	111	27519	9	53	0.7841	9	3	0.0060	131.63
100530	107009	43	42	100	5285	7	26	0.0619	7	2	0.0025	25.15
100530	107429	43	42	102	16266	7	38	0.2099	6	534	0.0043	49.32
100530	38064	43	42	115	9108	4	1643	0.0755	4	1500	0.0027	28.39
100530	99789	43	41	95	13556	7	375	0.1362	7	136	0.0033	41.6
100530	88589	43	41	105	4040	3	4040	0.0693	3	0	0.0013	53.68
100530	74414	43	40	95	32013	13	2	4.3814	12	4	0.0080	546.58
100530	87894	43	40	97	6955	4	2876	0.0657	4	2445	0.0025	26.43
100530	100937	43	40	92	24445	12	209	4.6161	10	1493	0.0101	455.77
100530	100652	43	40	95	11232	8	33	0.1761	7	417	0.0031	57.12
100530	74812	43	40	91	7889	6	347	0.0761	6	121	0.0023	32.53
100530	55634	43	40	111	2752	5	12	0.0414	5	10	0.0018	23.63
100530	100610	43	40	91	27065	14	6	6.1505	12	8	0.0072	855.43
100530	62617	43	40	103	6982	7	40	0.0752	7	36	0.0021	35.68
100530	56150	43	39	87	21879	10	124	2.6863	9	2198	0.0077	349.32
100530	104099	43	39	100	28831	11	230	2.4720	11	22	0.0071	348.02
100530	90603	43	39	92	16833	8	13	0.2053	7	170	0.0037	55.16
100530	106996	43	38	85	6687	7	70	0.0944	7	19	0.0025	38.35
100530	107220	43	38	97	2025	4	129	0.0268	4	100	0.0013	20.05
100530	107623	43	38	82	14511	9	2	0.3779	8	284	0.0040	93.41
100530	75001	43	38	94	7635	8	8	0.0710	8	3	0.0020	35.8
100530	88336	43	38	87	7839	7	206	0.1000	7	28	0.0022	46.37
100530	37353	43	38	110	26370	8	98	0.3881	7	463	0.0056	69.36
100530	105654	43	38	95	24497	11	16	2.0372	10	99	0.0059	344.24
55705	101685	43	43	150	21608	8	5	0.3457	7	49	0.0055	62.57
55705	48010	43	43	147	30750	8	20	0.4374	8	16	0.0062	70.28
55705	107009	43	42	124	4197	6	56	0.0637	6	22	0.0023	27.95
55705	107429	43	42	113	7546	6	75	0.0702	6	11	0.0025	28.21
55705	38064	43	42	160	21276	5	33	0.2255	5	13	0.0054	41.99
55705	99789	43	41	112	16032	8	28	0.1920	8	12	0.0035	54.49
55705	88589	43	41	164	14891	4	18	0.1931	4	15	0.0036	53.06
55705	74414	43	40	109	14881	9	1	0.1493	8	1	0.0034	44.02
55705	87894	43	40	150	19858	5	301	0.1845	5	158	0.0047	39.24
55705	100937	43	40	108	24264	9	128	0.4171	9	22	0.0058	72.18
55705	100652	43	40	109	4443	5	118	0.0416	5	74	0.0020	21.12
55705	74812	43	40	122	4894	5	117	0.0644	5	87	0.0023	28.3
55705	55634	43	40	147	7402	5	8	0.0961	5	2	0.0035	27.64
55705	100610	43	40	106	32364	9	31	0.7527	8	1811	0.0083	90.65
55705	62617	43	40	142	21574	8	4	0.3377	8	2	0.0049	69.16
55705	56150	43	39	101	12718	9	21	0.1160	9	21	0.0030	38.1
55705	104099	43	39	118	21497	8	1	0.2803	7	34	0.0042	66.25
55705	90603	43	39	119	11690	8	8	0.1225	7	29	0.0034	35.82
55705	106996	43	38	107	3633	5	133	0.0402	5	79	0.0018	21.82
55705	107220	43	38	144	7691	5	26	0.1020	5	14	0.0032	32.34
55705	107623	43	38	97	8929	7	257	0.0721	7	76	0.0027	26.35
55705	75001	43	38	136	12219	8	10	0.2216	7	50	0.0038	58.71
55705	88336	43	38	103	15221	6	110	0.1013	6	26	0.0029	34.53
55705	37353	43	38	131	21503	7	48	0.2369	7	18	0.0049	48.81
55705	105654	43	38	117	24377	8	501	0.3628	8	103	0.0057	63.41
101685	48010	43	43	180	39628	8	2	0.4273	7	50	0.0097	43.93
101685	107009	43	42	154	4916	5	132	0.0810	5	78	0.0030	26.57
101685	107429	43	42	134	3923	6	2	0.0617	5	105	0.0025	24.97
101685	38064	43	42	200	47591	6	743	0.5079	6	402	0.0104	48.9
101685	99789	43	41	130	11714	7	21	0.1342	6	152	0.0036	37.28
101685	88589	43	41	227	50552	4	1790	0.4744	4	1726	0.0099	47.75
101685	74414	43	40	124	13159	8	17	0.1732	8	5	0.0037	47.31
101685	87894	43	40	209	41819	7	52	0.4811	7	36	0.0104	46.31
101685	100937	43	40	125	8613	7	4	0.1098	7	4	0.0029	37.49
101685	100652	43	40	122	3945	7	1	0.0612	6	17	0.0023	26.82

Name1	**Name2**	**N**	**M**	**CV**	**TV**	**OS**	**OC**	**OT**	**NS**	**NC**	**NT**	**S**
101685	74812	43	40	160	9410	5	93	0.1087	5	53	0.0039	27.64
101685	55634	43	40	181	21668	6	21	0.2153	6	15	0.0061	35.25
101685	100610	43	40	115	13661	8	90	0.2065	8	73	0.0036	57.02
101685	62617	43	40	178	26109	9	5	0.3982	8	11	0.0074	54.14
101685	56150	43	39	108	8125	8	34	0.1097	8	10	0.0027	40.89
101685	104099	43	39	150	29196	8	33	0.3756	8	8	0.0066	56.72
101685	90603	43	39	146	9941	6	22	0.1075	6	12	0.0038	28.51
101685	106996	43	38	147	8653	6	8	0.0972	6	5	0.0035	28.06
101685	107220	43	38	200	21940	6	54	0.2245	6	9	0.0074	30.42
101685	107623	43	38	112	1451	5	31	0.0347	5	13	0.0016	21.9
101685	75001	43	38	175	25590	7	61	0.2698	7	27	0.0067	40.04
101685	88336	43	38	119	10541	8	4	0.1592	7	32	0.0032	49.56
101685	37353	43	38	152	36332	8	60	0.4445	7	345	0.0084	53.12
101685	105654	43	38	140	20825	7	120	0.3089	7	77	0.0051	60.08
48010	107009	43	42	151	6352	7	2	0.0975	6	108	0.0036	27.41
48010	107429	43	42	134	11980	7	18	0.1481	7	2	0.0038	38.61
48010	38064	43	42	194	52176	6	378	0.5533	6	201	0.0116	47.6
48010	99789	43	41	127	13670	7	12	0.1378	6	198	0.0039	35.58
48010	88589	43	41	186	47815	4	6820	0.4056	4	6363	0.0085	47.93
48010	74414	43	40	121	27962	9	2	0.6876	8	87	0.0062	110.87
48010	87894	43	40	178	58892	7	1	0.6472	6	333	0.0131	49.56
48010	100937	43	40	125	14644	6	36	0.1201	6	2	0.0038	31.38
48010	100652	43	40	125	13451	7	45	0.1814	7	18	0.0035	52.13
48010	74812	43	40	147	11263	7	63	0.1852	7	21	0.0041	45.64
48010	55634	43	40	178	5840	7	4	0.1075	7	4	0.0045	23.82
48010	100610	43	40	118	26195	7	64	0.3064	7	20	0.0051	59.8
48010	62617	43	40	169	35882	7	16	0.3487	7	4	0.0077	45.45
48010	56150	43	39	108	14693	8	16	0.1421	8	10	0.0036	39.93
48010	104099	43	39	139	31533	9	7	0.5281	9	2	0.0065	81.8
48010	90603	43	39	150	44675	7	382	0.5028	7	146	0.0089	56.4
48010	106996	43	38	142	9431	6	12	0.0976	6	12	0.0035	27.85
48010	107220	43	38	175	20297	6	1	0.1839	5	274	0.0063	29.28
48010	107623	43	38	107	3593	6	16	0.0492	6	10	0.0023	21.7
48010	75001	43	38	164	31633	8	2	0.3283	7	114	0.0082	40.05
48010	88336	43	38	123	16041	8	26	0.1380	7	26	0.0036	38.26
48010	37353	43	38	157	59486	9	35	1.1694	8	128	0.0134	87.34
48010	105654	43	38	136	41115	11	2	2.2275	10	8	0.0086	258.21
107009	107429	42	42	134	15496	8	9	0.3075	7	35	0.0047	66.05
107009	38064	42	42	158	13044	7	676	0.2283	7	408	0.0043	53.41
107009	99789	42	41	115	4611	6	183	0.0723	6	71	0.0022	32.16
107009	88589	42	41	185	12771	3	12771	0.3979	3	0	0.0032	124.38
107009	74414	42	40	108	8201	8	9	0.1618	7	66	0.0030	54.63
107009	87894	42	40	180	8704	6	112	0.1074	6	64	0.0041	26.06
107009	100937	42	40	114	5339	7	64	0.1002	7	12	0.0023	42.87
107009	100652	42	40	116	6049	7	154	0.1107	7	16	0.0027	41.04
107009	74812	42	40	151	7518	7	91	0.1342	7	56	0.0031	42.68
107009	55634	42	40	142	3586	4	361	0.0439	4	301	0.0022	20.1
107009	100610	42	40	105	9308	8	10	0.1834	8	4	0.0024	75.03
107009	62617	42	40	141	3205	5	10	0.0473	5	4	0.0023	20.36
107009	56150	42	39	98	4478	7	4	0.0575	6	43	0.0020	28.43
107009	104099	42	39	121	2390	8	30	0.0843	8	12	0.0020	42.7
107009	90603	42	39	142	7840	7	21	0.1156	7	8	0.0031	37.22
107009	106996	42	38	153	10913	8	14	0.1386	7	76	0.0034	40.56
107009	107220	42	38	159	5891	6	6	0.0634	6	4	0.0032	19.85
107009	107623	42	38	109	15418	8	24	0.3344	7	398	0.0038	86.98
107009	75001	42	38	140	4078	5	6	0.0488	5	2	0.0023	21.32
107009	88336	42	38	120	4023	7	10	0.0664	6	62	0.0020	33.08
107009	37353	42	38	122	3226	5	92	0.0429	5	37	0.0021	20.12
107009	105654	42	38	119	2854	6	54	0.0503	6	2	0.0020	25.25
107429	38064	42	42	133	6292	6	1	0.1116	5	160	0.0026	42.92
107429	99789	42	41	106	6267	6	62	0.0622	6	27	0.0021	29.41
107429	88589	42	41	163	6197	4	34	0.1060	3	0	0.0023	45.22
107429	74414	42	40	100	9009	6	141	0.0676	6	70	0.0023	29.26
107429	87894	42	40	159	10131	5	212	0.1771	5	112	0.0038	46.78
107429	100937	42	40	105	9402	7	84	0.0857	7	24	0.0026	32.55
107429	100652	42	40	112	12198	6	20	0.1004	6	14	0.0030	33.53
107429	74812	42	40	134	11329	7	8	0.1239	6	60	0.0033	37.89

Name1	**Name2**	**N**	**M**	**CV**	**TV**	**OS**	**OC**	**OT**	**NS**	**NC**	**NT**	**S**
107429	55634	42	40	124	1085	5	3	0.0418	5	3	0.0016	25.73
107429	100610	42	40	100	9444	7	19	0.0822	7	8	0.0025	32.81
107429	62617	42	40	122	3437	5	36	0.0653	5	27	0.0021	31.6
107429	56150	42	39	94	15980	7	102	0.1511	7	43	0.0033	45.73
107429	104099	42	39	112	4584	7	61	0.0665	7	17	0.0020	34.03
107429	90603	42	39	132	12891	7	105	0.1528	7	29	0.0034	45.1
107429	106996	42	38	143	21726	8	199	0.2971	8	104	0.0051	57.95
107429	107220	42	38	134	2779	5	144	0.0725	5	113	0.0021	35.09
107429	107623	42	38	104	16868	7	285	0.1738	7	123	0.0038	45.69
107429	75001	42	38	118	4294	6	8	0.0618	6	4	0.0020	30.2
107429	88336	42	38	112	6265	6	69	0.0698	6	32	0.0022	31.17
107429	37353	42	38	113	6553	7	42	0.0917	7	25	0.0022	41.31
107429	105654	42	38	107	6750	7	2	0.0634	6	49	0.0022	29.1
38064	99789	42	41	128	12956	6	94	0.1174	6	10	0.0030	38.68
38064	88589	42	41	175	96260	5	1857	8.7854	5	1669	0.0196	447.12
38064	74414	42	40	130	13293	6	38	0.1173	5	2225	0.0041	28.36
38064	87894	42	40	204	171149	8	75	5.1476	8	28	0.0377	136.46
38064	100937	42	40	130	4480	4	213	0.0532	4	192	0.0024	22.46
38064	100652	42	40	126	2399	4	57	0.0398	4	23	0.0019	20.56
38064	74812	42	40	157	5800	5	38	0.0898	5	25	0.0034	26.32
38064	55634	42	40	204	21421	5	559	0.2050	5	353	0.0085	24.16
38064	100610	42	40	116	8324	4	43	0.0557	4	37	0.0024	23.15
38064	62617	42	40	191	47571	6	64	0.4961	6	21	0.0097	50.89
38064	56150	42	39	107	6542	4	37	0.0462	4	6	0.0019	23.76
38064	104099	42	39	152	23113	4	8434	0.3604	4	6941	0.0072	49.96
38064	90603	42	39	148	13350	5	75	0.1021	5	37	0.0037	27.33
38064	106996	42	38	144	9251	7	6	0.1103	6	26	0.0033	33.09
38064	107220	42	38	224	106955	8	24	1.6126	8	10	0.0229	70.33
38064	107623	42	38	114	2593	5	28	0.0379	5	1	0.0017	21.69
38064	75001	42	38	185	54666	5	1636	0.4733	5	1108	0.0109	43.28
38064	88336	42	38	125	17324	7	934	0.3066	7	355	0.0046	66.09
38064	37353	42	38	171	44556	5	6	0.2281	5	3	0.0081	28.18
38064	105654	42	38	150	18988	5	29	0.1483	5	25	0.0047	31.88
99789	88589	41	41	141	4205	4	71	0.0488	4	68	0.0019	25.4
99789	74414	41	40	97	9164	7	30	0.0957	7	16	0.0023	41.87
99789	87894	41	40	123	6066	5	1	0.0592	4	393	0.0022	26.79
99789	100937	41	40	98	12684	7	58	0.1066	7	10	0.0026	40.56
99789	100652	41	40	98	3231	5	385	0.0336	5	284	0.0017	20.27
99789	74812	41	40	109	4268	6	114	0.0592	6	47	0.0019	31.1
99789	55634	41	40	121	4093	5	49	0.0549	5	33	0.0020	27.77
99789	100610	41	40	96	15773	8	47	0.2101	8	1	0.0032	66
99789	62617	41	40	120	9120	9	4	0.1491	9	1	0.0028	52.37
99789	56150	41	39	87	5581	6	160	0.0433	6	82	0.0016	27.19
99789	104099	41	39	107	10650	8	24	0.1729	8	2	0.0027	64.88
99789	90603	41	39	108	8381	7	12	0.0695	7	7	0.0023	30.02
99789	106996	41	38	97	3087	5	141	0.0311	5	97	0.0014	21.63
99789	107220	41	38	125	4345	5	48	0.0522	5	22	0.0020	25.95
99789	107623	41	38	89	6207	7	97	0.0503	7	16	0.0018	28.08
99789	75001	41	38	117	7072	7	4	0.0808	6	101	0.0023	35.77
99789	88336	41	38	91	6489	7	73	0.0662	7	47	0.0018	36.04
99789	37353	41	38	111	9693	6	105	0.0740	6	55	0.0025	29.65
99789	105654	41	38	100	8052	8	1	0.1144	7	67	0.0023	50.48
88589	74414	41	40	124	10793	3	10793	0.3700	3	0	0.0020	183.36
88589	87894	41	40	349	244042	6	987	3.2515	6	525	0.0603	53.89
88589	100937	41	40	118	3870	3	3870	0.0666	3	0	0.0014	46.68
88589	100652	41	40	137	1369	3	1369	0.0341	3	0	0.0017	20.51
88589	74812	41	40	228	15653	5	398	0.1517	5	120	0.0059	25.83
88589	55634	41	40	178	1928	4	37	0.0504	4	35	0.0028	17.97
88589	100610	41	40	123	12005	3	12005	0.4440	3	0	0.0020	219.13
88589	62617	41	40	196	17187	4	301	0.1256	4	266	0.0048	26.28
88589	56150	41	39	123	8164	3	8164	0.2451	3	0	0.0019	131.04
88589	104099	41	39	146	26354	4	4469	0.1983	4	4466	0.0050	39.89
88589	90603	41	39	181	6368	4	2026	0.0780	4	1860	0.0037	21.15
88589	106996	41	38	204	2233	4	6	0.0617	4	4	0.0031	19.74
88589	107220	41	38	150	15392	4	40	0.3482	4	33	0.0030	114.82
88589	107623	41	38	112	1250	3	1250	0.0247	3	0	0.0012	20.3
88589	75001	41	38	205	22260	4	76	0.5031	4	64	0.0060	84.39

Name1	Name2	N	M	CV	TV	OS	OC	OT	NS	NC	NT	S
88589	88336	41	38	140	13827	4	4845	0.1302	4	4420	0.0037	34.75
88589	37353	41	38	128	13514	4	4445	0.1284	4	4428	0.0037	34.82
88589	105654	41	38	146	18284	4	693	0.0949	4	659	0.0034	27.56
74414	87894	40	40	126	13023	5	45	0.1472	5	37	0.0036	40.62
74414	100937	40	40	98	15020	9	57	0.2246	9	25	0.0036	63.17
74414	100652	40	40	97	9944	8	264	0.1452	8	79	0.0034	43.01
74414	74812	40	40	105	5319	7	63	0.0820	7	27	0.0022	37.22
74414	55634	40	40	117	3316	5	2	0.0472	4	327	0.0020	23.4
74414	100610	40	40	94	31716	10	145	1.7870	10	12	0.0075	238.01
74414	62617	40	40	114	8876	6	158	0.1051	6	93	0.0027	38.85
74414	56150	40	39	92	13269	8	42	0.0943	8	8	0.0026	35.98
74414	104099	40	39	102	25137	9	463	0.6813	9	108	0.0053	129.05
74414	90603	40	39	101	15271	9	7	0.2101	8	110	0.0038	54.78
74414	106996	40	38	97	4851	6	40	0.0429	6	9	0.0019	23.06
74414	107220	40	38	129	3493	5	44	0.0623	5	25	0.0023	27.19
74414	107623	40	38	94	9642	9	9	0.1422	8	88	0.0028	51.3
74414	75001	40	38	110	5156	8	2	0.0916	8	2	0.0021	43.78
74414	88336	40	38	91	7584	7	25	0.0599	7	15	0.0019	32.16
74414	37353	40	38	104	15556	7	20	0.1427	7	4	0.0037	38.73
74414	105654	40	38	102	24319	10	11	0.7925	9	190	0.0055	143.42
87894	100937	40	40	123	3311	5	11	0.0487	5	4	0.0020	24.13
87894	100652	40	40	133	2364	4	112	0.0439	4	88	0.0022	19.98
87894	74812	40	40	214	21451	6	21	0.2530	6	5	0.0078	32.45
87894	55634	40	40	180	4823	4	226	0.0900	4	197	0.0041	22.06
87894	100610	40	40	115	10606	4	3573	0.1057	4	3258	0.0034	31.05
87894	62617	40	40	191	44438	6	21	0.3877	6	4	0.0097	39.94
87894	56150	40	39	110	6786	5	4	0.0477	5	4	0.0023	21.08
87894	104099	40	39	147	27014	6	145	0.2099	6	118	0.0058	36
87894	90603	40	39	178	18067	5	1297	0.2025	5	880	0.0062	32.91
87894	106996	40	38	210	28077	7	1	0.3442	6	39	0.0080	43.09
87894	107220	40	38	225	57468	6	116	0.5994	6	35	0.0133	45.18
87894	107623	40	38	137	3461	5	44	0.0554	5	34	0.0024	23.44
87894	75001	40	38	192	34818	6	216	0.3200	6	157	0.0086	37.36
87894	88336	40	38	142	16635	6	22	0.1427	6	6	0.0042	33.94
87894	37353	40	38	130	20595	6	119	0.1486	6	73	0.0047	31.32
87894	105654	40	38	142	21824	6	60	0.1427	6	30	0.0048	29.67
100937	100652	40	40	99	6946	7	22	0.0904	7	6	0.0020	45.14
100937	74812	40	40	112	4555	7	9	0.0858	7	6	0.0020	43.61
100937	55634	40	40	117	3547	5	57	0.0434	5	46	0.0017	24.82
100937	100610	40	40	95	30547	11	39	3.6993	10	159	0.0073	507.17
100937	62617	40	40	114	8008	7	79	0.0967	7	52	0.0023	42.71
100937	56150	40	39	93	19882	10	366	2.3454	9	574	0.0049	482.29
100937	104099	40	39	102	9003	10	31	0.6312	9	90	0.0030	211.65
100937	90603	40	39	109	16467	8	40	0.7143	7	1157	0.0050	142.03
100937	106996	40	38	110	8904	7	243	0.1909	7	99	0.0031	61.18
100937	107220	40	38	124	4055	4	401	0.0336	4	333	0.0019	17.48
100937	107623	40	38	93	17796	11	298	4.4722	11	36	0.0055	814.47
100937	75001	40	38	109	4795	6	46	0.0416	6	16	0.0017	24.81
100937	88336	40	38	96	10205	8	19	0.1114	7	179	0.0023	47.52
100937	37353	40	38	107	11983	9	242	0.8333	9	107	0.0036	234.4
100937	105654	40	38	102	19536	10	2	0.6695	8	140	0.0042	159.82
100652	74812	40	40	111	5996	6	141	0.0646	6	27	0.0023	28.58
100652	55634	40	40	116	2531	4	79	0.0364	4	73	0.0015	23.55
100652	100610	40	40	97	6602	8	29	0.0575	8	12	0.0022	26.11
100652	62617	40	40	113	2083	5	2	0.0380	5	2	0.0017	22.17
100652	56150	40	39	94	12977	8	174	0.1710	8	68	0.0034	49.79
100652	104099	40	39	100	2110	7	2	0.0313	6	39	0.0014	21.98
100652	90603	40	39	115	12651	6	55	0.0952	6	13	0.0033	28.79
100652	106996	40	38	111	7274	6	59	0.0529	6	7	0.0025	21.28
100652	107220	40	38	124	1769	4	83	0.0383	4	56	0.0017	22.91
100652	107623	40	38	97	5450	7	156	0.0422	7	57	0.0022	19.49
100652	75001	40	38	109	1793	4	174	0.0327	4	159	0.0015	21.66
100652	88336	40	38	99	4465	5	165	0.0381	5	135	0.0018	21.48
100652	37353	40	38	107	5051	6	21	0.0542	6	11	0.0019	28.23
100652	105654	40	38	101	5117	6	39	0.0456	6	25	0.0018	25.38
74812	55634	40	40	141	2876	5	6	0.0474	5	6	0.0022	21.78
74812	100610	40	40	100	3602	5	243	0.0453	5	138	0.0018	25.69

Name1	Name2	N	M	CV	TV	OS	OC	OT	NS	NC	NT	S
74812	62617	40	40	146	7159	6	3	0.0754	5	169	0.0032	23.64
74812	56150	40	39	95	5166	6	9	0.0548	6	1	0.0017	31.9
74812	104099	40	39	121	6181	6	20	0.0650	5	506	0.0028	23.11
74812	90603	40	39	145	9846	6	60	0.1082	6	28	0.0035	31.04
74812	106996	40	38	177	18675	7	5	0.1924	7	2	0.0055	35.3
74812	107220	40	38	151	6837	5	32	0.0686	5	17	0.0031	22.47
74812	107623	40	38	107	5004	7	54	0.0958	7	8	0.0021	45.97
74812	75001	40	38	144	7541	6	13	0.0858	6	4	0.0030	28.77
74812	88336	40	38	123	3416	6	8	0.0467	6	8	0.0022	21.52
74812	37353	40	38	112	5256	6	53	0.0590	6	32	0.0020	29.27
74812	105654	40	38	117	5670	6	36	0.0630	6	11	0.0023	27.42
55634	100610	40	40	109	2561	5	4	0.0345	5	3	0.0016	20.99
55634	62617	40	40	174	7966	5	61	0.1107	5	29	0.0038	28.77
55634	56150	40	39	97	1522	5	1	0.0216	4	218	0.0013	16.85
55634	104099	40	39	141	4480	4	321	0.0526	4	288	0.0027	19.84
55634	90603	40	39	137	2915	6	4	0.0436	6	2	0.0021	20.91
55634	106996	40	38	129	3132	4	240	0.0339	4	206	0.0018	19.31
55634	107220	40	38	180	9351	4	580	0.0877	4	479	0.0038	23.31
55634	107623	40	38	98	1110	4	49	0.0180	4	46	0.0010	17.52
55634	75001	40	38	166	5647	6	4	0.0905	6	4	0.0033	27.32
55634	88336	40	38	113	2707	5	7	0.0299	5	7	0.0017	17.81
55634	37353	40	38	162	8093	6	6	0.0853	5	111	0.0038	22.39
55634	105654	40	38	133	3624	5	1	0.0447	5	1	0.0023	19.59
100610	62617	40	40	107	9374	8	15	0.1155	8	6	0.0027	42.81
100610	56150	40	39	92	18676	11	84	1.9752	11	16	0.0054	367.62
100610	104099	40	39	94	25180	13	18	7.5637	12	78	0.0078	965.74
100610	90603	40	39	104	16209	8	76	0.3405	8	3	0.0047	73.15
100610	106996	40	38	94	6484	7	98	0.1083	7	15	0.0025	43.53
100610	107220	40	38	109	2247	4	89	0.0348	4	73	0.0016	22.19
100610	107623	40	38	91	15110	8	176	0.3507	8	52	0.0036	96.13
100610	75001	40	38	103	4177	7	8	0.0540	7	5	0.0018	30.13
100610	88336	40	38	90	11005	8	33	0.1180	8	10	0.0023	50.75
100610	37353	40	38	102	16126	7	125	0.1361	7	8	0.0035	38.36
100610	105654	40	38	94	25396	10	8	1.2358	10	1	0.0053	232.77
62617	56150	40	39	97	4994	7	17	0.0557	7	6	0.0018	31.7
62617	104099	40	39	135	22577	7	406	0.2169	7	127	0.0049	44.27
62617	90603	40	39	138	12204	7	7	0.1142	7	4	0.0036	32.02
62617	106996	40	38	132	5941	5	31	0.0633	5	23	0.0024	26.06
62617	107220	40	38	178	18772	6	6	0.1667	6	1	0.0057	29.41
62617	107623	40	38	100	1082	5	6	0.0256	5	6	0.0012	20.87
62617	75001	40	38	164	24752	7	7	0.2537	7	3	0.0057	44.26
62617	88336	40	38	113	9097	7	48	0.0752	7	5	0.0026	28.49
62617	37353	40	38	147	29976	8	13	0.3132	7	93	0.0066	47.48
62617	105654	40	38	128	13508	7	50	0.1120	7	31	0.0034	32.78
56150	104099	39	39	85	5047	10	5	0.1170	9	3	0.0017	67.24
56150	90603	39	39	97	20511	10	6	0.3575	9	2	0.0047	76.12
56150	106996	39	38	89	13590	7	11	0.1676	6	326	0.0033	50.32
56150	107220	39	38	104	1349	4	79	0.0271	4	63	0.0014	20.1
56150	107623	39	38	90	18782	8	331	0.4035	8	36	0.0048	83.33
56150	75001	39	38	94	5040	7	12	0.0440	7	2	0.0017	25.97
56150	88336	39	38	88	9309	7	304	0.0997	7	138	0.0021	47.6
56150	37353	39	38	90	19604	11	60	0.7588	11	54	0.0036	207.94
56150	105654	39	38	93	11962	8	34	0.1906	7	455	0.0027	70.86
104099	90603	39	39	112	11607	7	3	0.0973	6	421	0.0030	32.73
104099	106996	39	38	115	3216	6	4	0.0469	6	2	0.0019	25.2
104099	107220	39	38	149	9295	5	2	0.0633	5	2	0.0036	17.39
104099	107623	39	38	91	3756	8	148	0.1967	8	84	0.0019	103.61
104099	75001	39	38	128	12420	6	28	0.0814	6	18	0.0032	25.46
104099	88336	39	38	94	6340	9	20	0.0827	8	51	0.0018	44.91
104099	37353	39	38	126	35566	8	154	0.4564	8	76	0.0064	71.82
104099	105654	39	38	110	28674	11	115	1.4174	10	170	0.0055	259.69
90603	106996	39	38	153	12777	8	2	0.2165	8	2	0.0042	51.47
90603	107220	39	38	146	4777	5	27	0.0579	5	13	0.0025	23.21
90603	107623	39	38	105	9756	8	57	0.1717	7	168	0.0034	49.93
90603	75001	39	38	135	9654	6	61	0.0953	6	35	0.0031	31.06
90603	88336	39	38	121	8703	6	9	0.0740	6	2	0.0026	28.89
90603	37353	39	38	120	32091	10	4	1.1676	9	83	0.0085	137.43

Name1	Name2	N	M	CV	TV	OS	OC	OT	NS	NC	NT	S
90603	105654	39	38	112	13185	6	347	0.1135	6	237	0.0029	38.99
106996	107220	38	38	134	4785	5	120	0.0655	5	68	0.0023	28.87
106996	107623	38	38	105	12830	8	640	0.2523	8	78	0.0033	75.55
106996	75001	38	38	129	4443	5	139	0.0591	5	45	0.0022	27.08
106996	88336	38	38	130	7566	6	194	0.0850	6	40	0.0029	29.2
106996	37353	38	38	102	3899	6	30	0.0378	6	8	0.0016	23.77
106996	105654	38	38	110	2875	6	26	0.0483	6	22	0.0017	28.28
107220	107623	38	38	142	3968	5	81	0.0553	5	71	0.0023	23.72
107220	75001	38	38	182	15506	6	44	0.1813	6	25	0.0056	32.56
107220	88336	38	38	117	4506	5	68	0.0510	5	26	0.0020	25.19
107220	37353	38	38	143	7557	5	41	0.0641	5	13	0.0032	19.88
107220	105654	38	38	145	7514	5	8	0.0801	5	6	0.0033	24.32
107623	75001	38	38	100	1640	5	21	0.0271	5	18	0.0013	20.96
107623	88336	38	38	91	5239	7	184	0.0767	7	67	0.0017	45.77
107623	37353	38	38	86	3679	6	72	0.0265	5	842	0.0017	15.21
107623	105654	38	38	92	5891	8	18	0.0960	8	6	0.0018	53.65
75001	88336	38	38	112	6549	6	4	0.0494	5	95	0.0020	24.39
75001	37353	38	38	133	16691	7	3	0.1254	6	156	0.0040	31.27
75001	105654	38	38	125	8741	7	10	0.0922	7	1	0.0027	34.01
88336	37353	38	38	96	7394	6	78	0.0606	6	64	0.0020	30.58
88336	105654	38	38	99	10084	6	138	0.0745	6	58	0.0024	31.01
37353	105654	38 38	115	18808	8	78	0.1486	7	63	0.0036	41.4	

Table B.3: Output data for the TUBULIN_AB dataset

Name1	Name2	N	M	CV	TV	OS	OC	OT	NS	NC	NT	S
Tubulin Alpha	Tubulin Beta	516	485	4157	494535578	n/a	n/a	≥354780	9	54525	401	≥890

B.2 Software Profiling

This section contains the full results used in generating the software profiling results in Section 4.4 and the cache hit rate analysis in Section 4.2.8. Each row in Tables B.5 and B.6 lists the profile data for one MMM coevolution problem.

Table B.4: Column Legend

Column Name	**Description**
Name1	First matrix unique filename prefix
Name2	Second matrix unique filename prefix
S01	Non-max clique algorithm time ($\alpha = 0.1$)
M01	Max clique algorithm time ($\alpha = 0.1$)
T03	Total run time ($\alpha = 0.3$)
S03	Non-max clique algorithm time ($\alpha = 0.3$)
M03	Max clique algorithm time ($\alpha = 0.3$)
C1X	Simulated cache hit rate (1kbit cache lines)
C2X	Simulated cache hit rate (2kbit cache lines)

Table B.5: Software profile data for the BATCH50 dataset

Name1	**Name2**	**S01**	**M01**	**T03**	**S03**	**M03**	**C1X**	**C2X**
2506	106948	0.0630	0.0005	0.6328	0.1700	0.4533	0.9960	0.9960
2506	88748	0.2730	0.0330	3.6984	2.1029	1.5922	0.9983	0.9984
2506	106976	0.1258	0.0115	1.0717	0.4593	0.5945	0.9984	0.9984
2506	89932	0.0318	0.0003	0.5100	0.1395	0.2995	0.9964	0.9964
2506	107298	0.0151	0.0001	0.0624	0.0029	0.0567	0.9862	0.9862
2506	105282	0.0693	0.0007	0.7974	0.2577	0.5326	0.9967	0.9967
2506	90856	0.0225	0.0004	0.1856	0.0438	0.1409	0.9942	0.9942
2506	105323	0.0256	0.0002	0.1329	0.0152	0.1168	0.9966	0.9966
2506	107601	0.0163	0.0003	0.1389	0.0415	0.0895	0.9964	0.9964
2506	37889	0.0122	0.0002	0.0768	0.0294	0.0442	0.9972	0.9972
2506	74548	0.0297	0.0011	0.1919	0.0194	0.1711	0.9969	0.9969
2506	103997	0.0238	0.0004	0.1186	0.0051	0.1125	0.9954	0.9954
2506	88482	0.0479	0.0016	0.3550	0.0403	0.3109	0.9971	0.9971
2506	106838	0.0311	0.0004	0.2860	0.0329	0.2280	0.9967	0.9967
2506	103998	0.0126	0.0002	0.0700	0.0080	0.0612	0.9971	0.9971
2506	105677	0.0260	0.0004	0.1782	0.0114	0.1653	0.9967	0.9967
2506	81915	0.0278	0.0007	0.2217	0.0757	0.1448	0.9981	0.9981
2506	80191	0.0319	0.0031	0.3646	0.1940	0.1690	0.9985	0.9985
2506	100934	0.0235	0.0007	0.1372	0.0147	0.1217	0.9975	0.9975
2506	103789	0.0280	0.0003	0.1978	0.0101	0.1865	0.9945	0.9945
2506	90389	0.0179	0.0008	0.0821	0.0072	0.0740	0.9962	0.9962
2506	104370	0.0224	0.0001	0.1255	0.0028	0.1218	0.9744	0.9744
2506	100530	0.0147	0.0010	0.0934	0.0289	0.0636	0.9980	0.9980
2506	55705	0.0205	0.0003	0.1225	0.0126	0.1092	0.9965	0.9965
2506	101685	0.0286	0.0009	0.1263	0.0090	0.1162	0.9978	0.9978
2506	48010	0.0261	0.0008	0.2655	0.0989	0.1654	0.9963	0.9963
2506	107009	0.0113	0.0002	0.0429	0.0007	0.0415	0.9895	0.9895
2506	107429	0.0139	0.0001	0.1080	0.0294	0.0766	0.9950	0.9950
2506	38064	0.0262	0.0013	0.1804	0.0359	0.1366	0.9978	0.9978
2506	99789	0.0122	0.0003	0.0773	0.0054	0.0711	0.9965	0.9965
2506	88589	0.0210	0.0000	0.1042	0.0105	0.0913	0.9897	0.9897
2506	74414	0.0125	0.0001	0.1064	0.0377	0.0672	0.9977	0.9977
2506	87894	0.0236	0.0002	0.1990	0.0373	0.1606	0.9942	0.9942
2506	100937	0.0137	0.0003	0.0823	0.0214	0.0594	0.9979	0.9979
2506	100652	0.0114	0.0001	0.0630	0.0084	0.0536	0.9931	0.9931
2506	74812	0.0127	0.0001	0.0740	0.0054	0.0678	0.9805	0.9805
2506	55634	0.0305	0.0016	0.1205	0.0153	0.1044	0.9983	0.9983
2506	100610	0.0132	0.0002	0.1751	0.0909	0.0759	0.9973	0.9973
2506	62617	0.0158	0.0001	0.0987	0.0044	0.0936	0.9921	0.9921
2506	56150	0.0129	0.0007	0.0662	0.0093	0.0562	0.9975	0.9975
2506	104099	0.0107	0.0001	0.0458	0.0049	0.0403	0.9900	0.9900
2506	90603	0.0192	0.0005	0.1093	0.0158	0.0928	0.9976	0.9976
2506	106996	0.0139	0.0005	0.0934	0.0207	0.0717	0.9968	0.9968
2506	107220	0.0138	0.0003	0.0872	0.0114	0.0751	0.9890	0.9890
2506	107623	0.0088	0.0001	0.0368	0.0051	0.0304	0.9954	0.9954
2506	75001	0.0143	0.0001	0.0739	0.0032	0.0699	0.9930	0.9930
2506	88336	0.0143	0.0004	0.0782	0.0072	0.0700	0.9965	0.9965
2506	37353	0.0165	0.0003	0.0737	0.0060	0.0669	0.9974	0.9974
2506	105654	0.0148	0.0007	0.1121	0.0380	0.0714	0.9973	0.9973
106948	88748	0.1853	0.0030	17.9357	14.7431	3.0660	0.9981	0.9981
106948	106976	0.0092	0.0001	0.0711	0.0092	0.0609	0.9813	0.9813
106948	89932	0.0383	0.0003	0.5641	0.1762	0.3797	0.9959	0.9959
106948	107298	0.0250	0.0002	0.1459	0.0082	0.1367	0.9783	0.9783
106948	105282	0.0936	0.0032	37.6709	35.8580	1.8114	0.9984	0.9984
106948	90856	0.0208	0.0002	0.5953	0.4034	0.1879	0.9949	0.9949
106948	105323	0.0121	0.0002	0.0527	0.0057	0.0452	0.9970	0.9970
106948	107601	0.0270	0.0004	0.3312	0.1835	0.1459	0.9976	0.9981
106948	37889	0.0065	0.0002	0.0335	0.0058	0.0265	0.9954	0.9954
106948	74548	0.0163	0.0005	0.2089	0.0848	0.1222	0.9947	0.9947
106948	103997	0.0257	0.0016	0.3175	0.1414	0.1532	0.9981	0.9983
106948	88482	0.0467	0.0010	0.9265	0.3616	0.5635	0.9973	0.9973
106948	106838	0.0168	0.0003	0.9379	0.6143	0.2468	0.9911	0.9911
106948	103998	0.0077	0.0005	0.0712	0.0242	0.0451	0.9978	0.9978
106948	105677	0.0159	0.0002	0.1120	0.0018	0.1094	0.9776	0.9776

Name1	Name2	S01	M01	T03	S03	M03	C1X	C2X
106948	81915	0.0166	0.0008	0.1437	0.0593	0.0814	0.9980	0.9980
106948	80191	0.0178	0.0008	0.1182	0.0318	0.0826	0.9979	0.9979
106948	100934	0.0102	0.0001	0.0636	0.0122	0.0482	0.9966	0.9966
106948	103789	0.0460	0.0005	6.5758	5.7906	0.7799	0.9954	0.9954
106948	90389	0.0231	0.0005	0.1577	0.0337	0.1140	0.9970	0.9971
106948	104370	0.0439	0.0007	0.7699	0.2768	0.4907	0.9901	0.9901
106948	100530	0.0077	0.0003	0.1114	0.0505	0.0402	0.9975	0.9975
106948	55705	0.0095	0.0002	0.0372	0.0022	0.0344	0.9979	0.9979
106948	101685	0.0159	0.0001	0.1259	0.0089	0.1162	0.9778	0.9778
106948	48010	0.0138	0.0001	0.1401	0.0245	0.1147	0.9826	0.9826
106948	107009	0.0169	0.0006	0.1627	0.0576	0.1041	0.9983	0.9983
106948	107429	0.0155	0.0005	0.2268	0.1170	0.0994	0.9983	0.9983
106948	38064	0.0227	0.0003	0.4777	0.1909	0.2861	0.9941	0.9941
106948	99789	0.0093	0.0005	0.0432	0.0053	0.0372	0.9977	0.9977
106948	88589	0.0141	0.0004	0.0628	0.0008	0.0613	0.9900	0.9900
106948	74414	0.0072	0.0001	0.0534	0.0134	0.0351	0.9953	0.9953
106948	87894	0.0314	0.0009	0.8375	0.4277	0.4072	0.9938	0.9938
106948	100937	0.0112	0.0005	0.0402	0.0075	0.0319	0.9984	0.9984
106948	100652	0.0086	0.0004	0.0479	0.0108	0.0358	0.9971	0.9971
106948	74812	0.0160	0.0003	0.1608	0.0478	0.1116	0.9957	0.9957
106948	55634	0.0077	0.0000	0.0249	0.0003	0.0240	0.9462	0.9462
106948	100610	0.0074	0.0002	0.0273	0.0048	0.0218	0.9969	0.9969
106948	62617	0.0116	0.0001	0.0877	0.0026	0.0845	0.9820	0.9820
106948	56150	0.0087	0.0005	0.0672	0.0306	0.0358	0.9974	0.9974
106948	104099	0.0097	0.0001	0.0472	0.0044	0.0422	0.9922	0.9922
106948	90603	0.0129	0.0004	0.0919	0.0170	0.0592	0.9969	0.9969
106948	106996	0.0209	0.0008	0.4957	0.2997	0.1583	0.9976	0.9976
106948	107220	0.0242	0.0002	0.3850	0.1289	0.2552	0.9877	0.9877
106948	107623	0.0174	0.0018	0.5969	0.4853	0.0869	0.9984	0.9984
106948	75001	0.0120	0.0002	0.0937	0.0081	0.0845	0.9771	0.9771
106948	88336	0.0078	0.0001	0.0614	0.0130	0.0406	0.9907	0.9907
106948	37353	0.0067	0.0002	0.0317	0.0030	0.0282	0.9899	0.9899
106948	105654	0.0085	0.0002	0.0491	0.0063	0.0379	0.9943	0.9943
88748	106976	0.2293	0.0201	3.3347	1.8821	1.4011	0.9986	0.9986
88748	89932	0.1234	0.0015	8.5942	6.9603	1.6058	0.9982	0.9982
88748	107298	0.0332	0.0053	0.7944	0.5032	0.2182	0.9979	0.9979
88748	105282	1.0420	0.0063	99.5441	88.5970	10.6813	0.9983	0.9983
88748	90856	0.2661	0.0611	317.5450	316.3860	1.1200	0.9996	0.9996
88748	105323	0.0316	0.0017	0.1077	0.0054	0.1005	0.9971	0.9971
88748	107601	0.0198	0.0000	0.1514	0.0083	0.1420	0.9883	0.9883
88748	37889	0.0046	0.0000	0.0062	0.0000	0.0057	1.0000	1.0000
88748	74548	0.0313	0.0003	0.2275	0.0129	0.2075	0.9967	0.9967
88748	103997	0.0830	0.0013	23.0907	21.8610	1.1808	0.9978	0.9978
88748	88482	4.2625	0.2063	175.4860	161.9150	13.5255	0.9982	0.9993
88748	106838	0.1001	0.0016	1.2927	0.5506	0.6845	0.9985	0.9985
88748	103998	0.0042	0.0000	0.0071	0.0000	0.0065	1.0000	1.0000
88748	105677	0.0584	0.0037	1.8805	0.5793	0.8989	0.9978	0.9978
88748	81915	0.0154	0.0001	0.1260	0.0268	0.0983	0.9913	0.9913
88748	80191	0.0311	0.0029	0.0848	0.0075	0.0754	0.9939	0.9939
88748	100934	0.0224	0.0026	0.0967	0.0107	0.0707	0.9958	0.9958
88748	103789	0.6983	0.0055	4.1110	0.3085	3.8009	0.9988	0.9988
88748	90389	0.2544	0.0318	1.6598	0.9762	0.6800	0.9964	0.9985
88748	104370	0.6463	0.0403	932.9100	926.5330	6.3736	0.9961	0.9986
88748	100530	0.0049	0.0001	0.0104	0.0005	0.0087	0.9941	0.9941
88748	55705	0.0132	0.0000	0.1426	0.0157	0.1005	0.9822	0.9822
88748	101685	0.0651	0.0050	1.4013	0.8080	0.4660	0.9982	0.9982
88748	48010	0.0477	0.0009	0.4830	0.0704	0.3740	0.9976	0.9976
88748	107009	0.0182	0.0007	0.2618	0.0609	0.1683	0.9935	0.9935
88748	107429	0.0125	0.0001	0.1341	0.0316	0.1019	0.9923	0.9923
88748	38064	0.5448	0.1910	1306.8100	1303.5200	3.2879	0.9997	0.9997
88748	99789	0.0074	0.0001	0.0385	0.0045	0.0330	0.9927	0.9927
88748	88589	0.3087	0.0331	99.4090	96.9894	2.2097	0.9990	0.9990
88748	74414	0.0126	0.0001	0.0311	0.0003	0.0302	0.9954	0.9954
88748	87894	0.9928	0.7296	8812.3300	8805.6000	6.5801	0.9997	0.9997
88748	100937	0.0070	0.0000	0.0355	0.0022	0.0294	0.9487	0.9487
88748	100652	0.0060	0.0000	0.0238	0.0019	0.0210	0.8824	0.8824
88748	74812	0.0228	0.0001	0.2349	0.0238	0.2100	0.9826	0.9826

Name1	Name2	S01	M01	T03	S03	M03	C1X	C2X
88748	55634	0.0249	0.0016	0.1428	0.0314	0.1087	0.9968	0.9968
88748	100610	0.0071	0.0000	0.0293	0.0019	0.0206	0.9139	0.9139
88748	62617	0.0310	0.0009	0.2975	0.0309	0.2654	0.9966	0.9966
88748	56150	0.0050	0.0000	0.0245	0.0017	0.0176	0.9021	0.9021
88748	104099	0.0253	0.0016	0.1141	0.0104	0.1012	0.9926	0.9926
88748	90603	0.0166	0.0003	0.1678	0.0292	0.1369	0.9892	0.9892
88748	106996	0.0385	0.0013	1.2257	0.7892	0.4352	0.9970	0.9970
88748	107220	0.2718	0.0196	461.3960	457.6400	3.7069	0.9991	0.9991
88748	107623	0.0080	0.0002	0.0470	0.0027	0.0436	0.9898	0.9898
88748	75001	0.0574	0.0049	0.7084	0.2075	0.3813	0.9981	0.9981
88748	88336	0.0209	0.0002	0.1563	0.0314	0.0974	0.9982	0.9982
88748	37353	0.0131	0.0001	0.0459	0.0007	0.0448	0.9906	0.9906
88748	105654	0.0167	0.0001	0.0769	0.0010	0.0754	0.9869	0.9869
106976	89932	0.0260	0.0008	0.4185	0.1868	0.2307	0.9977	0.9977
106976	107298	0.0008	0.0000	0.0025	0.0001	0.0018	1.0000	1.0000
106976	105282	0.0869	0.0037	3.7889	2.9604	0.8249	0.9981	0.9981
106976	90856	0.0235	0.0014	0.5564	0.4038	0.0920	0.9989	0.9989
106976	105323	0.0114	0.0009	0.0479	0.0074	0.0394	0.9977	0.9977
106976	107601	0.0026	0.0000	0.0100	0.0003	0.0093	0.9309	0.9309
106976	37889	0.0022	0.0000	0.0036	0.0000	0.0032	1.0000	1.0000
106976	74548	0.0550	0.0071	5.9615	5.2545	0.4651	0.9987	0.9987
106976	103997	0.0017	0.0000	0.0047	0.0004	0.0038	0.9506	0.9506
106976	88482	0.2704	0.0210	3.4537	2.0440	1.3934	0.9990	0.9992
106976	106838	0.1580	0.0334	44.6531	43.5914	1.0306	0.9986	0.9986
106976	103998	0.0019	0.0000	0.0027	0.0000	0.0024	1.0000	1.0000
106976	105677	0.0226	0.0020	0.2433	0.0661	0.1450	0.9974	0.9974
106976	81915	0.0073	0.0002	0.0326	0.0015	0.0307	0.9808	0.9808
106976	80191	0.0044	0.0001	0.0147	0.0009	0.0130	0.9743	0.9743
106976	100934	0.0045	0.0001	0.0169	0.0013	0.0151	0.9899	0.9899
106976	103789	0.0550	0.0027	1.2069	0.7677	0.4378	0.9979	0.9979
106976	90389	0.0186	0.0006	0.1125	0.0070	0.1049	0.9966	0.9966
106976	104370	0.0658	0.0034	0.9638	0.6655	0.2886	0.9995	0.9995
106976	100530	0.0024	0.0000	0.0058	0.0001	0.0052	0.9744	0.9744
106976	55705	0.0073	0.0001	0.0489	0.0071	0.0392	0.9942	0.9942
106976	101685	0.0110	0.0007	0.0748	0.0151	0.0483	0.9956	0.9956
106976	48010	0.0135	0.0002	0.1258	0.0062	0.1191	0.9953	0.9953
106976	107009	0.0031	0.0000	0.0077	0.0001	0.0071	0.9652	0.9652
106976	107429	0.0028	0.0000	0.0163	0.0016	0.0143	0.9693	0.9693
106976	38064	0.2435	0.0819	836.7750	835.4320	1.2535	0.9995	0.9995
106976	99789	0.0027	0.0000	0.0062	0.0003	0.0055	0.9772	0.9772
106976	88589	0.0256	0.0004	0.1190	0.0052	0.1129	0.9917	0.9917
106976	74414	0.0027	0.0001	0.0086	0.0005	0.0065	0.9906	0.9906
106976	87894	0.0221	0.0005	0.3300	0.0996	0.2298	0.9972	0.9972
106976	100937	0.0021	0.0000	0.0048	0.0001	0.0042	0.9467	0.9467
106976	100652	0.0024	0.0000	0.0059	0.0003	0.0052	0.9772	0.9772
106976	74812	0.0052	0.0001	0.0291	0.0002	0.0286	0.9832	0.9832
106976	55634	0.0140	0.0009	0.3048	0.0427	0.1485	0.9961	0.9961
106976	100610	0.0021	0.0000	0.0048	0.0000	0.0044	1.0000	1.0000
106976	62617	0.0155	0.0009	0.1041	0.0180	0.0847	0.9982	0.9982
106976	56150	0.0017	0.0000	0.0042	0.0001	0.0037	1.0000	1.0000
106976	104099	0.0030	0.0002	0.0285	0.0029	0.0191	0.9769	0.9769
106976	90603	0.0051	0.0000	0.0256	0.0013	0.0238	0.9488	0.9488
106976	106996	0.0047	0.0000	0.0470	0.0082	0.0384	0.9747	0.9747
106976	107220	0.0018	0.0000	0.0087	0.0006	0.0078	0.9840	0.9840
106976	107623	0.0006	0.0000	0.0013	0.0000	0.0010	0.7895	0.7895
106976	75001	0.0163	0.0003	0.1311	0.0299	0.0856	0.9933	0.9933
106976	88336	0.0082	0.0002	0.0467	0.0012	0.0451	0.9970	0.9970
106976	37353	0.0055	0.0001	0.0274	0.0007	0.0263	0.9682	0.9682
106976	105654	0.0043	0.0000	0.0174	0.0010	0.0159	0.9811	0.9811
89932	107298	0.0043	0.0000	0.0106	0.0002	0.0099	0.7983	0.7983
89932	105282	0.0920	0.0304	66.9002	65.8233	1.0451	0.9991	0.9991
89932	90856	0.0098	0.0003	0.1556	0.0565	0.0955	0.9955	0.9955
89932	105323	0.0081	0.0000	0.0478	0.0057	0.0416	0.9890	0.9890
89932	107601	0.0129	0.0004	0.1453	0.0354	0.1060	0.9979	0.9979
89932	37889	0.0037	0.0001	0.0129	0.0005	0.0120	0.9823	0.9823
89932	74548	0.0113	0.0001	0.1448	0.0273	0.1170	0.9936	0.9936
89932	103997	0.0033	0.0001	0.0153	0.0022	0.0123	0.9898	0.9898

Name1	Name2	S01	M01	T03	S03	M03	C1X	C2X
89932	88482	0.0548	0.0008	0.4038	0.0339	0.3546	0.9979	0.9979
89932	106838	0.0100	0.0002	0.1448	0.0312	0.1126	0.9952	0.9952
89932	103998	0.0048	0.0002	0.0373	0.0096	0.0274	0.9947	0.9947
89932	105677	0.0111	0.0003	0.1124	0.0182	0.0936	0.9921	0.9921
89932	81915	0.0090	0.0004	0.1120	0.0375	0.0735	0.9957	0.9957
89932	80191	0.0148	0.0019	0.1212	0.0409	0.0782	0.9990	0.9990
89932	100934	0.0094	0.0002	0.0882	0.0230	0.0647	0.9973	0.9973
89932	103789	0.0499	0.0019	3.3765	2.7975	0.5765	0.9982	0.9982
89932	90389	0.0372	0.0011	0.2974	0.0663	0.2278	0.9977	0.9984
89932	104370	0.6433	0.6004	9895.8700	9890.9600	4.7512	0.9994	0.9997
89932	100530	0.0076	0.0004	0.0584	0.0205	0.0342	0.9970	0.9970
89932	55705	0.0095	0.0005	0.0933	0.0353	0.0573	0.9981	0.9981
89932	101685	0.0106	0.0001	0.0683	0.0026	0.0653	0.9939	0.9939
89932	48010	0.0131	0.0005	0.2616	0.1337	0.1254	0.9976	0.9976
89932	107009	0.0064	0.0000	0.0359	0.0010	0.0345	0.9697	0.9697
89932	107429	0.0085	0.0001	0.0927	0.0086	0.0836	0.9885	0.9885
89932	38064	0.0130	0.0004	0.2494	0.1327	0.1159	0.9967	0.9967
89932	99789	0.0050	0.0001	0.0356	0.0018	0.0333	0.9901	0.9901
89932	88589	0.0157	0.0006	0.1011	0.0098	0.0756	0.9948	0.9948
89932	74414	0.0053	0.0003	0.0444	0.0128	0.0293	0.9977	0.9977
89932	87894	0.0268	0.0010	0.5972	0.2654	0.3192	0.9975	0.9975
89932	100937	0.0074	0.0004	0.0555	0.0162	0.0389	0.9975	0.9975
89932	100652	0.0041	0.0001	0.0219	0.0017	0.0199	0.9947	0.9947
89932	74812	0.0152	0.0002	0.4053	0.2483	0.1562	0.9970	0.9970
89932	55634	0.0039	0.0000	0.0119	0.0005	0.0107	0.9076	0.9076
89932	100610	0.0071	0.0003	0.0766	0.0386	0.0372	0.9969	0.9969
89932	62617	0.0079	0.0001	0.0869	0.0155	0.0709	0.9885	0.9885
89932	56150	0.0037	0.0001	0.0230	0.0037	0.0188	0.9934	0.9934
89932	104099	0.0112	0.0007	0.1040	0.0372	0.0658	0.9989	0.9989
89932	90603	0.0099	0.0001	0.0769	0.0136	0.0625	0.9942	0.9942
89932	106996	0.0163	0.0004	0.4316	0.2143	0.2016	0.9949	0.9949
89932	107220	0.0061	0.0001	0.0481	0.0050	0.0427	0.9873	0.9873
89932	107623	0.0037	0.0000	0.0231	0.0052	0.0174	0.9771	0.9771
89932	75001	0.0062	0.0001	0.0659	0.0117	0.0500	0.9930	0.9930
89932	88336	0.0088	0.0002	0.0649	0.0078	0.0563	0.9906	0.9906
89932	37353	0.0062	0.0003	0.0495	0.0084	0.0408	0.9952	0.9952
89932	105654	0.0093	0.0008	0.1357	0.0848	0.0500	0.9982	0.9982
107298	105282	0.0110	0.0001	0.0560	0.0015	0.0535	0.9941	0.9941
107298	90856	0.0058	0.0003	0.0377	0.0076	0.0228	0.9967	0.9967
107298	105323	0.0096	0.0000	0.0322	0.0007	0.0307	0.9354	0.9354
107298	107601	0.0056	0.0002	0.0169	0.0012	0.0136	0.9874	0.9874
107298	37889	0.0024	0.0000	0.0036	0.0000	0.0032	1.0000	1.0000
107298	74548	0.0128	0.0004	0.0708	0.0041	0.0658	0.9902	0.9902
107298	103997	0.0016	0.0000	0.0026	0.0000	0.0022	0.9580	0.9580
107298	88482	0.0004	0.0000	0.0016	0.0001	0.0009	1.0000	1.0000
107298	106838	0.0260	0.0030	0.1279	0.0196	0.0826	0.9953	0.9953
107298	103998	0.0025	0.0000	0.0042	0.0000	0.0037	1.0000	1.0000
107298	105677	0.0115	0.0002	0.3107	0.0463	0.1727	0.9834	0.9834
107298	81915	0.0067	0.0000	0.0370	0.0019	0.0345	0.9780	0.9780
107298	80191	0.0032	0.0000	0.0078	0.0004	0.0068	0.9732	0.9732
107298	100934	0.0068	0.0002	0.0291	0.0003	0.0284	0.9660	0.9660
107298	103789	0.0641	0.0013	3.4467	1.9000	1.1899	0.9957	0.9957
107298	90389	0.0021	0.0001	0.0100	0.0012	0.0073	0.9948	0.9948
107298	104370	0.0023	0.0002	0.0117	0.0015	0.0086	0.9965	0.9965
107298	100530	0.0029	0.0000	0.0062	0.0001	0.0057	0.9882	0.9882
107298	55705	0.0067	0.0002	0.0295	0.0004	0.0287	0.9236	0.9236
107298	101685	0.0195	0.0002	0.5449	0.1424	0.3811	0.9922	0.9922
107298	48010	0.0146	0.0005	0.1793	0.0499	0.1281	0.9835	0.9835
107298	107009	0.0067	0.0001	0.0298	0.0024	0.0265	0.9913	0.9913
107298	107429	0.0031	0.0000	0.0086	0.0004	0.0078	0.9524	0.9524
107298	38064	0.0086	0.0004	0.0352	0.0039	0.0308	0.9970	0.9970
107298	99789	0.0086	0.0001	0.0302	0.0010	0.0287	0.9946	0.9946
107298	88589	0.1925	0.0220	49.5088	47.0047	2.3037	0.9986	0.9986
107298	74414	0.0030	0.0001	0.0060	0.0001	0.0055	0.9509	0.9509
107298	87894	0.0031	0.0001	0.0108	0.0004	0.0101	0.9774	0.9774
107298	100937	0.0026	0.0000	0.0055	0.0001	0.0050	0.7824	0.7824
107298	100652	0.0025	0.0000	0.0083	0.0006	0.0062	0.9203	0.9203

Name1	Name2	S01	M01	T03	S03	M03	C1X	C2X
107298	74812	0.0014	0.0000	0.0030	0.0001	0.0026	0.0000	0.0000
107298	55634	0.0049	0.0000	0.0148	0.0009	0.0129	0.9400	0.9400
107298	100610	0.0032	0.0001	0.0072	0.0004	0.0062	0.9306	0.9306
107298	62617	0.0067	0.0003	0.0264	0.0003	0.0257	0.9419	0.9419
107298	56150	0.0028	0.0000	0.0064	0.0002	0.0057	1.0000	1.0000
107298	104099	0.0080	0.0004	0.0385	0.0029	0.0352	0.9500	0.9500
107298	90603	0.0030	0.0000	0.0073	0.0002	0.0068	0.9603	0.9603
107298	106996	0.0002	0.0000	0.0005	0.0000	0.0003	0.8404	0.8404
107298	107220	0.0171	0.0002	0.3496	0.0808	0.2236	0.9880	0.9880
107298	107623	0.0011	0.0000	0.0020	0.0000	0.0016	0.9716	0.9716
107298	75001	0.0123	0.0004	0.1142	0.0271	0.0864	0.9861	0.9861
107298	88336	0.0012	0.0000	0.0024	0.0000	0.0021	0.7132	0.7132
107298	37353	0.0081	0.0004	0.0359	0.0011	0.0344	0.9473	0.9473
107298	105654	0.0082	0.0005	0.0345	0.0014	0.0326	0.9643	0.9643
105282	90856	0.0803	0.0022	3.1629	2.6453	0.5146	0.9987	0.9987
105282	105323	0.0150	0.0000	0.0417	0.0010	0.0400	0.9661	0.9661
105282	107601	0.0136	0.0000	0.0960	0.0104	0.0850	0.9829	0.9829
105282	37889	0.0034	0.0000	0.0045	0.0000	0.0041	1.0000	1.0000
105282	74548	0.0291	0.0006	0.6106	0.2967	0.3128	0.9979	0.9979
105282	103997	0.0298	0.0003	0.3087	0.0758	0.2306	0.9957	0.9957
105282	88482	0.8360	0.0255	177.3590	169.3680	7.9836	0.9992	0.9994
105282	106838	0.1382	0.0127	30.3400	29.2723	1.0615	0.9992	0.9992
105282	103998	0.0029	0.0000	0.0042	0.0000	0.0038	1.0000	1.0000
105282	105677	0.0327	0.0003	0.7265	0.1236	0.6014	0.9957	0.9957
105282	81915	0.0147	0.0001	0.1152	0.0038	0.1109	0.9950	0.9950
105282	80191	0.0229	0.0003	0.0648	0.0013	0.0630	0.9971	0.9971
105282	100934	0.0139	0.0003	0.0516	0.0013	0.0499	0.9969	0.9969
105282	103789	1.0596	0.4574	11894.0000	11886.9000	7.0398	0.9997	0.9997
105282	90389	0.0333	0.0014	0.2108	0.0098	0.2001	0.9975	0.9975
105282	104370	0.2435	0.0406	1218.8500	1217.1700	1.6772	0.9997	0.9997
105282	100530	0.0040	0.0000	0.0110	0.0003	0.0104	0.9838	0.9838
105282	55705	0.0177	0.0005	0.1254	0.0027	0.1223	0.9955	0.9955
105282	101685	0.0564	0.0008	0.3760	0.0548	0.3160	0.9976	0.9976
105282	48010	0.0803	0.0105	1.8732	1.4088	0.4635	0.9989	0.9989
105282	107009	0.0096	0.0002	0.1934	0.1163	0.0714	0.9954	0.9954
105282	107429	0.0081	0.0003	0.1198	0.0567	0.0622	0.9948	0.9948
105282	38064	0.1249	0.0039	363.1140	361.5400	1.4748	0.9988	0.9988
105282	99789	0.0051	0.0000	0.0281	0.0006	0.0272	0.9874	0.9874
105282	88589	0.1794	0.0211	0.6215	0.0329	0.5876	0.9988	0.9988
105282	74414	0.0142	0.0003	0.0402	0.0007	0.0391	0.9966	0.9966
105282	87894	0.2800	0.0240	280.4450	276.3380	3.9452	0.9987	0.9987
105282	100937	0.0042	0.0000	0.0174	0.0003	0.0166	0.9786	0.9786
105282	100652	0.0050	0.0002	0.0159	0.0009	0.0146	0.9813	0.9813
105282	74812	0.0150	0.0003	0.4384	0.2363	0.2013	0.9958	0.9958
105282	55634	0.0109	0.0002	0.0278	0.0017	0.0252	0.9885	0.9885
105282	100610	0.0095	0.0002	0.0185	0.0002	0.0180	0.9928	0.9928
105282	62617	0.0295	0.0006	0.5614	0.1412	0.4191	0.9960	0.9960
105282	56150	0.0066	0.0000	0.0178	0.0002	0.0173	0.9889	0.9889
105282	104099	0.0344	0.0009	0.1361	0.0037	0.1319	0.9978	0.9978
105282	90603	0.0093	0.0001	0.0528	0.0009	0.0514	0.9818	0.9818
105282	106996	0.0133	0.0001	0.3782	0.1764	0.2009	0.9913	0.9913
105282	107220	0.0302	0.0005	1.1103	0.6020	0.5059	0.9947	0.9947
105282	107623	0.0043	0.0000	0.0335	0.0030	0.0300	0.9775	0.9775
105282	75001	0.0329	0.0006	0.3327	0.0176	0.3144	0.9975	0.9975
105282	88336	0.0135	0.0003	0.0888	0.0062	0.0818	0.9953	0.9953
105282	37353	0.0240	0.0022	0.0789	0.0031	0.0753	0.9976	0.9976
105282	105654	0.0262	0.0008	0.1178	0.0026	0.1146	0.9975	0.9975
90856	105323	0.0064	0.0002	0.0501	0.0096	0.0298	0.9948	0.9948
90856	107601	0.0057	0.0002	0.0319	0.0050	0.0259	0.9975	0.9975
90856	37889	0.0023	0.0000	0.0067	0.0004	0.0056	0.9573	0.9573
90856	74548	0.0422	0.0036	1.7385	1.5430	0.1817	0.9993	0.9993
90856	103997	0.0158	0.0002	0.1216	0.0359	0.0845	0.9965	0.9965
90856	88482	0.0782	0.0206	4.7595	4.5782	0.1771	0.9997	0.9997
90856	106838	0.0186	0.0018	2.7603	2.4604	0.1802	0.9978	0.9978
90856	103998	0.0126	0.0025	0.2764	0.1163	0.0777	0.9993	0.9993
90856	105677	0.0069	0.0001	0.0531	0.0067	0.0453	0.9873	0.9873
90856	81915	0.0103	0.0006	0.2898	0.2058	0.0631	0.9982	0.9982

Name1	Name2	S01	M01	T03	S03	M03	C1X	C2X
90856	80191	0.0121	0.0025	0.0599	0.0167	0.0337	0.9986	0.9986
90856	100934	0.0083	0.0002	0.0446	0.0072	0.0332	0.9928	0.9928
90856	103789	0.0331	0.0039	1.5539	1.3285	0.2083	0.9986	0.9986
90856	90389	0.0052	0.0004	0.0237	0.0042	0.0183	0.9976	0.9976
90856	104370	0.0170	0.0006	0.1717	0.0721	0.0972	0.9977	0.9977
90856	100530	0.0126	0.0059	0.2431	0.2076	0.0229	0.9994	0.9994
90856	55705	0.0048	0.0001	0.0420	0.0078	0.0276	0.9906	0.9906
90856	101685	0.0086	0.0002	0.0416	0.0051	0.0352	0.9942	0.9942
90856	48010	0.0227	0.0046	0.8878	0.7907	0.0853	0.9992	0.9992
90856	107009	0.0061	0.0001	0.0195	0.0020	0.0172	0.9969	0.9969
90856	107429	0.0053	0.0004	0.1606	0.1105	0.0360	0.9977	0.9977
90856	38064	0.0428	0.0107	17.0178	16.7774	0.2366	0.9987	0.9987
90856	99789	0.0062	0.0004	0.1226	0.0782	0.0303	0.9968	0.9968
90856	88589	0.0116	0.0019	0.1199	0.0120	0.0604	0.9959	0.9959
90856	74414	0.0075	0.0006	0.0449	0.0173	0.0251	0.9986	0.9986
90856	87894	0.0198	0.0016	0.6645	0.5028	0.1601	0.9978	0.9978
90856	100937	0.0066	0.0007	0.1208	0.0613	0.0341	0.9982	0.9982
90856	100652	0.0030	0.0000	0.0111	0.0009	0.0099	0.9872	0.9872
90856	74812	0.0073	0.0006	0.0918	0.0472	0.0363	0.9980	0.9980
90856	55634	0.0038	0.0001	0.0099	0.0003	0.0093	0.9813	0.9813
90856	100610	0.0097	0.0009	0.2005	0.1237	0.0445	0.9984	0.9984
90856	62617	0.0073	0.0003	0.0753	0.0240	0.0488	0.9959	0.9959
90856	56150	0.0061	0.0004	0.2588	0.2098	0.0345	0.9973	0.9973
90856	104099	0.0063	0.0002	0.1002	0.0563	0.0328	0.9981	0.9981
90856	90603	0.0126	0.0007	1.1876	1.0574	0.0777	0.9983	0.9983
90856	106996	0.0034	0.0001	0.0421	0.0204	0.0213	0.9948	0.9948
90856	107220	0.0153	0.0005	0.3716	0.2358	0.1302	0.9974	0.9974
90856	107623	0.0048	0.0003	0.0310	0.0093	0.0183	0.9976	0.9976
90856	75001	0.0246	0.0059	0.4256	0.2023	0.1203	0.9988	0.9988
90856	88336	0.0046	0.0004	0.0342	0.0094	0.0192	0.9985	0.9985
90856	37353	0.0140	0.0017	0.2478	0.1725	0.0565	0.9988	0.9988
90856	105654	0.0054	0.0005	0.0340	0.0075	0.0221	0.9980	0.9980
105323	107601	0.0030	0.0000	0.0089	0.0005	0.0080	0.9861	0.9861
105323	37889	0.0022	0.0000	0.0065	0.0005	0.0057	0.9657	0.9657
105323	74548	0.0057	0.0001	0.0271	0.0023	0.0244	0.9816	0.9816
105323	103997	0.0071	0.0005	0.0233	0.0033	0.0192	0.9944	0.9944
105323	88482	0.0082	0.0001	0.0220	0.0007	0.0208	0.9949	0.9949
105323	106838	0.0060	0.0001	0.0237	0.0006	0.0226	0.9933	0.9933
105323	103998	0.0038	0.0006	0.0128	0.0032	0.0092	0.9982	0.9982
105323	105677	0.0071	0.0001	0.0271	0.0015	0.0250	0.9893	0.9893
105323	81915	0.0037	0.0000	0.0122	0.0004	0.0114	0.9852	0.9852
105323	80191	0.0034	0.0001	0.0146	0.0017	0.0123	0.9934	0.9934
105323	100934	0.0054	0.0002	0.0198	0.0020	0.0172	0.9969	0.9969
105323	103789	0.0073	0.0000	0.0254	0.0009	0.0239	0.9937	0.9937
105323	90389	0.0036	0.0000	0.0142	0.0009	0.0130	0.9964	0.9964
105323	104370	0.0064	0.0001	0.0158	0.0002	0.0152	0.9956	0.9956
105323	100530	0.0030	0.0001	0.0114	0.0022	0.0088	0.9935	0.9935
105323	55705	0.0048	0.0001	0.0263	0.0047	0.0210	0.9909	0.9909
105323	101685	0.0060	0.0001	0.0263	0.0034	0.0225	0.9965	0.9965
105323	48010	0.0041	0.0000	0.0139	0.0005	0.0131	0.9722	0.9722
105323	107009	0.0026	0.0000	0.0074	0.0004	0.0067	0.9785	0.9785
105323	107429	0.0025	0.0000	0.0088	0.0013	0.0072	0.9741	0.9741
105323	38064	0.0046	0.0000	0.0146	0.0011	0.0131	0.9771	0.9771
105323	99789	0.0034	0.0000	0.0156	0.0021	0.0133	0.9795	0.9795
105323	88589	0.0068	0.0002	0.0188	0.0011	0.0168	0.9937	0.9937
105323	74414	0.0024	0.0001	0.0085	0.0009	0.0073	0.9883	0.9883
105323	87894	0.0055	0.0000	0.0161	0.0001	0.0156	0.9659	0.9659
105323	100937	0.0027	0.0001	0.0113	0.0023	0.0082	0.9959	0.9959
105323	100652	0.0020	0.0000	0.0047	0.0001	0.0043	0.9170	0.9170
105323	74812	0.0031	0.0000	0.0092	0.0005	0.0084	0.9753	0.9753
105323	55634	0.0049	0.0001	0.0145	0.0003	0.0139	0.9960	0.9960
105323	100610	0.0021	0.0000	0.0095	0.0007	0.0086	0.9839	0.9839
105323	62617	0.0045	0.0001	0.0182	0.0004	0.0174	0.9923	0.9923
105323	56150	0.0018	0.0001	0.0045	0.0003	0.0040	0.9929	0.9929
105323	104099	0.0031	0.0000	0.0154	0.0014	0.0137	0.9682	0.9682
105323	90603	0.0026	0.0000	0.0074	0.0002	0.0069	0.9780	0.9780
105323	106996	0.0022	0.0000	0.0057	0.0002	0.0051	0.9077	0.9077

Name1	**Name2**	**S01**	**M01**	**T03**	**S03**	**M03**	**C1X**	**C2X**
105323	107220	0.0040	0.0000	0.0140	0.0007	0.0128	0.9719	0.9719
105323	107623	0.0016	0.0000	0.0045	0.0005	0.0037	0.9668	0.9668
105323	75001	0.0038	0.0000	0.0113	0.0002	0.0107	0.9679	0.9679
105323	88336	0.0024	0.0000	0.0083	0.0002	0.0078	0.9865	0.9865
105323	37353	0.0037	0.0001	0.0116	0.0002	0.0111	0.9887	0.9887
105323	105654	0.0025	0.0000	0.0103	0.0003	0.0097	0.9500	0.9500
107601	37889	0.0022	0.0000	0.0099	0.0010	0.0084	0.9615	0.9615
107601	74548	0.0033	0.0000	0.0152	0.0020	0.0128	0.9716	0.9716
107601	103997	0.0045	0.0001	0.0196	0.0029	0.0159	0.9744	0.9744
107601	88482	0.0083	0.0001	0.0270	0.0009	0.0252	0.9683	0.9683
107601	106838	0.0027	0.0000	0.0075	0.0002	0.0069	0.8960	0.8960
107601	103998	0.0026	0.0001	0.0166	0.0038	0.0123	0.9963	0.9963
107601	105677	0.0034	0.0000	0.0100	0.0003	0.0093	0.9190	0.9190
107601	81915	0.0052	0.0005	0.0271	0.0080	0.0185	0.9974	0.9974
107601	80191	0.0079	0.0003	0.0958	0.0481	0.0343	0.9977	0.9977
107601	100934	0.0031	0.0001	0.0155	0.0023	0.0128	0.9952	0.9952
107601	103789	0.0078	0.0000	0.0343	0.0038	0.0297	0.9634	0.9634
107601	90389	0.0062	0.0001	0.0370	0.0114	0.0226	0.9971	0.9971
107601	104370	0.0068	0.0000	0.0332	0.0016	0.0311	0.9588	0.9588
107601	100530	0.0035	0.0002	0.0196	0.0092	0.0101	0.9967	0.9967
107601	55705	0.0031	0.0002	0.0076	0.0007	0.0067	0.9937	0.9937
107601	101685	0.0034	0.0000	0.0116	0.0007	0.0103	0.9143	0.9143
107601	48010	0.0039	0.0001	0.0148	0.0014	0.0130	0.9824	0.9824
107601	107009	0.0037	0.0002	0.0324	0.0102	0.0153	0.9925	0.9925
107601	107429	0.0033	0.0000	0.0198	0.0015	0.0179	0.9926	0.9926
107601	38064	0.0031	0.0000	0.0088	0.0003	0.0081	0.8974	0.8974
107601	99789	0.0024	0.0001	0.0101	0.0017	0.0081	0.9951	0.9951
107601	88589	0.0039	0.0000	0.0091	0.0004	0.0078	1.0000	1.0000
107601	74414	0.0027	0.0000	0.0198	0.0067	0.0127	0.9938	0.9938
107601	87894	0.0053	0.0000	0.0183	0.0006	0.0173	0.9636	0.9636
107601	100937	0.0040	0.0004	0.0194	0.0063	0.0127	0.9961	0.9961
107601	100652	0.0026	0.0000	0.0177	0.0047	0.0126	0.9770	0.9770
107601	74812	0.0041	0.0001	0.0325	0.0092	0.0224	0.9897	0.9897
107601	55634	0.0019	0.0000	0.0041	0.0001	0.0037	0.7273	0.7273
107601	100610	0.0026	0.0000	0.0124	0.0035	0.0084	0.9842	0.9842
107601	62617	0.0025	0.0000	0.0069	0.0001	0.0065	0.8787	0.8787
107601	56150	0.0034	0.0001	0.0230	0.0086	0.0131	0.9932	0.9932
107601	104099	0.0024	0.0001	0.0089	0.0017	0.0069	0.9847	0.9847
107601	90603	0.0034	0.0001	0.0134	0.0009	0.0116	0.9861	0.9861
107601	106996	0.0046	0.0001	0.0280	0.0034	0.0236	0.9926	0.9926
107601	107220	0.0037	0.0000	0.0118	0.0003	0.0112	0.9480	0.9480
107601	107623	0.0036	0.0001	0.0203	0.0053	0.0126	0.9948	0.9948
107601	75001	0.0023	0.0000	0.0070	0.0005	0.0062	0.8993	0.8993
107601	88336	0.0028	0.0001	0.0103	0.0008	0.0091	0.9927	0.9927
107601	37353	0.0017	0.0000	0.0047	0.0003	0.0042	0.9732	0.9732
107601	105654	0.0034	0.0001	0.0138	0.0034	0.0098	0.9962	0.9962
37889	74548	0.0019	0.0000	0.0066	0.0006	0.0047	0.9526	0.9526
37889	103997	0.0021	0.0001	0.0077	0.0007	0.0060	0.9700	0.9700
37889	88482	0.0017	0.0000	0.0024	0.0000	0.0021	1.0000	1.0000
37889	106838	0.0017	0.0000	0.0043	0.0001	0.0039	0.8696	0.8696
37889	103998	0.0029	0.0000	0.0168	0.0030	0.0133	0.9884	0.9884
37889	105677	0.0017	0.0000	0.0033	0.0001	0.0030	0.8970	0.8970
37889	81915	0.0022	0.0001	0.0065	0.0004	0.0057	0.9941	0.9941
37889	80191	0.0021	0.0000	0.0112	0.0015	0.0091	0.9942	0.9942
37889	100934	0.0023	0.0000	0.0088	0.0004	0.0082	0.9833	0.9833
37889	103789	0.0016	0.0000	0.0022	0.0000	0.0019	1.0000	1.0000
37889	90389	0.0016	0.0000	0.0047	0.0003	0.0040	0.9906	0.9906
37889	104370	0.0015	0.0000	0.0029	0.0001	0.0025	1.0000	1.0000
37889	100530	0.0017	0.0000	0.0082	0.0005	0.0074	0.9942	0.9942
37889	55705	0.0016	0.0000	0.0048	0.0001	0.0045	0.9683	0.9683
37889	101685	0.0015	0.0000	0.0026	0.0001	0.0022	0.9359	0.9359
37889	48010	0.0017	0.0000	0.0034	0.0001	0.0031	0.9507	0.9507
37889	107009	0.0019	0.0001	0.0093	0.0020	0.0069	0.9886	0.9886
37889	107429	0.0020	0.0000	0.0092	0.0012	0.0065	0.9921	0.9921
37889	38064	0.0013	0.0000	0.0037	0.0002	0.0026	1.0000	1.0000
37889	99789	0.0016	0.0001	0.0052	0.0002	0.0047	0.9801	0.9801
37889	88589	0.0010	0.0000	0.0016	0.0000	0.0013	1.0000	1.0000

Name1	**Name2**	**S01**	**M01**	**T03**	**S03**	**M03**	**C1X**	**C2X**
37889	74414	0.0015	0.0000	0.0050	0.0001	0.0046	0.9309	0.9309
37889	87894	0.0012	0.0000	0.0017	0.0000	0.0014	1.0000	1.0000
37889	100937	0.0014	0.0000	0.0056	0.0004	0.0049	0.9762	0.9762
37889	100652	0.0016	0.0000	0.0062	0.0006	0.0052	0.9899	0.9899
37889	74812	0.0014	0.0000	0.0043	0.0003	0.0036	0.9846	0.9846
37889	55634	0.0012	0.0000	0.0021	0.0001	0.0018	0.9285	0.9285
37889	100610	0.0015	0.0000	0.0053	0.0003	0.0048	0.9901	0.9901
37889	62617	0.0012	0.0000	0.0024	0.0001	0.0021	0.8246	0.8246
37889	56150	0.0014	0.0000	0.0061	0.0003	0.0054	0.9748	0.9748
37889	104099	0.0012	0.0000	0.0031	0.0001	0.0027	0.9806	0.9806
37889	90603	0.0012	0.0000	0.0026	0.0001	0.0023	0.9338	0.9338
37889	106996	0.0014	0.0001	0.0037	0.0003	0.0032	0.9731	0.9731
37889	107220	0.0010	0.0000	0.0015	0.0000	0.0013	1.0000	1.0000
37889	107623	0.0017	0.0001	0.0072	0.0011	0.0058	0.9915	0.9915
37889	75001	0.0012	0.0000	0.0026	0.0002	0.0022	0.9206	0.9206
37889	88336	0.0014	0.0000	0.0055	0.0004	0.0041	0.9710	0.9710
37889	37353	0.0012	0.0000	0.0025	0.0001	0.0022	0.9474	0.9474
37889	105654	0.0013	0.0000	0.0034	0.0001	0.0031	0.9572	0.9572
74548	103997	0.0068	0.0001	0.0380	0.0122	0.0252	0.9944	0.9944
74548	88482	0.0107	0.0002	0.1109	0.0135	0.0967	0.9954	0.9954
74548	106838	0.0301	0.0003	0.3909	0.1526	0.2376	0.9957	0.9957
74548	103998	0.0033	0.0003	0.0151	0.0037	0.0105	0.9965	0.9965
74548	105677	0.0093	0.0002	0.0630	0.0061	0.0549	0.9929	0.9929
74548	81915	0.0111	0.0009	0.1233	0.0591	0.0560	0.9975	0.9975
74548	80191	0.0054	0.0001	0.0210	0.0014	0.0192	0.9944	0.9944
74548	100934	0.0052	0.0001	0.0243	0.0024	0.0204	0.9959	0.9959
74548	103789	0.0133	0.0002	0.2296	0.0728	0.1546	0.9960	0.9960
74548	90389	0.0053	0.0002	0.0162	0.0005	0.0154	0.9831	0.9831
74548	104370	0.0239	0.0009	0.2836	0.1061	0.1766	0.9988	0.9988
74548	100530	0.0052	0.0004	0.0370	0.0106	0.0193	0.9988	0.9988
74548	55705	0.0047	0.0000	0.0260	0.0018	0.0230	0.9838	0.9838
74548	101685	0.0089	0.0002	0.0411	0.0030	0.0377	0.9936	0.9936
74548	48010	0.0102	0.0002	0.0759	0.0109	0.0646	0.9950	0.9950
74548	107009	0.0046	0.0002	0.0191	0.0023	0.0165	0.9962	0.9962
74548	107429	0.0050	0.0004	0.0648	0.0252	0.0328	0.9972	0.9972
74548	38064	0.0409	0.0064	28.2310	28.0479	0.1809	0.9995	0.9995
74548	99789	0.0047	0.0002	0.0351	0.0074	0.0229	0.9963	0.9963
74548	88589	0.0056	0.0000	0.0323	0.0020	0.0298	0.9948	0.9948
74548	74414	0.0052	0.0002	0.0428	0.0150	0.0195	0.9955	0.9955
74548	87894	0.0074	0.0002	0.0708	0.0094	0.0609	0.9842	0.9842
74548	100937	0.0048	0.0003	0.0756	0.0314	0.0264	0.9979	0.9979
74548	100652	0.0027	0.0000	0.0091	0.0007	0.0082	0.9783	0.9783
74548	74812	0.0052	0.0002	0.0611	0.0262	0.0344	0.9939	0.9939
74548	55634	0.0043	0.0000	0.0152	0.0008	0.0139	0.9910	0.9910
74548	100610	0.0043	0.0001	0.0505	0.0191	0.0210	0.9938	0.9938
74548	62617	0.0089	0.0003	0.0625	0.0106	0.0490	0.9961	0.9961
74548	56150	0.0043	0.0000	0.0377	0.0170	0.0203	0.9864	0.9864
74548	104099	0.0073	0.0003	0.0323	0.0048	0.0262	0.9968	0.9968
74548	90603	0.0103	0.0006	0.3689	0.2675	0.0491	0.9985	0.9985
74548	106996	0.0040	0.0001	0.0264	0.0056	0.0204	0.9942	0.9942
74548	107220	0.0045	0.0000	0.0316	0.0036	0.0272	0.9796	0.9796
74548	107623	0.0037	0.0004	0.0200	0.0065	0.0112	0.9978	0.9978
74548	75001	0.0073	0.0002	0.0583	0.0140	0.0425	0.9953	0.9953
74548	88336	0.0033	0.0000	0.0176	0.0033	0.0132	0.9891	0.9891
74548	37353	0.0138	0.0002	0.1663	0.0899	0.0586	0.9973	0.9973
74548	105654	0.0050	0.0002	0.0221	0.0023	0.0195	0.9982	0.9982
103997	88482	0.0105	0.0001	0.0995	0.0191	0.0776	0.9901	0.9901
103997	106838	0.0043	0.0002	0.0352	0.0066	0.0241	0.9950	0.9950
103997	103998	0.0029	0.0000	0.0096	0.0014	0.0076	0.9958	0.9958
103997	105677	0.0057	0.0001	0.0226	0.0005	0.0217	0.9901	0.9901
103997	81915	0.0048	0.0003	0.0179	0.0028	0.0147	0.9964	0.9964
103997	80191	0.0045	0.0002	0.0142	0.0012	0.0127	0.9971	0.9971
103997	100934	0.0065	0.0004	0.0187	0.0030	0.0154	0.9983	0.9983
103997	103789	0.0077	0.0001	0.0654	0.0077	0.0556	0.9957	0.9957
103997	90389	0.0013	0.0001	0.0028	0.0001	0.0025	0.9859	0.9859
103997	104370	0.0019	0.0000	0.0071	0.0006	0.0063	0.9178	0.9178
103997	100530	0.0030	0.0003	0.0096	0.0018	0.0069	0.9964	0.9964

Name1	Name2	S01	M01	T03	S03	M03	C1X	C2X
103997	55705	0.0042	0.0002	0.0189	0.0027	0.0143	0.9964	0.9964
103997	101685	0.0050	0.0001	0.0172	0.0006	0.0162	0.9860	0.9860
103997	48010	0.0038	0.0001	0.0186	0.0016	0.0166	0.9808	0.9808
103997	107009	0.0039	0.0002	0.0738	0.0569	0.0138	0.9973	0.9973
103997	107429	0.0028	0.0001	0.0135	0.0026	0.0097	0.9958	0.9958
103997	38064	0.0111	0.0005	0.1556	0.0749	0.0799	0.9954	0.9954
103997	99789	0.0029	0.0001	0.0103	0.0006	0.0094	0.9941	0.9941
103997	88589	0.0012	0.0000	0.0062	0.0006	0.0040	1.0000	1.0000
103997	74414	0.0040	0.0001	0.0139	0.0011	0.0118	0.9945	0.9945
103997	87894	0.0093	0.0002	0.0735	0.0099	0.0617	0.9953	0.9953
103997	100937	0.0028	0.0001	0.0104	0.0017	0.0079	0.9972	0.9972
103997	100652	0.0024	0.0001	0.0066	0.0002	0.0062	0.9928	0.9928
103997	74812	0.0026	0.0001	0.0096	0.0006	0.0087	0.9889	0.9889
103997	55634	0.0034	0.0001	0.0104	0.0006	0.0090	0.9674	0.9674
103997	100610	0.0032	0.0001	0.0122	0.0017	0.0098	0.9958	0.9958
103997	62617	0.0042	0.0001	0.0149	0.0003	0.0143	0.9913	0.9913
103997	56150	0.0026	0.0001	0.0127	0.0027	0.0081	0.9947	0.9947
103997	104099	0.0029	0.0000	0.0118	0.0007	0.0107	0.9895	0.9895
103997	90603	0.0034	0.0002	0.0112	0.0019	0.0083	0.9969	0.9969
103997	106996	0.0016	0.0001	0.0050	0.0006	0.0038	0.9944	0.9944
103997	107220	0.0216	0.0006	0.6676	0.3965	0.2250	0.9965	0.9965
103997	107623	0.0074	0.0008	0.1041	0.0367	0.0357	0.9981	0.9981
103997	75001	0.0042	0.0001	0.0142	0.0009	0.0130	0.9936	0.9936
103997	88336	0.0025	0.0001	0.0116	0.0029	0.0072	0.9877	0.9877
103997	37353	0.0030	0.0001	0.0096	0.0003	0.0090	0.9952	0.9952
103997	105654	0.0032	0.0001	0.0124	0.0012	0.0107	0.9958	0.9958
88482	106838	0.0433	0.0019	1.1200	0.7425	0.3248	0.9984	0.9984
88482	103998	0.0016	0.0000	0.0022	0.0000	0.0019	1.0000	1.0000
88482	105677	0.0170	0.0002	0.5299	0.1080	0.2832	0.9962	0.9962
88482	81915	0.0053	0.0000	0.0349	0.0032	0.0302	0.9814	0.9814
88482	80191	0.0081	0.0001	0.0274	0.0009	0.0260	0.9890	0.9890
88482	100934	0.0047	0.0001	0.0148	0.0007	0.0138	0.9905	0.9905
88482	103789	0.4329	0.0402	1077.3400	1073.7000	3.4827	0.9993	0.9998
88482	90389	0.0619	0.0025	0.9120	0.4275	0.4804	0.9981	0.9982
88482	104370	0.1124	0.0020	0.4319	0.0228	0.3995	0.9981	0.9990
88482	100530	0.0022	0.0001	0.0042	0.0001	0.0037	0.9913	0.9913
88482	55705	0.0073	0.0003	0.0368	0.0028	0.0330	0.9948	0.9948
88482	101685	0.0187	0.0005	0.1112	0.0114	0.0936	0.9963	0.9963
88482	48010	0.0192	0.0005	0.6269	0.3431	0.1970	0.9978	0.9978
88482	107009	0.0061	0.0002	0.0328	0.0012	0.0310	0.9872	0.9872
88482	107429	0.0067	0.0004	0.0585	0.0125	0.0418	0.9970	0.9970
88482	38064	0.1479	0.0206	36.1382	35.5637	0.4823	0.9997	0.9997
88482	99789	0.0026	0.0000	0.0076	0.0001	0.0069	0.9823	0.9823
88482	88589	0.0781	0.0011	0.4586	0.0701	0.3871	0.9979	0.9979
88482	74414	0.0047	0.0000	0.0105	0.0002	0.0101	0.9727	0.9727
88482	87894	0.2110	0.0044	14.5483	12.5176	2.0265	0.9986	0.9986
88482	100937	0.0027	0.0001	0.0084	0.0004	0.0075	0.9763	0.9763
88482	100652	0.0024	0.0000	0.0127	0.0010	0.0096	0.9714	0.9714
88482	74812	0.0102	0.0002	0.0804	0.0055	0.0741	0.9844	0.9844
88482	55634	0.0056	0.0000	0.0133	0.0006	0.0120	0.9929	0.9929
88482	100610	0.0032	0.0000	0.0068	0.0001	0.0065	0.9796	0.9796
88482	62617	0.0134	0.0004	0.1421	0.0238	0.1177	0.9968	0.9968
88482	56150	0.0023	0.0000	0.0080	0.0007	0.0070	0.9612	0.9612
88482	104099	0.0092	0.0002	0.0671	0.0133	0.0475	0.9963	0.9963
88482	90603	0.0076	0.0000	0.0461	0.0034	0.0400	0.9935	0.9935
88482	106996	0.0144	0.0001	0.1441	0.0038	0.1397	0.9876	0.9876
88482	107220	0.0167	0.0003	0.1822	0.0396	0.1412	0.9972	0.9972
88482	107623	0.0021	0.0000	0.0090	0.0005	0.0079	0.8246	0.8246
88482	75001	0.0141	0.0001	0.1072	0.0166	0.0901	0.9945	0.9945
88482	88336	0.0075	0.0001	0.0437	0.0044	0.0384	0.9951	0.9951
88482	37353	0.0059	0.0004	0.0238	0.0019	0.0204	0.9969	0.9969
88482	105654	0.0089	0.0003	0.0382	0.0038	0.0338	0.9972	0.9972
106838	103998	0.0022	0.0000	0.0063	0.0009	0.0050	0.9802	0.9802
106838	105677	0.0155	0.0002	0.1036	0.0088	0.0941	0.9901	0.9901
106838	81915	0.0100	0.0003	0.0962	0.0164	0.0697	0.9934	0.9934
106838	80191	0.0038	0.0001	0.0146	0.0004	0.0139	0.9584	0.9584
106838	100934	0.0047	0.0001	0.0187	0.0009	0.0175	0.9873	0.9873

Name1	Name2	S01	M01	T03	S03	M03	C1X	C2X
106838	103789	0.0425	0.0021	3.3795	2.9495	0.4210	0.9982	0.9982
106838	90389	0.0053	0.0004	0.0248	0.0051	0.0192	0.9957	0.9957
106838	104370	0.0796	0.0112	2.2886	1.7990	0.4331	0.9996	0.9996
106838	100530	0.0033	0.0001	0.0325	0.0055	0.0244	0.9811	0.9811
106838	55705	0.0083	0.0002	0.0933	0.0251	0.0581	0.9953	0.9953
106838	101685	0.0098	0.0001	0.0994	0.0178	0.0739	0.9952	0.9952
106838	48010	0.0143	0.0003	0.2201	0.0738	0.1422	0.9946	0.9946
106838	107009	0.0041	0.0001	0.0281	0.0034	0.0224	0.9950	0.9950
106838	107429	0.0027	0.0000	0.0159	0.0013	0.0138	0.9830	0.9830
106838	38064	0.0825	0.0054	3.8379	3.2755	0.5423	0.9987	0.9987
106838	99789	0.0041	0.0001	0.0178	0.0018	0.0154	0.9887	0.9887
106838	88589	0.0207	0.0007	0.1887	0.0419	0.1307	0.9966	0.9966
106838	74414	0.0038	0.0002	0.0221	0.0016	0.0198	0.9817	0.9817
106838	87894	0.0165	0.0004	0.2747	0.1193	0.1532	0.9965	0.9965
106838	100937	0.0024	0.0000	0.0058	0.0001	0.0053	0.9792	0.9792
106838	100652	0.0020	0.0000	0.0054	0.0002	0.0049	0.9047	0.9047
106838	74812	0.0032	0.0000	0.0208	0.0020	0.0183	0.9638	0.9638
106838	55634	0.0066	0.0000	0.0250	0.0005	0.0240	0.9639	0.9639
106838	100610	0.0026	0.0000	0.0200	0.0024	0.0169	0.9287	0.9287
106838	62617	0.0111	0.0002	0.0893	0.0056	0.0833	0.9959	0.9959
106838	56150	0.0020	0.0000	0.0106	0.0013	0.0089	0.9475	0.9475
106838	104099	0.0067	0.0001	0.0740	0.0093	0.0638	0.9816	0.9816
106838	90603	0.0047	0.0001	0.0350	0.0089	0.0248	0.9956	0.9956
106838	106996	0.0026	0.0001	0.0139	0.0009	0.0127	0.9347	0.9347
106838	107220	0.0058	0.0001	0.0520	0.0059	0.0454	0.9881	0.9881
106838	107623	0.0013	0.0000	0.0066	0.0004	0.0060	0.9782	0.9782
106838	75001	0.0103	0.0003	0.1148	0.0336	0.0764	0.9941	0.9941
106838	88336	0.0027	0.0000	0.0201	0.0028	0.0151	0.9844	0.9844
106838	37353	0.0122	0.0008	0.1690	0.0272	0.1326	0.9916	0.9916
106838	105654	0.0052	0.0001	0.0400	0.0047	0.0345	0.9863	0.9863
103998	105677	0.0018	0.0000	0.0044	0.0002	0.0039	0.9924	0.9924
103998	81915	0.0038	0.0002	0.0132	0.0022	0.0107	0.9953	0.9953
103998	80191	0.0030	0.0001	0.0144	0.0018	0.0123	0.9805	0.9805
103998	100934	0.0047	0.0001	0.0260	0.0086	0.0167	0.9969	0.9969
103998	103789	0.0016	0.0000	0.0021	0.0000	0.0019	1.0000	1.0000
103998	90389	0.0016	0.0000	0.0056	0.0006	0.0048	0.9847	0.9847
103998	104370	0.0017	0.0001	0.0074	0.0007	0.0050	0.9798	0.9798
103998	100530	0.0038	0.0001	0.0729	0.0337	0.0218	0.9932	0.9932
103998	55705	0.0025	0.0001	0.0117	0.0012	0.0088	0.9958	0.9958
103998	101685	0.0017	0.0000	0.0045	0.0003	0.0039	0.9744	0.9744
103998	48010	0.0020	0.0000	0.0066	0.0012	0.0051	0.9943	0.9943
103998	107009	0.0020	0.0000	0.0073	0.0015	0.0053	0.9924	0.9924
103998	107429	0.0028	0.0001	0.0392	0.0166	0.0135	0.9956	0.9956
103998	38064	0.0014	0.0000	0.0022	0.0000	0.0020	1.0000	1.0000
103998	99789	0.0024	0.0001	0.0113	0.0016	0.0094	0.9919	0.9919
103998	88589	0.0011	0.0000	0.0016	0.0000	0.0013	1.0000	1.0000
103998	74414	0.0027	0.0002	0.0168	0.0046	0.0096	0.9924	0.9924
103998	87894	0.0012	0.0000	0.0020	0.0000	0.0017	1.0000	1.0000
103998	100937	0.0026	0.0001	0.0137	0.0032	0.0085	0.9945	0.9945
103998	100652	0.0022	0.0001	0.0077	0.0009	0.0064	0.9908	0.9908
103998	74812	0.0018	0.0001	0.0057	0.0004	0.0050	0.9901	0.9901
103998	55634	0.0016	0.0001	0.0029	0.0002	0.0025	0.9932	0.9932
103998	100610	0.0029	0.0002	0.0106	0.0010	0.0092	0.9966	0.9966
103998	62617	0.0013	0.0000	0.0031	0.0001	0.0027	0.9881	0.9881
103998	56150	0.0030	0.0001	0.0307	0.0121	0.0118	0.9942	0.9942
103998	104099	0.0019	0.0001	0.0061	0.0006	0.0051	0.9930	0.9930
103998	90603	0.0015	0.0000	0.0076	0.0016	0.0045	0.9765	0.9765
103998	106996	0.0016	0.0001	0.0042	0.0004	0.0036	0.9865	0.9865
103998	107220	0.0010	0.0000	0.0017	0.0000	0.0015	1.0000	1.0000
103998	107623	0.0025	0.0002	0.0083	0.0008	0.0068	0.9959	0.9959
103998	75001	0.0011	0.0000	0.0025	0.0002	0.0021	0.9609	0.9609
103998	88336	0.0017	0.0000	0.0096	0.0015	0.0074	0.9868	0.9868
103998	37353	0.0016	0.0000	0.0043	0.0004	0.0037	0.9904	0.9904
103998	105654	0.0015	0.0000	0.0057	0.0003	0.0051	0.9884	0.9884
105677	81915	0.0054	0.0001	0.0351	0.0029	0.0317	0.9885	0.9885
105677	80191	0.0036	0.0001	0.0173	0.0012	0.0157	0.9919	0.9919
105677	100934	0.0046	0.0001	0.0216	0.0006	0.0206	0.9939	0.9939

Name1	Name2	S01	M01	T03	S03	M03	C1X	C2X
105677	103789	0.0165	0.0004	0.3364	0.0880	0.2462	0.9909	0.9909
105677	90389	0.0039	0.0000	0.0159	0.0003	0.0152	0.9813	0.9813
105677	104370	0.0141	0.0001	0.1756	0.0310	0.1419	0.9916	0.9916
105677	100530	0.0026	0.0001	0.0106	0.0005	0.0099	0.9887	0.9887
105677	55705	0.0058	0.0001	0.0481	0.0101	0.0360	0.9948	0.9948
105677	101685	0.0095	0.0001	0.0914	0.0300	0.0606	0.9957	0.9957
105677	48010	0.0082	0.0001	0.0757	0.0047	0.0704	0.9943	0.9943
105677	107009	0.0031	0.0001	0.0130	0.0010	0.0115	0.9403	0.9403
105677	107429	0.0026	0.0000	0.0132	0.0012	0.0114	0.9686	0.9686
105677	38064	0.0105	0.0003	0.2043	0.0369	0.1132	0.9911	0.9911
105677	99789	0.0038	0.0001	0.0226	0.0046	0.0175	0.9901	0.9901
105677	88589	0.0058	0.0000	0.0348	0.0017	0.0325	0.9319	0.9319
105677	74414	0.0026	0.0000	0.0150	0.0011	0.0135	0.9828	0.9828
105677	87894	0.0112	0.0002	0.1611	0.0396	0.1206	0.9923	0.9923
105677	100937	0.0027	0.0001	0.0103	0.0008	0.0092	0.9924	0.9924
105677	100652	0.0020	0.0000	0.0068	0.0003	0.0063	0.9879	0.9879
105677	74812	0.0038	0.0000	0.0250	0.0026	0.0220	0.9592	0.9592
105677	55634	0.0053	0.0000	0.0173	0.0004	0.0165	0.9684	0.9684
105677	100610	0.0023	0.0000	0.0141	0.0008	0.0130	0.9760	0.9760
105677	62617	0.0091	0.0001	0.0777	0.0098	0.0676	0.9922	0.9922
105677	56150	0.0017	0.0000	0.0061	0.0002	0.0056	0.9713	0.9713
105677	104099	0.0045	0.0001	0.0317	0.0013	0.0301	0.9858	0.9858
105677	90603	0.0036	0.0000	0.0151	0.0003	0.0145	0.9686	0.9686
105677	106996	0.0031	0.0000	0.0201	0.0025	0.0168	0.9671	0.9671
105677	107220	0.0076	0.0002	0.0854	0.0181	0.0593	0.9870	0.9870
105677	107623	0.0014	0.0000	0.0045	0.0003	0.0039	0.8676	0.8676
105677	75001	0.0068	0.0001	0.0372	0.0017	0.0348	0.9937	0.9937
105677	88336	0.0027	0.0001	0.0130	0.0004	0.0124	0.9344	0.9344
105677	37353	0.0054	0.0000	0.0416	0.0018	0.0394	0.9768	0.9768
105677	105654	0.0038	0.0001	0.0228	0.0008	0.0218	0.9860	0.9860
81915	80191	0.0097	0.0011	0.4124	0.3712	0.0395	0.9988	0.9988
81915	100934	0.0045	0.0001	0.0161	0.0015	0.0144	0.9957	0.9957
81915	103789	0.0078	0.0002	0.0582	0.0037	0.0541	0.9854	0.9854
81915	90389	0.0034	0.0001	0.0175	0.0033	0.0125	0.9953	0.9953
81915	104370	0.0122	0.0007	0.1255	0.0448	0.0782	0.9968	0.9968
81915	100530	0.0073	0.0011	0.0668	0.0376	0.0256	0.9993	0.9993
81915	55705	0.0043	0.0001	0.0230	0.0034	0.0192	0.9953	0.9953
81915	101685	0.0049	0.0001	0.0261	0.0022	0.0235	0.9918	0.9918
81915	48010	0.0090	0.0006	0.0711	0.0158	0.0548	0.9979	0.9979
81915	107009	0.0030	0.0001	0.0102	0.0008	0.0091	0.9966	0.9966
81915	107429	0.0051	0.0004	0.0507	0.0275	0.0226	0.9973	0.9973
81915	38064	0.0070	0.0005	0.0447	0.0069	0.0335	0.9859	0.9859
81915	99789	0.0029	0.0001	0.0147	0.0033	0.0110	0.9932	0.9932
81915	88589	0.0024	0.0000	0.0128	0.0013	0.0088	0.9863	0.9863
81915	74414	0.0043	0.0001	0.0317	0.0127	0.0187	0.9937	0.9937
81915	87894	0.0042	0.0001	0.0498	0.0103	0.0308	0.9875	0.9875
81915	100937	0.0064	0.0004	0.0243	0.0083	0.0157	0.9984	0.9984
81915	100652	0.0034	0.0001	0.0165	0.0026	0.0136	0.9960	0.9960
81915	74812	0.0031	0.0001	0.0193	0.0026	0.0164	0.9908	0.9908
81915	55634	0.0033	0.0000	0.0088	0.0002	0.0084	0.9882	0.9882
81915	100610	0.0044	0.0004	0.0483	0.0287	0.0192	0.9978	0.9978
81915	62617	0.0045	0.0001	0.0295	0.0029	0.0262	0.9923	0.9923
81915	56150	0.0088	0.0011	0.1171	0.0904	0.0254	0.9991	0.9991
81915	104099	0.0041	0.0001	0.0336	0.0103	0.0223	0.9967	0.9967
81915	90603	0.0055	0.0002	0.0403	0.0161	0.0236	0.9973	0.9973
81915	106996	0.0041	0.0002	0.0272	0.0103	0.0164	0.9975	0.9975
81915	107220	0.0032	0.0000	0.0185	0.0018	0.0165	0.9522	0.9522
81915	107623	0.0051	0.0005	0.0141	0.0040	0.0097	0.9982	0.9982
81915	75001	0.0034	0.0000	0.0208	0.0022	0.0182	0.9755	0.9755
81915	88336	0.0028	0.0001	0.0090	0.0006	0.0082	0.9955	0.9955
81915	37353	0.0076	0.0004	0.0518	0.0177	0.0337	0.9983	0.9983
81915	105654	0.0045	0.0004	0.0378	0.0174	0.0200	0.9979	0.9979
80191	100934	0.0052	0.0001	0.0226	0.0021	0.0202	0.9962	0.9962
80191	103789	0.0101	0.0004	0.0331	0.0017	0.0311	0.9917	0.9917
80191	90389	0.0081	0.0002	0.0526	0.0258	0.0252	0.9963	0.9963
80191	104370	0.0071	0.0002	0.0260	0.0019	0.0237	0.9940	0.9940
80191	100530	0.0113	0.0044	0.0494	0.0224	0.0197	0.9997	0.9997

Name1	Name2	S01	M01	T03	S03	M03	C1X	C2X
80191	55705	0.0049	0.0003	0.0254	0.0049	0.0203	0.9977	0.9977
80191	101685	0.0048	0.0001	0.0173	0.0028	0.0142	0.9928	0.9928
80191	48010	0.0117	0.0014	0.0534	0.0203	0.0326	0.9990	0.9990
80191	107009	0.0029	0.0002	0.0108	0.0014	0.0079	0.9934	0.9934
80191	107429	0.0046	0.0003	0.0343	0.0137	0.0198	0.9971	0.9971
80191	38064	0.0042	0.0002	0.0244	0.0023	0.0167	0.9903	0.9903
80191	99789	0.0029	0.0001	0.0134	0.0023	0.0108	0.9956	0.9956
80191	88589	0.0027	0.0000	0.0069	0.0004	0.0056	0.7500	0.7500
80191	74414	0.0081	0.0007	0.0992	0.0762	0.0208	0.9988	0.9988
80191	87894	0.0043	0.0000	0.0176	0.0012	0.0161	0.9894	0.9894
80191	100937	0.0071	0.0007	0.0607	0.0389	0.0202	0.9988	0.9988
80191	100652	0.0050	0.0004	0.0395	0.0192	0.0199	0.9977	0.9977
80191	74812	0.0028	0.0000	0.0228	0.0064	0.0156	0.9921	0.9921
80191	55634	0.0023	0.0000	0.0048	0.0001	0.0045	0.9929	0.9929
80191	100610	0.0081	0.0010	0.0838	0.0613	0.0219	0.9993	0.9993
80191	62617	0.0027	0.0000	0.0130	0.0005	0.0122	0.9867	0.9867
80191	56150	0.0098	0.0013	0.0904	0.0596	0.0300	0.9994	0.9994
80191	104099	0.0052	0.0005	0.0152	0.0030	0.0119	0.9982	0.9982
80191	90603	0.0065	0.0005	0.0343	0.0097	0.0241	0.9979	0.9979
80191	106996	0.0056	0.0004	0.0866	0.0326	0.0346	0.9984	0.9984
80191	107220	0.0026	0.0000	0.0115	0.0010	0.0102	0.9285	0.9285
80191	107623	0.0069	0.0012	0.0310	0.0098	0.0153	0.9983	0.9983
80191	75001	0.0025	0.0000	0.0082	0.0004	0.0076	0.9892	0.9892
80191	88336	0.0037	0.0002	0.0163	0.0021	0.0139	0.9974	0.9974
80191	37353	0.0031	0.0001	0.0150	0.0030	0.0116	0.9941	0.9941
80191	105654	0.0072	0.0008	0.0382	0.0211	0.0166	0.9988	0.9988
100934	103789	0.0057	0.0001	0.0310	0.0054	0.0251	0.9953	0.9953
100934	90389	0.0029	0.0001	0.0167	0.0030	0.0131	0.9909	0.9909
100934	104370	0.0063	0.0005	0.0171	0.0009	0.0158	0.9827	0.9827
100934	100530	0.0041	0.0003	0.0138	0.0007	0.0128	0.9962	0.9962
100934	55705	0.0064	0.0003	0.0428	0.0113	0.0311	0.9969	0.9969
100934	101685	0.0039	0.0001	0.0169	0.0014	0.0152	0.9860	0.9860
100934	48010	0.0051	0.0002	0.0294	0.0036	0.0254	0.9964	0.9964
100934	107009	0.0032	0.0002	0.0109	0.0015	0.0079	0.9969	0.9969
100934	107429	0.0035	0.0001	0.0175	0.0036	0.0134	0.9933	0.9933
100934	38064	0.0043	0.0003	0.0161	0.0015	0.0124	0.9890	0.9890
100934	99789	0.0036	0.0001	0.0266	0.0058	0.0204	0.9909	0.9909
100934	88589	0.0021	0.0000	0.0063	0.0005	0.0050	0.5714	0.5714
100934	74414	0.0032	0.0002	0.0157	0.0016	0.0139	0.9963	0.9963
100934	87894	0.0032	0.0000	0.0130	0.0010	0.0117	0.9695	0.9695
100934	100937	0.0038	0.0003	0.0160	0.0012	0.0145	0.9962	0.9962
100934	100652	0.0028	0.0002	0.0103	0.0010	0.0090	0.9960	0.9960
100934	74812	0.0021	0.0000	0.0099	0.0010	0.0085	0.9558	0.9558
100934	55634	0.0024	0.0000	0.0066	0.0003	0.0060	0.9716	0.9716
100934	100610	0.0046	0.0005	0.0262	0.0039	0.0221	0.9978	0.9978
100934	62617	0.0030	0.0000	0.0138	0.0005	0.0130	0.9658	0.9658
100934	56150	0.0030	0.0001	0.0137	0.0027	0.0108	0.9882	0.9882
100934	104099	0.0026	0.0000	0.0124	0.0008	0.0114	0.9805	0.9805
100934	90603	0.0040	0.0003	0.0097	0.0002	0.0092	0.9941	0.9941
100934	106996	0.0023	0.0001	0.0076	0.0009	0.0063	0.9919	0.9919
100934	107220	0.0025	0.0001	0.0117	0.0011	0.0101	0.9263	0.9263
100934	107623	0.0027	0.0001	0.0111	0.0017	0.0088	0.9933	0.9933
100934	75001	0.0027	0.0001	0.0076	0.0003	0.0071	0.9933	0.9933
100934	88336	0.0041	0.0001	0.0227	0.0053	0.0163	0.9963	0.9963
100934	37353	0.0037	0.0002	0.0113	0.0004	0.0106	0.9914	0.9914
100934	105654	0.0029	0.0001	0.0217	0.0047	0.0167	0.9945	0.9945
103789	90389	0.0329	0.0025	0.2032	0.0198	0.1809	0.9978	0.9978
103789	104370	0.1211	0.0048	5.8153	4.9604	0.8541	0.9991	0.9991
103789	100530	0.0022	0.0000	0.0056	0.0002	0.0051	0.9861	0.9861
103789	55705	0.0084	0.0002	0.0580	0.0048	0.0528	0.9920	0.9920
103789	101685	0.0234	0.0002	0.1738	0.0189	0.1543	0.9931	0.9931
103789	48010	0.0335	0.0018	0.7450	0.4955	0.2485	0.9981	0.9981
103789	107009	0.0053	0.0001	0.0674	0.0259	0.0366	0.9801	0.9801
103789	107429	0.0044	0.0001	0.0487	0.0146	0.0338	0.9844	0.9844
103789	38064	0.0514	0.0016	9.6711	9.1510	0.5045	0.9983	0.9983
103789	99789	0.0034	0.0000	0.0139	0.0004	0.0132	0.9723	0.9723
103789	88589	0.1102	0.0081	0.5344	0.0262	0.5071	0.9993	0.9994

Name1	Name2	S01	M01	T03	S03	M03	C1X	C2X
103789	74414	0.0055	0.0001	0.0184	0.0011	0.0170	0.9901	0.9901
103789	87894	0.1052	0.0064	12.6008	11.4231	1.1733	0.9984	0.9984
103789	100937	0.0026	0.0000	0.0092	0.0002	0.0087	0.9600	0.9600
103789	100652	0.0024	0.0000	0.0098	0.0008	0.0086	0.9417	0.9417
103789	74812	0.0083	0.0002	0.1827	0.0834	0.0984	0.9910	0.9910
103789	55634	0.0049	0.0000	0.0092	0.0001	0.0088	0.9935	0.9935
103789	100610	0.0042	0.0000	0.0096	0.0001	0.0092	0.9635	0.9635
103789	62617	0.0134	0.0002	0.2472	0.0751	0.1714	0.9909	0.9909
103789	56150	0.0031	0.0001	0.0079	0.0002	0.0074	0.9857	0.9857
103789	104099	0.0162	0.0009	0.0785	0.0086	0.0690	0.9950	0.9950
103789	90603	0.0054	0.0000	0.0260	0.0009	0.0247	0.9820	0.9820
103789	106996	0.0087	0.0001	0.2183	0.0941	0.1227	0.9924	0.9924
103789	107220	0.0180	0.0004	0.5013	0.2506	0.2501	0.9949	0.9949
103789	107623	0.0021	0.0000	0.0105	0.0006	0.0096	0.9330	0.9330
103789	75001	0.0157	0.0005	0.1506	0.0160	0.1318	0.9974	0.9974
103789	88336	0.0081	0.0003	0.0574	0.0146	0.0424	0.9973	0.9973
103789	37353	0.0097	0.0004	0.0399	0.0013	0.0382	0.9958	0.9958
103789	105654	0.0122	0.0003	0.0592	0.0038	0.0551	0.9959	0.9959
90389	104370	0.0176	0.0001	0.2255	0.0107	0.2133	0.9645	0.9645
90389	100530	0.0041	0.0003	0.0109	0.0026	0.0079	0.9981	0.9981
90389	55705	0.0023	0.0001	0.0092	0.0005	0.0084	0.9907	0.9907
90389	101685	0.0038	0.0000	0.0137	0.0006	0.0126	0.9817	0.9817
90389	48010	0.0064	0.0002	0.0281	0.0026	0.0251	0.9968	0.9968
90389	107009	0.0034	0.0002	0.0110	0.0011	0.0093	0.9950	0.9950
90389	107429	0.0035	0.0000	0.0204	0.0029	0.0163	0.9657	0.9657
90389	38064	0.0042	0.0001	0.0179	0.0030	0.0142	0.9953	0.9953
90389	99789	0.0019	0.0001	0.0084	0.0016	0.0062	0.9890	0.9890
90389	88589	0.0091	0.0004	0.0729	0.0124	0.0540	0.9969	0.9969
90389	74414	0.0033	0.0002	0.0083	0.0009	0.0070	0.9925	0.9925
90389	87894	0.0109	0.0001	0.0789	0.0113	0.0660	0.9956	0.9956
90389	100937	0.0037	0.0003	0.0179	0.0081	0.0086	0.9978	0.9978
90389	100652	0.0021	0.0000	0.0069	0.0002	0.0064	0.9914	0.9914
90389	74812	0.0051	0.0001	0.0268	0.0019	0.0244	0.9936	0.9936
90389	55634	0.0020	0.0000	0.0044	0.0002	0.0040	0.9225	0.9225
90389	100610	0.0038	0.0003	0.0359	0.0181	0.0093	0.9984	0.9984
90389	62617	0.0030	0.0000	0.0148	0.0011	0.0133	0.9713	0.9713
90389	56150	0.0020	0.0002	0.0103	0.0039	0.0060	0.9962	0.9962
90389	104099	0.0050	0.0003	0.0220	0.0061	0.0138	0.9977	0.9977
90389	90603	0.0051	0.0001	0.0209	0.0009	0.0197	0.9780	0.9780
90389	106996	0.0087	0.0006	0.0491	0.0051	0.0392	0.9975	0.9976
90389	107220	0.0020	0.0000	0.0077	0.0007	0.0067	0.9060	0.9060
90389	107623	0.0023	0.0002	0.0109	0.0032	0.0054	0.9972	0.9972
90389	75001	0.0031	0.0001	0.0120	0.0010	0.0107	0.9737	0.9737
90389	88336	0.0037	0.0001	0.0151	0.0007	0.0141	0.9961	0.9961
90389	37353	0.0018	0.0001	0.0077	0.0004	0.0069	0.9830	0.9830
90389	105654	0.0043	0.0003	0.0197	0.0077	0.0109	0.9964	0.9964
104370	100530	0.0029	0.0001	0.0122	0.0004	0.0115	0.9877	0.9877
104370	55705	0.0057	0.0002	0.0475	0.0130	0.0338	0.9926	0.9926
104370	101685	0.0149	0.0003	0.1061	0.0165	0.0880	0.9963	0.9963
104370	48010	0.0232	0.0015	0.2025	0.0376	0.1644	0.9968	0.9968
104370	107009	0.0075	0.0001	0.0424	0.0027	0.0386	0.9777	0.9777
104370	107429	0.0106	0.0003	0.1928	0.0717	0.1195	0.9921	0.9921
104370	38064	0.0508	0.0020	4.8279	4.4567	0.3679	0.9988	0.9988
104370	99789	0.0025	0.0000	0.0091	0.0006	0.0082	0.9905	0.9905
104370	88589	0.0086	0.0000	0.0306	0.0016	0.0276	0.9749	0.9749
104370	74414	0.0032	0.0001	0.0142	0.0011	0.0129	0.9904	0.9904
104370	87894	0.0441	0.0009	1.4151	0.9586	0.4549	0.9969	0.9969
104370	100937	0.0028	0.0000	0.0090	0.0004	0.0083	0.9331	0.9331
104370	100652	0.0024	0.0000	0.0067	0.0001	0.0063	0.9823	0.9823
104370	74812	0.0159	0.0002	0.2467	0.0517	0.1943	0.9945	0.9945
104370	55634	0.0055	0.0000	0.0192	0.0017	0.0167	0.9881	0.9881
104370	100610	0.0027	0.0001	0.0167	0.0029	0.0123	0.9900	0.9900
104370	62617	0.0101	0.0004	0.0940	0.0068	0.0868	0.9910	0.9910
104370	56150	0.0018	0.0001	0.0062	0.0006	0.0054	0.9671	0.9671
104370	104099	0.0126	0.0003	0.1189	0.0289	0.0835	0.9942	0.9942
104370	90603	0.0095	0.0002	0.0729	0.0108	0.0616	0.9968	0.9968
104370	106996	0.0292	0.0025	3.1429	2.6500	0.4716	0.9981	0.9981

Name1	Name2	S01	M01	T03	S03	M03	C1X	C2X
104370	107220	0.0118	0.0001	0.2090	0.0576	0.1481	0.9934	0.9934
104370	107623	0.0024	0.0001	0.0203	0.0038	0.0135	0.9840	0.9840
104370	75001	0.0150	0.0014	0.1898	0.0833	0.0915	0.9981	0.9981
104370	88336	0.0083	0.0000	0.0262	0.0010	0.0249	0.9901	0.9901
104370	37353	0.0139	0.0005	0.1117	0.0188	0.0922	0.9950	0.9950
104370	105654	0.0072	0.0001	0.0455	0.0059	0.0393	0.9909	0.9909
100530	55705	0.0033	0.0001	0.0141	0.0017	0.0122	0.9957	0.9957
100530	101685	0.0024	0.0001	0.0073	0.0004	0.0066	0.9900	0.9900
100530	48010	0.0053	0.0004	0.0259	0.0075	0.0179	0.9982	0.9982
100530	107009	0.0022	0.0001	0.0066	0.0013	0.0049	0.9965	0.9965
100530	107429	0.0036	0.0003	0.0304	0.0148	0.0153	0.9962	0.9962
100530	38064	0.0022	0.0001	0.0111	0.0009	0.0079	0.9748	0.9748
100530	99789	0.0029	0.0002	0.0267	0.0151	0.0096	0.9959	0.9959
100530	88589	0.0011	0.0000	0.0025	0.0001	0.0019	1.0000	1.0000
100530	74414	0.0068	0.0010	0.0216	0.0058	0.0155	0.9991	0.9991
100530	87894	0.0019	0.0001	0.0053	0.0004	0.0044	0.9412	0.9412
100530	100937	0.0071	0.0024	0.0570	0.0230	0.0160	0.9993	0.9993
100530	100652	0.0026	0.0002	0.0118	0.0030	0.0082	0.9969	0.9969
100530	74812	0.0020	0.0001	0.0134	0.0054	0.0076	0.9925	0.9925
100530	55634	0.0015	0.0000	0.0039	0.0001	0.0035	0.9922	0.9922
100530	100610	0.0062	0.0008	0.1186	0.0876	0.0163	0.9991	0.9991
100530	62617	0.0019	0.0000	0.0098	0.0012	0.0084	0.9788	0.9788
100530	56150	0.0059	0.0011	0.0859	0.0679	0.0170	0.9991	0.9991
100530	104099	0.0060	0.0009	0.0315	0.0134	0.0163	0.9990	0.9990
100530	90603	0.0031	0.0003	0.0122	0.0032	0.0087	0.9980	0.9980
100530	106996	0.0022	0.0001	0.0095	0.0034	0.0058	0.9952	0.9952
100530	107220	0.0011	0.0000	0.0036	0.0002	0.0032	0.8910	0.8910
100530	107623	0.0036	0.0002	0.0400	0.0302	0.0079	0.9981	0.9981
100530	75001	0.0018	0.0000	0.0062	0.0002	0.0058	0.9908	0.9908
100530	88336	0.0019	0.0001	0.0065	0.0005	0.0057	0.9948	0.9948
100530	37353	0.0049	0.0004	0.0397	0.0204	0.0164	0.9984	0.9984
100530	105654	0.0050	0.0007	0.0190	0.0068	0.0120	0.9989	0.9989
55705	101685	0.0051	0.0001	0.0264	0.0028	0.0231	0.9935	0.9935
55705	48010	0.0059	0.0001	0.0553	0.0109	0.0439	0.9935	0.9935
55705	107009	0.0020	0.0001	0.0055	0.0003	0.0049	0.9924	0.9924
55705	107429	0.0022	0.0000	0.0101	0.0015	0.0083	0.9902	0.9902
55705	38064	0.0050	0.0001	0.0345	0.0049	0.0274	0.9847	0.9847
55705	99789	0.0032	0.0001	0.0282	0.0103	0.0174	0.9931	0.9931
55705	88589	0.0034	0.0000	0.0233	0.0026	0.0156	0.5600	0.5600
55705	74414	0.0031	0.0001	0.0257	0.0074	0.0172	0.9905	0.9905
55705	87894	0.0044	0.0001	0.0304	0.0034	0.0266	0.9802	0.9802
55705	100937	0.0053	0.0003	0.0185	0.0056	0.0126	0.9983	0.9983
55705	100652	0.0017	0.0000	0.0070	0.0006	0.0061	0.9385	0.9385
55705	74812	0.0020	0.0001	0.0088	0.0004	0.0082	0.9620	0.9620
55705	55634	0.0031	0.0001	0.0085	0.0003	0.0079	0.9721	0.9721
55705	100610	0.0065	0.0013	0.0751	0.0498	0.0217	0.9988	0.9988
55705	62617	0.0046	0.0001	0.0418	0.0096	0.0310	0.9824	0.9824
55705	56150	0.0028	0.0000	0.0153	0.0039	0.0093	0.9912	0.9912
55705	104099	0.0039	0.0001	0.0271	0.0041	0.0227	0.9915	0.9915
55705	90603	0.0031	0.0001	0.0151	0.0018	0.0130	0.9965	0.9965
55705	106996	0.0015	0.0000	0.0057	0.0004	0.0051	0.9901	0.9901
55705	107220	0.0029	0.0000	0.0157	0.0015	0.0138	0.9527	0.9527
55705	107623	0.0024	0.0001	0.0064	0.0010	0.0050	0.9961	0.9961
55705	75001	0.0035	0.0001	0.0164	0.0013	0.0148	0.9940	0.9940
55705	88336	0.0027	0.0000	0.0189	0.0050	0.0134	0.9890	0.9890
55705	37353	0.0045	0.0001	0.0257	0.0026	0.0228	0.9957	0.9957
55705	105654	0.0050	0.0005	0.0303	0.0084	0.0216	0.9980	0.9980
101685	48010	0.0092	0.0002	0.0494	0.0034	0.0457	0.9957	0.9957
101685	107009	0.0027	0.0000	0.0106	0.0005	0.0097	0.9715	0.9715
101685	107429	0.0022	0.0000	0.0102	0.0009	0.0090	0.9746	0.9746
101685	38064	0.0098	0.0002	0.0735	0.0131	0.0563	0.9949	0.9949
101685	99789	0.0033	0.0001	0.0136	0.0015	0.0117	0.9906	0.9906
101685	88589	0.0093	0.0001	0.0257	0.0015	0.0236	0.9755	0.9755
101685	74414	0.0034	0.0000	0.0110	0.0006	0.0101	0.9932	0.9932
101685	87894	0.0099	0.0001	0.0763	0.0118	0.0641	0.9924	0.9924
101685	100937	0.0026	0.0001	0.0087	0.0006	0.0079	0.9909	0.9909
101685	100652	0.0020	0.0000	0.0058	0.0002	0.0053	0.9945	0.9945

Name1	**Name2**	**S01**	**M01**	**T03**	**S03**	**M03**	**C1X**	**C2X**
101685	74812	0.0036	0.0000	0.0201	0.0022	0.0176	0.9652	0.9652
101685	55634	0.0057	0.0001	0.0169	0.0012	0.0152	0.9955	0.9955
101685	100610	0.0032	0.0001	0.0094	0.0007	0.0084	0.9970	0.9970
101685	62617	0.0070	0.0001	0.0449	0.0038	0.0407	0.9843	0.9843
101685	56150	0.0023	0.0001	0.0079	0.0012	0.0065	0.9960	0.9960
101685	104099	0.0063	0.0001	0.0256	0.0040	0.0213	0.9958	0.9958
101685	90603	0.0034	0.0001	0.0129	0.0017	0.0108	0.9952	0.9952
101685	106996	0.0031	0.0001	0.0170	0.0024	0.0143	0.9831	0.9831
101685	107220	0.0069	0.0001	0.0535	0.0093	0.0437	0.9884	0.9884
101685	107623	0.0014	0.0000	0.0038	0.0001	0.0034	0.9283	0.9283
101685	75001	0.0064	0.0001	0.0308	0.0022	0.0275	0.9865	0.9865
101685	88336	0.0029	0.0001	0.0098	0.0007	0.0088	0.9912	0.9912
101685	37353	0.0076	0.0005	0.0293	0.0057	0.0233	0.9977	0.9977
101685	105654	0.0048	0.0001	0.0162	0.0009	0.0150	0.9934	0.9934
48010	107009	0.0032	0.0001	0.0118	0.0006	0.0109	0.9935	0.9935
48010	107429	0.0035	0.0001	0.0351	0.0140	0.0208	0.9937	0.9937
48010	38064	0.0109	0.0003	0.1456	0.0594	0.0851	0.9915	0.9915
48010	99789	0.0034	0.0002	0.0199	0.0032	0.0154	0.9945	0.9945
48010	88589	0.0072	0.0004	0.0207	0.0003	0.0200	0.9944	0.9944
48010	74414	0.0056	0.0003	0.0268	0.0037	0.0228	0.9973	0.9973
48010	87894	0.0121	0.0006	0.2290	0.1276	0.0961	0.9961	0.9961
48010	100937	0.0034	0.0002	0.0238	0.0079	0.0151	0.9927	0.9927
48010	100652	0.0032	0.0001	0.0104	0.0008	0.0093	0.9899	0.9899
48010	74812	0.0037	0.0001	0.0432	0.0167	0.0254	0.9941	0.9941
48010	55634	0.0042	0.0000	0.0113	0.0002	0.0108	0.9912	0.9912
48010	100610	0.0046	0.0003	0.0353	0.0119	0.0231	0.9953	0.9953
48010	62617	0.0073	0.0001	0.0762	0.0127	0.0632	0.9878	0.9878
48010	56150	0.0033	0.0001	0.0262	0.0078	0.0181	0.9937	0.9937
48010	104099	0.0059	0.0003	0.0428	0.0060	0.0361	0.9964	0.9964
48010	90603	0.0084	0.0002	0.0542	0.0151	0.0382	0.9969	0.9969
48010	106996	0.0032	0.0001	0.0287	0.0053	0.0230	0.9903	0.9903
48010	107220	0.0058	0.0001	0.0646	0.0161	0.0481	0.9819	0.9819
48010	107623	0.0019	0.0001	0.0090	0.0015	0.0066	0.9940	0.9940
48010	75001	0.0077	0.0002	0.0571	0.0077	0.0491	0.9966	0.9966
48010	88336	0.0033	0.0000	0.0188	0.0008	0.0175	0.9834	0.9834
48010	37353	0.0122	0.0009	0.1367	0.0689	0.0663	0.9983	0.9983
48010	105654	0.0078	0.0006	0.0467	0.0109	0.0354	0.9986	0.9986
107009	107429	0.0042	0.0002	0.0182	0.0055	0.0123	0.9975	0.9975
107009	38064	0.0038	0.0001	0.0926	0.0434	0.0284	0.9969	0.9969
107009	99789	0.0020	0.0000	0.0052	0.0002	0.0048	0.9928	0.9928
107009	88589	0.0029	0.0000	0.0231	0.0027	0.0138	1.0000	1.0000
107009	74414	0.0026	0.0001	0.0065	0.0012	0.0045	0.9963	0.9963
107009	87894	0.0038	0.0000	0.0300	0.0069	0.0211	0.9815	0.9815
107009	100937	0.0021	0.0000	0.0083	0.0021	0.0058	0.9858	0.9858
107009	100652	0.0024	0.0001	0.0072	0.0011	0.0058	0.9930	0.9930
107009	74812	0.0028	0.0000	0.0127	0.0027	0.0096	0.9884	0.9884
107009	55634	0.0019	0.0000	0.0043	0.0001	0.0039	0.9418	0.9418
107009	100610	0.0022	0.0000	0.0063	0.0014	0.0045	0.9907	0.9907
107009	62617	0.0021	0.0000	0.0065	0.0001	0.0061	0.8329	0.8329
107009	56150	0.0018	0.0000	0.0059	0.0008	0.0048	0.9920	0.9920
107009	104099	0.0017	0.0000	0.0034	0.0000	0.0031	0.9807	0.9807
107009	90603	0.0028	0.0001	0.0088	0.0008	0.0077	0.9900	0.9900
107009	106996	0.0031	0.0000	0.0211	0.0060	0.0129	0.9877	0.9877
107009	107220	0.0029	0.0000	0.0162	0.0013	0.0144	0.9446	0.9446
107009	107623	0.0033	0.0003	0.0389	0.0186	0.0105	0.9965	0.9965
107009	75001	0.0020	0.0000	0.0079	0.0006	0.0066	0.8614	0.8614
107009	88336	0.0018	0.0000	0.0043	0.0002	0.0038	0.9809	0.9809
107009	37353	0.0019	0.0000	0.0048	0.0004	0.0042	0.9900	0.9900
107009	105654	0.0018	0.0000	0.0042	0.0003	0.0037	0.9872	0.9872
107429	38064	0.0023	0.0000	0.0116	0.0013	0.0100	0.9698	0.9698
107429	99789	0.0019	0.0000	0.0088	0.0019	0.0067	0.9893	0.9893
107429	88589	0.0021	0.0000	0.0089	0.0008	0.0066	1.0000	1.0000
107429	74414	0.0020	0.0001	0.0129	0.0049	0.0075	0.9926	0.9926
107429	87894	0.0034	0.0001	0.0213	0.0019	0.0191	0.9703	0.9703
107429	100937	0.0024	0.0001	0.0109	0.0031	0.0075	0.9931	0.9931
107429	100652	0.0027	0.0001	0.0134	0.0031	0.0095	0.9922	0.9922
107429	74812	0.0030	0.0001	0.0202	0.0047	0.0148	0.9905	0.9905

Name1	**Name2**	**S01**	**M01**	**T03**	**S03**	**M03**	**C1X**	**C2X**
107429	55634	0.0014	0.0000	0.0033	0.0001	0.0030	0.9000	0.9000
107429	100610	0.0022	0.0000	0.0116	0.0031	0.0081	0.9836	0.9836
107429	62617	0.0018	0.0000	0.0086	0.0010	0.0072	0.8868	0.8868
107429	56150	0.0029	0.0002	0.0617	0.0355	0.0140	0.9953	0.9953
107429	104099	0.0017	0.0000	0.0067	0.0009	0.0054	0.9848	0.9848
107429	90603	0.0031	0.0000	0.0155	0.0022	0.0130	0.9858	0.9858
107429	106996	0.0047	0.0001	0.0295	0.0072	0.0213	0.9942	0.9942
107429	107220	0.0018	0.0000	0.0065	0.0003	0.0059	0.9524	0.9524
107429	107623	0.0034	0.0002	0.0140	0.0034	0.0103	0.9973	0.9973
107429	75001	0.0018	0.0000	0.0102	0.0020	0.0074	0.9647	0.9647
107429	88336	0.0020	0.0001	0.0060	0.0003	0.0055	0.9936	0.9936
107429	37353	0.0020	0.0001	0.0105	0.0020	0.0081	0.9910	0.9910
107429	105654	0.0019	0.0001	0.0070	0.0010	0.0057	0.9921	0.9921
38064	99789	0.0028	0.0000	0.0092	0.0006	0.0083	0.9816	0.9816
38064	88589	0.0173	0.0017	0.0990	0.0138	0.0620	0.9968	0.9968
38064	74414	0.0035	0.0002	0.0173	0.0020	0.0118	0.9880	0.9880
38064	87894	0.0355	0.0019	8.6991	8.3321	0.3639	0.9984	0.9984
38064	100937	0.0021	0.0000	0.0062	0.0003	0.0049	0.9712	0.9712
38064	100652	0.0017	0.0000	0.0041	0.0001	0.0037	0.9074	0.9074
38064	74812	0.0031	0.0000	0.0214	0.0022	0.0188	0.9804	0.9804
38064	55634	0.0077	0.0004	0.0280	0.0030	0.0246	0.9974	0.9974
38064	100610	0.0021	0.0000	0.0050	0.0000	0.0047	0.9401	0.9401
38064	62617	0.0092	0.0002	0.1031	0.0187	0.0633	0.9944	0.9944
38064	56150	0.0017	0.0000	0.0042	0.0000	0.0039	0.8462	0.8462
38064	104099	0.0058	0.0005	0.0269	0.0024	0.0240	0.9750	0.9750
38064	90603	0.0034	0.0000	0.0166	0.0014	0.0143	0.9707	0.9707
38064	106996	0.0030	0.0001	0.0291	0.0072	0.0204	0.9812	0.9812
38064	107220	0.0221	0.0005	0.9529	0.7030	0.2454	0.9965	0.9965
38064	107623	0.0015	0.0000	0.0078	0.0004	0.0071	0.9630	0.9630
38064	75001	0.0101	0.0004	0.1213	0.0251	0.0728	0.9913	0.9913
38064	88336	0.0041	0.0002	0.0429	0.0116	0.0193	0.9985	0.9985
38064	37353	0.0077	0.0001	0.0350	0.0020	0.0326	0.9721	0.9721
38064	105654	0.0043	0.0001	0.0326	0.0051	0.0245	0.9838	0.9838
99789	88589	0.0017	0.0000	0.0054	0.0005	0.0047	0.0000	0.0000
99789	74414	0.0020	0.0000	0.0114	0.0018	0.0093	0.9860	0.9860
99789	87894	0.0019	0.0000	0.0067	0.0002	0.0063	0.9456	0.9456
99789	100937	0.0024	0.0001	0.0372	0.0228	0.0104	0.9872	0.9872
99789	100652	0.0014	0.0001	0.0046	0.0003	0.0041	0.9859	0.9859
99789	74812	0.0017	0.0000	0.0056	0.0004	0.0050	0.9876	0.9876
99789	55634	0.0017	0.0000	0.0048	0.0002	0.0043	0.9833	0.9833
99789	100610	0.0029	0.0001	0.0280	0.0140	0.0138	0.9922	0.9922
99789	62617	0.0026	0.0000	0.0156	0.0018	0.0135	0.9677	0.9677
99789	56150	0.0014	0.0000	0.0072	0.0015	0.0050	0.9826	0.9826
99789	104099	0.0024	0.0001	0.0148	0.0023	0.0121	0.9882	0.9882
99789	90603	0.0021	0.0000	0.0089	0.0012	0.0071	0.9845	0.9845
99789	106996	0.0012	0.0000	0.0037	0.0003	0.0031	0.9413	0.9413
99789	107220	0.0018	0.0000	0.0065	0.0005	0.0058	0.9567	0.9567
99789	107623	0.0015	0.0001	0.0069	0.0020	0.0042	0.9919	0.9919
99789	75001	0.0020	0.0001	0.0068	0.0002	0.0064	0.9849	0.9849
99789	88336	0.0015	0.0001	0.0087	0.0012	0.0074	0.9901	0.9901
99789	37353	0.0022	0.0000	0.0121	0.0014	0.0105	0.9875	0.9875
99789	105654	0.0020	0.0001	0.0126	0.0028	0.0094	0.9896	0.9896
88589	74414	0.0018	0.0000	0.0045	0.0003	0.0035	1.0000	1.0000
88589	87894	0.0566	0.0031	1.3210	0.6778	0.6422	0.9979	0.9979
88589	100937	0.0012	0.0000	0.0025	0.0000	0.0022	1.0000	1.0000
88589	100652	0.0014	0.0000	0.0022	0.0000	0.0020	1.0000	1.0000
88589	74812	0.0055	0.0000	0.0394	0.0052	0.0266	0.9863	0.9863
88589	55634	0.0025	0.0000	0.0085	0.0008	0.0070	0.9940	0.9940
88589	100610	0.0018	0.0000	0.0033	0.0001	0.0028	1.0000	1.0000
88589	62617	0.0045	0.0000	0.0430	0.0066	0.0351	0.9390	0.9390
88589	56150	0.0017	0.0000	0.0033	0.0001	0.0027	1.0000	1.0000
88589	104099	0.0041	0.0002	0.0194	0.0023	0.0134	0.9911	0.9911
88589	90603	0.0032	0.0001	0.0198	0.0019	0.0128	0.9927	0.9927
88589	106996	0.0028	0.0000	0.0066	0.0002	0.0057	0.6000	0.6000
88589	107220	0.0028	0.0000	0.0173	0.0004	0.0165	0.6316	0.6316
88589	107623	0.0010	0.0000	0.0050	0.0005	0.0035	1.0000	1.0000
88589	75001	0.0056	0.0000	0.0235	0.0012	0.0217	0.9182	0.9182

Name1	Name2	S01	M01	T03	S03	M03	C1X	C2X
88589	88336	0.0029	0.0002	0.0157	0.0023	0.0098	0.9970	0.9970
88589	37353	0.0029	0.0002	0.0115	0.0013	0.0076	0.9973	0.9973
88589	105654	0.0031	0.0000	0.0198	0.0025	0.0138	0.9788	0.9788
74414	87894	0.0032	0.0001	0.0085	0.0002	0.0080	0.9755	0.9755
74414	100937	0.0032	0.0002	0.0366	0.0192	0.0123	0.9971	0.9971
74414	100652	0.0029	0.0003	0.0120	0.0035	0.0079	0.9977	0.9977
74414	74812	0.0019	0.0001	0.0097	0.0016	0.0079	0.9943	0.9943
74414	55634	0.0017	0.0000	0.0035	0.0000	0.0032	0.9739	0.9739
74414	100610	0.0061	0.0012	0.0339	0.0199	0.0128	0.9986	0.9986
74414	62617	0.0024	0.0001	0.0122	0.0011	0.0109	0.9855	0.9855
74414	56150	0.0023	0.0001	0.0170	0.0055	0.0113	0.9917	0.9917
74414	104099	0.0045	0.0005	0.0210	0.0080	0.0126	0.9982	0.9982
74414	90603	0.0033	0.0003	0.0307	0.0159	0.0140	0.9970	0.9970
74414	106996	0.0016	0.0000	0.0079	0.0017	0.0060	0.9926	0.9926
74414	107220	0.0021	0.0000	0.0073	0.0002	0.0068	0.9367	0.9367
74414	107623	0.0024	0.0002	0.0125	0.0050	0.0060	0.9972	0.9972
74414	75001	0.0019	0.0000	0.0091	0.0005	0.0084	0.9831	0.9831
74414	88336	0.0016	0.0000	0.0082	0.0012	0.0063	0.9912	0.9912
74414	37353	0.0032	0.0002	0.0140	0.0013	0.0125	0.9950	0.9950
74414	105654	0.0048	0.0004	0.0159	0.0034	0.0122	0.9976	0.9976
87894	100937	0.0018	0.0000	0.0056	0.0001	0.0052	0.9077	0.9077
87894	100652	0.0019	0.0000	0.0070	0.0004	0.0063	0.8995	0.8995
87894	74812	0.0074	0.0001	0.0795	0.0139	0.0651	0.9805	0.9805
87894	55634	0.0037	0.0000	0.0091	0.0004	0.0083	0.9470	0.9470
87894	100610	0.0027	0.0002	0.0073	0.0004	0.0064	0.9482	0.9482
87894	62617	0.0092	0.0002	0.0866	0.0069	0.0794	0.9891	0.9891
87894	56150	0.0020	0.0001	0.0050	0.0001	0.0046	0.9791	0.9791
87894	104099	0.0054	0.0001	0.0322	0.0035	0.0282	0.9927	0.9927
87894	90603	0.0055	0.0002	0.0268	0.0022	0.0241	0.9927	0.9927
87894	106996	0.0075	0.0001	0.1073	0.0385	0.0681	0.9836	0.9836
87894	107220	0.0128	0.0001	0.2137	0.0713	0.1418	0.9901	0.9901
87894	107623	0.0021	0.0000	0.0116	0.0010	0.0103	0.9411	0.9411
87894	75001	0.0081	0.0001	0.0646	0.0067	0.0574	0.9933	0.9933
87894	88336	0.0039	0.0001	0.0233	0.0021	0.0204	0.9785	0.9785
87894	37353	0.0044	0.0002	0.0256	0.0048	0.0203	0.9955	0.9955
87894	105654	0.0044	0.0001	0.0243	0.0008	0.0232	0.9836	0.9836
100937	100652	0.0018	0.0000	0.0077	0.0007	0.0068	0.9766	0.9766
100937	74812	0.0017	0.0000	0.0081	0.0010	0.0068	0.9915	0.9915
100937	55634	0.0015	0.0000	0.0035	0.0001	0.0032	0.9610	0.9610
100937	100610	0.0061	0.0010	0.0450	0.0264	0.0136	0.9990	0.9990
100937	62617	0.0020	0.0000	0.0081	0.0007	0.0071	0.9837	0.9837
100937	56150	0.0041	0.0004	0.0215	0.0117	0.0096	0.9989	0.9989
100937	104099	0.0026	0.0002	0.0122	0.0035	0.0081	0.9966	0.9966
100937	90603	0.0040	0.0005	0.0210	0.0083	0.0124	0.9981	0.9981
100937	106996	0.0028	0.0001	0.0143	0.0038	0.0078	0.9974	0.9974
100937	107220	0.0017	0.0000	0.0043	0.0002	0.0037	0.9099	0.9099
100937	107623	0.0043	0.0010	0.0162	0.0064	0.0068	0.9992	0.9992
100937	75001	0.0014	0.0000	0.0038	0.0001	0.0035	0.9849	0.9849
100937	88336	0.0020	0.0001	0.0080	0.0005	0.0073	0.9927	0.9927
100937	37353	0.0030	0.0004	0.0104	0.0014	0.0083	0.9986	0.9986
100937	105654	0.0037	0.0002	0.0140	0.0034	0.0103	0.9981	0.9981
100652	74812	0.0020	0.0001	0.0099	0.0022	0.0069	0.9865	0.9865
100652	55634	0.0013	0.0000	0.0030	0.0001	0.0026	0.9277	0.9277
100652	100610	0.0020	0.0000	0.0071	0.0010	0.0059	0.9923	0.9923
100652	62617	0.0015	0.0000	0.0047	0.0002	0.0043	0.8298	0.8298
100652	56150	0.0030	0.0002	0.0151	0.0055	0.0091	0.9971	0.9971
100652	104099	0.0012	0.0000	0.0032	0.0002	0.0028	0.9576	0.9576
100652	90603	0.0029	0.0002	0.0105	0.0015	0.0087	0.9972	0.9972
100652	106996	0.0022	0.0001	0.0090	0.0012	0.0076	0.9956	0.9956
100652	107220	0.0014	0.0000	0.0038	0.0001	0.0034	0.8462	0.8462
100652	107623	0.0018	0.0002	0.0072	0.0014	0.0053	0.9965	0.9965
100652	75001	0.0013	0.0000	0.0028	0.0001	0.0025	0.9561	0.9561
100652	88336	0.0015	0.0001	0.0042	0.0001	0.0038	0.9891	0.9891
100652	37353	0.0017	0.0000	0.0046	0.0002	0.0042	0.9936	0.9936
100652	105654	0.0016	0.0000	0.0051	0.0005	0.0044	0.9602	0.9602
74812	55634	0.0019	0.0000	0.0049	0.0001	0.0045	0.8407	0.8407
74812	100610	0.0015	0.0000	0.0056	0.0009	0.0045	0.9831	0.9831

Name1	Name2	S01	M01	T03	S03	M03	C1X	C2X
74812	62617	0.0029	0.0000	0.0143	0.0010	0.0129	0.9489	0.9489
74812	56150	0.0015	0.0000	0.0068	0.0010	0.0056	0.9940	0.9940
74812	104099	0.0024	0.0001	0.0085	0.0007	0.0075	0.9951	0.9951
74812	90603	0.0032	0.0000	0.0142	0.0015	0.0125	0.9857	0.9857
74812	106996	0.0051	0.0001	0.0418	0.0105	0.0308	0.9860	0.9860
74812	107220	0.0028	0.0000	0.0138	0.0006	0.0129	0.8778	0.8778
74812	107623	0.0018	0.0001	0.0081	0.0014	0.0063	0.9941	0.9941
74812	75001	0.0027	0.0000	0.0134	0.0014	0.0116	0.9523	0.9523
74812	88336	0.0019	0.0000	0.0068	0.0001	0.0065	0.9691	0.9691
74812	37353	0.0018	0.0000	0.0080	0.0010	0.0067	0.9516	0.9516
74812	105654	0.0020	0.0000	0.0081	0.0010	0.0068	0.9816	0.9816
55634	100610	0.0014	0.0000	0.0028	0.0000	0.0025	0.9819	0.9819
55634	62617	0.0036	0.0000	0.0116	0.0002	0.0112	0.9704	0.9704
55634	56150	0.0010	0.0000	0.0020	0.0000	0.0018	0.9701	0.9701
55634	104099	0.0024	0.0000	0.0053	0.0003	0.0047	0.9671	0.9671
55634	90603	0.0018	0.0000	0.0042	0.0001	0.0039	0.9639	0.9639
55634	106996	0.0015	0.0000	0.0038	0.0002	0.0033	0.9049	0.9049
55634	107220	0.0034	0.0001	0.0143	0.0014	0.0119	0.9513	0.9513
55634	107623	0.0008	0.0000	0.0017	0.0000	0.0014	0.8733	0.8733
55634	75001	0.0030	0.0000	0.0096	0.0001	0.0092	0.9896	0.9896
55634	88336	0.0014	0.0000	0.0033	0.0001	0.0030	0.9825	0.9825
55634	37353	0.0035	0.0001	0.0105	0.0002	0.0100	0.9947	0.9947
55634	105654	0.0020	0.0000	0.0049	0.0001	0.0046	0.9568	0.9568
100610	62617	0.0025	0.0000	0.0123	0.0013	0.0108	0.9875	0.9875
100610	56150	0.0047	0.0005	0.0242	0.0116	0.0124	0.9987	0.9987
100610	104099	0.0058	0.0018	0.0293	0.0167	0.0123	0.9994	0.9994
100610	90603	0.0042	0.0002	0.0417	0.0246	0.0159	0.9975	0.9975
100610	106996	0.0022	0.0001	0.0056	0.0008	0.0046	0.9965	0.9965
100610	107220	0.0013	0.0000	0.0062	0.0006	0.0048	0.7936	0.7936
100610	107623	0.0033	0.0001	0.0450	0.0205	0.0110	0.9969	0.9969
100610	75001	0.0016	0.0000	0.0062	0.0002	0.0058	0.9833	0.9833
100610	88336	0.0021	0.0000	0.0099	0.0009	0.0087	0.9925	0.9925
100610	37353	0.0032	0.0001	0.0400	0.0220	0.0170	0.9932	0.9932
100610	105654	0.0050	0.0001	0.0293	0.0168	0.0114	0.9961	0.9961
62617	56150	0.0015	0.0000	0.0069	0.0007	0.0060	0.9791	0.9791
62617	104099	0.0045	0.0001	0.0379	0.0090	0.0280	0.9943	0.9943
62617	90603	0.0033	0.0000	0.0154	0.0004	0.0147	0.9891	0.9891
62617	106996	0.0022	0.0000	0.0132	0.0011	0.0118	0.9458	0.9458
62617	107220	0.0053	0.0001	0.0416	0.0063	0.0350	0.9841	0.9841
62617	107623	0.0010	0.0000	0.0027	0.0000	0.0025	0.8182	0.8182
62617	75001	0.0054	0.0001	0.0342	0.0016	0.0322	0.9844	0.9844
62617	88336	0.0024	0.0001	0.0114	0.0006	0.0106	0.9844	0.9844
62617	37353	0.0061	0.0002	0.0407	0.0040	0.0364	0.9969	0.9969
62617	105654	0.0032	0.0000	0.0198	0.0013	0.0182	0.9763	0.9763
56150	104099	0.0015	0.0001	0.0053	0.0006	0.0045	0.9946	0.9946
56150	90603	0.0043	0.0002	0.0684	0.0456	0.0164	0.9977	0.9977
56150	106996	0.0029	0.0002	0.0163	0.0062	0.0082	0.9976	0.9976
56150	107220	0.0011	0.0000	0.0032	0.0001	0.0029	0.8793	0.8793
56150	107623	0.0043	0.0004	0.0362	0.0169	0.0122	0.9983	0.9983
56150	75001	0.0015	0.0000	0.0048	0.0003	0.0043	0.9902	0.9902
56150	88336	0.0018	0.0001	0.0048	0.0006	0.0040	0.9951	0.9951
56150	37353	0.0032	0.0002	0.0163	0.0076	0.0084	0.9982	0.9982
56150	105654	0.0022	0.0002	0.0073	0.0008	0.0063	0.9963	0.9963
104099	90603	0.0026	0.0001	0.0100	0.0009	0.0087	0.9963	0.9963
104099	106996	0.0016	0.0000	0.0084	0.0007	0.0075	0.9779	0.9779
104099	107220	0.0033	0.0001	0.0211	0.0027	0.0181	0.9357	0.9357
104099	107623	0.0015	0.0002	0.0035	0.0005	0.0027	0.9973	0.9973
104099	75001	0.0030	0.0000	0.0162	0.0002	0.0158	0.9906	0.9906
104099	88336	0.0016	0.0001	0.0048	0.0001	0.0044	0.9904	0.9904
104099	37353	0.0059	0.0003	0.0460	0.0201	0.0256	0.9968	0.9968
104099	105654	0.0048	0.0004	0.0254	0.0092	0.0154	0.9982	0.9982
90603	106996	0.0039	0.0001	0.0242	0.0052	0.0181	0.9936	0.9936
90603	107220	0.0022	0.0000	0.0082	0.0004	0.0073	0.9120	0.9120
90603	107623	0.0030	0.0002	0.0093	0.0023	0.0063	0.9977	0.9977
90603	75001	0.0028	0.0000	0.0133	0.0012	0.0119	0.9863	0.9863
90603	88336	0.0023	0.0000	0.0098	0.0011	0.0082	0.9641	0.9641
90603	37353	0.0076	0.0007	0.0253	0.0057	0.0192	0.9989	0.9989

Name1	**Name2**	**S01**	**M01**	**T03**	**S03**	**M03**	**C1X**	**C2X**
90603	105654	0.0026	0.0001	0.0101	0.0012	0.0085	0.9880	0.9880
106996	107220	0.0020	0.0000	0.0090	0.0006	0.0081	0.9612	0.9612
106996	107623	0.0028	0.0003	0.0227	0.0089	0.0089	0.9975	0.9975
106996	75001	0.0019	0.0000	0.0085	0.0007	0.0076	0.9271	0.9271
106996	88336	0.0026	0.0001	0.0104	0.0019	0.0082	0.9937	0.9937
106996	37353	0.0014	0.0000	0.0040	0.0001	0.0038	0.9782	0.9782
106996	105654	0.0015	0.0000	0.0056	0.0005	0.0048	0.9623	0.9623
107220	107623	0.0021	0.0000	0.0084	0.0004	0.0076	0.9775	0.9775
107220	75001	0.0052	0.0001	0.0504	0.0109	0.0358	0.9803	0.9803
107220	88336	0.0018	0.0000	0.0078	0.0004	0.0072	0.9615	0.9615
107220	37353	0.0030	0.0000	0.0184	0.0015	0.0167	0.9237	0.9237
107220	105654	0.0030	0.0000	0.0189	0.0016	0.0170	0.9312	0.9312
107623	75001	0.0011	0.0000	0.0028	0.0001	0.0025	0.9814	0.9814
107623	88336	0.0014	0.0000	0.0058	0.0010	0.0039	0.9900	0.9900
107623	37353	0.0014	0.0001	0.0028	0.0003	0.0023	0.9945	0.9945
107623	105654	0.0016	0.0000	0.0040	0.0008	0.0030	0.9959	0.9959
75001	88336	0.0018	0.0000	0.0075	0.0005	0.0067	0.9782	0.9782
75001	37353	0.0037	0.0001	0.0222	0.0027	0.0191	0.9852	0.9852
75001	105654	0.0025	0.0001	0.0120	0.0008	0.0109	0.9866	0.9866
88336	37353	0.0017	0.0000	0.0065	0.0007	0.0056	0.9900	0.9900
88336	105654	0.0021	0.0001	0.0103	0.0004	0.0098	0.9943	0.9943
37353	105654	0.0033	0.0001	0.0237	0.0068	0.0162	0.9811	0.9811

Table B.6: Software profile data for the TUBULIN_AB dataset

Name1	**Name2**	**S01**	**M01**	**T03**	**S03**	**M03**	**C1X**	**C2X**
Tubulin A	Tubulin B	368.7650	33	n/a	n/a	n/a	0.9355	0.9784

B.3 Hardware vs. Software

This section contains the full results used in Section 4.4 for comparing the software-only and hardware-accelerated implementations of the new algorithm presented in Chapter 3. Each row in Tables B.8 and B.9 lists the output for one MMM coevolution problem.

Table B.7: Column Legend

Column Name	**Description**
Name1	First matrix unique filename prefix
Name2	Second matrix unique filename prefix
T	Total execution time
MC	Time spent finding maximum cliques
F	Total non-idle FPGA time
WU	Time for which at least one work unit was not idle
U	Fraction of work units not idle during any 16 clock cycle cycle window

Table B.8: Hardware output data for the BATCH50 data set

Name1	**Name2**	**T**	**MC**	**F**	**WU**	**U**
2506	106948	0.0864	0.0189	0.0088	0.0010	0.0770
2506	88748	0.5925	0.3086	0.1988	0.1039	0.0809
2506	106976	0.2447	0.1135	0.0615	0.0328	0.0937
2506	89932	0.0512	0.0163	0.0077	0.0006	0.0796
2506	107298	0.0404	0.0225	0.0094	0.0001	0.0745
2506	105282	0.1356	0.0626	0.0308	0.0015	0.0679
2506	90856	0.0635	0.0377	0.0195	0.0005	0.0756
2506	105323	0.0384	0.0098	0.0044	0.0007	0.0681
2506	107601	0.0408	0.0213	0.0114	0.0006	0.0860
2506	37889	0.0201	0.0052	0.0033	0.0004	0.0912
2506	74548	0.0964	0.0628	0.0307	0.0025	0.0746
2506	103997	0.0680	0.0407	0.0207	0.0007	0.0843
2506	88482	0.1466	0.0945	0.0478	0.0038	0.0654
2506	106838	0.0683	0.0342	0.0170	0.0009	0.0661
2506	103998	0.0275	0.0122	0.0058	0.0005	0.0863
2506	105677	0.0677	0.0383	0.0195	0.0008	0.0716
2506	81915	0.0493	0.0185	0.0091	0.0019	0.0821
2506	80191	0.0984	0.0621	0.0338	0.0057	0.1236
2506	100934	0.0700	0.0425	0.0228	0.0013	0.0807
2506	103789	0.0906	0.0590	0.0292	0.0005	0.0709
2506	90389	0.0912	0.0694	0.0383	0.0014	0.0830
2506	104370	0.0500	0.0247	0.0129	0.0001	0.0878
2506	100530	0.0588	0.0406	0.0209	0.0017	0.0879
2506	55705	0.0395	0.0161	0.0078	0.0006	0.0685
2506	101685	0.0548	0.0231	0.0103	0.0020	0.0790
2506	48010	0.0831	0.0535	0.0272	0.0012	0.0811
2506	107009	0.0498	0.0353	0.0188	0.0003	0.0777
2506	107429	0.0248	0.0082	0.0035	0.0003	0.0723
2506	38064	0.0885	0.0587	0.0301	0.0032	0.0734
2506	99789	0.0439	0.0289	0.0138	0.0007	0.0726
2506	88589	0.0479	0.0240	0.0127	0.0001	0.0737
2506	74414	0.0196	0.0046	0.0019	0.0002	0.0768
2506	87894	0.0607	0.0341	0.0170	0.0004	0.0745
2506	100937	0.0300	0.0136	0.0065	0.0006	0.0748
2506	100652	0.0248	0.0108	0.0055	0.0002	0.0825
2506	74812	0.0354	0.0199	0.0103	0.0002	0.0793
2506	55634	0.0779	0.0437	0.0261	0.0039	0.0924
2506	100610	0.0317	0.0157	0.0075	0.0005	0.0750
2506	62617	0.0406	0.0220	0.0109	0.0002	0.0697
2506	56150	0.0459	0.0299	0.0156	0.0012	0.0844
2506	104099	0.0309	0.0174	0.0092	0.0002	0.0822
2506	90603	0.0561	0.0334	0.0168	0.0015	0.0662
2506	106996	0.0463	0.0295	0.0149	0.0011	0.0846
2506	107220	0.0797	0.0626	0.0325	0.0004	0.0758
2506	107623	0.0167	0.0054	0.0021	0.0002	0.0901
2506	75001	0.0367	0.0197	0.0102	0.0002	0.0702
2506	88336	0.0472	0.0298	0.0144	0.0007	0.0737
2506	37353	0.0427	0.0233	0.0119	0.0006	0.0679
2506	105654	0.0550	0.0367	0.0178	0.0013	0.0947
106948	88748	0.2734	0.0820	0.0340	0.0053	0.0906
106948	106976	0.0406	0.0287	0.0148	0.0001	0.0811
106948	89932	0.0617	0.0199	0.0098	0.0007	0.0733
106948	107298	0.0426	0.0148	0.0073	0.0002	0.0896
106948	105282	0.1541	0.0561	0.0221	0.0038	0.0929
106948	90856	0.0351	0.0114	0.0057	0.0004	0.0862
106948	105323	0.0281	0.0133	0.0061	0.0004	0.0665
106948	107601	0.0463	0.0159	0.0086	0.0010	0.0949
106948	37889	0.0328	0.0234	0.0124	0.0005	0.0679
106948	74548	0.0500	0.0305	0.0138	0.0008	0.0804
106948	103997	0.0628	0.0339	0.0208	0.0044	0.0721
106948	88482	0.1159	0.0655	0.0309	0.0021	0.0793
106948	106838	0.0394	0.0198	0.0102	0.0004	0.0834
106948	103998	0.0297	0.0193	0.0095	0.0015	0.0750
106948	105677	0.0835	0.0641	0.0330	0.0003	0.0823

Name1	**Name2**	**T**	**MC**	**F**	**WU**	**U**
106948	81915	0.0386	0.0191	0.0102	0.0022	0.0825
106948	80191	0.0488	0.0280	0.0140	0.0022	0.0723
106948	100934	0.0281	0.0151	0.0075	0.0002	0.0644
106948	103789	0.0755	0.0261	0.0115	0.0005	0.0802
106948	90389	0.0735	0.0470	0.0246	0.0012	0.0663
106948	104370	0.1612	0.1128	0.0542	0.0010	0.0801
106948	100530	0.0283	0.0179	0.0090	0.0008	0.0728
106948	55705	0.0260	0.0140	0.0069	0.0005	0.0674
106948	101685	0.0485	0.0296	0.0137	0.0001	0.0884
106948	48010	0.0374	0.0209	0.0098	0.0002	0.0825
106948	107009	0.0448	0.0252	0.0120	0.0013	0.0822
106948	107429	0.0266	0.0087	0.0041	0.0014	0.0807
106948	38064	0.0528	0.0272	0.0123	0.0003	0.0834
106948	99789	0.0327	0.0206	0.0104	0.0012	0.0914
106948	88589	0.0916	0.0731	0.0425	0.0006	0.0747
106948	74414	0.0247	0.0149	0.0075	0.0002	0.0725
106948	87894	0.1251	0.0896	0.0440	0.0009	0.0782
106948	100937	0.0234	0.0098	0.0059	0.0018	0.0844
106948	100652	0.0376	0.0262	0.0143	0.0011	0.0659
106948	74812	0.0305	0.0118	0.0055	0.0005	0.0783
106948	55634	0.0167	0.0065	0.0035	0.0000	0.1016
106948	100610	0.0321	0.0220	0.0113	0.0006	0.0649
106948	62617	0.0895	0.0742	0.0393	0.0002	0.0763
106948	56150	0.0294	0.0181	0.0089	0.0013	0.0771
106948	104099	0.0272	0.0150	0.0081	0.0002	0.0768
106948	90603	0.0541	0.0381	0.0202	0.0009	0.0675
106948	106996	0.0408	0.0171	0.0094	0.0014	0.0929
106948	107220	0.0514	0.0243	0.0107	0.0002	0.0814
106948	107623	0.0510	0.0307	0.0167	0.0054	0.0719
106948	75001	0.0574	0.0423	0.0208	0.0002	0.0819
106948	88336	0.0274	0.0171	0.0089	0.0001	0.0809
106948	37353	0.0665	0.0567	0.0294	0.0003	0.0718
106948	105654	0.0425	0.0311	0.0162	0.0003	0.0704
88748	106976	0.4089	0.1722	0.1154	0.0670	0.0852
88748	89932	0.1605	0.0329	0.0118	0.0035	0.0784
88748	107298	0.1619	0.1226	0.0777	0.0153	0.0680
88748	105282	1.1406	0.0845	0.0335	0.0108	0.0880
88748	90856	0.4477	0.1712	0.1385	0.1243	0.1580
88748	105323	0.1313	0.0944	0.0490	0.0035	0.0727
88748	107601	0.0282	0.0057	0.0029	0.0000	0.0764
88748	37889	0.0068	0.0000	0.0000	0.0000	0.0000
88748	74548	0.0512	0.0168	0.0085	0.0007	0.0687
88748	103997	0.1225	0.0363	0.0184	0.0025	0.0859
88748	88482	4.9748	0.6272	0.5917	0.5123	0.1392
88748	106838	0.1577	0.0514	0.0271	0.0040	0.0863
88748	103998	0.0064	0.0000	0.0000	0.0000	0.0000
88748	105677	0.1749	0.1110	0.0560	0.0096	0.0771
88748	81915	0.0413	0.0230	0.0117	0.0002	0.0707
88748	80191	0.2155	0.1736	0.1065	0.0047	0.0785
88748	100934	0.2140	0.1787	0.1122	0.0044	0.0888
88748	103789	0.7606	0.0751	0.0395	0.0154	0.0929
88748	90389	0.4453	0.1842	0.1658	0.1243	0.0867
88748	104370	0.8421	0.1904	0.1264	0.0975	0.1120
88748	100530	0.0312	0.0236	0.0123	0.0002	0.0706
88748	55705	0.0255	0.0099	0.0047	0.0000	0.0700
88748	101685	0.1574	0.0874	0.0432	0.0119	0.0872
88748	48010	0.0966	0.0450	0.0209	0.0019	0.0900
88748	107009	0.0904	0.0678	0.0369	0.0010	0.0842
88748	107429	0.0606	0.0450	0.0214	0.0002	0.0678
88748	38064	1.2273	0.6183	0.5513	0.4838	0.1679
88748	99789	0.0401	0.0256	0.0138	0.0002	0.0759
88748	88589	0.7032	0.2068	0.1673	0.0849	0.1335
88748	74414	0.0474	0.0254	0.0140	0.0002	0.0670
88748	87894	3.0250	1.5520	1.4347	1.3254	0.3875
88748	100937	0.0553	0.0412	0.0225	0.0001	0.0815
88748	100652	0.0199	0.0082	0.0043	0.0000	0.0860
88748	74812	0.0567	0.0193	0.0096	0.0001	0.0818

Name1	**Name2**	**T**	**MC**	**F**	**WU**	**U**
88748	55634	0.1633	0.1212	0.0580	0.0036	0.0707
88748	100610	0.0460	0.0331	0.0169	0.0000	0.0802
88748	62617	0.1129	0.0644	0.0338	0.0016	0.0776
88748	56150	0.0204	0.0111	0.0060	0.0000	0.0754
88748	104099	0.1405	0.0999	0.0605	0.0028	0.0751
88748	90603	0.0710	0.0490	0.0269	0.0004	0.0739
88748	106996	0.1172	0.0749	0.0358	0.0017	0.0750
88748	107220	0.3951	0.1148	0.0623	0.0374	0.1294
88748	107623	0.0735	0.0620	0.0351	0.0004	0.0776
88748	75001	0.2190	0.1529	0.0991	0.0122	0.0882
88748	88336	0.0311	0.0068	0.0040	0.0004	0.0831
88748	37353	0.0266	0.0109	0.0053	0.0001	0.0749
88748	105654	0.0312	0.0119	0.0065	0.0001	0.0798
106976	89932	0.0634	0.0349	0.0158	0.0016	0.0827
106976	107298	0.0029	0.0000	0.0000	0.0000	0.0000
106976	105282	0.1477	0.0569	0.0274	0.0091	0.0859
106976	90856	0.0412	0.0146	0.0076	0.0030	0.1149
106976	105323	0.0585	0.0440	0.0211	0.0026	0.0666
106976	107601	0.0299	0.0249	0.0141	0.0000	0.0868
106976	37889	0.0045	0.0000	0.0000	0.0000	0.0000
106976	74548	0.1214	0.0629	0.0297	0.0161	0.1003
106976	103997	0.0097	0.0059	0.0032	0.0000	0.0880
106976	88482	0.4414	0.1599	0.1157	0.0667	0.0936
106976	106838	0.3689	0.2000	0.1393	0.0824	0.1064
106976	103998	0.0040	0.0000	0.0000	0.0000	0.0000
106976	105677	0.0974	0.0715	0.0308	0.0053	0.0739
106976	81915	0.1184	0.1074	0.0593	0.0004	0.0815
106976	80191	0.0603	0.0530	0.0298	0.0002	0.0862
106976	100934	0.0402	0.0330	0.0178	0.0001	0.0722
106976	103789	0.1186	0.0601	0.0273	0.0060	0.0820
106976	90389	0.0641	0.0425	0.0207	0.0013	0.0737
106976	104370	0.0954	0.0265	0.0142	0.0072	0.1256
106976	100530	0.0181	0.0134	0.0073	0.0000	0.0722
106976	55705	0.0285	0.0188	0.0090	0.0002	0.0671
106976	101685	0.0818	0.0677	0.0354	0.0010	0.0711
106976	48010	0.0394	0.0234	0.0116	0.0003	0.0694
106976	107009	0.0215	0.0161	0.0088	0.0000	0.0809
106976	107429	0.0220	0.0169	0.0087	0.0001	0.0886
106976	38064	0.4807	0.2291	0.1772	0.1518	0.2327
106976	99789	0.0118	0.0068	0.0036	0.0000	0.0625
106976	88589	0.0868	0.0575	0.0312	0.0006	0.0870
106976	74414	0.0410	0.0354	0.0199	0.0002	0.0694
106976	87894	0.0503	0.0260	0.0117	0.0011	0.0714
106976	100937	0.0124	0.0081	0.0045	0.0000	0.0743
106976	100652	0.0145	0.0099	0.0053	0.0000	0.0841
106976	74812	0.0278	0.0203	0.0109	0.0001	0.0890
106976	55634	0.0803	0.0627	0.0343	0.0018	0.0738
106976	100610	0.0042	0.0000	0.0000	0.0000	0.0000
106976	62617	0.0591	0.0403	0.0230	0.0021	0.0704
106976	56150	0.0039	0.0000	0.0000	0.0000	0.0000
106976	104099	0.0529	0.0469	0.0268	0.0004	0.0869
106976	90603	0.0713	0.0632	0.0343	0.0001	0.0814
106976	106996	0.0121	0.0052	0.0027	0.0000	0.0850
106976	107220	0.0075	0.0036	0.0019	0.0000	0.0861
106976	107623	0.0066	0.0039	0.0022	0.0000	0.0805
106976	75001	0.0437	0.0250	0.0132	0.0005	0.0870
106976	88336	0.0235	0.0130	0.0071	0.0006	0.0669
106976	37353	0.0922	0.0836	0.0488	0.0002	0.0863
106976	105654	0.0205	0.0138	0.0073	0.0001	0.0845
89932	107298	0.0489	0.0418	0.0243	0.0001	0.0920
89932	105282	0.2187	0.1227	0.0689	0.0356	0.2224
89932	90856	0.0431	0.0305	0.0166	0.0007	0.0896
89932	105323	0.0159	0.0055	0.0027	0.0001	0.0712
89932	107601	0.0321	0.0168	0.0088	0.0008	0.0976
89932	37889	0.0371	0.0308	0.0173	0.0001	0.0791
89932	74548	0.0289	0.0150	0.0070	0.0001	0.0699
89932	103997	0.0303	0.0245	0.0136	0.0002	0.0805

Name1	**Name2**	**T**	**MC**	**F**	**WU**	**U**
89932	88482	0.0950	0.0360	0.0207	0.0014	0.1952
89932	106838	0.0444	0.0317	0.0169	0.0004	0.0726
89932	103998	0.0240	0.0168	0.0087	0.0002	0.0790
89932	105677	0.0724	0.0581	0.0316	0.0004	0.0732
89932	81915	0.0627	0.0505	0.0275	0.0008	0.0713
89932	80191	0.0417	0.0241	0.0134	0.0044	0.1739
89932	100934	0.0255	0.0138	0.0070	0.0004	0.0941
89932	103789	0.0987	0.0456	0.0173	0.0036	0.0882
89932	90389	0.0692	0.0285	0.0159	0.0033	0.0717
89932	104370	1.6750	1.0167	0.9162	0.8916	0.3431
89932	100530	0.0406	0.0302	0.0150	0.0008	0.0783
89932	55705	0.0332	0.0215	0.0112	0.0012	0.0662
89932	101685	0.0417	0.0294	0.0154	0.0002	0.0678
89932	48010	0.0453	0.0296	0.0130	0.0008	0.0712
89932	107009	0.0295	0.0205	0.0114	0.0000	0.0769
89932	107429	0.0268	0.0159	0.0077	0.0001	0.0765
89932	38064	0.0491	0.0336	0.0172	0.0006	0.0757
89932	99789	0.0274	0.0200	0.0108	0.0001	0.0799
89932	88589	0.0728	0.0516	0.0342	0.0010	0.0840
89932	74414	0.0210	0.0134	0.0064	0.0007	0.0772
89932	87894	0.0905	0.0600	0.0310	0.0021	0.0744
89932	100937	0.0303	0.0206	0.0112	0.0007	0.0909
89932	100652	0.0318	0.0253	0.0137	0.0002	0.0708
89932	74812	0.0249	0.0073	0.0032	0.0005	0.0734
89932	55634	0.0228	0.0166	0.0095	0.0000	0.0818
89932	100610	0.0312	0.0216	0.0107	0.0006	0.0770
89932	62617	0.0239	0.0137	0.0067	0.0001	0.0727
89932	56150	0.0246	0.0187	0.0105	0.0002	0.0715
89932	104099	0.0251	0.0117	0.0056	0.0016	0.0967
89932	90603	0.0301	0.0178	0.0096	0.0003	0.0693
89932	106996	0.0598	0.0403	0.0191	0.0005	0.0838
89932	107220	0.0462	0.0376	0.0199	0.0002	0.0779
89932	107623	0.0203	0.0143	0.0082	0.0001	0.0925
89932	75001	0.0255	0.0169	0.0089	0.0002	0.0795
89932	88336	0.0433	0.0320	0.0174	0.0002	0.0753
89932	37353	0.0463	0.0376	0.0194	0.0005	0.0703
89932	105654	0.0396	0.0278	0.0140	0.0016	0.0859
107298	105282	0.0615	0.0474	0.0247	0.0002	0.0642
107298	90856	0.0636	0.0548	0.0310	0.0010	0.0705
107298	105323	0.0243	0.0122	0.0068	0.0000	0.0970
107298	107601	0.1009	0.0915	0.0529	0.0005	0.0796
107298	37889	0.0047	0.0000	0.0000	0.0000	0.0000
107298	74548	0.1002	0.0839	0.0463	0.0006	0.0770
107298	103997	0.0292	0.0254	0.0145	0.0000	0.0693
107298	88482	0.0025	0.0000	0.0000	0.0000	0.0000
107298	106838	0.2291	0.1935	0.1227	0.0081	0.0690
107298	103998	0.0047	0.0000	0.0000	0.0000	0.0000
107298	105677	0.0767	0.0622	0.0335	0.0002	0.0777
107298	81915	0.0276	0.0185	0.0082	0.0001	0.0767
107298	80191	0.0403	0.0346	0.0196	0.0001	0.0813
107298	100934	0.1263	0.1158	0.0666	0.0004	0.0929
107298	103789	0.1830	0.1146	0.0547	0.0020	0.0734
107298	90389	0.0372	0.0326	0.0186	0.0001	0.0653
107298	104370	0.0574	0.0523	0.0295	0.0004	0.0632
107298	100530	0.0180	0.0128	0.0070	0.0000	0.0621
107298	55705	0.1412	0.1294	0.0740	0.0004	0.1009
107298	101685	0.0555	0.0333	0.0163	0.0003	0.0768
107298	48010	0.1368	0.1184	0.0645	0.0007	0.0804
107298	107009	0.0281	0.0191	0.0089	0.0002	0.0722
107298	107429	0.0596	0.0537	0.0307	0.0001	0.0800
107298	38064	0.0686	0.0569	0.0312	0.0011	0.0662
107298	99789	0.0353	0.0242	0.0132	0.0001	0.0730
107298	88589	0.3404	0.1419	0.0862	0.0439	0.0959
107298	74414	0.0828	0.0767	0.0442	0.0002	0.0926
107298	87894	0.0872	0.0812	0.0461	0.0001	0.0800
107298	100937	0.0326	0.0276	0.0156	0.0000	0.0896
107298	100652	0.0368	0.0319	0.0183	0.0000	0.0655

Name1	**Name2**	**T**	**MC**	**F**	**WU**	**U**
107298	74812	0.0051	0.0015	0.0008	0.0000	0.0551
107298	55634	0.0588	0.0512	0.0287	0.0001	0.0858
107298	100610	0.1078	0.1013	0.0579	0.0002	0.1035
107298	62617	0.1303	0.1196	0.0681	0.0005	0.1012
107298	56150	0.0048	0.0000	0.0000	0.0000	0.0000
107298	104099	0.1360	0.1239	0.0708	0.0008	0.1004
107298	90603	0.0206	0.0153	0.0086	0.0000	0.0968
107298	106996	0.0073	0.0050	0.0029	0.0000	0.0921
107298	107220	0.0904	0.0701	0.0379	0.0003	0.0748
107298	107623	0.0326	0.0291	0.0166	0.0000	0.0622
107298	75001	0.1050	0.0893	0.0480	0.0005	0.0808
107298	88336	0.0238	0.0204	0.0117	0.0000	0.0733
107298	37353	0.1335	0.1213	0.0690	0.0008	0.1013
107298	105654	0.1582	0.1455	0.0836	0.0011	0.0968
105282	90856	0.1101	0.0246	0.0096	0.0046	0.0864
105282	105323	0.0310	0.0136	0.0072	0.0000	0.0957
105282	107601	0.0372	0.0233	0.0126	0.0000	0.0717
105282	37889	0.0056	0.0000	0.0000	0.0000	0.0000
105282	74548	0.0448	0.0132	0.0046	0.0010	0.0757
105282	103997	0.0556	0.0232	0.0113	0.0005	0.0837
105282	88482	0.9656	0.1126	0.0825	0.0678	0.1267
105282	106838	0.2056	0.0616	0.0382	0.0216	0.1510
105282	103998	0.0050	0.0000	0.0000	0.0000	0.0000
105282	105677	0.0576	0.0221	0.0111	0.0004	0.0696
105282	81915	0.0271	0.0101	0.0054	0.0002	0.0682
105282	80191	0.0484	0.0229	0.0120	0.0006	0.0679
105282	100934	0.0473	0.0307	0.0165	0.0006	0.0670
105282	103789	1.8735	0.7828	0.6761	0.6447	0.3806
105282	90389	0.1235	0.0869	0.0480	0.0031	0.0705
105282	104370	0.3576	0.1106	0.0814	0.0755	0.1592
105282	100530	0.0137	0.0074	0.0042	0.0000	0.0701
105282	55705	0.0899	0.0690	0.0369	0.0008	0.0704
105282	101685	0.0794	0.0210	0.0099	0.0018	0.0704
105282	48010	0.1542	0.0703	0.0333	0.0151	0.1356
105282	107009	0.0214	0.0095	0.0050	0.0003	0.0877
105282	107429	0.0329	0.0224	0.0110	0.0003	0.0780
105282	38064	0.1584	0.0294	0.0126	0.0082	0.0990
105282	99789	0.0191	0.0118	0.0067	0.0001	0.0768
105282	88589	0.5358	0.3319	0.2376	0.0490	0.0874
105282	74414	0.0416	0.0246	0.0128	0.0006	0.0646
105282	87894	0.4372	0.1453	0.0757	0.0435	0.1123
105282	100937	0.0284	0.0218	0.0119	0.0000	0.0774
105282	100652	0.0722	0.0640	0.0359	0.0003	0.0815
105282	74812	0.0340	0.0165	0.0073	0.0003	0.0862
105282	55634	0.0696	0.0558	0.0307	0.0004	0.0799
105282	100610	0.0596	0.0471	0.0259	0.0004	0.0664
105282	62617	0.0970	0.0644	0.0334	0.0011	0.0698
105282	56150	0.0209	0.0122	0.0065	0.0001	0.0710
105282	104099	0.0741	0.0370	0.0173	0.0019	0.0757
105282	90603	0.0267	0.0150	0.0082	0.0001	0.0789
105282	106996	0.0233	0.0077	0.0037	0.0001	0.0819
105282	107220	0.0859	0.0528	0.0241	0.0006	0.0735
105282	107623	0.0231	0.0165	0.0092	0.0000	0.0727
105282	75001	0.0658	0.0302	0.0144	0.0014	0.0648
105282	88336	0.0456	0.0291	0.0159	0.0007	0.0726
105282	37353	0.1058	0.0776	0.0415	0.0038	0.0791
105282	105654	0.0737	0.0446	0.0232	0.0015	0.0750
90856	105323	0.0394	0.0304	0.0163	0.0005	0.0694
90856	107601	0.0210	0.0130	0.0071	0.0005	0.0657
90856	37889	0.0172	0.0125	0.0071	0.0000	0.0771
90856	74548	0.0792	0.0344	0.0221	0.0113	0.0850
90856	103997	0.0316	0.0133	0.0071	0.0005	0.0783
90856	88482	0.1913	0.1082	0.0871	0.0447	0.1581
90856	106838	0.0773	0.0562	0.0295	0.0031	0.0852
90856	103998	0.0939	0.0712	0.0602	0.0041	0.1552
90856	105677	0.0355	0.0259	0.0134	0.0002	0.0845
90856	81915	0.0280	0.0154	0.0081	0.0015	0.0774

Name1	**Name2**	**T**	**MC**	**F**	**WU**	**U**
90856	80191	0.0891	0.0710	0.0468	0.0041	0.1156
90856	100934	0.0214	0.0107	0.0064	0.0003	0.0821
90856	103789	0.0784	0.0430	0.0223	0.0054	0.1106
90856	90389	0.0395	0.0317	0.0173	0.0010	0.0725
90856	104370	0.0363	0.0167	0.0088	0.0011	0.0896
90856	100530	0.1061	0.0851	0.0627	0.0119	0.1247
90856	55705	0.0125	0.0055	0.0029	0.0001	0.0910
90856	101685	0.0399	0.0288	0.0146	0.0004	0.0721
90856	48010	0.0565	0.0307	0.0192	0.0091	0.1233
90856	107009	0.0183	0.0098	0.0054	0.0002	0.0740
90856	107429	0.0200	0.0124	0.0061	0.0008	0.0725
90856	38064	0.1244	0.0786	0.0559	0.0233	0.1054
90856	99789	0.0240	0.0153	0.0088	0.0005	0.0920
90856	88589	0.0987	0.0787	0.0545	0.0032	0.0701
90856	74414	0.0271	0.0173	0.0093	0.0018	0.0717
90856	87894	0.0641	0.0415	0.0212	0.0020	0.1025
90856	100937	0.0378	0.0286	0.0168	0.0022	0.0815
90856	100652	0.0155	0.0103	0.0058	0.0001	0.0848
90856	74812	0.0337	0.0241	0.0136	0.0011	0.0818
90856	55634	0.0700	0.0633	0.0371	0.0002	0.0805
90856	100610	0.0396	0.0270	0.0150	0.0017	0.0904
90856	62617	0.0214	0.0117	0.0060	0.0003	0.1125
90856	56150	0.0216	0.0132	0.0068	0.0010	0.0797
90856	104099	0.0203	0.0115	0.0064	0.0006	0.0692
90856	90603	0.0364	0.0213	0.0115	0.0021	0.0753
90856	106996	0.0190	0.0133	0.0074	0.0002	0.0754
90856	107220	0.0332	0.0155	0.0072	0.0009	0.0808
90856	107623	0.0241	0.0168	0.0100	0.0011	0.0661
90856	75001	0.1652	0.1287	0.0948	0.0098	0.1278
90856	88336	0.0241	0.0169	0.0097	0.0005	0.1212
90856	37353	0.0600	0.0425	0.0224	0.0038	0.0931
90856	105654	0.0289	0.0207	0.0119	0.0006	0.1229
105323	107601	0.0319	0.0264	0.0149	0.0001	0.0675
105323	37889	0.0161	0.0116	0.0066	0.0000	0.0845
105323	74548	0.0426	0.0342	0.0193	0.0001	0.0862
105323	103997	0.0634	0.0529	0.0308	0.0010	0.0747
105323	88482	0.0266	0.0160	0.0084	0.0002	0.0775
105323	106838	0.0453	0.0367	0.0202	0.0002	0.0697
105323	103998	0.0297	0.0231	0.0138	0.0008	0.0950
105323	105677	0.0327	0.0232	0.0126	0.0001	0.0734
105323	81915	0.0218	0.0157	0.0086	0.0000	0.0690
105323	80191	0.0408	0.0348	0.0195	0.0002	0.0683
105323	100934	0.0239	0.0161	0.0084	0.0004	0.0742
105323	103789	0.0208	0.0111	0.0062	0.0001	0.0709
105323	90389	0.0119	0.0062	0.0033	0.0001	0.0641
105323	104370	0.0326	0.0239	0.0131	0.0001	0.0659
105323	100530	0.0232	0.0178	0.0099	0.0003	0.0702
105323	55705	0.0140	0.0072	0.0036	0.0001	0.0750
105323	101685	0.0317	0.0232	0.0115	0.0003	0.0674
105323	48010	0.0168	0.0103	0.0056	0.0000	0.0813
105323	107009	0.0300	0.0248	0.0142	0.0001	0.0786
105323	107429	0.0413	0.0363	0.0204	0.0001	0.0762
105323	38064	0.0370	0.0299	0.0172	0.0000	0.0790
105323	99789	0.0125	0.0069	0.0040	0.0000	0.0834
105323	88589	0.0581	0.0481	0.0277	0.0004	0.0733
105323	74414	0.0255	0.0207	0.0115	0.0001	0.0871
105323	87894	0.0139	0.0062	0.0035	0.0000	0.0724
105323	100937	0.0239	0.0188	0.0107	0.0002	0.0737
105323	100652	0.0118	0.0077	0.0043	0.0000	0.0854
105323	74812	0.0235	0.0177	0.0101	0.0001	0.0810
105323	55634	0.0443	0.0348	0.0190	0.0003	0.0680
105323	100610	0.0257	0.0204	0.0116	0.0001	0.0852
105323	62617	0.0434	0.0341	0.0180	0.0001	0.0694
105323	56150	0.0154	0.0103	0.0058	0.0001	0.0858
105323	104099	0.0234	0.0164	0.0091	0.0000	0.0880
105323	90603	0.0129	0.0069	0.0037	0.0000	0.0751
105323	106996	0.0236	0.0177	0.0099	0.0000	0.0902

Name1	**Name2**	**T**	**MC**	**F**	**WU**	**U**
105323	107220	0.0362	0.0277	0.0158	0.0001	0.0971
105323	107623	0.0206	0.0158	0.0091	0.0001	0.0801
105323	75001	0.0185	0.0107	0.0054	0.0000	0.0806
105323	88336	0.0160	0.0100	0.0056	0.0000	0.0813
105323	37353	0.0398	0.0317	0.0168	0.0001	0.0749
105323	105654	0.0160	0.0102	0.0054	0.0000	0.0704
107601	37889	0.0313	0.0254	0.0140	0.0001	0.0808
107601	74548	0.0137	0.0064	0.0032	0.0000	0.0946
107601	103997	0.0365	0.0269	0.0145	0.0001	0.0841
107601	88482	0.0484	0.0331	0.0173	0.0001	0.0849
107601	106838	0.0088	0.0024	0.0012	0.0000	0.1059
107601	103998	0.0343	0.0276	0.0149	0.0002	0.0658
107601	105677	0.0220	0.0146	0.0078	0.0000	0.0972
107601	81915	0.0474	0.0365	0.0194	0.0010	0.0733
107601	80191	0.0251	0.0111	0.0051	0.0008	0.0631
107601	100934	0.0152	0.0086	0.0044	0.0002	0.0692
107601	103789	0.0303	0.0163	0.0089	0.0001	0.0857
107601	90389	0.0207	0.0094	0.0044	0.0004	0.0672
107601	104370	0.0349	0.0227	0.0124	0.0000	0.0762
107601	100530	0.0265	0.0189	0.0091	0.0005	0.0749
107601	55705	0.0580	0.0501	0.0279	0.0004	0.0802
107601	101685	0.0257	0.0179	0.0096	0.0000	0.0943
107601	48010	0.0192	0.0111	0.0059	0.0001	0.0839
107601	107009	0.0321	0.0238	0.0128	0.0003	0.0824
107601	107429	0.0104	0.0032	0.0016	0.0001	0.0693
107601	38064	0.0357	0.0283	0.0158	0.0000	0.0955
107601	99789	0.0175	0.0115	0.0060	0.0001	0.0658
107601	88589	0.0076	0.0000	0.0000	0.0000	0.0000
107601	74414	0.0141	0.0077	0.0041	0.0001	0.0678
107601	87894	0.0285	0.0181	0.0095	0.0000	0.0781
107601	100937	0.0633	0.0544	0.0295	0.0009	0.0707
107601	100652	0.0112	0.0053	0.0024	0.0001	0.0694
107601	74812	0.0236	0.0153	0.0082	0.0002	0.0857
107601	55634	0.0313	0.0258	0.0141	0.0000	0.0835
107601	100610	0.0180	0.0117	0.0062	0.0000	0.0882
107601	62617	0.0154	0.0096	0.0051	0.0000	0.0912
107601	56150	0.0178	0.0104	0.0052	0.0003	0.0695
107601	104099	0.0552	0.0488	0.0267	0.0001	0.0728
107601	90603	0.0343	0.0269	0.0140	0.0001	0.0732
107601	106996	0.0128	0.0041	0.0020	0.0002	0.0760
107601	107220	0.0151	0.0075	0.0040	0.0000	0.0956
107601	107623	0.0216	0.0139	0.0075	0.0002	0.0744
107601	75001	0.0093	0.0038	0.0021	0.0000	0.0881
107601	88336	0.0455	0.0388	0.0212	0.0002	0.0737
107601	37353	0.0191	0.0144	0.0079	0.0000	0.0787
107601	105654	0.0265	0.0191	0.0102	0.0003	0.0674
37889	74548	0.0338	0.0284	0.0152	0.0001	0.0892
37889	103997	0.0323	0.0267	0.0144	0.0001	0.0817
37889	88482	0.0047	0.0000	0.0000	0.0000	0.0000
37889	106838	0.0094	0.0045	0.0025	0.0000	0.0896
37889	103998	0.0120	0.0055	0.0029	0.0000	0.0808
37889	105677	0.0228	0.0184	0.0102	0.0000	0.0862
37889	81915	0.0209	0.0164	0.0091	0.0001	0.0668
37889	80191	0.0133	0.0089	0.0047	0.0001	0.0653
37889	100934	0.0158	0.0112	0.0061	0.0000	0.0851
37889	103789	0.0039	0.0000	0.0000	0.0000	0.0000
37889	90389	0.0221	0.0183	0.0104	0.0000	0.0708
37889	104370	0.0036	0.0000	0.0000	0.0000	0.0000
37889	100530	0.0210	0.0169	0.0095	0.0001	0.0650
37889	55705	0.0194	0.0155	0.0085	0.0000	0.0769
37889	101685	0.0257	0.0219	0.0122	0.0000	0.0991
37889	48010	0.0181	0.0141	0.0078	0.0000	0.0757
37889	107009	0.0202	0.0160	0.0091	0.0001	0.0942
37889	107429	0.0135	0.0094	0.0051	0.0001	0.0789
37889	38064	0.0033	0.0000	0.0000	0.0000	0.0000
37889	99789	0.0375	0.0334	0.0186	0.0001	0.0755
37889	88589	0.0031	0.0000	0.0000	0.0000	0.0000

Name1	Name2	T	MC	F	WU	U
37889	74414	0.0172	0.0134	0.0073	0.0000	0.0944
37889	87894	0.0033	0.0000	0.0000	0.0000	0.0000
37889	100937	0.0281	0.0244	0.0136	0.0000	0.0758
37889	100652	0.0148	0.0109	0.0061	0.0001	0.0682
37889	74812	0.0190	0.0153	0.0080	0.0001	0.0771
37889	55634	0.0237	0.0201	0.0111	0.0000	0.0831
37889	100610	0.0168	0.0131	0.0071	0.0000	0.0706
37889	62617	0.0072	0.0038	0.0022	0.0000	0.0769
37889	56150	0.0120	0.0085	0.0046	0.0000	0.0759
37889	104099	0.0194	0.0160	0.0090	0.0000	0.0798
37889	90603	0.0303	0.0267	0.0153	0.0000	0.0853
37889	106996	0.0285	0.0248	0.0139	0.0001	0.0868
37889	107220	0.0031	0.0000	0.0000	0.0000	0.0000
37889	107623	0.0153	0.0114	0.0059	0.0001	0.0776
37889	75001	0.0102	0.0069	0.0039	0.0000	0.0826
37889	88336	0.0157	0.0121	0.0066	0.0000	0.0881
37889	37353	0.0206	0.0171	0.0096	0.0000	0.0936
37889	105654	0.0158	0.0123	0.0068	0.0000	0.0870
74548	103997	0.0185	0.0094	0.0054	0.0001	0.0928
74548	88482	0.0387	0.0254	0.0132	0.0004	0.0677
74548	106838	0.0502	0.0176	0.0079	0.0006	0.0737
74548	103998	0.0309	0.0249	0.0142	0.0006	0.0776
74548	105677	0.0411	0.0292	0.0156	0.0002	0.0687
74548	81915	0.0633	0.0488	0.0273	0.0016	0.0832
74548	80191	0.0118	0.0040	0.0021	0.0001	0.0948
74548	100934	0.0187	0.0110	0.0060	0.0002	0.1002
74548	103789	0.0328	0.0172	0.0092	0.0003	0.0809
74548	90389	0.0500	0.0418	0.0224	0.0004	0.0799
74548	104370	0.0391	0.0128	0.0072	0.0018	0.1165
74548	100530	0.0137	0.0061	0.0035	0.0009	0.0903
74548	55705	0.0087	0.0015	0.0009	0.0000	0.0974
74548	101685	0.0363	0.0248	0.0132	0.0002	0.0782
74548	48010	0.0237	0.0110	0.0060	0.0003	0.0878
74548	107009	0.0248	0.0175	0.0095	0.0005	0.0679
74548	107429	0.0238	0.0156	0.0085	0.0009	0.0741
74548	38064	0.1048	0.0443	0.0231	0.0141	0.1148
74548	99789	0.0234	0.0142	0.0075	0.0003	0.0888
74548	88589	0.0280	0.0170	0.0094	0.0001	0.0655
74548	74414	0.0204	0.0107	0.0056	0.0003	0.0901
74548	87894	0.0690	0.0554	0.0301	0.0002	0.0787
74548	100937	0.0228	0.0135	0.0072	0.0008	0.0784
74548	100652	0.0149	0.0083	0.0043	0.0000	0.0993
74548	74812	0.0255	0.0155	0.0083	0.0003	0.0720
74548	55634	0.0242	0.0157	0.0079	0.0000	0.0663
74548	100610	0.0118	0.0035	0.0018	0.0001	0.0874
74548	62617	0.0386	0.0235	0.0123	0.0005	0.0738
74548	56150	0.0106	0.0022	0.0012	0.0000	0.1023
74548	104099	0.0263	0.0130	0.0070	0.0005	0.0883
74548	90603	0.0313	0.0134	0.0073	0.0020	0.0708
74548	106996	0.0250	0.0164	0.0082	0.0003	0.0701
74548	107220	0.0238	0.0145	0.0077	0.0001	0.0848
74548	107623	0.0193	0.0111	0.0067	0.0014	0.0804
74548	75001	0.0277	0.0140	0.0073	0.0003	0.0866
74548	88336	0.0157	0.0085	0.0046	0.0001	0.0774
74548	37353	0.0295	0.0064	0.0029	0.0005	0.0773
74548	105654	0.0141	0.0049	0.0025	0.0007	0.0795
103997	88482	0.0376	0.0197	0.0108	0.0001	0.0775
103997	106838	0.0226	0.0136	0.0080	0.0003	0.0917
103997	103998	0.0144	0.0078	0.0042	0.0001	0.0642
103997	105677	0.0406	0.0298	0.0160	0.0001	0.0724
103997	81915	0.0444	0.0345	0.0192	0.0008	0.0797
103997	80191	0.0248	0.0157	0.0084	0.0006	0.0649
103997	100934	0.0443	0.0318	0.0177	0.0012	0.0793
103997	103789	0.0476	0.0335	0.0176	0.0002	0.0660
103997	90389	0.0525	0.0475	0.0273	0.0002	0.0692
103997	104370	0.0543	0.0485	0.0279	0.0001	0.0863
103997	100530	0.0369	0.0295	0.0163	0.0005	0.0813

Name1	**Name2**	**T**	**MC**	**F**	**WU**	**U**
103997	55705	0.0239	0.0152	0.0080	0.0005	0.0762
103997	101685	0.0396	0.0297	0.0163	0.0001	0.0790
103997	48010	0.0538	0.0453	0.0246	0.0001	0.0847
103997	107009	0.0253	0.0170	0.0088	0.0006	0.0905
103997	107429	0.0324	0.0255	0.0137	0.0003	0.0657
103997	38064	0.0853	0.0653	0.0356	0.0011	0.0747
103997	99789	0.0213	0.0145	0.0076	0.0002	0.0742
103997	88589	0.0040	0.0000	0.0000	0.0000	0.0000
103997	74414	0.0235	0.0154	0.0082	0.0002	0.0719
103997	87894	0.0417	0.0254	0.0149	0.0004	0.0678
103997	100937	0.0233	0.0164	0.0090	0.0003	0.0897
103997	100652	0.0130	0.0071	0.0037	0.0002	0.0759
103997	74812	0.0409	0.0342	0.0191	0.0002	0.0750
103997	55634	0.0603	0.0523	0.0283	0.0001	0.0863
103997	100610	0.0151	0.0081	0.0043	0.0001	0.0794
103997	62617	0.0249	0.0163	0.0083	0.0002	0.0689
103997	56150	0.0199	0.0137	0.0073	0.0002	0.0681
103997	104099	0.0234	0.0168	0.0089	0.0001	0.0682
103997	90603	0.0240	0.0164	0.0092	0.0005	0.0691
103997	106996	0.0157	0.0110	0.0062	0.0001	0.0666
103997	107220	0.0570	0.0226	0.0133	0.0015	0.0825
103997	107623	0.0480	0.0336	0.0200	0.0024	0.0806
103997	75001	0.0426	0.0338	0.0178	0.0003	0.0665
103997	88336	0.0475	0.0411	0.0221	0.0002	0.0785
103997	37353	0.0236	0.0165	0.0094	0.0002	0.0639
103997	105654	0.0329	0.0257	0.0142	0.0003	0.0690
88482	106838	0.1122	0.0449	0.0248	0.0056	0.0805
88482	103998	0.0047	0.0000	0.0000	0.0000	0.0000
88482	105677	0.0589	0.0309	0.0164	0.0003	0.0703
88482	81915	0.0181	0.0079	0.0041	0.0000	0.0781
88482	80191	0.0412	0.0268	0.0145	0.0002	0.0731
88482	100934	0.0662	0.0559	0.0308	0.0002	0.0730
88482	103789	0.8341	0.1987	0.1741	0.1207	0.1207
88482	90389	0.1327	0.0370	0.0223	0.0087	0.0742
88482	104370	0.2131	0.0354	0.0210	0.0057	0.0693
88482	100530	0.0388	0.0327	0.0175	0.0002	0.0695
88482	55705	0.0541	0.0399	0.0215	0.0004	0.0723
88482	101685	0.0690	0.0385	0.0185	0.0010	0.0727
88482	48010	0.0538	0.0233	0.0101	0.0010	0.0796
88482	107009	0.0755	0.0624	0.0334	0.0003	0.0789
88482	107429	0.0532	0.0401	0.0219	0.0006	0.0676
88482	38064	0.2882	0.0765	0.0555	0.0440	0.1955
88482	99789	0.0107	0.0045	0.0025	0.0000	0.0737
88482	88589	0.1354	0.0177	0.0121	0.0033	0.0641
88482	74414	0.0312	0.0221	0.0116	0.0001	0.0817
88482	87894	0.3580	0.0543	0.0293	0.0129	0.0947
88482	100937	0.0429	0.0359	0.0192	0.0001	0.0841
88482	100652	0.0119	0.0061	0.0032	0.0000	0.0704
88482	74812	0.1030	0.0847	0.0449	0.0003	0.0780
88482	55634	0.0237	0.0134	0.0070	0.0001	0.0672
88482	100610	0.0245	0.0177	0.0096	0.0000	0.0636
88482	62617	0.0431	0.0218	0.0110	0.0007	0.0736
88482	56150	0.0146	0.0092	0.0050	0.0000	0.0713
88482	104099	0.0559	0.0400	0.0198	0.0006	0.0682
88482	90603	0.0237	0.0109	0.0058	0.0001	0.0679
88482	106996	0.0529	0.0300	0.0164	0.0001	0.0781
88482	107220	0.0445	0.0184	0.0093	0.0009	0.0699
88482	107623	0.0120	0.0067	0.0036	0.0000	0.0978
88482	75001	0.0353	0.0125	0.0063	0.0001	0.0787
88482	88336	0.0428	0.0295	0.0154	0.0002	0.0711
88482	37353	0.0471	0.0355	0.0187	0.0007	0.0846
88482	105654	0.0364	0.0214	0.0111	0.0007	0.0811
106838	103998	0.0168	0.0111	0.0060	0.0000	0.0827
106838	105677	0.0567	0.0316	0.0160	0.0003	0.0762
106838	81915	0.0652	0.0476	0.0245	0.0005	0.0731
106838	80191	0.0779	0.0693	0.0367	0.0002	0.0882
106838	100934	0.0811	0.0713	0.0379	0.0002	0.0731

Name1	Name2	T	MC	F	WU	U
106838	103789	0.1210	0.0606	0.0273	0.0047	0.0842
106838	90389	0.0524	0.0410	0.0239	0.0007	0.0790
106838	104370	0.2180	0.0925	0.0766	0.0258	0.1723
106838	100530	0.0660	0.0597	0.0324	0.0002	0.0755
106838	55705	0.0383	0.0276	0.0140	0.0004	0.0742
106838	101685	0.0186	0.0065	0.0036	0.0002	0.0948
106838	48010	0.0547	0.0378	0.0186	0.0004	0.0753
106838	107009	0.0299	0.0234	0.0117	0.0002	0.0721
106838	107429	0.0083	0.0036	0.0020	0.0000	0.0807
106838	38064	0.1607	0.0739	0.0373	0.0120	0.1074
106838	99789	0.0341	0.0276	0.0145	0.0002	0.0778
106838	88589	0.0477	0.0246	0.0157	0.0013	0.0662
106838	74414	0.0813	0.0742	0.0410	0.0003	0.0818
106838	87894	0.0507	0.0317	0.0135	0.0007	0.0701
106838	100937	0.0149	0.0102	0.0055	0.0000	0.0741
106838	100652	0.0228	0.0186	0.0102	0.0000	0.0869
106838	74812	0.0293	0.0237	0.0128	0.0000	0.0697
106838	55634	0.0186	0.0097	0.0051	0.0000	0.0846
106838	100610	0.0141	0.0093	0.0050	0.0000	0.0865
106838	62617	0.0207	0.0073	0.0050	0.0002	0.1166
106838	56150	0.0222	0.0180	0.0098	0.0000	0.0780
106838	104099	0.0289	0.0200	0.0107	0.0001	0.0827
106838	90603	0.0220	0.0149	0.0080	0.0002	0.0682
106838	106996	0.0371	0.0321	0.0175	0.0001	0.0935
106838	107220	0.0181	0.0102	0.0054	0.0001	0.0764
106838	107623	0.0150	0.0115	0.0062	0.0000	0.0692
106838	75001	0.0492	0.0363	0.0172	0.0004	0.0704
106838	88336	0.0193	0.0144	0.0075	0.0001	0.0798
106838	37353	0.1326	0.1158	0.0654	0.0015	0.0716
106838	105654	0.0384	0.0308	0.0161	0.0002	0.0777
103998	105677	0.0105	0.0066	0.0035	0.0000	0.0717
103998	81915	0.0255	0.0197	0.0097	0.0004	0.0729
103998	80191	0.0253	0.0199	0.0109	0.0001	0.0948
103998	100934	0.0190	0.0123	0.0066	0.0002	0.0909
103998	103789	0.0036	0.0000	0.0000	0.0000	0.0000
103998	90389	0.0108	0.0072	0.0039	0.0001	0.0731
103998	104370	0.0448	0.0405	0.0218	0.0001	0.0837
103998	100530	0.0116	0.0057	0.0031	0.0001	0.0699
103998	55705	0.0223	0.0177	0.0096	0.0002	0.0672
103998	101685	0.0112	0.0074	0.0039	0.0000	0.0862
103998	48010	0.0111	0.0072	0.0039	0.0000	0.0786
103998	107009	0.0099	0.0058	0.0032	0.0001	0.0742
103998	107429	0.0136	0.0087	0.0043	0.0002	0.0779
103998	38064	0.0034	0.0000	0.0000	0.0000	0.0000
103998	99789	0.0181	0.0135	0.0074	0.0001	0.0757
103998	88589	0.0032	0.0000	0.0000	0.0000	0.0000
103998	74414	0.0184	0.0135	0.0075	0.0002	0.0838
103998	87894	0.0032	0.0000	0.0000	0.0000	0.0000
103998	100937	0.0154	0.0106	0.0058	0.0002	0.0807
103998	100652	0.0072	0.0029	0.0017	0.0001	0.1006
103998	74812	0.0168	0.0129	0.0067	0.0001	0.0758
103998	55634	0.0132	0.0094	0.0050	0.0001	0.0719
103998	100610	0.0128	0.0079	0.0040	0.0004	0.1017
103998	62617	0.0128	0.0095	0.0051	0.0000	0.0684
103998	56150	0.0090	0.0038	0.0019	0.0001	0.1008
103998	104099	0.0307	0.0264	0.0143	0.0003	0.0777
103998	90603	0.0153	0.0117	0.0062	0.0001	0.0894
103998	106996	0.0320	0.0281	0.0152	0.0002	0.0776
103998	107220	0.0029	0.0000	0.0000	0.0000	0.0000
103998	107623	0.0163	0.0118	0.0063	0.0003	0.0728
103998	75001	0.0066	0.0036	0.0020	0.0000	0.0904
103998	88336	0.0130	0.0093	0.0051	0.0001	0.0828
103998	37353	0.0101	0.0066	0.0035	0.0001	0.0743
103998	105654	0.0201	0.0165	0.0087	0.0001	0.0727
105677	81915	0.0255	0.0177	0.0093	0.0001	0.0754
105677	80191	0.0171	0.0114	0.0058	0.0001	0.0748
105677	100934	0.0169	0.0101	0.0054	0.0001	0.0723

Name1	**Name2**	**T**	**MC**	**F**	**WU**	**U**
105677	103789	0.0625	0.0434	0.0229	0.0007	0.0744
105677	90389	0.0161	0.0100	0.0054	0.0001	0.0768
105677	104370	0.0439	0.0273	0.0135	0.0002	0.0705
105677	100530	0.0335	0.0284	0.0154	0.0001	0.0738
105677	55705	0.0186	0.0106	0.0053	0.0001	0.0659
105677	101685	0.0187	0.0070	0.0034	0.0002	0.0707
105677	48010	0.0188	0.0083	0.0043	0.0001	0.0777
105677	107009	0.0539	0.0481	0.0263	0.0001	0.0989
105677	107429	0.0154	0.0106	0.0060	0.0000	0.0781
105677	38064	0.0694	0.0559	0.0287	0.0004	0.0776
105677	99789	0.0246	0.0184	0.0099	0.0001	0.0789
105677	88589	0.0543	0.0458	0.0248	0.0001	0.0877
105677	74414	0.0222	0.0174	0.0095	0.0000	0.0792
105677	87894	0.0347	0.0210	0.0102	0.0003	0.0758
105677	100937	0.0172	0.0123	0.0064	0.0001	0.0777
105677	100652	0.0070	0.0030	0.0016	0.0000	0.0791
105677	74812	0.0241	0.0180	0.0097	0.0000	0.0892
105677	55634	0.0321	0.0244	0.0132	0.0001	0.0831
105677	100610	0.0096	0.0052	0.0026	0.0000	0.0785
105677	62617	0.0282	0.0168	0.0081	0.0002	0.0704
105677	56150	0.0300	0.0260	0.0142	0.0000	0.0746
105677	104099	0.0487	0.0417	0.0226	0.0002	0.0805
105677	90603	0.0287	0.0228	0.0126	0.0001	0.0845
105677	106996	0.0250	0.0197	0.0104	0.0000	0.0765
105677	107220	0.0550	0.0449	0.0232	0.0002	0.0755
105677	107623	0.0309	0.0272	0.0148	0.0000	0.0939
105677	75001	0.0292	0.0199	0.0106	0.0002	0.0746
105677	88336	0.0276	0.0226	0.0124	0.0001	0.1058
105677	37353	0.0104	0.0030	0.0016	0.0000	0.0919
105677	105654	0.0434	0.0371	0.0198	0.0001	0.0734
81915	80191	0.0322	0.0200	0.0109	0.0032	0.0825
81915	100934	0.0182	0.0116	0.0062	0.0003	0.0715
81915	103789	0.0362	0.0260	0.0129	0.0003	0.0777
81915	90389	0.0174	0.0118	0.0062	0.0002	0.0702
81915	104370	0.0690	0.0539	0.0286	0.0011	0.0762
81915	100530	0.0282	0.0182	0.0107	0.0023	0.0991
81915	55705	0.0200	0.0133	0.0069	0.0002	0.0761
81915	101685	0.0343	0.0271	0.0143	0.0002	0.0725
81915	48010	0.0239	0.0125	0.0068	0.0016	0.0671
81915	107009	0.0127	0.0075	0.0041	0.0001	0.0637
81915	107429	0.0282	0.0208	0.0094	0.0007	0.0744
81915	38064	0.0582	0.0485	0.0271	0.0009	0.0775
81915	99789	0.0289	0.0237	0.0128	0.0002	0.0711
81915	88589	0.0210	0.0164	0.0090	0.0000	0.0675
81915	74414	0.0189	0.0126	0.0065	0.0002	0.0758
81915	87894	0.0330	0.0264	0.0138	0.0001	0.0744
81915	100937	0.0204	0.0119	0.0063	0.0009	0.0894
81915	100652	0.0140	0.0084	0.0044	0.0002	0.0682
81915	74812	0.0152	0.0100	0.0052	0.0001	0.0881
81915	55634	0.0294	0.0238	0.0126	0.0001	0.0761
81915	100610	0.0239	0.0174	0.0088	0.0010	0.0722
81915	62617	0.0248	0.0181	0.0095	0.0002	0.0785
81915	56150	0.0235	0.0124	0.0064	0.0028	0.0996
81915	104099	0.0110	0.0047	0.0024	0.0004	0.0786
81915	90603	0.0157	0.0080	0.0042	0.0005	0.0732
81915	106996	0.0194	0.0131	0.0062	0.0005	0.0642
81915	107220	0.0092	0.0040	0.0018	0.0000	0.0854
81915	107623	0.0254	0.0180	0.0094	0.0013	0.0814
81915	75001	0.0156	0.0101	0.0055	0.0000	0.0807
81915	88336	0.0226	0.0175	0.0092	0.0002	0.0664
81915	37353	0.0197	0.0102	0.0056	0.0008	0.0898
81915	105654	0.0218	0.0150	0.0079	0.0012	0.0688
80191	100934	0.0190	0.0115	0.0059	0.0002	0.0661
80191	103789	0.0401	0.0275	0.0144	0.0007	0.0724
80191	90389	0.0176	0.0072	0.0034	0.0003	0.0846
80191	104370	0.0308	0.0212	0.0110	0.0003	0.0685
80191	100530	0.0427	0.0286	0.0185	0.0130	0.0802

Name1	**Name2**	**T**	**MC**	**F**	**WU**	**U**
80191	55705	0.0152	0.0081	0.0044	0.0007	0.0740
80191	101685	0.0116	0.0046	0.0023	0.0001	0.1252
80191	48010	0.0372	0.0230	0.0125	0.0028	0.0959
80191	107009	0.0401	0.0348	0.0188	0.0003	0.0714
80191	107429	0.0192	0.0122	0.0065	0.0007	0.0807
80191	38064	0.0284	0.0220	0.0123	0.0003	0.0843
80191	99789	0.0285	0.0233	0.0120	0.0003	0.0772
80191	88589	0.0114	0.0066	0.0035	0.0000	0.0859
80191	74414	0.0268	0.0164	0.0085	0.0017	0.0759
80191	87894	0.0173	0.0109	0.0055	0.0000	0.0705
80191	100937	0.0197	0.0104	0.0057	0.0018	0.1056
80191	100652	0.0360	0.0284	0.0149	0.0009	0.0841
80191	74812	0.0114	0.0065	0.0031	0.0001	0.0705
80191	55634	0.0190	0.0145	0.0075	0.0001	0.0687
80191	100610	0.0180	0.0077	0.0042	0.0016	0.0998
80191	62617	0.0130	0.0082	0.0043	0.0000	0.0756
80191	56150	0.0299	0.0176	0.0104	0.0033	0.0866
80191	104099	0.0283	0.0206	0.0111	0.0011	0.0801
80191	90603	0.0341	0.0255	0.0136	0.0013	0.0678
80191	106996	0.0235	0.0156	0.0085	0.0014	0.0786
80191	107220	0.0515	0.0463	0.0253	0.0001	0.0945
80191	107623	0.0361	0.0264	0.0155	0.0032	0.0977
80191	75001	0.0120	0.0073	0.0039	0.0001	0.0743
80191	88336	0.0167	0.0110	0.0058	0.0004	0.0713
80191	37353	0.0111	0.0059	0.0031	0.0001	0.0873
80191	105654	0.0193	0.0098	0.0051	0.0016	0.1068
100934	103789	0.0255	0.0176	0.0093	0.0001	0.0669
100934	90389	0.0285	0.0232	0.0125	0.0003	0.0799
100934	104370	0.0568	0.0466	0.0290	0.0008	0.0875
100934	100530	0.0215	0.0152	0.0079	0.0003	0.0966
100934	55705	0.0246	0.0160	0.0082	0.0004	0.0757
100934	101685	0.0170	0.0109	0.0058	0.0001	0.0792
100934	48010	0.0270	0.0196	0.0104	0.0005	0.0721
100934	107009	0.0190	0.0134	0.0078	0.0004	0.0859
100934	107429	0.0102	0.0045	0.0023	0.0000	0.1021
100934	38064	0.0589	0.0512	0.0310	0.0004	0.0914
100934	99789	0.0162	0.0105	0.0054	0.0001	0.0838
100934	88589	0.0057	0.0014	0.0007	0.0000	0.0681
100934	74414	0.0150	0.0095	0.0052	0.0004	0.0846
100934	87894	0.0196	0.0141	0.0066	0.0000	0.0817
100934	100937	0.0298	0.0236	0.0124	0.0005	0.0964
100934	100652	0.0246	0.0196	0.0106	0.0003	0.0688
100934	74812	0.0173	0.0129	0.0069	0.0001	0.0960
100934	55634	0.0225	0.0179	0.0097	0.0001	0.0872
100934	100610	0.0206	0.0138	0.0076	0.0011	0.0841
100934	62617	0.0133	0.0082	0.0042	0.0000	0.0919
100934	56150	0.0284	0.0230	0.0126	0.0002	0.0877
100934	104099	0.0073	0.0027	0.0013	0.0000	0.1009
100934	90603	0.0429	0.0365	0.0202	0.0005	0.0740
100934	106996	0.0364	0.0318	0.0173	0.0003	0.0714
100934	107220	0.0477	0.0426	0.0232	0.0001	0.0957
100934	107623	0.0162	0.0112	0.0060	0.0002	0.0774
100934	75001	0.0124	0.0075	0.0040	0.0001	0.0684
100934	88336	0.0125	0.0061	0.0030	0.0002	0.0715
100934	37353	0.0429	0.0365	0.0198	0.0003	0.0780
100934	105654	0.0235	0.0182	0.0095	0.0003	0.0691
103789	90389	0.1318	0.0940	0.0544	0.0058	0.0759
103789	104370	0.1670	0.0421	0.0212	0.0124	0.0891
103789	100530	0.0086	0.0043	0.0023	0.0000	0.0844
103789	55705	0.0427	0.0317	0.0156	0.0002	0.0764
103789	101685	0.0420	0.0161	0.0079	0.0003	0.0799
103789	48010	0.0782	0.0418	0.0181	0.0033	0.0849
103789	107009	0.0373	0.0296	0.0160	0.0001	0.0768
103789	107429	0.0169	0.0104	0.0049	0.0001	0.0833
103789	38064	0.0811	0.0268	0.0128	0.0028	0.0894
103789	99789	0.0127	0.0071	0.0036	0.0000	0.0855
103789	88589	0.1979	0.0811	0.0553	0.0185	0.0930

Name1	**Name2**	**T**	**MC**	**F**	**WU**	**U**
103789	74414	0.0280	0.0201	0.0105	0.0002	0.0683
103789	87894	0.1786	0.0702	0.0336	0.0110	0.1016
103789	100937	0.0165	0.0118	0.0062	0.0000	0.0850
103789	100652	0.0372	0.0324	0.0176	0.0000	0.0875
103789	74812	0.0388	0.0281	0.0139	0.0002	0.0804
103789	55634	0.0255	0.0182	0.0097	0.0001	0.0687
103789	100610	0.0272	0.0208	0.0109	0.0000	0.0850
103789	62617	0.0321	0.0162	0.0080	0.0002	0.0743
103789	56150	0.0484	0.0429	0.0234	0.0001	0.0705
103789	104099	0.0989	0.0795	0.0397	0.0013	0.0766
103789	90603	0.0207	0.0131	0.0069	0.0000	0.0805
103789	106996	0.0335	0.0225	0.0104	0.0002	0.0722
103789	107220	0.0582	0.0377	0.0179	0.0006	0.0774
103789	107623	0.0365	0.0319	0.0175	0.0000	0.0829
103789	75001	0.0421	0.0241	0.0079	0.0010	0.0666
103789	88336	0.0342	0.0237	0.0126	0.0006	0.0733
103789	37353	0.0371	0.0253	0.0113	0.0006	0.0750
103789	105654	0.0280	0.0133	0.0048	0.0006	0.0791
90389	104370	0.0803	0.0598	0.0302	0.0002	0.0933
90389	100530	0.0248	0.0186	0.0092	0.0007	0.0668
90389	55705	0.0246	0.0200	0.0109	0.0001	0.0763
90389	101685	0.0257	0.0196	0.0103	0.0001	0.0776
90389	48010	0.0372	0.0284	0.0150	0.0004	0.0700
90389	107009	0.0391	0.0333	0.0184	0.0005	0.0709
90389	107429	0.0198	0.0140	0.0076	0.0000	0.0913
90389	38064	0.0267	0.0202	0.0105	0.0003	0.0689
90389	99789	0.0391	0.0346	0.0189	0.0002	0.0729
90389	88589	0.0487	0.0372	0.0194	0.0010	0.0654
90389	74414	0.0450	0.0393	0.0212	0.0003	0.0775
90389	87894	0.0198	0.0065	0.0032	0.0002	0.0747
90389	100937	0.0279	0.0219	0.0115	0.0007	0.0800
90389	100652	0.0218	0.0176	0.0095	0.0001	0.0749
90389	74812	0.0273	0.0199	0.0106	0.0002	0.0713
90389	55634	0.0481	0.0438	0.0238	0.0001	0.0872
90389	100610	0.0143	0.0085	0.0040	0.0010	0.0765
90389	62617	0.0300	0.0248	0.0136	0.0001	0.0831
90389	56150	0.0237	0.0195	0.0106	0.0003	0.0776
90389	104099	0.0495	0.0420	0.0232	0.0009	0.0713
90389	90603	0.0575	0.0498	0.0268	0.0002	0.0821
90389	106996	0.0517	0.0404	0.0232	0.0021	0.0664
90389	107220	0.0296	0.0253	0.0136	0.0000	0.0910
90389	107623	0.0209	0.0164	0.0087	0.0006	0.0731
90389	75001	0.0764	0.0707	0.0382	0.0002	0.0822
90389	88336	0.0102	0.0044	0.0023	0.0002	0.0656
90389	37353	0.0195	0.0155	0.0086	0.0001	0.0799
90389	105654	0.0346	0.0279	0.0147	0.0006	0.0821
104370	100530	0.0519	0.0465	0.0253	0.0001	0.0698
104370	55705	0.0550	0.0466	0.0241	0.0003	0.0727
104370	101685	0.0494	0.0318	0.0160	0.0005	0.0687
104370	48010	0.0999	0.0728	0.0337	0.0023	0.0844
104370	107009	0.0507	0.0405	0.0214	0.0002	0.0817
104370	107429	0.0374	0.0246	0.0094	0.0003	0.0738
104370	38064	0.0670	0.0134	0.0078	0.0046	0.0951
104370	99789	0.0287	0.0240	0.0129	0.0000	0.0644
104370	88589	0.0479	0.0367	0.0194	0.0001	0.0827
104370	74414	0.0261	0.0206	0.0113	0.0002	0.0748
104370	87894	0.0748	0.0275	0.0135	0.0018	0.0791
104370	100937	0.0249	0.0197	0.0108	0.0000	0.0885
104370	100652	0.0242	0.0195	0.0106	0.0000	0.0739
104370	74812	0.0431	0.0249	0.0105	0.0002	0.0740
104370	55634	0.0258	0.0181	0.0098	0.0000	0.0671
104370	100610	0.0194	0.0145	0.0078	0.0002	0.0733
104370	62617	0.0874	0.0742	0.0392	0.0005	0.0777
104370	56150	0.0399	0.0356	0.0195	0.0001	0.0960
104370	104099	0.0370	0.0218	0.0103	0.0005	0.0777
104370	90603	0.0336	0.0219	0.0102	0.0004	0.0778
104370	106996	0.0837	0.0512	0.0240	0.0036	0.0968

Name1	Name2	T	MC	F	WU	U
104370	107220	0.0268	0.0126	0.0057	0.0002	0.0678
104370	107623	0.0523	0.0472	0.0259	0.0002	0.0806
104370	75001	0.0726	0.0545	0.0287	0.0029	0.0786
104370	88336	0.0217	0.0111	0.0058	0.0000	0.0673
104370	37353	0.0796	0.0630	0.0258	0.0009	0.0690
104370	105654	0.0178	0.0086	0.0044	0.0002	0.0781
100530	55705	0.0115	0.0060	0.0031	0.0002	0.0679
100530	101685	0.0117	0.0072	0.0039	0.0001	0.1007
100530	48010	0.0207	0.0132	0.0072	0.0009	0.1021
100530	107009	0.0086	0.0044	0.0024	0.0002	0.0666
100530	107429	0.0310	0.0251	0.0130	0.0006	0.0754
100530	38064	0.0274	0.0228	0.0127	0.0001	0.0927
100530	99789	0.0222	0.0172	0.0090	0.0003	0.0771
100530	88589	0.0030	0.0000	0.0000	0.0000	0.0000
100530	74414	0.0192	0.0104	0.0057	0.0029	0.0879
100530	87894	0.0594	0.0548	0.0296	0.0002	0.0990
100530	100937	0.0311	0.0214	0.0123	0.0052	0.1243
100530	100652	0.0184	0.0135	0.0070	0.0004	0.0705
100530	74812	0.0271	0.0228	0.0118	0.0002	0.0714
100530	55634	0.0087	0.0051	0.0027	0.0000	0.0728
100530	100610	0.0174	0.0092	0.0042	0.0015	0.1010
100530	62617	0.0105	0.0066	0.0035	0.0000	0.1046
100530	56150	0.0288	0.0202	0.0123	0.0028	0.0909
100530	104099	0.0232	0.0150	0.0079	0.0028	0.0727
100530	90603	0.0213	0.0159	0.0074	0.0009	0.0700
100530	106996	0.0163	0.0121	0.0064	0.0002	0.0725
100530	107220	0.0248	0.0216	0.0117	0.0000	0.0829
100530	107623	0.0143	0.0086	0.0042	0.0006	0.0658
100530	75001	0.0066	0.0029	0.0016	0.0000	0.0683
100530	88336	0.0141	0.0102	0.0054	0.0001	0.0829
100530	37353	0.0241	0.0171	0.0089	0.0010	0.0773
100530	105654	0.0176	0.0106	0.0059	0.0016	0.0878
55705	101685	0.0151	0.0078	0.0039	0.0002	0.0757
55705	48010	0.0143	0.0063	0.0029	0.0002	0.0717
55705	107009	0.0165	0.0123	0.0066	0.0001	0.0768
55705	107429	0.0112	0.0069	0.0037	0.0000	0.0755
55705	38064	0.0209	0.0136	0.0058	0.0001	0.0838
55705	99789	0.0210	0.0156	0.0083	0.0001	0.0797
55705	88589	0.0119	0.0066	0.0035	0.0000	0.0694
55705	74414	0.0139	0.0088	0.0047	0.0001	0.0780
55705	87894	0.0303	0.0237	0.0125	0.0001	0.0793
55705	100937	0.0134	0.0060	0.0029	0.0009	0.0736
55705	100652	0.0428	0.0388	0.0210	0.0001	0.0903
55705	74812	0.0305	0.0263	0.0138	0.0001	0.0919
55705	55634	0.0650	0.0593	0.0323	0.0002	0.0847
55705	100610	0.0418	0.0329	0.0181	0.0019	0.1002
55705	62617	0.0173	0.0106	0.0058	0.0001	0.0860
55705	56150	0.0122	0.0073	0.0039	0.0000	0.0849
55705	104099	0.0128	0.0068	0.0034	0.0001	0.0722
55705	90603	0.0142	0.0090	0.0048	0.0002	0.0749
55705	106996	0.0182	0.0144	0.0078	0.0001	0.0758
55705	107220	0.0173	0.0123	0.0065	0.0001	0.0936
55705	107623	0.0180	0.0135	0.0070	0.0002	0.0735
55705	75001	0.0191	0.0135	0.0074	0.0001	0.0694
55705	88336	0.0124	0.0076	0.0037	0.0001	0.0791
55705	37353	0.0275	0.0207	0.0106	0.0003	0.0695
55705	105654	0.0236	0.0164	0.0082	0.0012	0.0820
101685	48010	0.0268	0.0155	0.0080	0.0003	0.0824
101685	107009	0.0174	0.0125	0.0066	0.0000	0.0824
101685	107429	0.0195	0.0151	0.0080	0.0000	0.0830
101685	38064	0.0305	0.0182	0.0088	0.0002	0.0881
101685	99789	0.0248	0.0193	0.0100	0.0002	0.0694
101685	88589	0.0607	0.0488	0.0261	0.0002	0.0703
101685	74414	0.0128	0.0072	0.0039	0.0001	0.0675
101685	87894	0.0212	0.0091	0.0045	0.0001	0.0754
101685	100937	0.0120	0.0073	0.0040	0.0001	0.0787
101685	100652	0.0104	0.0064	0.0035	0.0001	0.0684

Name1	**Name2**	**T**	**MC**	**F**	**WU**	**U**
101685	74812	0.0203	0.0145	0.0076	0.0001	0.0844
101685	55634	0.0182	0.0103	0.0052	0.0002	0.0723
101685	100610	0.0195	0.0141	0.0073	0.0005	0.0675
101685	62617	0.0128	0.0038	0.0019	0.0001	0.0879
101685	56150	0.0209	0.0165	0.0086	0.0002	0.0786
101685	104099	0.0152	0.0067	0.0035	0.0001	0.0685
101685	90603	0.0152	0.0095	0.0054	0.0002	0.0704
101685	106996	0.0226	0.0173	0.0090	0.0001	0.0848
101685	107220	0.0250	0.0156	0.0078	0.0001	0.0790
101685	107623	0.0056	0.0022	0.0011	0.0000	0.1089
101685	75001	0.0185	0.0099	0.0049	0.0001	0.0722
101685	88336	0.0194	0.0144	0.0075	0.0001	0.0779
101685	37353	0.0334	0.0235	0.0125	0.0007	0.1078
101685	105654	0.0189	0.0120	0.0062	0.0001	0.0753
48010	107009	0.0168	0.0114	0.0060	0.0001	0.0729
48010	107429	0.0150	0.0093	0.0046	0.0002	0.0706
48010	38064	0.0474	0.0340	0.0164	0.0004	0.0817
48010	99789	0.0266	0.0209	0.0112	0.0003	0.0709
48010	88589	0.0512	0.0410	0.0230	0.0007	0.0787
48010	74414	0.0201	0.0124	0.0065	0.0005	0.0815
48010	87894	0.0624	0.0475	0.0226	0.0008	0.0783
48010	100937	0.0501	0.0442	0.0241	0.0003	0.0722
48010	100652	0.0174	0.0121	0.0066	0.0001	0.0893
48010	74812	0.0141	0.0083	0.0035	0.0002	0.0791
48010	55634	0.0145	0.0082	0.0043	0.0000	0.0803
48010	100610	0.0233	0.0166	0.0083	0.0005	0.0738
48010	62617	0.0175	0.0080	0.0040	0.0001	0.0779
48010	56150	0.0110	0.0057	0.0031	0.0001	0.0798
48010	104099	0.0228	0.0146	0.0071	0.0005	0.0710
48010	90603	0.0218	0.0109	0.0051	0.0003	0.0774
48010	106996	0.0265	0.0212	0.0108	0.0001	0.0698
48010	107220	0.0611	0.0526	0.0281	0.0001	0.0778
48010	107623	0.0229	0.0189	0.0101	0.0002	0.0739
48010	75001	0.0288	0.0191	0.0097	0.0003	0.0733
48010	88336	0.0197	0.0141	0.0078	0.0001	0.0868
48010	37353	0.0308	0.0163	0.0084	0.0020	0.1026
48010	105654	0.0177	0.0077	0.0044	0.0016	0.0776
107009	107429	0.0250	0.0187	0.0098	0.0007	0.0713
107009	38064	0.0151	0.0093	0.0051	0.0002	0.0956
107009	99789	0.0178	0.0137	0.0074	0.0001	0.0663
107009	88589	0.0049	0.0000	0.0000	0.0000	0.0000
107009	74414	0.0149	0.0103	0.0054	0.0003	0.0749
107009	87894	0.0145	0.0086	0.0047	0.0000	0.0807
107009	100937	0.0118	0.0077	0.0040	0.0001	0.0812
107009	100652	0.0124	0.0079	0.0043	0.0002	0.0676
107009	74812	0.0218	0.0167	0.0090	0.0001	0.0753
107009	55634	0.0277	0.0235	0.0128	0.0000	0.0860
107009	100610	0.0143	0.0101	0.0055	0.0001	0.0840
107009	62617	0.0294	0.0251	0.0136	0.0000	0.0963
107009	56150	0.0118	0.0080	0.0043	0.0001	0.0704
107009	104099	0.0075	0.0036	0.0019	0.0000	0.0892
107009	90603	0.0231	0.0181	0.0097	0.0002	0.0775
107009	106996	0.0162	0.0110	0.0058	0.0001	0.0780
107009	107220	0.0071	0.0021	0.0012	0.0000	0.0961
107009	107623	0.0276	0.0220	0.0115	0.0008	0.0818
107009	75001	0.0120	0.0079	0.0043	0.0000	0.1119
107009	88336	0.0121	0.0083	0.0044	0.0000	0.0727
107009	37353	0.0207	0.0166	0.0087	0.0001	0.0752
107009	105654	0.0140	0.0100	0.0055	0.0001	0.0723
107429	38064	0.0301	0.0256	0.0140	0.0001	0.0822
107429	99789	0.0176	0.0137	0.0074	0.0001	0.0746
107429	88589	0.0042	0.0000	0.0000	0.0000	0.0000
107429	74414	0.0143	0.0102	0.0053	0.0001	0.0710
107429	87894	0.0378	0.0321	0.0167	0.0001	0.0831
107429	100937	0.0132	0.0088	0.0045	0.0001	0.0715
107429	100652	0.0121	0.0073	0.0035	0.0001	0.0727
107429	74812	0.0187	0.0136	0.0068	0.0001	0.0735

Name1	Name2	T	MC	F	WU	U
107429	55634	0.0063	0.0029	0.0016	0.0000	0.0795
107429	100610	0.0128	0.0086	0.0044	0.0001	0.0783
107429	62617	0.0156	0.0116	0.0062	0.0000	0.0886
107429	56150	0.0180	0.0129	0.0065	0.0002	0.0821
107429	104099	0.0146	0.0107	0.0059	0.0001	0.0721
107429	90603	0.0118	0.0066	0.0032	0.0000	0.0807
107429	106996	0.0182	0.0113	0.0058	0.0003	0.0725
107429	107220	0.0214	0.0175	0.0094	0.0000	0.0851
107429	107623	0.0202	0.0147	0.0074	0.0005	0.0769
107429	75001	0.0263	0.0224	0.0117	0.0001	0.0892
107429	88336	0.0148	0.0108	0.0055	0.0001	0.0695
107429	37353	0.0136	0.0096	0.0049	0.0001	0.0718
107429	105654	0.0201	0.0160	0.0084	0.0002	0.0710
38064	99789	0.0057	0.0008	0.0004	0.0000	0.1005
38064	88589	0.0669	0.0467	0.0343	0.0035	0.0856
38064	74414	0.0344	0.0280	0.0156	0.0002	0.0996
38064	87894	0.0699	0.0318	0.0131	0.0029	0.0938
38064	100937	0.0143	0.0101	0.0055	0.0000	0.0791
38064	100652	0.0082	0.0045	0.0023	0.0000	0.0809
38064	74812	0.0138	0.0086	0.0047	0.0000	0.0759
38064	55634	0.0399	0.0298	0.0125	0.0012	0.0637
38064	100610	0.0092	0.0051	0.0027	0.0000	0.0862
38064	62617	0.0277	0.0162	0.0083	0.0003	0.0763
38064	56150	0.0067	0.0029	0.0016	0.0000	0.0736
38064	104099	0.0863	0.0769	0.0429	0.0007	0.0876
38064	90603	0.0250	0.0193	0.0105	0.0001	0.0776
38064	106996	0.0136	0.0084	0.0044	0.0001	0.0917
38064	107220	0.0336	0.0092	0.0039	0.0007	0.0899
38064	107623	0.0065	0.0029	0.0016	0.0000	0.0906
38064	75001	0.0766	0.0637	0.0326	0.0006	0.0770
38064	88336	0.0156	0.0093	0.0050	0.0004	0.1012
38064	37353	0.0338	0.0238	0.0125	0.0002	0.0881
38064	105654	0.0214	0.0150	0.0064	0.0001	0.0726
99789	88589	0.0287	0.0248	0.0133	0.0000	0.0866
99789	74414	0.0122	0.0081	0.0042	0.0001	0.0873
99789	87894	0.0541	0.0497	0.0269	0.0001	0.0840
99789	100937	0.0146	0.0102	0.0053	0.0001	0.0802
99789	100652	0.0263	0.0227	0.0118	0.0001	0.0781
99789	74812	0.0168	0.0131	0.0070	0.0001	0.0727
99789	55634	0.0186	0.0148	0.0072	0.0000	0.0741
99789	100610	0.0117	0.0067	0.0034	0.0001	0.0909
99789	62617	0.0067	0.0021	0.0012	0.0000	0.1104
99789	56150	0.0112	0.0079	0.0043	0.0000	0.0769
99789	104099	0.0110	0.0065	0.0035	0.0001	0.0848
99789	90603	0.0070	0.0029	0.0015	0.0000	0.0958
99789	106996	0.0295	0.0260	0.0140	0.0001	0.0981
99789	107220	0.0177	0.0139	0.0075	0.0000	0.0865
99789	107623	0.0187	0.0151	0.0082	0.0001	0.0787
99789	75001	0.0220	0.0179	0.0098	0.0001	0.0709
99789	88336	0.0178	0.0141	0.0075	0.0001	0.0743
99789	37353	0.0159	0.0115	0.0062	0.0001	0.0723
99789	105654	0.0171	0.0131	0.0070	0.0001	0.0751
88589	74414	0.0038	0.0000	0.0000	0.0000	0.0000
88589	87894	0.1131	0.0530	0.0252	0.0095	0.0655
88589	100937	0.0032	0.0000	0.0000	0.0000	0.0000
88589	100652	0.0035	0.0000	0.0000	0.0000	0.0000
88589	74812	0.0188	0.0111	0.0059	0.0001	0.0737
88589	55634	0.0091	0.0044	0.0024	0.0000	0.0617
88589	100610	0.0038	0.0000	0.0000	0.0000	0.0000
88589	62617	0.0331	0.0263	0.0146	0.0000	0.0772
88589	56150	0.0037	0.0000	0.0000	0.0000	0.0000
88589	104099	0.0374	0.0305	0.0174	0.0003	0.0785
88589	90603	0.0197	0.0140	0.0076	0.0001	0.0710
88589	106996	0.0072	0.0022	0.0012	0.0000	0.0676
88589	107220	0.0149	0.0100	0.0055	0.0000	0.0880
88589	107623	0.0030	0.0000	0.0000	0.0000	0.0000
88589	75001	0.0239	0.0161	0.0087	0.0000	0.0758

Name1	**Name2**	**T**	**MC**	**F**	**WU**	**U**
88589	88336	0.0418	0.0359	0.0206	0.0005	0.0630
88589	37353	0.0305	0.0248	0.0144	0.0004	0.0672
88589	105654	0.0319	0.0264	0.0141	0.0001	0.0788
74414	87894	0.0365	0.0309	0.0159	0.0002	0.0860
74414	100937	0.0128	0.0076	0.0038	0.0003	0.0871
74414	100652	0.0166	0.0115	0.0061	0.0008	0.0843
74414	74812	0.0154	0.0115	0.0052	0.0001	0.0729
74414	55634	0.0406	0.0364	0.0199	0.0001	0.0796
74414	100610	0.0350	0.0266	0.0132	0.0013	0.1014
74414	62617	0.0266	0.0221	0.0120	0.0001	0.0751
74414	56150	0.0145	0.0101	0.0054	0.0001	0.0777
74414	104099	0.0196	0.0131	0.0062	0.0010	0.1002
74414	90603	0.0200	0.0144	0.0069	0.0006	0.0704
74414	106996	0.0140	0.0104	0.0053	0.0001	0.0723
74414	107220	0.0151	0.0110	0.0058	0.0000	0.0921
74414	107623	0.0193	0.0147	0.0078	0.0004	0.0718
74414	75001	0.0067	0.0028	0.0016	0.0000	0.0714
74414	88336	0.0115	0.0079	0.0043	0.0000	0.0780
74414	37353	0.0344	0.0289	0.0151	0.0004	0.0692
74414	105654	0.0238	0.0168	0.0085	0.0006	0.0936
87894	100937	0.0053	0.0015	0.0008	0.0000	0.0866
87894	100652	0.0292	0.0251	0.0137	0.0000	0.0825
87894	74812	0.0387	0.0286	0.0152	0.0001	0.0829
87894	55634	0.0462	0.0399	0.0219	0.0000	0.0827
87894	100610	0.0701	0.0643	0.0351	0.0003	0.1043
87894	62617	0.0338	0.0221	0.0105	0.0003	0.0923
87894	56150	0.0274	0.0232	0.0129	0.0001	0.0835
87894	104099	0.0311	0.0235	0.0127	0.0002	0.0880
87894	90603	0.0456	0.0375	0.0206	0.0003	0.0796
87894	106996	0.0322	0.0223	0.0110	0.0001	0.0839
87894	107220	0.0290	0.0139	0.0066	0.0001	0.0764
87894	107623	0.0140	0.0099	0.0052	0.0000	0.0801
87894	75001	0.0234	0.0130	0.0064	0.0002	0.0808
87894	88336	0.0304	0.0242	0.0131	0.0001	0.0903
87894	37353	0.0178	0.0113	0.0056	0.0002	0.0830
87894	105654	0.0249	0.0182	0.0097	0.0001	0.0787
100937	100652	0.0090	0.0051	0.0028	0.0000	0.0825
100937	74812	0.0052	0.0014	0.0008	0.0000	0.0821
100937	55634	0.0102	0.0065	0.0036	0.0000	0.0929
100937	100610	0.0282	0.0199	0.0100	0.0023	0.0796
100937	62617	0.0126	0.0085	0.0045	0.0001	0.0857
100937	56150	0.0226	0.0162	0.0090	0.0010	0.0704
100937	104099	0.0163	0.0116	0.0061	0.0005	0.0704
100937	90603	0.0320	0.0253	0.0138	0.0012	0.0909
100937	106996	0.0205	0.0154	0.0079	0.0004	0.0673
100937	107220	0.0197	0.0160	0.0087	0.0000	0.1005
100937	107623	0.0207	0.0141	0.0079	0.0020	0.0900
100937	75001	0.0144	0.0109	0.0060	0.0000	0.0760
100937	88336	0.0229	0.0187	0.0103	0.0001	0.0713
100937	37353	0.0183	0.0131	0.0073	0.0011	0.0723
100937	105654	0.0206	0.0149	0.0083	0.0006	0.0697
100652	74812	0.0138	0.0098	0.0048	0.0001	0.0773
100652	55634	0.0170	0.0134	0.0076	0.0000	0.0841
100652	100610	0.0077	0.0036	0.0020	0.0001	0.0717
100652	62617	0.0186	0.0150	0.0084	0.0000	0.0914
100652	56150	0.0112	0.0061	0.0033	0.0006	0.0848
100652	104099	0.0170	0.0137	0.0076	0.0000	0.0852
100652	90603	0.0143	0.0093	0.0047	0.0004	0.0665
100652	106996	0.0134	0.0092	0.0043	0.0002	0.0659
100652	107220	0.0186	0.0150	0.0084	0.0000	0.0837
100652	107623	0.0241	0.0201	0.0112	0.0004	0.0749
100652	75001	0.0300	0.0264	0.0149	0.0000	0.0797
100652	88336	0.0262	0.0225	0.0122	0.0001	0.0745
100652	37353	0.0066	0.0030	0.0016	0.0001	0.0708
100652	105654	0.0126	0.0090	0.0048	0.0000	0.0789
74812	55634	0.0195	0.0153	0.0084	0.0000	0.0867
74812	100610	0.0233	0.0195	0.0109	0.0001	0.0885

Name1	**Name2**	**T**	**MC**	**F**	**WU**	**U**
74812	62617	0.0332	0.0279	0.0154	0.0001	0.0886
74812	56150	0.0077	0.0041	0.0021	0.0001	0.0879
74812	104099	0.0379	0.0330	0.0184	0.0003	0.0689
74812	90603	0.0190	0.0137	0.0073	0.0001	0.0771
74812	106996	0.0222	0.0149	0.0076	0.0001	0.0889
74812	107220	0.0242	0.0193	0.0108	0.0000	0.0947
74812	107623	0.0215	0.0175	0.0096	0.0002	0.0751
74812	75001	0.0161	0.0113	0.0062	0.0000	0.0939
74812	88336	0.0104	0.0064	0.0036	0.0000	0.0777
74812	37353	0.0139	0.0101	0.0054	0.0000	0.0764
74812	105654	0.0137	0.0097	0.0051	0.0001	0.0855
55634	100610	0.0186	0.0149	0.0084	0.0000	0.0795
55634	62617	0.0198	0.0140	0.0076	0.0000	0.0824
55634	56150	0.0241	0.0209	0.0117	0.0000	0.0819
55634	104099	0.0371	0.0324	0.0181	0.0001	0.0783
55634	90603	0.0084	0.0045	0.0024	0.0000	0.0697
55634	106996	0.0233	0.0196	0.0109	0.0000	0.0925
55634	107220	0.0546	0.0485	0.0269	0.0001	0.0874
55634	107623	0.0108	0.0080	0.0044	0.0000	0.0817
55634	75001	0.0095	0.0044	0.0024	0.0000	0.0834
55634	88336	0.0283	0.0245	0.0137	0.0001	0.0741
55634	37353	0.0271	0.0214	0.0115	0.0001	0.0660
55634	105654	0.0401	0.0357	0.0201	0.0001	0.0917
100610	62617	0.0087	0.0042	0.0021	0.0000	0.0774
100610	56150	0.0157	0.0090	0.0049	0.0013	0.0780
100610	104099	0.0274	0.0193	0.0118	0.0046	0.0813
100610	90603	0.0176	0.0112	0.0055	0.0007	0.0656
100610	106996	0.0145	0.0101	0.0057	0.0004	0.0705
100610	107220	0.0283	0.0246	0.0137	0.0000	0.0808
100610	107623	0.0094	0.0040	0.0019	0.0002	0.1005
100610	75001	0.0124	0.0088	0.0048	0.0000	0.0751
100610	88336	0.0090	0.0050	0.0025	0.0001	0.0802
100610	37353	0.0120	0.0067	0.0036	0.0003	0.0734
100610	105654	0.0085	0.0015	0.0008	0.0001	0.1518
62617	56150	0.0066	0.0030	0.0016	0.0000	0.0754
62617	104099	0.0176	0.0108	0.0057	0.0002	0.0922
62617	90603	0.0171	0.0116	0.0064	0.0001	0.0702
62617	106996	0.0169	0.0126	0.0068	0.0000	0.0909
62617	107220	0.0569	0.0490	0.0270	0.0001	0.0748
62617	107623	0.0125	0.0094	0.0052	0.0000	0.0925
62617	75001	0.0170	0.0094	0.0052	0.0001	0.0795
62617	88336	0.0235	0.0188	0.0104	0.0001	0.0788
62617	37353	0.0211	0.0126	0.0060	0.0004	0.0814
62617	105654	0.0171	0.0118	0.0064	0.0000	0.0837
56150	104099	0.0085	0.0050	0.0028	0.0002	0.0745
56150	90603	0.0141	0.0078	0.0035	0.0004	0.0796
56150	106996	0.0193	0.0141	0.0076	0.0003	0.0737
56150	107220	0.0237	0.0203	0.0113	0.0000	0.0723
56150	107623	0.0136	0.0072	0.0042	0.0007	0.1319
56150	75001	0.0144	0.0108	0.0060	0.0000	0.0705
56150	88336	0.0119	0.0080	0.0044	0.0001	0.0854
56150	37353	0.0100	0.0046	0.0026	0.0005	0.0849
56150	105654	0.0280	0.0235	0.0132	0.0004	0.0852
104099	90603	0.0242	0.0193	0.0102	0.0003	0.0687
104099	106996	0.0176	0.0137	0.0077	0.0000	0.0831
104099	107220	0.0645	0.0585	0.0330	0.0002	0.0970
104099	107623	0.0161	0.0125	0.0068	0.0005	0.0667
104099	75001	0.0132	0.0081	0.0041	0.0000	0.0731
104099	88336	0.0123	0.0086	0.0048	0.0001	0.0958
104099	37353	0.0223	0.0141	0.0070	0.0004	0.0748
104099	105654	0.0202	0.0131	0.0067	0.0006	0.0948
90603	106996	0.0150	0.0088	0.0049	0.0002	0.0679
90603	107220	0.0120	0.0078	0.0044	0.0000	0.1052
90603	107623	0.0120	0.0069	0.0038	0.0005	0.0759
90603	75001	0.0161	0.0113	0.0059	0.0001	0.0758
90603	88336	0.0120	0.0076	0.0041	0.0000	0.0749
90603	37353	0.0215	0.0116	0.0064	0.0019	0.0914

Name1	Name2	T	MC	F	WU	U
90603	105654	0.0213	0.0165	0.0092	0.0002	0.0763
106996	107220	0.0156	0.0116	0.0062	0.0000	0.0885
106996	107623	0.0179	0.0130	0.0069	0.0006	0.1039
106996	75001	0.0199	0.0158	0.0082	0.0000	0.0839
106996	88336	0.0233	0.0185	0.0101	0.0001	0.0752
106996	37353	0.0117	0.0083	0.0044	0.0000	0.0822
106996	105654	0.0092	0.0056	0.0029	0.0000	0.0813
107220	107623	0.0175	0.0133	0.0070	0.0000	0.0803
107220	75001	0.0234	0.0161	0.0083	0.0001	0.0835
107220	88336	0.0238	0.0199	0.0105	0.0000	0.0774
107220	37353	0.0211	0.0159	0.0086	0.0001	0.1057
107220	105654	0.0203	0.0151	0.0082	0.0000	0.0912
107623	75001	0.0089	0.0059	0.0032	0.0000	0.0788
107623	88336	0.0113	0.0079	0.0043	0.0001	0.0862
107623	37353	0.0298	0.0260	0.0143	0.0003	0.0736
107623	105654	0.0101	0.0066	0.0035	0.0001	0.0656
75001	88336	0.0214	0.0174	0.0094	0.0000	0.0807
75001	37353	0.0342	0.0282	0.0152	0.0002	0.0794
75001	105654	0.0176	0.0130	0.0069	0.0001	0.0711
88336	37353	0.0102	0.0065	0.0035	0.0001	0.0841
88336	105654	0.0184	0.0141	0.0076	0.0002	0.0731
37353	105654	0.0175	0.0121	0.0065	0.0001	0.0950

Table B.9: Hardware output data for the TUBULIN_AB data set

Name1	Name2	T	MC	F	WU	U
Tubulin A	Tubulin B	417	47	46.8352	44.5991	0.6345