Statistical Mappings of Social Choice Rules*

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ABSTRACT:
This paper presents a statistical analysis of 21 social choice rules. Under a wide variety of profile assumptions, similarity matrices were generated which contained pairwise similarity data for every pair of the 21 rules (Monte Carlo simulations were run to indicate how often any pair of rules picked the same winner). The techniques of hierarchical clustering and multidimensional scaling were then applied to these similarity data in order to create clusterings and visual mappings of the rules. Through the clusters and sub-clusters generated by hierarchical clustering, we gained an overall picture of the relationships between these rules. By varying the assumptions on our profile type, we investigated how these clusters change as we alter the number of alternatives, the number of voters, and the distribution of preferences. Through the plots generated by multidimensional scaling, we were able to begin an investigation of which rule properties have the greatest effect on rule behavior.

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As a reader of this paper, I submit my approval of the work contained herein as sufficient for a M.S. thesis in Symbolic Systems.

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Introduction

In "On the probability that all decision rules select the same winner", Merlin, Tataru, and Valognes (2000) correctly point out that since the publication of Kenneth Arrow's strongly negative Impossibility theorem, the discussion within the social choice literature of the relative merits and drawbacks of various social choice rules has, perhaps unexpectedly, only intensified. Arrow's theorem is concerned with the problem of selecting an ideal procedure for deciding the outcome of an election in which voters submit their preferences over the contending candidates, or alternatives. His impossibility result essentially says that no social choice rule exists which satisfies certain (arguably) desirable properties (Arrow 1963).

If we are skeptical of Arrow's assumptions, then we are back to where we started, faced with a slew of potentially desirable social choice rules to choose from. But, as Merlin et al. argue, even if we accept Arrow's argument, we are still left with the task of sorting through the available rules, flawed as they may be, to determine which imperfect rule best suits our current purposes. Depending on one's ideological bent, the collection of social choice rules either live together or die together, but either way, it becomes necessary at the end of the day to choose amongst these rules one which is acceptable to the members of whatever community will be implementing it as the procedure of choice. Thus, though Arrow's theorem fails to parcel up the space of rules into smaller groups that can be ruled out or in, en masse, it has succeeded in bringing greater attention to the more general problem of studying the properties of, and relationships among, the various social choice rules that have been proposed in the literature.

Perhaps due in part to the theoretical nature of Arrow's theorem and the profound influence it has had on the field, the bulk of analysis done on social choice rules and their relationships to one another has also been governed by an a priori theoretical approach. However, for some time, and increasingly so recently, the "empirical" (or computational) branch of social choice has endeavored to apply the power and robustness of various computational and statistical techniques to the problem of analyzing a host of social choice rules.

One of the earlier computational studies in which a variety of social choice rules were compared was carried out by Bordley (1983). Bordley developed a comprehensive approach by testing rules with a variety of electorate and candidate pool sizes. However, rather than analyzing rules in a descriptive framework, he focused instead on evaluating rules based on a somewhat arbitrary welfare function from which he attempted to assess the 'desirability' of each of the rules. Nurmi (1990) extended this work and also incorporated the normative component by calculating Condorcet efficiencies[1] for a variety of rules (using Condorcet efficiency as a measure of desirability), but he also engaged in descriptive analysis by calculating the frequencies with which various pairs of social choice rules select the same winner by running Monte Carlo simulations on a large number of profiles generated with the so-called "impartial culture assumption" (see description in *Methodology* section below).

The aforementioned paper by Merlin et al. and a paper by Lepelley, Pierron, and Valognes (2000) also concern themselves with the questions of how often certain rules select the same winner and how

[1] The Condorcet winner, if one exists, is the alternative that beats all other alternatives in pairwise head-to-head contests. The Condorcet efficiency of a rule is the frequency with which that rule selects the Condorcet winner as the winning alternative, whenever a Condorcet winner exists.

often they select the Condorcet winner, respectively. Their aim is similar to Nurmi's, although, unlike Nurmi, they rely on analytic and classical computational techniques to arrive at these results.

Each of the studies mentioned above breaks new ground, but at the same time is lacking in an area better attended to by one of the other papers. Merlin et al. include more rules in their analysis than any of the other papers mentioned; however, they carry out their computations only for the 3 alternative case. Nurmi looks at a variety of profile sizes, but only compares a relatively small set of social choice rules. Thus, though Merlin et al. find that weighted scoring rules have a relatively high probability of choosing the same winner in the three alternative case, work by Nurmi and also by Gehrlein and Lepelley (2000) involving Monte Carlo simulations indicate that this probability drops off rapidly as the number of alternatives increases. Unfortunately, these simulations are only carried out for a fairly circumscribed set of social choice rules and so, it is difficult to make any broader statements about deeper relationships that may exist among the set of commonly discussed social choice rules.

The purpose of this paper is to build upon the computational analyses that have already been done, but also to extend this work in two significant ways. First, we aim to achieve a level of robustness that has seldom been attained in computational work of this sort. By combining the insights gleaned from the existing literature, we report here results that pertain to the behavior of a large number of social choice rules across a variety of profile sizes. Second, we go beyond "How often do these rules pick the same winner?" studies by using similarity data to investigate more complex relationships among the social choice rules studied. Specifically, we use the techniques of hierarchical clustering and multidimensional scaling to process similarity data into richer, more structured models of the relationships between social choice rules. Hierarchical clustering uses similarity data to group rules into sets and subsets, allowing us to examine the set of choice procedures holistically. Multidimensional scaling uses similarity data to create a visual mapping of the choice procedures – we interpret the dimensions of this mapping to give ourselves a clearer idea of how the internal structure of the choice procedures affects the winner that it ultimately selects. Both of these procedures will be described in further detail below.

Definitions

We consider situations in which a group of n voters, $V = \{v_1, \ldots, v_n\}$ must collectively choose one alternative from a set of m alternatives, $A = \{a_1, \ldots, a_m\}$. Each voter i submits his/her preferences over the alternatives, from most preferred to least preferred, as an m-tuple, P_i. The set of preferences of the group as a whole $\{P_1, \ldots, P_n\}$, is denoted by P and is also known as a *preference profile*. The domain of preference profiles P is called D. We now define a Social Choice Function (SCF), F, as a mapping from D to A:

SCF: $F: D \rightarrow A$

Thus, for any preference profile, an SCF, also known informally as a social choice rule, voting rule, or voting procedure, selects one alternative a_i as the 'winner'. For the purposes of this paper, it is assumed that voters' preferences are strict – no ties are allowed.

Descriptions of Computational Techniques

Hierarchical Clustering

Hierarchical clustering is a technique that has traditionally been used to classify groups of input patterns into clusters of distinct groups, with each cluster containing sub-clusters of increasingly similar patterns. For example, given similarity data about a variety of biological organisms, a hierarchical clustering algorithm might first group the organisms together into clusters of organisms of the same species. It would then group together those clusters of species that belong to the same genus, then those genera that belong to the same family, and so on (this example, and a deeper discussion of this technique, can be found in Duda, Hart, and Stork 2001). Thus, at the first 'level' of clustering, we would have as many distinct clusters as we do organisms being classified. At the second level, we would have fewer clusters – each cluster corresponding to a particular species. At the third level, some of the clusters would merge because they are part of the same genus – at the top of this hierarchy, we would be left with one large cluster that contained all of the organisms being classified. The lower the level, the more similar are the objects that are clustered together; nonetheless, by looking at the whole map of hierarchical clusters (such a map is called a *dendrogram*), we can get a more comprehensive picture of organism similarity than is provided by merely looking at pairwise similarity data.

In our study, we applied the technique of hierarchical clustering to 21 social choice rules. We gathered similarity data for the social choice rules by generating, for a variety of profile sizes, 10000 random preference profiles (see the *Methodology* section below concerning the assumptions governing these profile cultures) and determined how often each pair of rules picked the same winning alternative. This defines a *similarity matrix*: entry [i,j] indicates how often rule i and rule j pick the same winner. The statistical/computing software suite Matlab provides functionality for performing hierarchical clustering analysis on such similarity matrices. We used Matlab to perform the clustering analysis, and to generate dendrogram plots with which to analyze the results.

Though the biological taxonomy example above gives the gist of how hierarchical clustering works, a bit more needs to be said about the specific algorithm that is used to create the successively higher-level clusters. The following pseudo-code describes a bit more precisely how this technique proceeds at each step of the clustering process:

At step r:

For each pair of pre-existing clusters (if a sub-cluster in some earlier step has since been merged into a larger cluster, consider only the larger cluster), determine how dissimilar the two clusters, A and B, are by finding the average dissimilarity between all pairs x, y in which $x \in A$ and $y \in B$. Find the two clusters that are most similar and merge them, making note of their average dissimilarity (to be used in the analysis, later). If, after this merge, there are still more than 2 clusters remaining, proceed to step r+1. Otherwise, stop the procedure.

Notice that in order to measure the dissimilarity between any two clusters we calculate the *average* dissimilarity between their respective members. In fact, a variety of metrics could be used instead – we could find the minimum dissimilarity between objects of each cluster or, in turn, we could base this measure on the maximum dissimilarity between the members of each cluster (i.e. for any pair of clusters, dissimilarity could be measured by the minimum/maximum dissimilarity between members of the two clusters). The *cophenetic correlation coefficient* is a measure of how well a particular clustering fits the original similarity data – the closer the coefficient is to '1', the better the clustering (Sokal and Sneath 1973, 278). We found that employing the average dissimilarity metric provided higher values for the cophenetic correlation coefficient than either the minimum or maximum dissimilarity metrics. Further details about the procedure used to create the similarity matrices and clustering dendrograms is provided in the *Methodology* section.

Multidimensional scaling

Multidimensional scaling (MDS) has often been described in the following way: suppose you are given the pairwise distances between a group of cities in the U.S. and would like to reconstruct a map of the country based on these distances. The multidimensional scaling algorithm takes as inputs these pairwise distances and generates as output a map of each of the original points to which the distances refer (Kruskal and Wish 1978). It is up to the analyst to determine what the dimensions of the map represent (in the case of the U.S. map, we might infer that one axis corresponds to East-West distances while the other axis refers to North-South distances). Nevertheless, MDS allows us to turn a mass of unstructured pairwise similarity data into a map which visually displays the relationship of each of the points in question to the other points. In essence, MDS is a technique for transforming complex data into a simplified form by using approximations to reduce the number of dimensions that are required to convey the relationships contained in the data.

We applied MDS to 21 social choice rules by using the same similarity matrices described above. Again, we generated random profiles for a variety of profile sizes (described in further detail below), created similarity matrices for each of the profile sizes, and generated mappings of the social choice rules using a newly available Matlab multidimensional scaling function. By looking at the dimensions along which the rules differed from each other, we could create interpretations for each of the significant dimensions, thereby gaining an understanding of the relative contribution of a particular characteristic (or dimension) to the overall social choice. For example, if the most salient dimension turns out to measure *Condorcet efficiency* (how often a rule selects the alternative that beats all other alternatives in head-to-head, pairwise contests, provided that such an alternative exists), then we can conclude that the degree to which a rule takes into account pairwise contests is the most significant factor in determining the way in which it will behave. Whereas hierarchical clustering gives us insight into the degree to which various rules behave similarly (i.e. how often they pick the same winner), MDS helps us understand *why* different rules behave as they do.

Again, some more explanation is needed regarding the procedure used by the version of MDS we employed. The Matlab scaling function takes as input a matrix of similarity data (just the same similarity matrix described in the hierarchical clustering section above) and generates as output a set of points of dimensionality d. It creates these points and determines the number of dimensions necessary by minimizing a sum squared error criterion function – it chooses the set of points such that the distances between these points correspond most closely to the input similarity data. In addition, it creates a vector of eigenvalues[2] of length d – each eigenvalue corresponds to one of the dimensions of the set of points.

[2] This vector of eigenvalues contains the sorted eigenvalues of the matrix equal to Y*Y', where Y is the r x d output of the scaling function, r is the number of rules (points), and d is the number of dimensions.

The eigenvalues are ordered from high to low and range from 1 to 0. Each eigenvalue gives a measure of the relative importance of the corresponding dimension in determining the layout of the points (again, each point corresponds to a different social choice rule). Thus, if after the first 6 dimensions the magnitude of the eigenvalues drops off sharply, we can deduce that we can get a reasonable understanding of the data by concerning ourselves only with the first 6 dimensions of each point.

As described in further detail below, we created a variety of rule plots by varying our starting assumptions regarding number of voters, number of alternatives, etc. We were able to compare the plots generated in each of these cases by using *procrustes* analysis[3]. The procrustes algorithm takes two sets of points (in which the ith point of the first set corresponds to the ith point of the second set) and transforms the second set so that it more closely 'matches up' to the first set – the algorithm proceeds by reducing a sum squared error criterion. By using procrustes analysis, it was possible to compare plots of points created with differing assumptions on the initial conditions.

Methodology

The rules

We chose to investigate the relationships among 21 social choice rules – we attempted to include as many of those rules that have appeared in the social choice literature as was feasible. The list of rules we included in the study appears in the Appendix, along with descriptions of how each of these rules chooses a winner. Also in the Appendix are listings and descriptions of those rules that we omitted because of considerations of computational complexity. We hope that the rules in the Appendix can form the basis of a repository for all social choice rules, as we have yet to come across a comprehensive listing of all of the rules that are commonly (and less commonly) discussed in the literature – with the informed feedback of the social choice community, we hope that this list can serve as a public resource for interested researchers. Moreover, because we have saved all of the profiles and results of the experiments described below, we invite other researchers to add to our work and add as many rules as they wish to the mappings discussed below. Because the data from our experiments will be publicly available, it should be possible to add new rules to the mappings without having to rerun the pre-existing rules on the data.

A note on tie-breaking

Many of the rules included do not necessarily choose a unique winner but rather result in a 'choice set', or group of alternatives that are determined to be superior to all other alternatives but tied amongst themselves. In general, it is standard convention for ties to be broken randomly. However, we have chosen to break ties non-randomly[4] – unless otherwise specified, we break ties among winning alternatives by choosing in accordance with the preferences of the first voter, v_1. Had we chosen to break ties randomly, we would risk losing relationships between rules that pick the same set of winners – if two rules always picked the same set of x winners, then the probability that they would actually pick the same winner with random tie-breaking would only be 1/x, whereas with non-random tie-breaking, these two

[3] Thanks to David Donoho and Carrie Grimes for their assistance with using this technique.

[4] Thanks to Arkadii Slinko and Wayland Leung for their work on this method.

rules will always pick the same winner. In addition, in cases when two rules pick similar, but slightly different, sets of winners, this method of tie-breaking will result in the two rules choosing the same, unique winner more often than random tie-breaking, though some randomness will be preserved due to the different possible permutations of v_1's rankings (Choice sets {x,y,z} and {x,y} will be deemed the same when v_1 ranks z below x or y; they'll result in different winners when v_1 ranks z ahead of both x and y). We believe that, even if two rules don't pick the exact same set of winners, the similarity in their choice sets should be reflected by our clustering and scaling procedures. This method reflects such similarities while preserving enough randomness to prevent the extreme case in which two choice sets are always judged to be the same whenever they contain only one alternative in common.

Parameters

In order to carry out the clustering and scaling procedures described above, it is first necessary to generate a similarity matrix which contains, for every pair of social choice rules, data indicating how often, given a large number of randomly generated profiles, that pair of rules selects the same winner. Clearly, this similarity value can depend on a number of parameters – how many voters and alternatives do we assume for our randomly generated profiles? And, what assumptions should we make about the distribution of voters' preferences within these profiles?

We created similarity matrices under a wide range of assumptions so that we could study the effect of varying these parameters on the resultant clusters and mappings. Specifically, we studied two types of preference distributions – the impartial culture hypothesis (IC) and the clustered culture hypothesis (CC) – both described below. For each type of culture, we created 20 different similarity matrices, corresponding to 20 different profile sizes. We considered profile sizes in which we varied the number of alternatives from 3 to 15 in increments of 4 [3, 7, 11, 15], and for each of these numbers of alternatives, we created similarity matrices in which we varied the number of voters from 5 to 85 in increments of 20 [5, 25, 45, 65, 85] (from the four alternative sizes and the five voter sizes we get the 20 different profile sizes). With 20 similarity matrices for each of the two cultures, we have a total of 40 different similarity matrices, i.e. 40 dendrograms from hierarchical clustering and 40 mappings from the MDS procedure. A significant portion of the analysis involved determining the effect of varying these parameters.

For each of the 40 profile types, we randomly generated 10000 instances of the profile type and determined the winning alternative according to each of the 21 rules studied. By seeing how often each pair of rules picked the same winner for each profile type, we were then able to create 40 similarity matrices, one for each of the profile types. We determined that 10000 is a sufficient number of profiles by steadily increasing the number of profiles used until the data in our similarity matrices became sufficiently stable. In fact, for relatively small profile sizes (3 alternatives, 5 voters; 7 alternatives, 5 voters, 3 alternatives, 25 voters), multiple 10000 profile runs resulted in similarity matrices that were identical with previous runs of the same sizes to four significant digits. We used a sum squared error criterion on pairs of similarity matrices to quantitatively measure of the differences between any two runs. This technique allowed us to test for stability when both members of the pair were of the same profile type and also to test the effect of varying the numbers of alternatives and voters and the type of preference distribution when the members of the pair were of different profile types.

Cultures Explained

Impartial Culture hypothesis

The impartial culture hypothesis (IC) assumes that for each voter, every possible preference ordering on the alternatives is equally likely. As a result, there are no dependencies between voters, i.e. no voting blocs – every voter's preferences are generated independently of the other voters' preferences.

Clustered Culture hypothesis

The clustered culture hypothesis (CC) assumes that the electorate is divided into voting blocs who have similar preferences[5]. In fact, there are an infinite number of ways in which we could divide up the electorate, but for our purposes, we made a somewhat arbitrary choice for the purpose of seeing whether the results changed at all. Specifically, we divided the electorate into four groups, consisting of 35%, 30%, 20%, and 15% of the total number of voters, respectively. We assumed that the 20%-voting bloc consisted of independent voters whose preferences were determined according to the impartial culture hypothesis. For each of the other voting blocs, we randomly generated one preference ordering, and then introduced some randomness into the bloc by, for each voter in that bloc, starting with the initial preference ordering and then swapping m randomly chosen pairs of alternatives, where m is the total number of alternatives. The result is that, for each of these blocs, we have a modal distribution, peaking at the initial randomly generated order. Had we swapped 0 pairs, we would have had no randomness within the voting blocs. And, as Diaconis and Shahshahani (1981) have shown, we, in general, need to swap m*ln(m) pairs in order to ensure a uniform distribution (bringing us back to the Impartial Culture hypothesis) . As a result, we decided to choose a value between these two extremes, albeit biased toward the random side.

Clearly, the choice of number of voting blocs, size of voting blocs, and level of randomness within the voting blocs is arbitrary and a number of other reasonable starting assumptions could have been made. We wish to stress that the purpose of carrying out the study with this alternate preference distribution assumption was not to exhaustively examine the effect of varying the distribution assumption, but rather to make an initial inquiry into whether altering this assumption would make a difference – of course, if it had made no difference, then we would not be able to conclusively say that the distribution assumption is unimportant. But, we hypothesized (correctly) that it would make some difference, and as a result, we hope that this study will lay the groundwork for future studies in which the distribution assumption can be examined more closely.

Results

Sensitivity Analysis

Before analyzing the various rule clusters formed by hierarchical clustering or interpreting the dimensions of the plots created by MDS, we first give a brief account of the effect of varying the number

[5] Thanks to Arkadii Slinko and David Donoho for their suggestions regarding this culture.

of alternatives and number of voters on the results. We will first examine the effect of varying the number of alternatives and number of voters in the IC hypothesis. After giving a sensitivity analysis for the IC case and indicating the Clustering Results for the IC case, we will then discuss the significant ways in which the CC results differed from the IC results.
We measure the difference between the clusters and MDS plots associated with any pair of profile types in three ways:

1) Quantitatively - we use a sum squared error criterion (henceforth denoted as 'SSE') to measure the difference between the similarity matrices of the two profile types in question

2) Visual inspection of plots – after determining the number of dimensions required to represent the data associated with the pair of profile types, we examine the MDS plots associated with these profile types and visually gauge how similar or different they appear

3) Visual inspection of dendrograms – we compare the dendrograms associated with the two profile types in question and determine whether the dendrograms represent similar or different clusters and sub-clusters of rules

As mentioned in the above description of MDS, we determine the number of dimensions required to 'capture' the relationships within the similarity matrix by examining the spread of eigenvalues – if the jth eigenvalue represents a sharp drop-off and is relatively close to 0, then we can safely assume that only j-1 dimensions are required to represent the data.

In general, when the number of alternatives in a profile is held constant, the number of dimensions required to represent the data increases with the number of voters, reaching a plateau when the number of voters is 25 (i.e. the 5-voter case differs from the other voter sizes tested). Similarly, when the number of voters in a profile is held constant, the number of dimensions required to represent the data increases with the number of alternatives, reaching a plateau when the number of alternatives reaches 11.

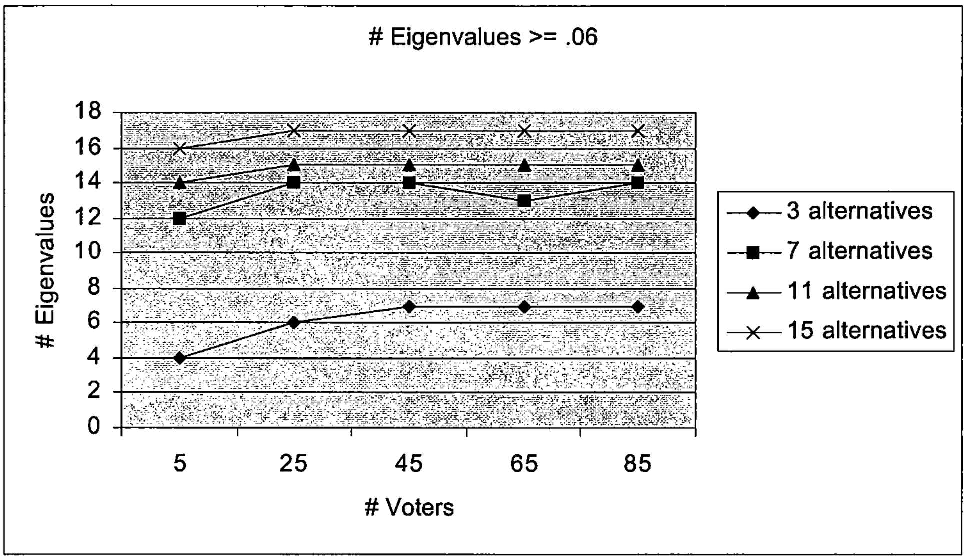
Table 1 below indicates the number of dimensions deemed necessary to represent the data for each profile size tested under the IC hypothesis. Though this decision was based on a combination of eigenvalue size and the relative difference between successive eigenvalues, the trend in these numbers corresponds roughly with the number of eigenvalues for a particular profile size that are greater than or equal to .06 (a measure that is based only on eigenvalue size)[6] – a graph of these numbers is provided for the sake of giving a quantitative measure of the trend in the vectors of eigenvalues produced by MDS (Graph 1).

Table 1 – # of Dimensions deemed necessary for representing the data based on eigenvalue analysis

	5 voters	**25 voters**	**45 voters**	**65 voters**	**85 voters**
3 alternatives	4	6	7	7	7
7 alternatives	8	13	13	13	13
11 alternatives	12	15	15	15	15
15 alternatives	14	15	15	15	15

[6] Because the dissimilarities are Euclidean, all eigenvalues fall between 1 and 0, with .06 being a common cutoff value.

Graph 1 – # Non-small eigenvalues corresponds roughly to # Dimensions



Findings

In general, we found that when we held the number of alternatives constant and increased the number of voters, the clusters and plots would become relatively stable once the number of voters reached 45; though, even the 25-voter case was often quite similar to the 45-voter (and above) scenarios. Also, the 5-voter case tended to be quite different from all other cases. Perhaps this is not surprising as profiles involving only 5 voters are capable of representing a much less complex electorate than is possible in the other, higher voter size cases. Table 2 indicates the SSE, averaged across all alternative sizes, between the 5 voter and 25 voter cases, the 25 voter and 45 voter cases, etc, for the IC hypothesis. As can be seen, as the number of voters increases, the SSE between each voting size and the preceding voting size gets smaller, indicating that the plots and clusters created by MDS and hierarchical clustering, respectively, become more and more similar.

Table 2 – Sum squared error b/n similarity matrices of adjoining voter sizes – IC

	5 vs. 25 voters	**25 vs. 45 voters**	**45 vs. 65 voters**	**65 vs. 85 voters**
SSE	2.1940	.0554	.0194	.0124

When the number of voters is held constant, the resultant plots and clusters stabilize a bit when the number of alternatives is increased, but not as much stabilization occurs as when the number of voters is increased and the number of alternatives is held constant. The 3 alternative case is significantly different from all other cases – in comparison to the 3 alternative case, all other cases look relatively similar. Again, this is perhaps not surprising, as with only 3 alternatives, many of the rules that would produce different results if there were more alternatives are instead constrained to choose the same winner. However, there are important differences between the 7, 11, and 15 alternative cases as well – the substantive differences among all these cases will be discussed in more detail in the Clustering Analysis section below. But, one reassuring observation is that, with a few exceptions, there seem to be negligible interaction effects between number of voters and number of alternatives. Thus, though the 7-alternative 25-voter case differs from the 11-alternative 25-voter case, these cases differ in much the same way that the 7-alternative 45-voter case differs from the 11-alternative 45-voter case. The pairwise SSE values for adjoining alternative sizes in the IC hypothesis, averaged across number of voters, are given in Table 3 below.

Table 3 – Sum squared error b/n similarity matrices of adjoining alternative sizes – IC

	3 vs. 7 alternatives	**7 vs. 11 alternatives**	**11 vs. 15 alternatives**
SSE	11.0536	2.4757	.8936

Clustering Results

General observations

Throughout the results, certain clusters of rules appeared in which all rules in the cluster picked the same winner the majority of the time. The Impartial Culture 11 alternative 45 voter case (henceforth denoted as 'IC-11-45') gives a good indication of the general layout of the social choice rule clusters, and I discuss that case in detail here. Later, I will indicate significant differences between this case and other cases. All dendrograms appear in the Appendix.

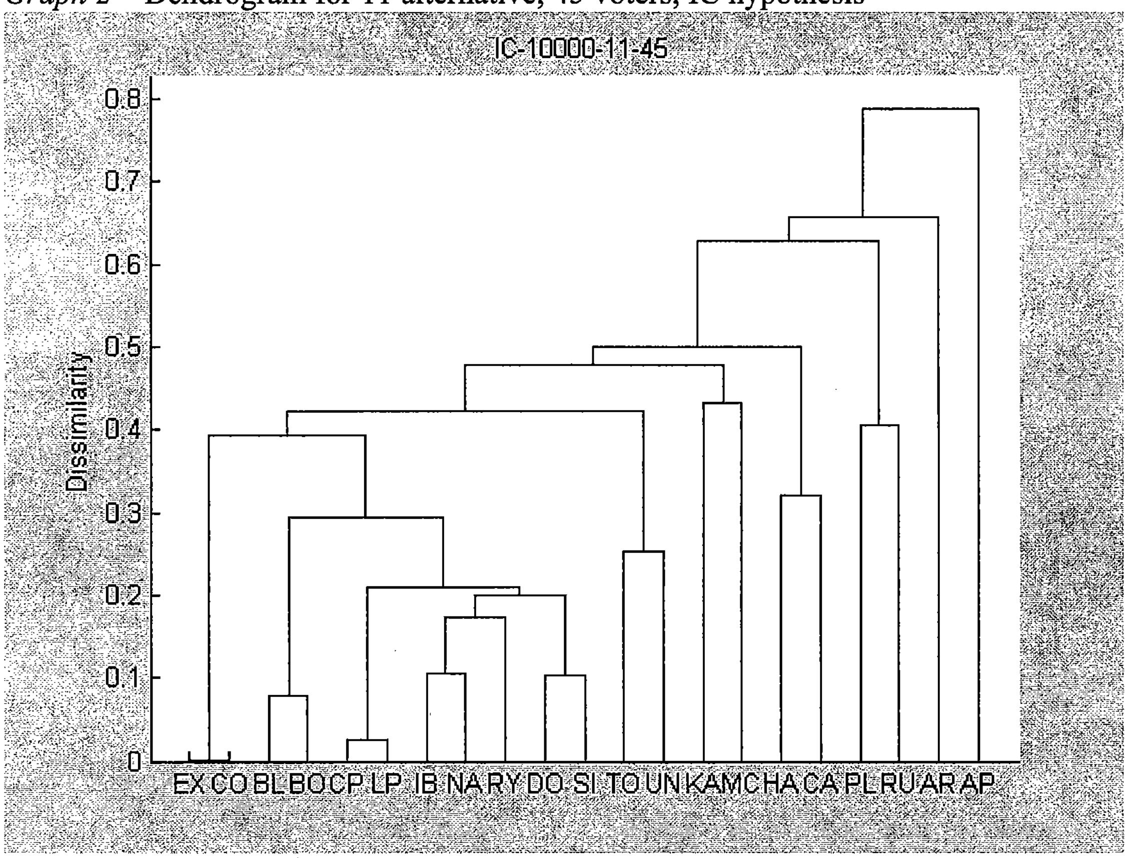
Remember that the clustering algorithm creates clusters by looking at all pre-existing clusters (including singleton sets) and determining which pair of clusters is most similar. As described above, we used the 'average distance' metric, which measures the average dissimilarity between members of one cluster and members of the other cluster. Below, I list the clusters whose similarity values are greater than .55 (the algorithm continues forming clusters below this value, but it is questionable whether the clusters at this low level of similarity are any longer meaningful), in the order that they were formed by the algorithm (i.e. in order of decreasing similarity) along with a brief analysis. I include in parentheses the average similarity metric (1 – Dissimilarity, as it appears on the y-axis of Graph 2) that was used to create this cluster from its two constituent clusters (in the case of clusters of size 2, this will simply be the similarity between the two rules). Graph 2 contains the dendrogram for this profile type (Impartial culture, 10000 profiles, 11 alternatives, 45 voters). Table 4 gives the rule abbreviations used in this and all other graphs.

Table 4 – Rule Abbreviations

Rule	**Abbreviation**
Antiplurality	AP
k-Approval	KA
Approval	AR
Black	BL
Borda	BO

Exhaustive	EX
Copeland	CP
Hare	HA
Inverse Borda	IB
Longpath	LP
Majoritarian compromise	MC
Dodgson	DO
Nanson	NA
Plurality	PL
Plurality Runoff	RU
Simpsons	SI
Top cycle	TO
Uncovered set	UN
Raynaud	RY
Coombs	CO
Carey	CA

Graph 2 – Dendrogram for 11 alternative, 45 voters, IC hypothesis



-*Cluster 1*: Exhaustive and Coombs (.9996) – These rules are understandably close as they are both elimination rules which eliminate the alternative that receives the most last place votes. They differ only in their criterion for stopping the elimination procedure – Coombs stops when one alternative receives more than 50% of the first-place votes, Exhaustive stops when there is only one alternative remaining.

-*Cluster 2*: Copeland and Longpath (.9742) – This clustering can be understood by the fact that the Longpath method is essentially a variation on Copeland.

-*Cluster 3*: Black and Borda (.9224) – Again, this cluster is not unexpected, as Black simply picks the Borda winner when there is no Condorcet winner. As will be discussed below, the similarity between these rules necessarily depends on the likelihood of a Condorcet winner, which in turn, depends on the profile type.

-*Cluster 4*: Dodgson and Simpson (.8969) – These rules are both concerned with the amount by which an alternative loses to all other alternatives – Simpson picks the alternative with the smallest such defeat (as measured by number of voters who prefer other alternatives to the alternative in question) whereas Dodgson sums up each alternative's margins of defeat and chooses the alternative with the smallest such sum.

-*Cluster 5*: Inverse Borda and Nanson (.8941) – These rules also use a very similar procedure – Inverse Borda eliminates the alternative with the lowest borda score whereas Nanson eliminates all alternatives with below average borda scores.

-*Cluster 6*: (Inverse Borda, Nanson) and Raynaud (.8274) – Raynaud is similar to the other two rules in that it is also an elimination procedure which considers each alternative's relationship to the other alternatives.

-*Cluster 7*: (Inverse Borda, Nanson, Raynaud) and (Dodgson, Simpson) (.7997) – With the exception of Raynaud, all of these rules always pick the Condorcet winner, if one exists. Raynaud picks the Condorcet winner the vast majority of the time (99%, averaged across all profile sizes).

-*Cluster 8*: (Copeland, Longpath) and (Inverse Borda, Nanson, Raynaud, Dodgson, Simpson) (.7895) – With the exception of Raynaud and Longpath, all of these rules also pick the Condorcet winner, if one exists (note the close values of similarity metrics between this and the preceding cluster). Longpath picks the Condorcet winner 99.95% of the time, averaged across all profile sizes.

-*Cluster 9*: Top Cycle and Uncovered Set (.7463) – Both of these rules are concerned with choosing an alternative x such that if yMx for some y, then x and y are part of the topmost cycle (Top Cycle rule) or y is beaten by some other alternative z which does not beat x (Uncovered Set). But, these two criteria will often amount to the same thing.

-*Cluster 10*: (Black, Borda) and (Copeland, Longpath, Inverse Borda, Nanson, Raynaud, Dodgson, Simpson) (.7050) – All of these rules deal, in varying degrees, with the whole profile, rather than constraining their attention to only one part of it. In addition, all of these rules are highly Condorcet efficient (for this profile size, Borda has the lowest Condorcet efficiency among these rules, at 84%).

Note however, that only 49% of the profiles of this type (IC-11-45) had a Condorcet winner. So, even when there was no Condorcet winner, these rules picked the same alternative a significant percent of the time.

-*Cluster 11*: Hare and Carey (.6786) – Again, these rules use a similar algorithm – Hare eliminates the alternative with the fewest first-place votes (lowest plurality score) whereas Carey eliminates all alternatives with below average plurality scores.

-*Cluster 12*: (Black, Borda, Copeland, Longpath, Inverse Borda, Nanson, Raynaud, Dodgson, Simpson) and (Exhaustive, Coombs) (.6056)

-*Cluster 13*: Plurality and Runoff (.5956) – Both of these rules rely heavily on the top row of voters' profiles.

-*Cluster 14*: (Black, Borda, Copeland, Longpath, Inverse Borda, Nanson, Raynaud, Dodgson, Simpson, Exhaustive, Coombs) and (Topcycle, Uncovered Set) (.5772)

-*Cluster 15*: k-Approval and Majoritarian Compromise (.5688) – Both of these rules involve looking only at the some upper portion of the preference profile

Rules that don't appear in sub-clusters: Approval, Antiplurality

Cluster analysis

While most of the clusters above appeared in most of the dendrograms in roughly the same order as above, the behavior of some of the rules, and hence the size and shape of some of the clusters, did clearly depend on the size of profile tested. While all distinct dendrograms are given in the Appendix, I will discuss here some of the more interesting cluster behavior. In this analysis, I will give emphasis to clusters in the IC hypothesis that differed when the number of alternatives varied among [7, 11, 15] and the number of voters varied among [25, 45, 65, 85] – I pay a bit less attention to the 3 alternative and 5 voter cases. Though these cases often differed significantly from the other cases, it seems that a good portion of these differences are due to the relatively homogenous nature of the profiles of this type. I will discuss how the CC results differed from the IC results after this section. The analysis and tables immediately below are confined to the results of the IC experiments.

Exhaustive and Coombs

As mentioned above, these rules use very similar procedures and it is therefore not surprising that they usually pick the same winner. However, the likelihood that they do choose the same alternative does seem to depend significantly upon the number of voters in the profile (it depends relatively less on the number of alternatives). One explanation for this behavior is the idea that the two rules are most likely to pick different winners if a majority winner exists at any point in the elimination process (Coombs will stop and pick this alternative, Exhaustive will continue eliminating alternatives based on the last row of the profile, perhaps even eliminating the majority winner), and we would expect the likelihood of such a situation occurring to be correlated with situations in which a Condorcet winner exists (whenever a Condorcet winner exists, the probability is higher that there exists some step in which there is also a majority winner).

Table 5 below gives for each voter size the percent of profiles with a Condorcet winner (averaged across all alternative sizes) and also the similarity value for Coombs and Exhaustive. As expected, the similarity values vary inversely with the frequency of Condorcet-winning profiles.

Table 5 – Results averaged across all alternative sizes

# Voters	% Condorcet profiles	Exhaustive/Coombs Sim
5	68	.91
25	62	.99
45	61	~1.00
65	60	1.00
85	61	1.00

Black and Borda

These rules differ only in that Black will always choose the Condorcet winner if one exists. Thus, we can expect that their similarity values should depend on the likelihood of a Condorcet winner existing (and, in smaller part, the Condorcet efficiency of the Borda winner, depending on profile type). In fact, this is exactly what we find. The percentage of profiles with a Condorcet winner depends most heavily on the number of alternatives, declining significantly as the number of alternatives is increased. Table 6 below gives the following values for each alternative size (results are averaged across all voter sizes): percent of profiles with a Condorcet winner, the similarity values for the Black and Borda rules (BL/BO), and the Condorcet efficiency of the Borda rule.

We would expect that the similarity between Black and Borda should increase as the percentage of Condorcet-winning profiles decreases (because if there is no Condorcet winner, Black simply picks the Borda winner). This is what we find below, except in the 3 alternative case. But, this result is explained by the fact that Borda's Condorcet efficiency is highest when there are only 3 alternatives. So, when there are 3 alternatives, though Black and Borda use different procedures, they still usually (92% of the time) choose the same winning alternative.

Table 6 – Results are averaged across all voter sizes

# Alts	% Condorcet Profiles	BL/BO Sim.	Borda Condorcet Eff.	DO/SI Sim.	IB/NA Sim.	TO/UN Sim.	HA/CA Sim.	PL/RU Sim.
3	92	.92	.92	1.00	.99	1.00	.95	.80
7	54	.90	.85	.93	.93	.90	.76	.65
11	51	.92	.84	.87	.90	.77	.66	.61
15	41	.93	.84	.82	.87	.68	.59	.59

Dodgson and Simpson

As mentioned above and discussed in more depth in the Appendix, Simpson's procedure is essentially a type of minimax algorithm which picks the alternative with the smallest maximum defeat. Dodgson (the simplified version of which we have implemented) sums up the margins by which alternative x loses to other alternatives (ignoring alternatives against which x is the winner) to score each alternative negatively. Simpsons procedure essentially only considers alternative x's results against its most superior rival, whereas Dodgson considers x's results against all of its superior rivals. Thus, the fewer the alternatives, the smaller the discrepancy between the amount of information considered by Simpson and Dodgson. Table 6 corroborates this explanation, listing, for each alternative size (averaged across all voter sizes) the similarity values for Dodgson and Simpson (DO/SI). As expected, the similarity value decreases as the number of alternatives increases because the discrepancy between the amount of information considered by each rule increases with the number of alternatives.

Inverse Borda and Nanson

Because both of these rules are elimination procedures based on the Borda count, it is not surprising that their similarity values are virtually identical across voter sizes (when number of alternatives is held constant) – no matter how many voters there are, both rules eliminate alternatives based on their relative 'strength' in the rankings.

However, the similarity value for these rules does depend significantly on the number of alternatives as can be seen in Table 6 (IB/NA). Perhaps the best explanation for this phenomenon is the idea that with more alternatives, there will be more elimination rounds. And, because the two rules use different criteria for eliminating alternatives, there are more opportunities for one of the rules to eliminate the alternative that will eventually be chosen by the other rule.

Raynaud

Though the cluster results above report that Raynaud first joins the {Inverse Borda, Nanson} cluster, its location in the dendrogram actually depends on the number of alternatives. For lower numbers of alternatives (3 and 7), Raynaud first joins up with the {Dodgson, Simpson} cluster. For higher numbers of alternatives (11 and 15), Raynaud first joins up with the {Inverse Borda, Nanson} cluster, as reported above for the 11-45 case.

This behavior is perhaps best explained by the fact that Raynaud is an elimination procedure (like Inverse Borda and Nanson) whose criterion for eliminating alternatives is much more similar to the Dodgson and Simpson methods of choosing the winner than the Inverse Borda and Nanson methods' criteria for eliminating alternatives. Thus, for lower numbers of alternatives, there are fewer rounds of elimination, and the criterion function is the dominant factor in determining the clustering behavior of Raynaud. But, for higher numbers of alternatives, there are many rounds of elimination, and thus the fact of going through an elimination procedure becomes relatively more important than the actual criterion for eliminating alternatives.

Copeland, Longpath, Inverse Borda, Nanson, Raynaud, Dodgson, and Simpson

These rules (appearing in Cluster 8 above), have high Condorcet efficiencies (as mentioned above, all but Longpath and Raynaud are 100% efficient). Thus, we would expect that the average similarity metric used to link them in the dendrograms would depend on the percent of profiles of each type in which a Condorcet winner exists (if a Condorcet winner exists, then these rules are guaranteed to pick the same winner, whereas if one does not exist, they may choose differently). This is what we found. The likelihood of a Condorcet winner depends much more on the number of alternatives than the number of voters. In Table 7 below, for the 45-voter case, we give the percentage of profiles in which a Condorcet winner exists for alternative sizes 7, 11, and 15 along with the average similarity metric used to cluster these rules together (1 – Dissimilarity, as it appears on the y-axis of the dendrograms).

Table 7 – Results given for 45 voter case (IC hypothesis) – Avg. similarity pertains to Cluster 8

# Alternatives (45 voters)	% Condorcet profiles	Average similarity
7	64	.84
11	49	.79
15	40	.75

Top cycle and Uncovered set

As both of these rules are 100% Condorcet efficient, we would expect their similarity values to depend on the likelihood of a Condorcet winner occurring – and this is precisely what we found. Table 6 lists the percent of Condorcet-winning profiles for each alternative size along with the similarity values for Top cycle and Uncovered set (TO/UN – averaged across all voter sizes).

Hare and Carey

The relationship between Hare and Carey is similar to the relationship between Inverse Borda and Nanson – both use an elimination procedure (in this case, based on plurality scores) with slightly different criteria for eliminating alternatives. Just as with Inverse Borda and Nanson, the similarity values for Hare and Carey depend considerably on the number of alternatives, presumably because with more alternatives, there are more rounds of elimination, and thus more opportunities for one rule to eliminate the alternative chosen by the other rule. Table 6 lists the similarity values for Hare and Carey (HA/CA) for each number of alternatives (averaging across all voter sizes). Note that the discrepancy between Hare and Carey tends to be much larger than that between Inverse Borda and Nanson, presumably because the difference between the criteria for eliminating alternatives is greater in the Hare/Carey case (Hare and Carey use plurality scores, Inverse Borda and Nanson use Borda scores).

Plurality and Runoff

These rules often pick the same winner, but again, the frequency with which they do so depends heavily on the number of alternatives in the profile. This effect can be understood in the following way. Plurality picks the alternative, x, with the highest plurality score, s(x). Runoff first narrows down the field to the two alternatives, x and y, with the highest plurality scores s(x) and s(y). If the winner between the two Runoff finalists were to be determined at chance, then Plurality and Runoff would only have a .50 similarity value. But in fact, the winner is not determined by chance – the alternative that would win a head-to-head contest between x and y is the winner.

Now, after looking only at the voters' top row of preferences, we know that s(x) voters prefer x to y and s(y) voters prefer y to x, where $s(x) > s(y)$. We do not yet know (after looking only at the first row of preferences) how many of the remaining $n - s(x) - s(y)$ voters prefer either x to y or y to x, but, we do know that, before examining these other voters' preferences, x is ahead in the head-to-head competition with y, and the smaller the percentage of voters that make up the currently uninvestigated n – s(x) – s(y) bloc, the less chance y will have of overtaking x.

When the number of alternatives is relatively low, the number of voters in the currently uninvestigated n – s(x) – s(y) bloc will be lower, i.e. when there are fewer alternatives, the chances are higher that either x or y has appeared in the top row of voters' preferences. As a result, y will have a harder time coming up with enough votes to overtake x, and the likelihood is higher that the Runoff winner will remain the same as the Plurality winner. This trend is observed in Table 6, which lists the Plurality/Runoff similarity values (PL/RU) along with the number of alternatives in the profile (results are averaged across all voter sizes).

IC vs. CC Clustering Results

For many of the profile sizes tested, the results of the two profile distribution hypotheses were virtually identical – this was especially the case for the 7 and 11 alternative cases. However, results differed significantly for the 3 alternative case, and they were somewhat different for the 15 alternative case. Table 8 below indicates, for each profile size, the SSE between the similarity matrices generated under each preference distribution hypothesis. For example, the 3 alternatives 5 voters cell indicates the sum squared error between the similarity values generated for this profile size under the IC assumption and the similarity values generated for this profile size under the CC assumption.

Table 8 – For each profile size, SSE b/n IC and CC hypotheses

	5 voters	**25 voters**	**45 voters**	**65 voters**	**85 voters**
3 alternatives	0.2866	1.8009	3.8584	5.5722	6.4889
7 alternatives	0.016	0.0042	0.0092	0.0053	0.0124
11 alternatives	0.011	0.0145	0.0267	0.0906	0.06
15 alternatives	0.0244	0.0485	0.0575	0.1826	0.1613

Visual inspection will corroborate the information in the above table: with few exceptions, the graphs for the 7 alternatives and 11 alternatives cases are almost identical. We will avoid a detailed analysis of the differences for the 3 alternative case, as this case tends to produce generally instable results; however, we put forth a partial explanation for the fact of the discrepancies themselves – namely, that the differences are due to the percentage of profiles in which a Condorcet winner exists. Table 9 indicates the following term for each of the profile sizes:
|(% profiles with Condorcet winner in IC) – (% profiles with Condorcet winner in CC)|

Table 9 – For each profile size, the difference in % Condorcet-winning profiles b/n IC and CC

	5 voters	**25 voters**	**45 voters**	**65 voters**	**85 voters**
3 alternatives	0.0757	0.2587	0.3610	0.4368	0.4689
7 alternatives	0.0103	0.0036	0.0006	0.0095	0.0067
11 alternatives	0.0025	0.0118	0.0251	0.0440	0.0366
15 alternatives	0.0193	0.0279	0.0348	0.0652	0.0647

Notice that the difference in percentage of profiles with a Condorcet winner corresponds roughly with the SSE values in Table 8. Thus, one hypothesis to be tested in further studies is that altering the distribution assumption effects the clustering results insofar as it changes the likelihood of a Condorcet winner existing in any given profile from that distribution.

Multidimensional Scaling Results

As discussed above, the MDS function takes the similarity matrix as input and produces a plot of points (each point representing a different social choice rule) whose interpoint distances correspond to the dissimilarity between each pair of rules. If the distances are Euclidean, then it will plot these points in enough dimensions to exactly match the dissimilarities found from the similarity matrix. We consult the eigenvalue output to determine how many of these dimensions we need to consider in order to get a fairly accurate representation of the data.

When the number of dimensions is low (1, 2 or 3), then we can examine a visual plot of the data and attempt to give interpretations of each dimension. Of course, there is no guarantee that the properties which determine the location of the points will correspond with the x, y, and z coordinate axes, as given by the MDS function. In fact, it may be the case that we need to rotate the plot before the coordinate axes match up with our posited property interpretations.

However, when the number of dimensions required to represent the data is much higher than 3, it becomes much more difficult to create interpretations for the dimensions. It is no longer easy to imagine what sorts of rotations will cause the coordinate axes to represent salient rule properties. Examining parallel plots of the data (plots which display the points one dimension at a time) is of little help as well, as these plots assume that the data has already been rotated so that the salient rule properties are aligned with the coordinate axes.

Unfortunately, most of the profile types examined require far more than 3 dimensions to represent the data, and thus we are faced with the dilemma of how to address the above problem. Throughout the following discussion, I will again focus my attention on the Impartial Culture 11-45 case. In fact, with MDS, there is much less to be gained by analyzing the results from other profile types than was the case with hierarchical clustering. This is because our purpose here is to improve our understanding of abstract rule properties (such as Condorcet efficiency, etc.) rather than to learn more about individual rules themselves, as was the case with hierarchical clustering. Thus, though individual rules may shift around from profile type to profile type, the interpretations of the dimensions should remain roughly the same (remember, before analyzing any of the plots, we performed procrustes analysis to force the axes of all plots to more or less 'match up'). Consulting the plots produced from other profile types will be useful for testing our dimension interpretations, but we should not expect the interpretations of the dimensions to change significantly, if at all, from profile type to profile type.

That said, we must still deal with the fact that there are more than 3 dimensions and that it will thus be difficult to make an informed decision regarding how to rotate the plots (a cursory examination of the initial rotation produced by scaling function seems to confirm that none of the axes correspond closely to any easily identifiable rule property). The approach used here is one suggested by Kruskal and Wish (1978). Rather than rotating the plot at all, we instead posit specific rule properties that we may expect to be important determinants of rule position and then test the extent to which these properties are in fact significant factors in deciding the ultimate position of a rule. We test these hypothesized correspondences by first creating, for each rule property we wish to examine, a numerical scale on which we rank every rule tested. We then run a multiple linear regression over the significant dimensions (as determined by eigenvalue analysis) of the point plot.

By examining the coefficient of determination of the regression and its significance value, we can determine to what extent this property is an important determine of overall rule location at all. Further, by examining the resultant dimension coefficients, we can examine which dimensions are associated with the property being tested, and in what degree. Finally, by seeing which dimensions appear to be correlated with the property in question, we can make a conjecture regarding the relative importance of this property in determining overall rule location – if the dimensions associated with the property are among the first few (i.e. dimensions 1, 2, 3, ...), then we can say that this property is fairly important in determining rule behavior. However, if this property is associated with higher dimensions, then we may say that this property is less important in determining rule behavior. Thus, though we may not be able to rotate the data so that there is a one-to-one correspondence between rule properties and dimensions, we will get an idea of which rule properties are more significant than the others.

For example, suppose we wish to test which dimensions, if any, measure Condorcet efficiency. First, we find the Condorcet efficiency of each rule (as measured by determining how often each rule picked the Condorcet winner, when one existed, in the trials from which we generated the similarity data). Then, we run a multiple linear regression in which Condorcet efficiency is the dependent variable and the dimensions of the MDS plot are the independent variables (though our MDS plot contains 20 dimensions, we only examine the first 15 because the eigenvalues for the 5 highest dimensions drop off towards zero). The regression produces a coefficient associated with each dimension – it also gives us the coefficient of determination (R^2) associated with the regression (the higher the value, the better the ability of the regression to explain the independent variable, Condorcet efficiency). Finally, it gives us the significance value (p) for the regression – we follow the general rule that .01 is the maximum acceptable value (Kruskal and Wish 1978, 39).

We posited 6 rule properties which we wanted to test against the MDS plots in order to determine their relative importance in determining rule behavior: Condorcet efficiency, whether the rule used an elimination procedure, the degree to which the rule relied on Borda scores, the degree to which the rule relied on information regarding alternatives' defeat margins, the amount of the profile considered by each rule, and the portion of the profile considered by each rule (top, middle, bottom). Table 10 gives the ratings that we assigned each rule according to these scales. Note that only Condorcet efficiency is an objective measure, obtained from the trials from which we obtained the similarity data. We produced all other ratings by judging the degree to which each rule satisfied the property in question.

Table 10 – Rule property scales (Condorcet efficiency pertains to IC, 11 alternatives, 45 voters)

Rule/Scale	**Condorcet efficiency**	**Elimination**	**Borda**	**Defeat**	**Amount of profile**	**Portion of profile**
Antiplurality	0.2616	0	0	0	0	-1
k-Approval	0.7306	0	0	0	.5	.5
Approval	0.4611	0	0	0	.5	.5
Black	1.0000	0	.5	0	1	0
Borda	0.8418	0	1	0	1	0
Exhaustive	0.8055	1	0	0	.25	-1

Copeland	1.0000	0	0	0	1	0
Hare	0.7747	1	0	0	.25	1
Inverse Borda	1.0000	1	.5	0	1	0
Longpath	0.9984	0	0	0	1	0
Majoritarian compromise	0.6601	0	0	0	.5	.5
Dodgson	1.0000	0	0	1	1	0
Nanson	1.0000	1	.5	0	1	0
Plurality	0.3783	0	0	0	0	1
Plurality Runoff	0.5597	.5	0	0	.1	1
Simpsons	1.0000	0	0	1	1	0
Top cycle	1.0000	0	0	0	1	0
Uncovered set	1.0000	0	0	0	1	0
Raynaud	0.9859	1	0	1	1	0
Coombs	0.8061	1	0	0	.25	-1
Carey	0.6743	1	0	0	.25	1

Table 11 gives the results of regressing each of these properties over the dimensions of the MDS plot (considering only the first 15 dimensions) for the 11-45 case. Next to each dimension it lists the regression coefficient associated with this dimension. Regression coefficients have been normalized so that the sum of their squares adds up to 1. The table also gives the coefficient of determination (R^2) and the p value of the significance test for this regression.

Table 11 – Regression results

	Condorcet efficiency	**Elimination**	**Borda**	**Defeat**	**Amount of profile**	**Portion of profile**
Dim #1	-0.7247	0.0501	-0.2078	-0.0330	-0.6659	0.2266
Dim #2	0.1630	0.1891	-0.1809	0.2160	0.0061	-0.7461
Dim #3	-0.5254	-0.2911	0.0942	-0.1062	-0.1775	-0.2136
Dim #4	-0.0279	0.3337	-0.0601	-0.0829	-0.0756	0.2706
Dim #5	-0.0513	-0.3031	-0.2166	0.1083	0.3241	0.1580
Dim #6	0.1543	-0.2585	0.3374	0.0162	0.4585	-0.2325
Dim #7	-0.3005	0.1866	-0.1842	-0.2068	-0.3785	-0.2761
Dim #8	-0.1624	-0.0446	0.0102	-0.0997	-0.1506	-0.3018
Dim #9	-0.0767	0.6384	0.7253	-0.1756	0.0412	-0.0090
Dim #10	-0.0884	0.1789	-0.3117	0.5469	0.0623	0.0024
Dim #11	0.0166	0.0750	-0.1024	-0.0300	-0.1132	-0.1192
Dim #12	0.0425	0.2738	-0.2269	0.3041	-0.0552	0.1075
Dim #13	-0.0881	-0.1790	-0.1209	0.3959	-0.0728	0.0303
Dim #14	0.0612	0.0643	0.1125	-0.5356	0.1038	0.0046
Dim #15	0.0307	-0.1175	-0.0655	-0.0508	0.0218	0.0050
R^2	0.9922	0.9367	0.9490	0.9345	0.9965	0.9998
p	0.0003	0.0436	0.0270	0.0471	0	0

I now consider each of these rule properties in turn.

Condorcet efficiency

It appears that Condorcet efficiency is a significant factor in determining the behavior of social choice rules. Its high coefficient of determination value is statistically significant at the .0003 level. Moreover, it appears to be primarily associated with two dimensions: 1 and 3, with dimension 1 having the highest absolute coefficient value.

Elimination

Whether or not a rule uses an elimination procedure does not appear to be a significant factor in determining rule behavior – though the coefficient of determination is above .90, it is not statistically significant better than the .01 level. This finding is inconsistent with the explanation given above of why Raynaud joins different clusters depending on the profile type – it appears that further investigation is necessary to explain the behavior of that rule.

Borda and Defeat

Whether or not a rule uses some variation of the Borda count in choosing a winning alternative is not significant better than the .01 level. Similarly, whether the rule explicitly takes into account the magnitude by which a particular alternative loses to other alternatives also seems to be a statistically insignificant determinant of rule position.

Amount of profile

The amount of information considered by the rule (does it look at only the top half of the profile, or only the first row?) does seem to be an important determinant of rule position. And, this property seems to be associated most closely with the first dimension, as is the case with Condorcet efficiency – this is not too surprising as, in general, Condorcet efficient rules need to take into account all of the information in the profile.

Portion of profile

In addition to the amount of the profile considered, it seems that the portion of the profile examined is also an important determinant of rule behavior. For example, the plurality rule looks at only the first row of voters' preferences, while the antiplurality rule looks at only the last row; the k-Approval rule looks at roughly the top half of voters' preferences. These differences apparently make enough of a difference that the second dimension is highly (negatively) correlated with rules' behavior with respect to this property (the stronger the bias of the rule to consider the top of the profile, the lower its value along the second dimension).

Discussion/Future Studies

It seems that hierarchical clustering is a powerful technique and one that can be put to further use in the field of social choice. The dendrograms generated in this study give a strong indication that indeed there is much to be learned about the relationships among the various social choice rules that have been proposed in the literature. Significantly, it appears that, though distinct clusters and sub-clusters do emerge for any particular profile size or type, the actual clustering formation does depend on the type of profile used – both profile size and preference distribution have an effect on the resultant dendrogram. Interestingly but perhaps not unexpectedly, the likelihood that there will be a Condorcet winner for any given profile type seems to have a significant effect on the clustering associated with this profile type. Although we only tested two preference distributions, our initial findings regarding the relationship between clustering results and Condorcet-likelihood indicate that further research investigating this relationship could be fruitful. If the effect suggested here regarding the influence of preference distribution on clustering results is robust, it might suggest that the procedure for selecting the 'appropriate' social choice rule for a particular situation ought to place a high weight on the type of preference distribution expected.

While varying the type of profile used suggests that the likelihood of a Condorcet winner has an effect on the resultant dendrogram, visual inspection of any one dendrogram shows that the Condorcet efficiency of a rule largely determines a rule's general placement within the dendrogram clusters. The importance of Condorcet efficiency as a determinant of rule behavior is also supported by our multidimensional scaling results. The Condorcet efficiency scale is the only scale used in our multilinear regression analysis that is completely objective. And, this analysis strongly suggests that Condorcet efficiency plays a significant role in determining the location of a rule in the overall MDS plot.

As just noted, most of the scales used to look for trends in the MDS plots were generated by considering the definitions of the rules and making a 'best guess' as to how a particular rule measures on the scale under consideration. Clearly, this process is a bit subjective and open to improvement. The underlying problem with the MDS technique is that eigenvalue analysis indicates that far more than 3 dimensions are necessary to properly represent the relationships contained in the similarity matrix. As such, it is difficult to find the proper rotation of the data and discover which combinations of dimensions to look at without knowing in advance where to look. We suggest that MDS will become significantly more useful in analyzing the hidden structure of social choice rules once an objective framework has been developed in which we can rate each rule along a variety of dimensions. Such a framework will (hopefully) allow for further investigations in which multilinear regressions, of the sort presented above, can lead the way to a better understanding of those properties which significantly affect rule behavior, and those that do not.

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Appendix

Definitions of Social Choice Rules

Notes:

-Because the experiments described here assume that voters rank all alternatives, the definitions provided below will make use of the same assumption.

-Ties are broken by consulting the preferences of Voter 1. This non-random tie-breaking procedure was chosen to preserve the relationships between rules that often result in ties, yet choose the same set of possible winners.

Antiplurality rule - Voters rank all alternatives. The alternative with the fewest number of last place votes is the winner.

k-Approval - k is taken as a parameter to this social choice rule - in this case, k was set to floor(#alternatives/2) – this choice of k was based on work by Pritchard and Slinko (2003). An alternative receives a 'vote' anytime it is among the top k choices of a voter. The alternative with the most votes is the winner.

Approval - This rule operates similarly to k-Approval described above, except that, for each profile, the choice of k is randomly selected from the set {1,...,m} where m is the number of alternatives.

Black's rule - If a Condorcet winner exists (one alternative beats all other alternatives in simple majority contests), then the the Black winner is the Condorcet winner. If no Condorcet winner exists, then the Black winner is the Borda winner (described below) (Richelson 1975, 332).

Borda rule - From each voter, alternative x receives r points, where r is the number of alternatives ranked below x by that particular voter. The total number of points received by alternative x from all voters is x's Borda score. The alternative that has the highest Borda score is the winner (Borda (1781) cited in Richelson, 1975, 332).

Exhaustive procedure - The following procedure is repeated until only one alternative remains: eliminate the candidate that receives the largest number of last place ranks. The voters' rankings of alternatives are readjusted such that, whereas before voters ranked all m alternatives from 1 to m, voters now rank the remaining m-1 alternatives from 1 to m-1. This is similar to Coombs procedure except that the procedure is repeated until all but one of the alternatives are eliminated, rather than stopping when one alternative is ranked first by more than 50% of voters, as is the case with Coombs. The distinction between the two rules is noted in Tideman (1987, 191).

Copeland rule - The Copeland winner is the alternative that most often beats the other alternatives in simple majority contests. More precisely, if the number of voters who prefer x to y is greater than the number of voters who prefer y to x, then x beats y in a simple majority contest, or xMy. The Copeland score for alternative x is simply the number of alternatives that defeat x in a simple majority contest subtracted from the number of alternatives that x defeats in a simple majority contest. The Copeland winner is the alternative with the highest Copeland score. In the version of Copeland used here, in case of a tie, a Second Copeland score is computed for each of the tied alternatives by adding to the original score the Copeland scores of every alternative beaten by the alternative in question. The tied alternative with the highest Second Copeland score is declared the winner. If there is still a tie, then the tie is broken by consulting the preferences of Voter 1 (Tideman 1987, 194; Slinko 2002).

Hare's rule (also known as Single Transferable Vote or Alternative Vote) - If one alternative is ranked first by more than 50% of voters, then that alternative is the Hare's winner. Otherwise, the following procedure is carried out: eliminate the candidate that receives the fewest number of first place ranks. The voters' rankings of alternatives are readjusted such that, whereas before voters ranked all m alternatives from 1 to m, voters now rank the remaining m-1 alternatives from 1 to m-1. If any alternative is now ranked first by more than 50% of voters, then that alternative is the Hare's winner. Otherwise, the procedure just described is repeated - eliminating one alternative, readjusting the rankings, and checking if any alternative receives a majority of first-place ranks - until a Hare's winner is identified (Tideman 1987, 190).

Inverse Borda rule - This rule first checks to see whether any alternative is a plurality winner - if so, then that alternative is the Inverse Borda winner. Otherwise, the following procedure is repeated until only one alternative remains: eliminate the candidate with the lowest Borda score. The voters' rankings of alternatives are readjusted such that, whereas before voters ranked all m alternatives from 1 to m, voters now rank the remaining m-1 alternatives from 1 to m-1. The last alternative remaining is the Inverse Borda winner.

Long path rule – To give an intuition behind the long path rule, consider the following: the Copeland rule considers the number of simple majority contests won by each alternative (i.e. it sums the rows of the majority matrix). But, we could instead give points to each alternative for the quality of the alternatives that it beats by scoring each alternative by summing the Copeland scores of the alternatives it beats – if the Copeland method considers paths of length 1, then the method just described considers paths of length 2. Similarly, we could consider paths of length 3 by scoring each alternative by the quality of the alternatives beaten by the alternatives beaten by the alternative in question. Call the length of the path t. In effect, the long path rule scores alternatives by considering paths of length t, for large values of t, and then choosing the alternative with the highest score.

This rule uses the following procedure: create a pairwise majority matrix (entry [i, j] = 1 iff alternative i beats alternative j in a simple majority contest; otherwise it equals 0). Find the eigenvalues and eigenvectors associated with this matrix – then, isolate the eigenvector associated with the maximum eigenvalue. Element i of this vector is associated with alternative i. Normalize each element of the eigenvector by the sum of the eigenvector elements and find the alternative associated with the largest such value. This alternative is the long path winner (Laslier 1997, 55).

Majoritarian Compromise (also known as the Bucklin rule) - The rule proceeds by first examining the top row (first choice) of each voter's preferences. If an alternative appears in the top row of more than 50% of voters' preferences, then that alternative is the majoritarian compromise winner. Otherwise, we look at the top two rows (first and second choices) of voters' preferences. If any alternatives appear in the top two rows of more than 50% of voters' preferences, then we choose the alternative among this set that appears in the top two rows most often. If no alternative appears in the top two rows of voters' preferences for more than 50% of voters, then we examine the top three rows (first, second, and third choices), and so on (Sertel and Yilmaz, 1999, 620).

Dodgson's procedure - Formally, Dodgson's procedure says to pick the alternative which requires the minimum number of voter preference reversals to make it the Condorcet winner (or tied Condorcet winner). However, this procedure is computationally intensive, and a simplification has been suggested that is very similar to the rule actually proposed by Dodgson. For each alternative x, determine x's simplified Dodgson score by determining which alternatives beat x in a pairwise majority contest. x's score is equal to the sum of x's margins of defeat in all such losing contests. The simplified Dodgson winner is the alternative with the lowest such score. In effect, this rule chooses the alternative with the smallest sum of margins of defeat (Tideman 1987, 194).

Nanson's procedure - The following procedure is repeated until only one alternative remains: calculate the Borda score for each alternative. Eliminate those alternatives with below average Borda scores. Continue this process until one alternative remains or until all remaining alternatives have tied Borda scores, in which case the tie should be broken by choosing in accordance with Voter 1's preferences. Note: Other definitions of Nanson exist (Richelson 1981, 346) in which Nanson is defined exactly the same as the Inverse Borda rule above – that definition was not used in this paper. The definition we used is the one used by Tideman (1987, 194).

Plurality rule - The alternative with the greatest number of first place votes is the plurality winner. Ties are broken by choosing in accordance with Voter 1's preferences (Tideman 1987, 189).

Plurality Runoff procedure - If any alternative is ranked first by more than 50% of voters, then that alternative is the Plurality Runoff winner. Otherwise, all but the two alternatives that are ranked first by the most voters are eliminated. Among these two remaining alternatives, the alternative that is ranked ahead of the other alternative by the most voters is selected as the Plurality Runoff winner.

Simpsons Rule (also known as the minimax/maximin rule) - This rule picks the alternative with the smallest maximum margin of defeat. To compute the winner, we first we create an m-by-m matrix S, where m is the number of alternatives, and S(i,j) indicates the number of voters who rank alternative i ahead of alternative j. Simpsons rule first determines the maximum number of voters by which any rule is defeated by any other rule (by examining the maximum values in each of the columns of S). It selects the rule whose maximum margin of defeat is smallest (Tideman 1987, 195).

Top cycle rule (also known as GOCHA [general optimal choice axiom] and Schwartz's rule) – Let xMy denote that alternative x beats alternative y in a simple majority contest. A subset X of A (A being the set of all alternatives) is M-undominated iff for all x ε X: ~yMx, for all y ε A – X. X is minimum M-undominated if there is no proper subset of X which is also M-undominated. The union of minimum M-undominated subsets of A is the set of top cycle winners – ties are broken by consulting Voter 1's preferences (Richelson 1978, 170).

Uncovered set rule (also known as Miller's procedure) – This rule chooses those alternatives x ε A such that whenever yMx, there exists a z ε A such that zMy and ~zMx. Again ties are broken in accordance with Voter 1's preferences (Brams and Fishburn 2002, 210).

Raynaud procedure (also known as the Arrow-Raynaud procedure) – The following process is repeated until only one alternative remains: for each pair of alternatives x and y, determine the number of voters that prefer x over y. For each alternative x, determine the maximum number of voters that prefer x to any other alternative y. Eliminate the alternative with the smallest such maximum. The voters' rankings of alternatives are readjusted such that, whereas before voters ranked all m alternatives from 1 to m, voters now rank the remaining m-1 alternatives from 1 to m-1. The last remaining candidate is the Raynaud winner (Lansdowne 1997, 126).

Coombs procedure - If one alternative is ranked first by more than 50% of voters, then that alternative is the Coombs winner. Otherwise, the following procedure is carried out: eliminate the candidate that receives the largest number of last place ranks. The voters' rankings of alternatives are readjusted such that, whereas before voters ranked all m alternatives from 1 to m, voters now rank the remaining m-1 alternatives from 1 to m-1. If any alternative is now ranked first by more than 50% of voters, then that alternative is the Coombs winner. Otherwise, the procedure just described is repeated - eliminating one alternative, readjusting the rankings, and checking if any alternative receives a majority of first-place ranks - until a Coombs winner is identified (Tideman 1987, 191).

Carey rule - The following procedure is repeated until only one alternative remains: calculate the plurality score (number of voters that rank this alternative first) for each alternative. Eliminate those alternatives with below average plurality scores. Continue this process until one alternative remains or until all remaining alternatives have tied plurality scores, in which case the tie should be broken by choosing in accordance with Voter 1's preferences.

Social Choice Rules not included because of computational complexity constraints

Young's rule – From Tideman (1987, 196): "...the score for any candidate, x, is the cardinality of the largest subset of rankings for which x is a dominant candidate, and the candidate with largest score wins". Remember that x is a dominant candidate in a set A if it is a Condorcet winner amongst all of the alternatives in A.

Kemeny's rule – From Brams and Fishburn (2002, 211) – this procedure "takes $x \varepsilon F$ if x is a maximum candidate in a linear ordering L of X that maximizes $\Sigma\{v(a, b)L(a,b): a,b \varepsilon X\}$, where $L(a,b) = 1$ if aLb and $L(a,b) = 0$ otherwise." Here F is the social choice set and v(x,y) indicates the number of voters who prefer x to y.

Fishburn's procedure – From Brams and Fishburn (2002, 210) – define "$>'_M$ by $a >'_M b$ if $z >_M a \Rightarrow z >_M b$ for all $z \varepsilon X$, and for some z, $a \geq_M z >_M b$. Then $x \varepsilon F$ if no y has $y >'_M x$." Here, F is the social choice set, X is the set of alternatives, and $>_M$ is the majority relation.

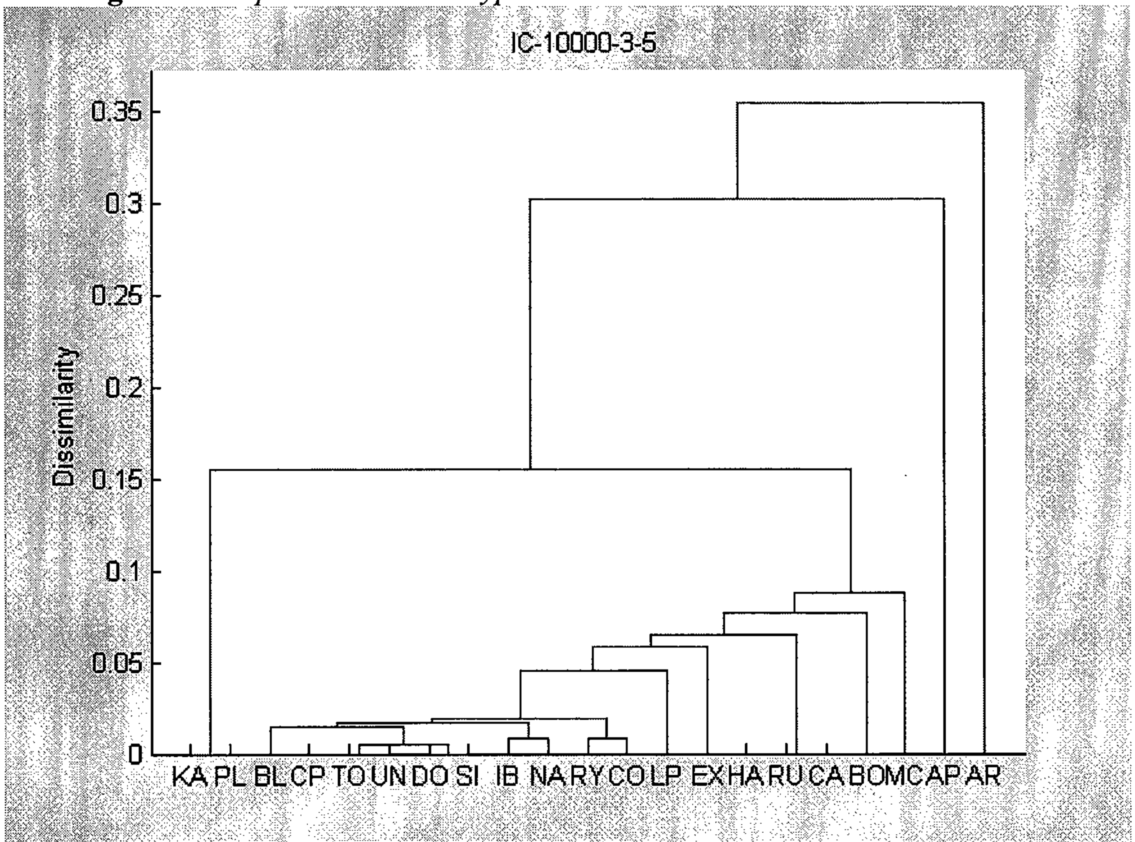
Graphs and Data

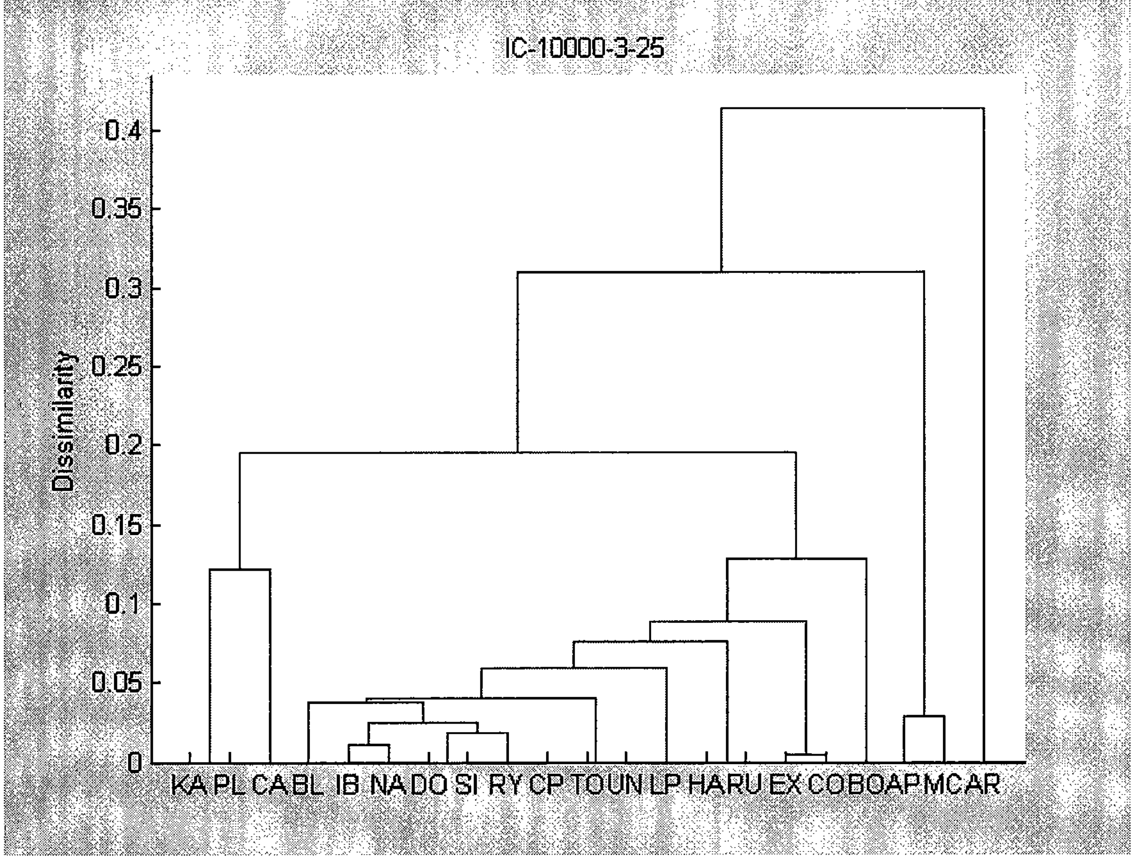
On the following pages are the dendrograms for all 40 profile types, labeled data matrices (eigenvalues, percent of Condorcet-winning profiles, similarity matrices), and MDS plots for the relevant dimensions, 3 dimensions at a time.

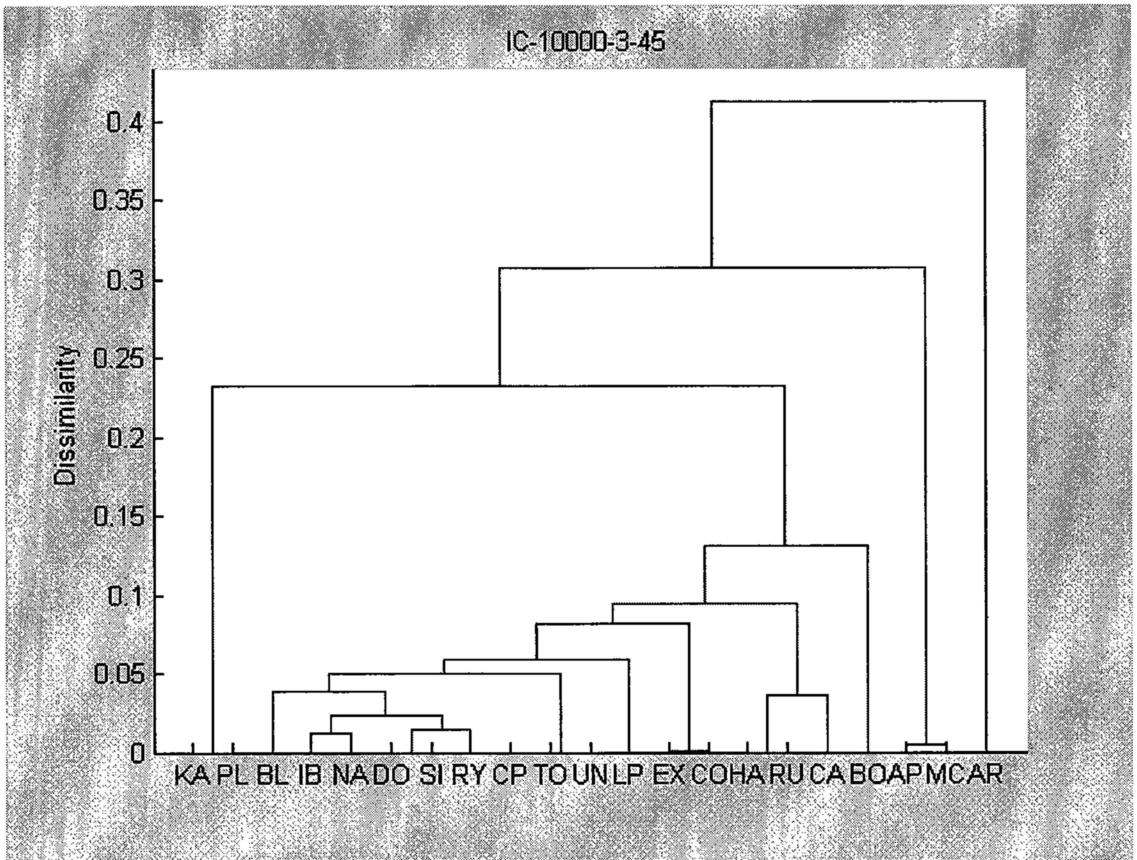
Titles for graphs generally use the following format: *'Culture type-#profiles-#alternatives-#voters'*
Here again are all rule abbreviations:

Rule	Abbreviation
Antiplurality	AP
k-Approval	KA
Approval	AR
Black	BL
Borda	BO
Exhaustive	EX
Copeland	CP
Hare	HA
Inverse Borda	IB
Longpath	LP
Majoritarian compromise	MC
Dodgson	DO
Nanson	NA
Plurality	PL
Plurality Runoff	RU
Simpsons	SI
Top cycle	TO
Uncovered set	UN
Raynaud	RY
Coombs	CO
Carey	CA

Dendrograms – *Impartial Culture Hypothesis – 3 alternatives*



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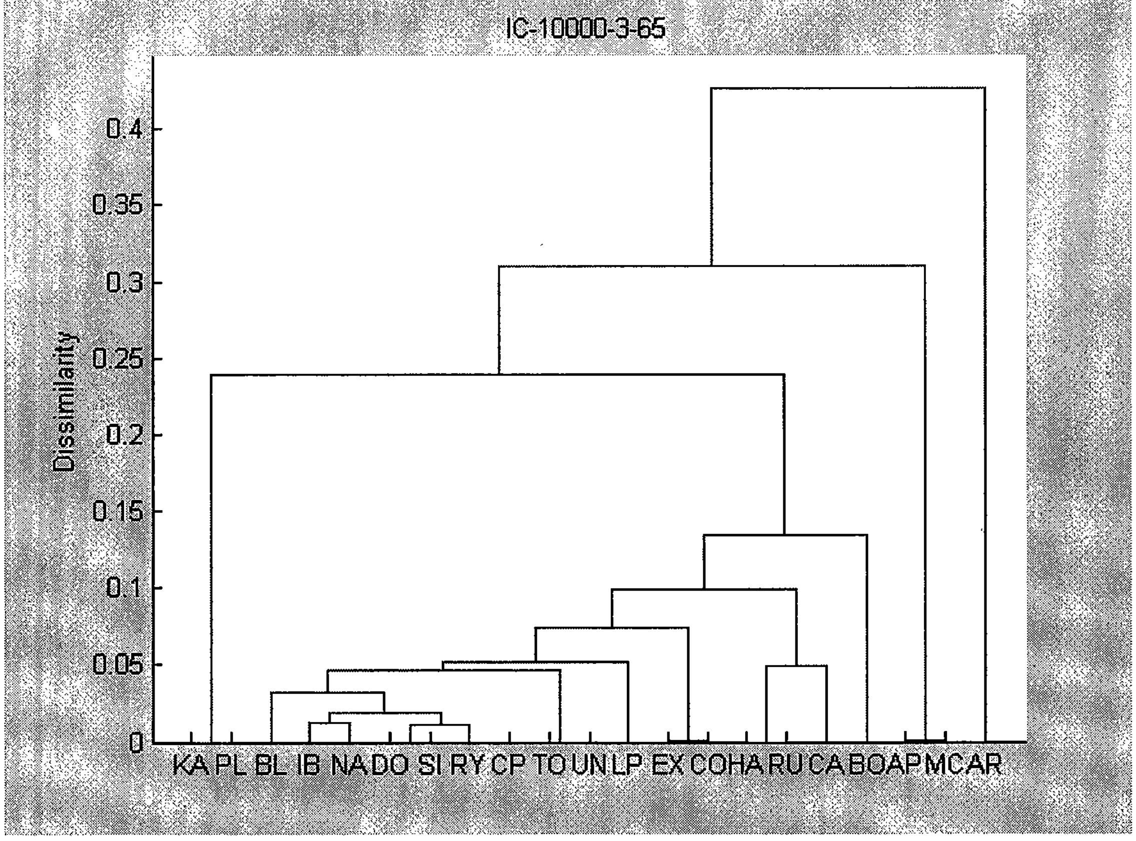
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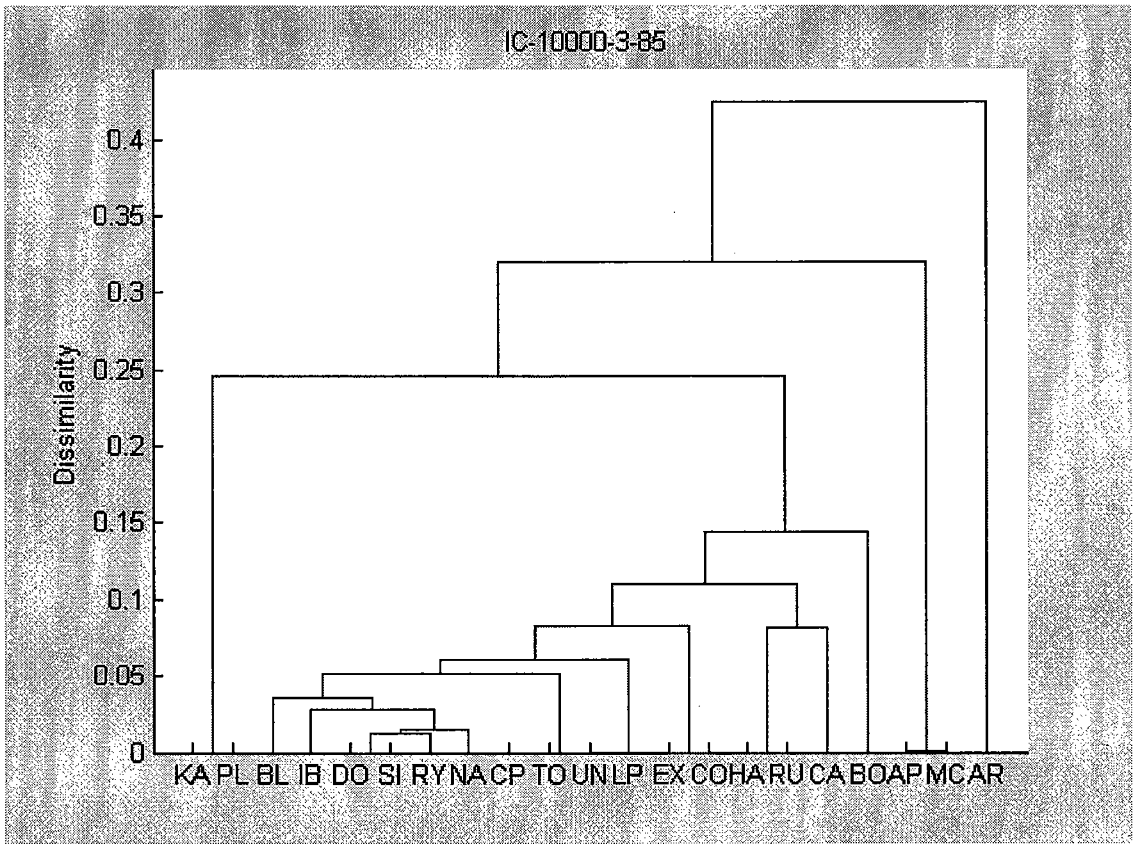

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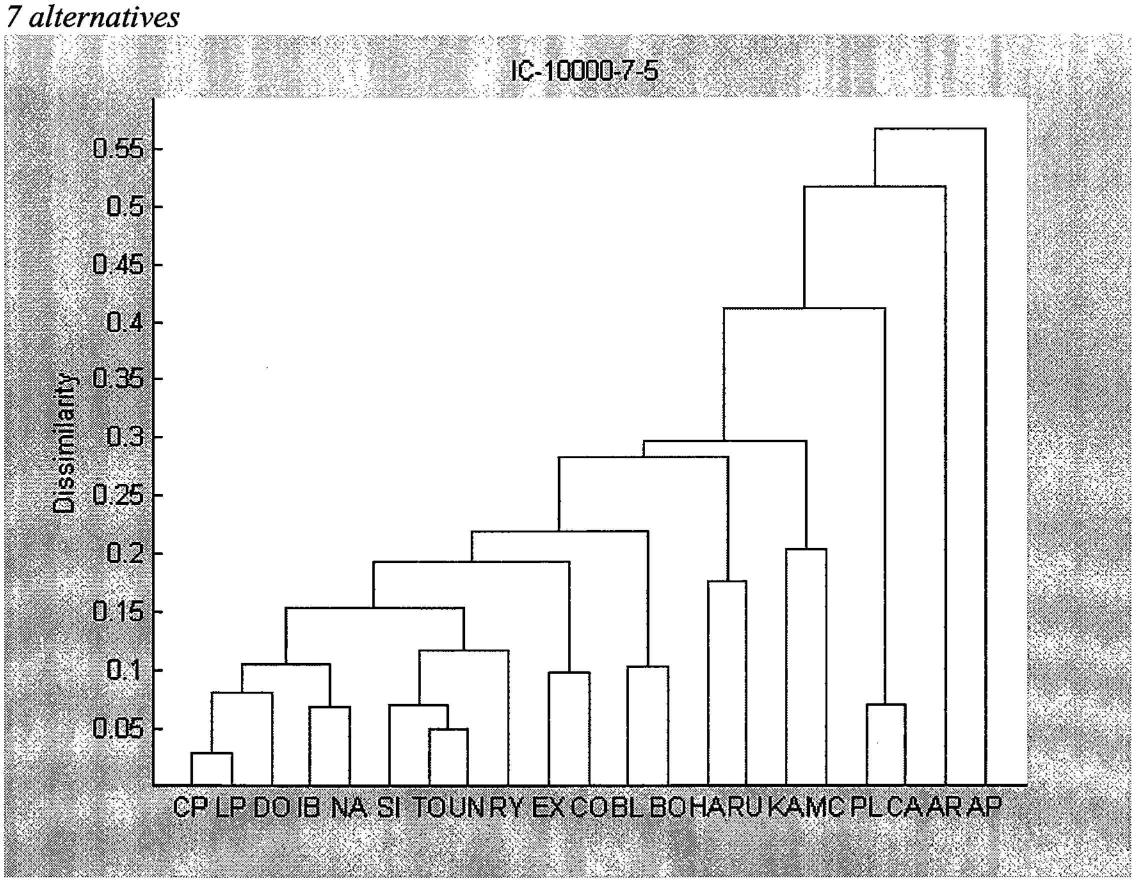

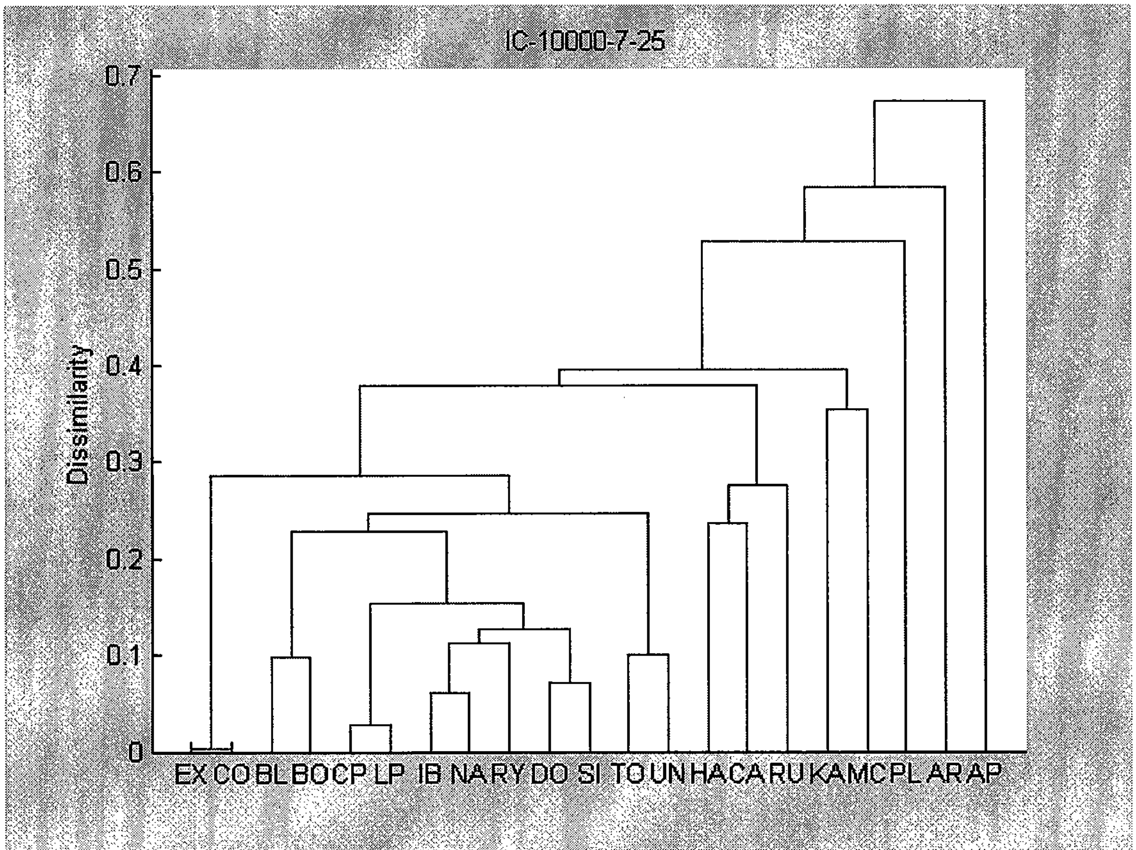
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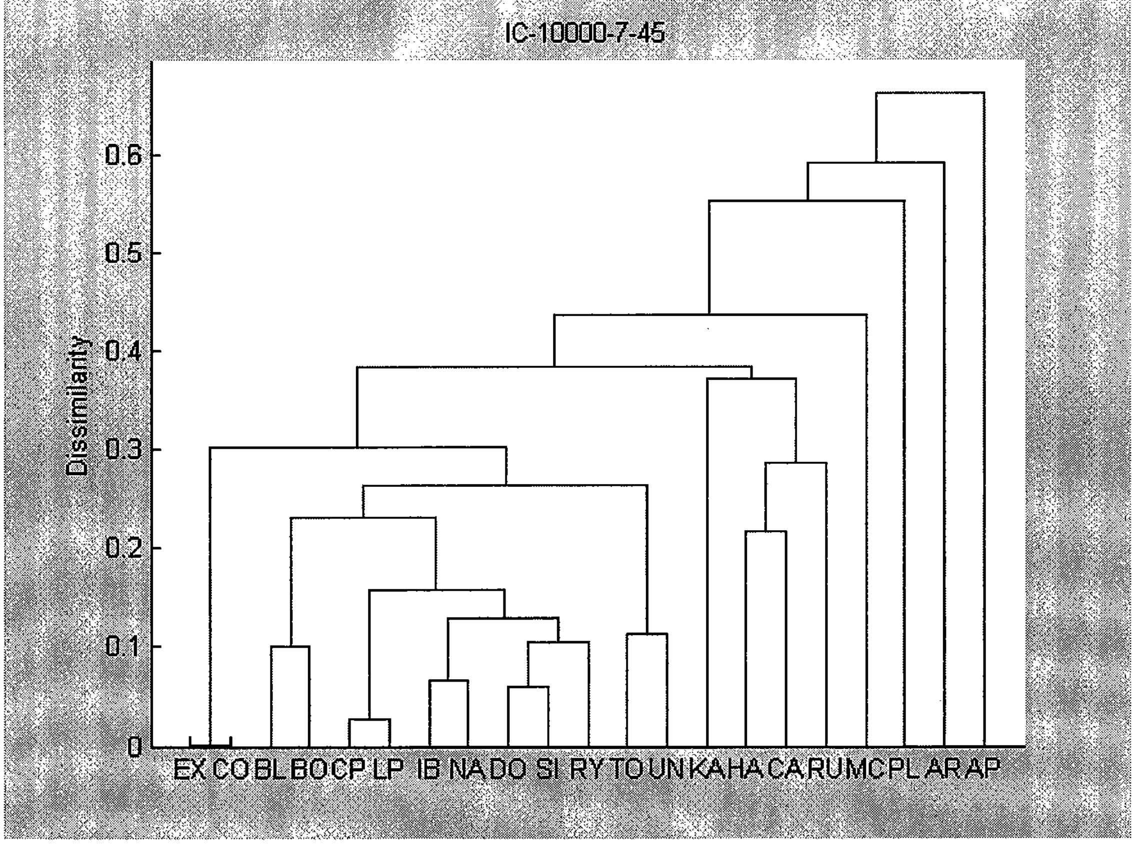
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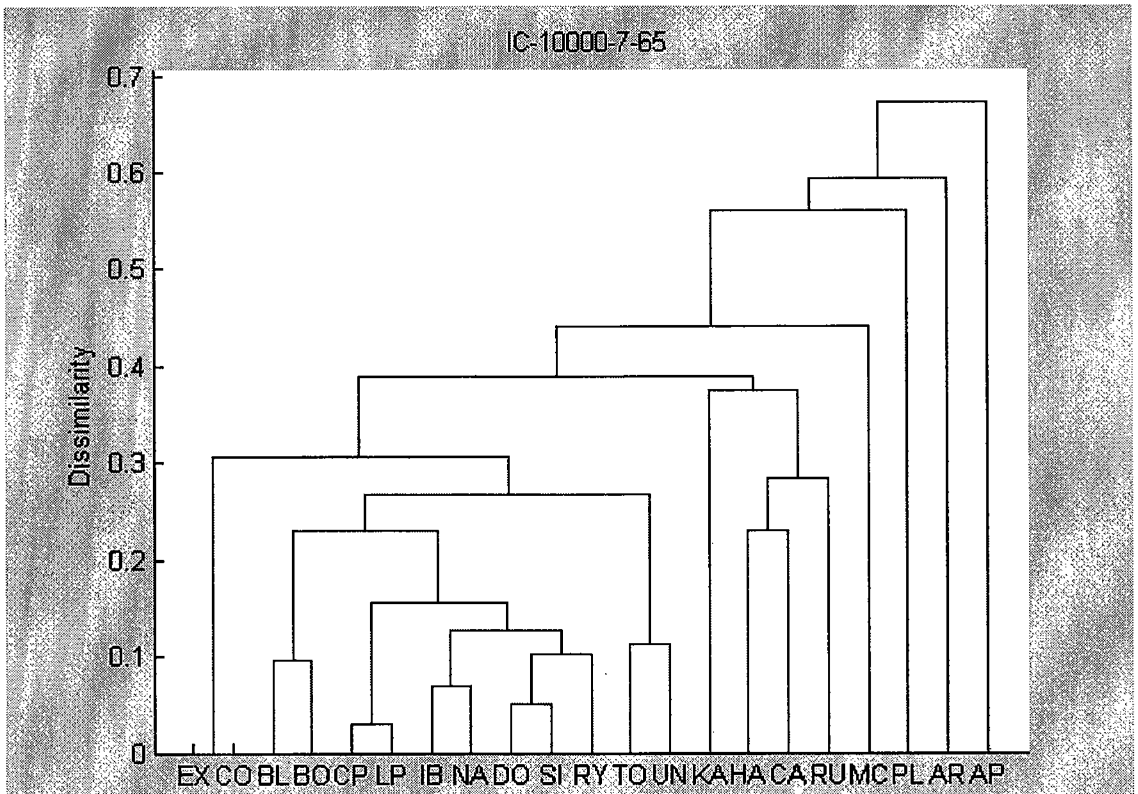
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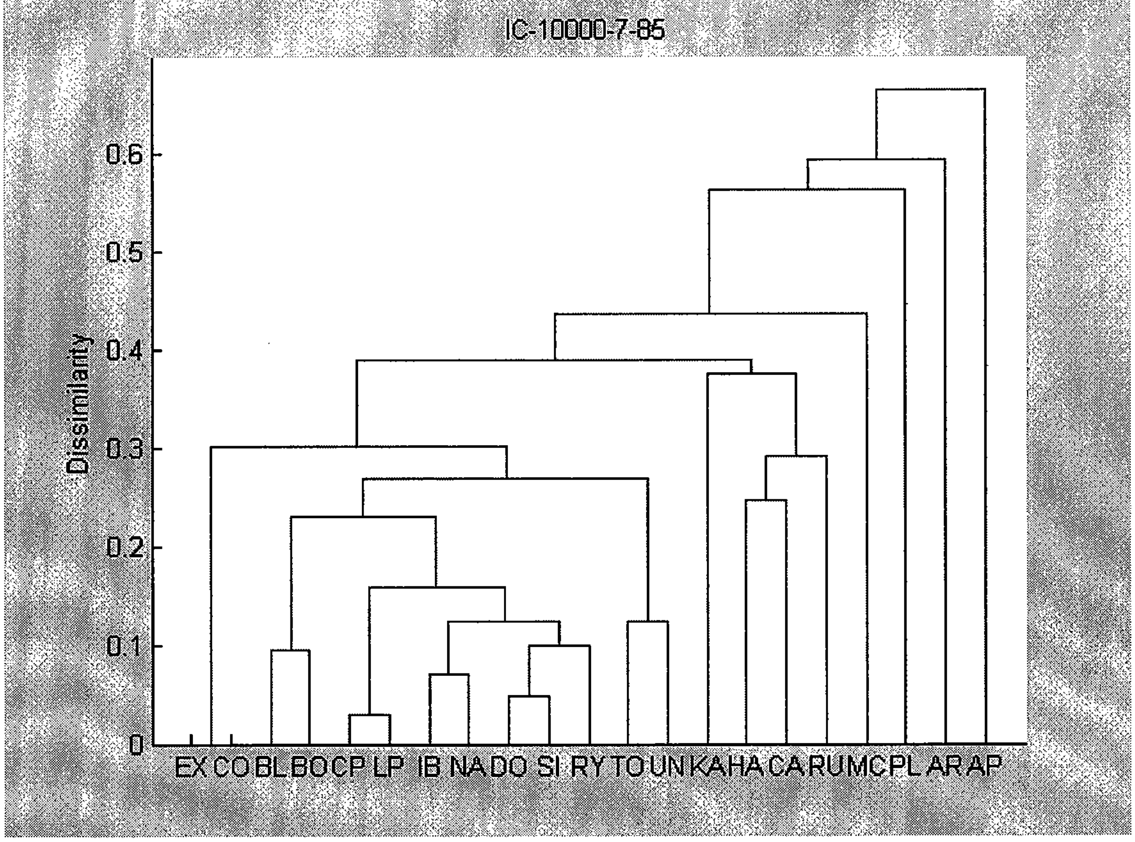
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11 alternatives

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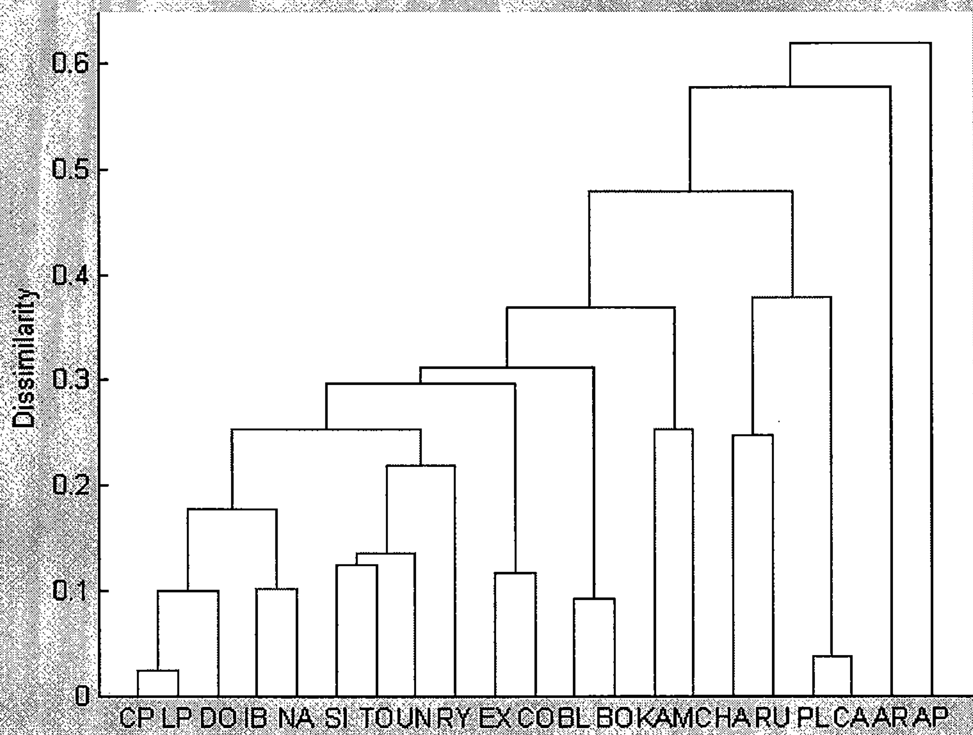

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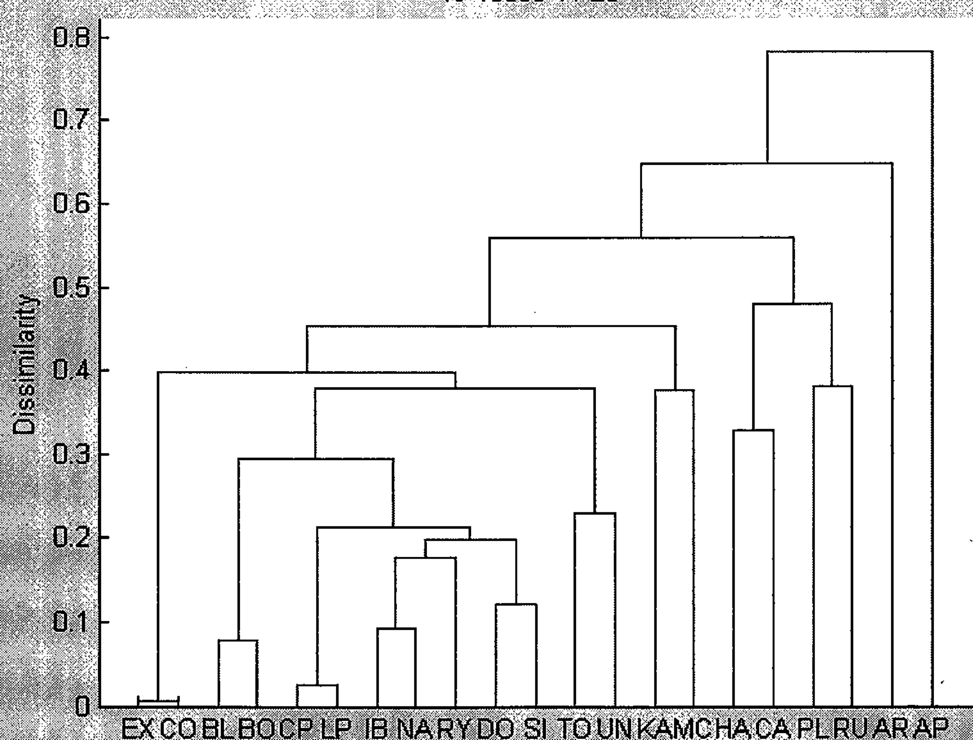

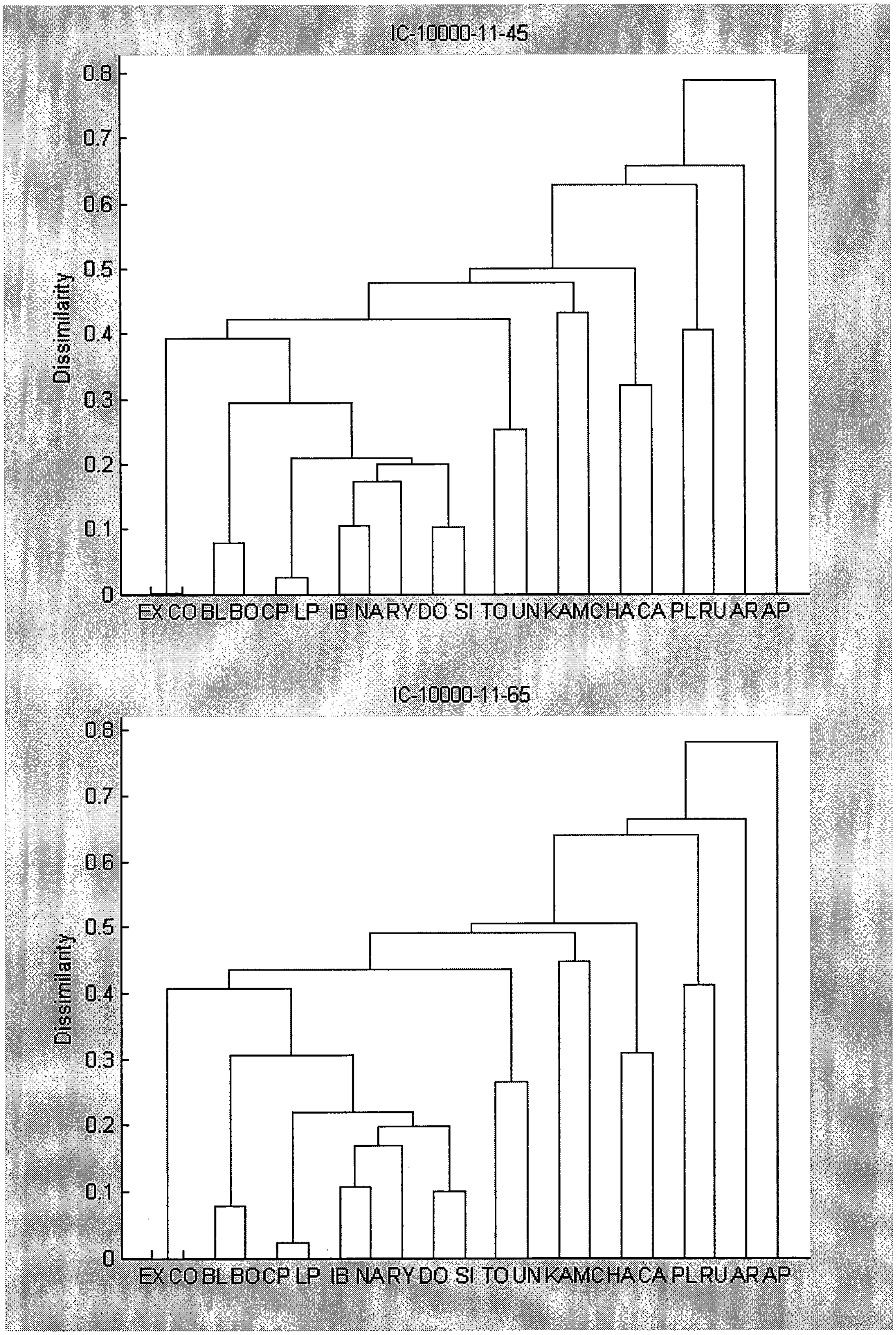

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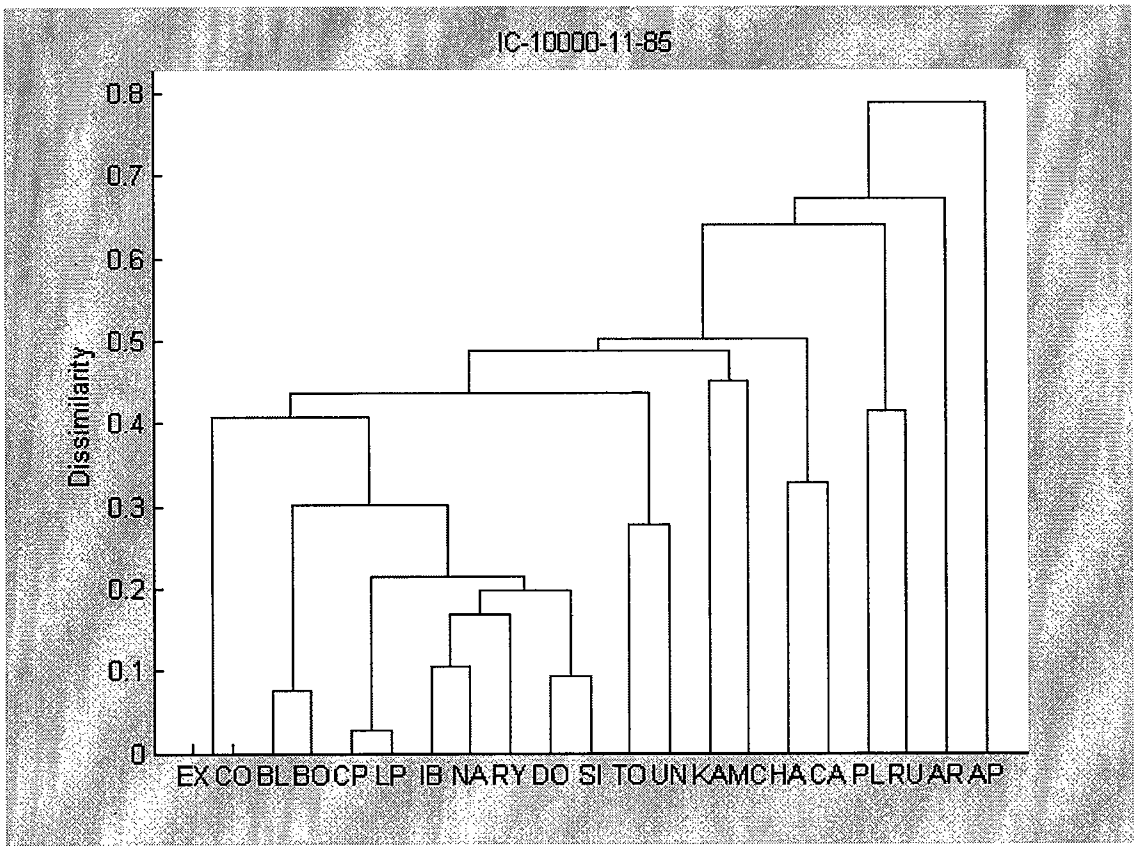

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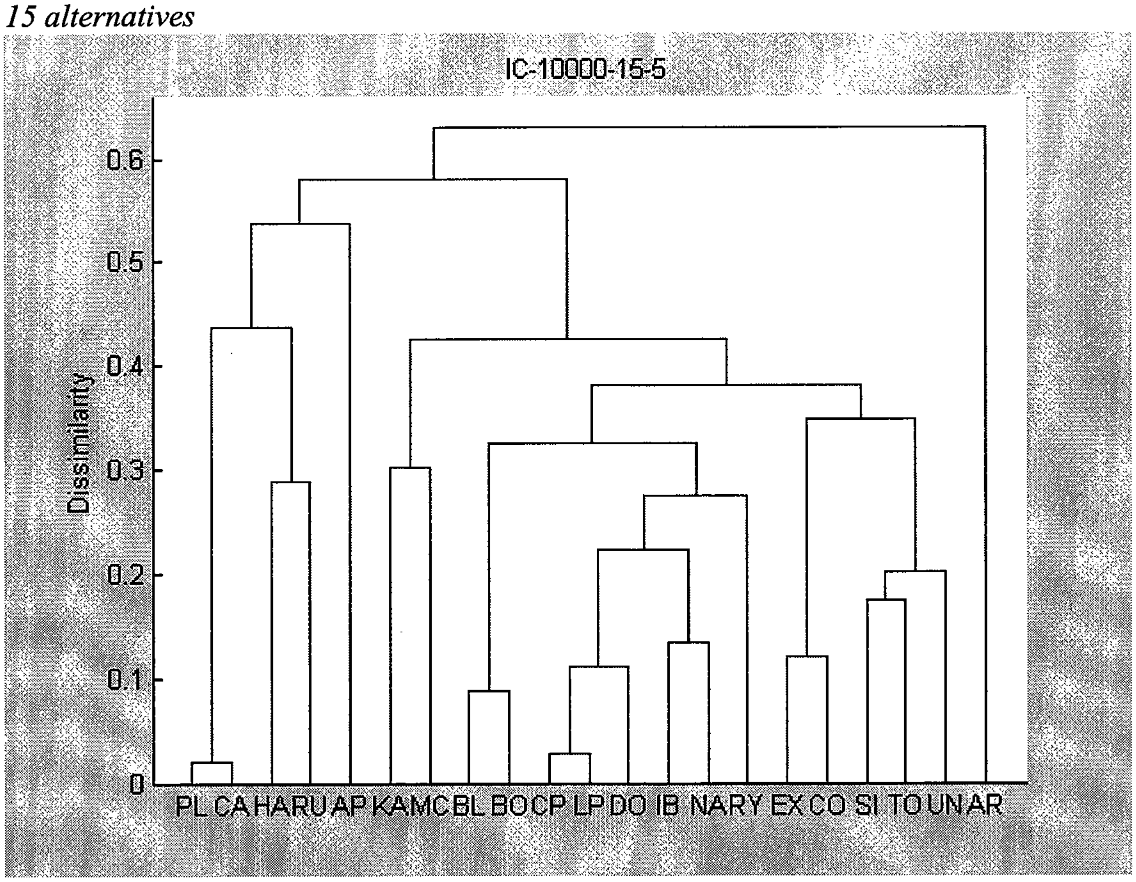

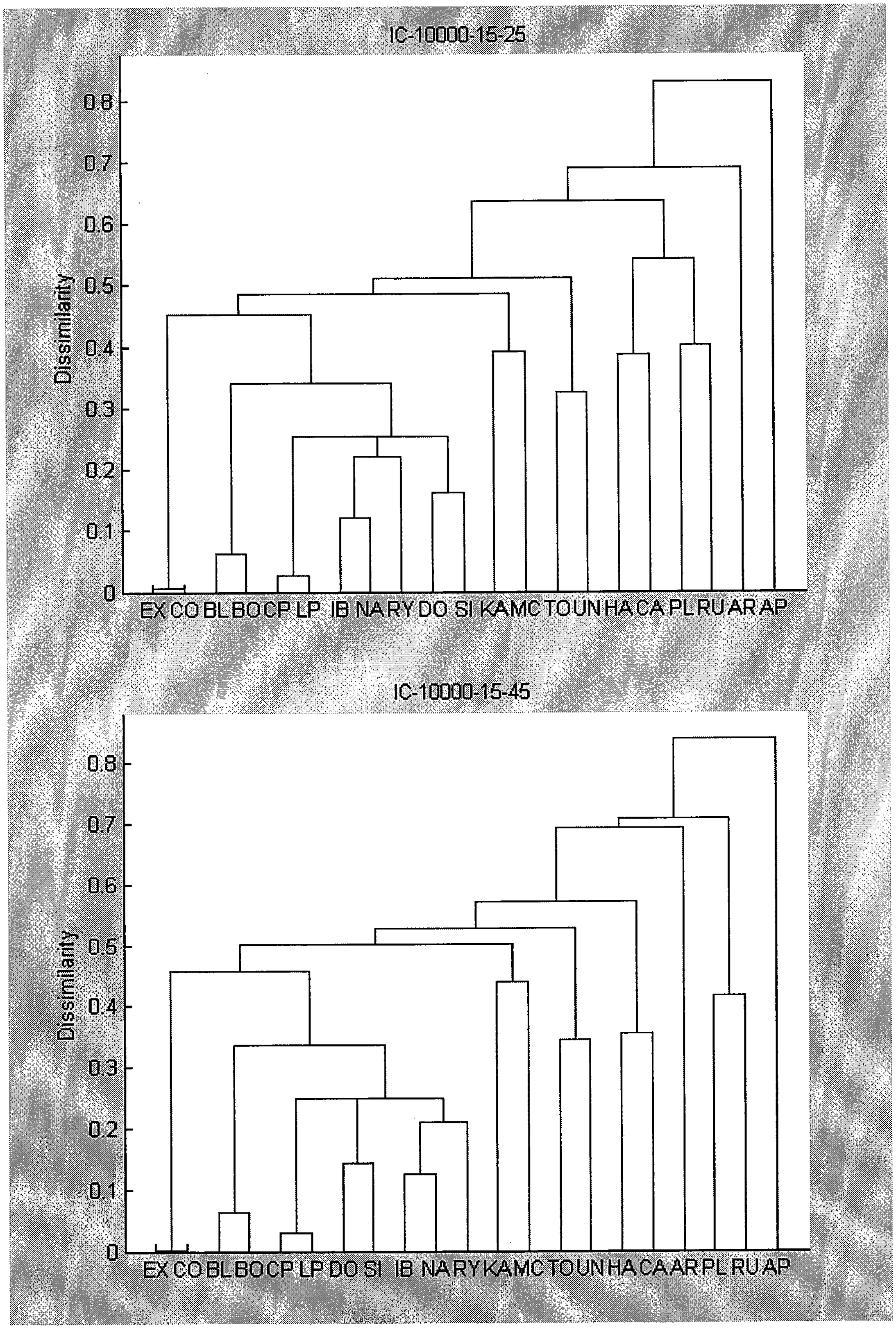
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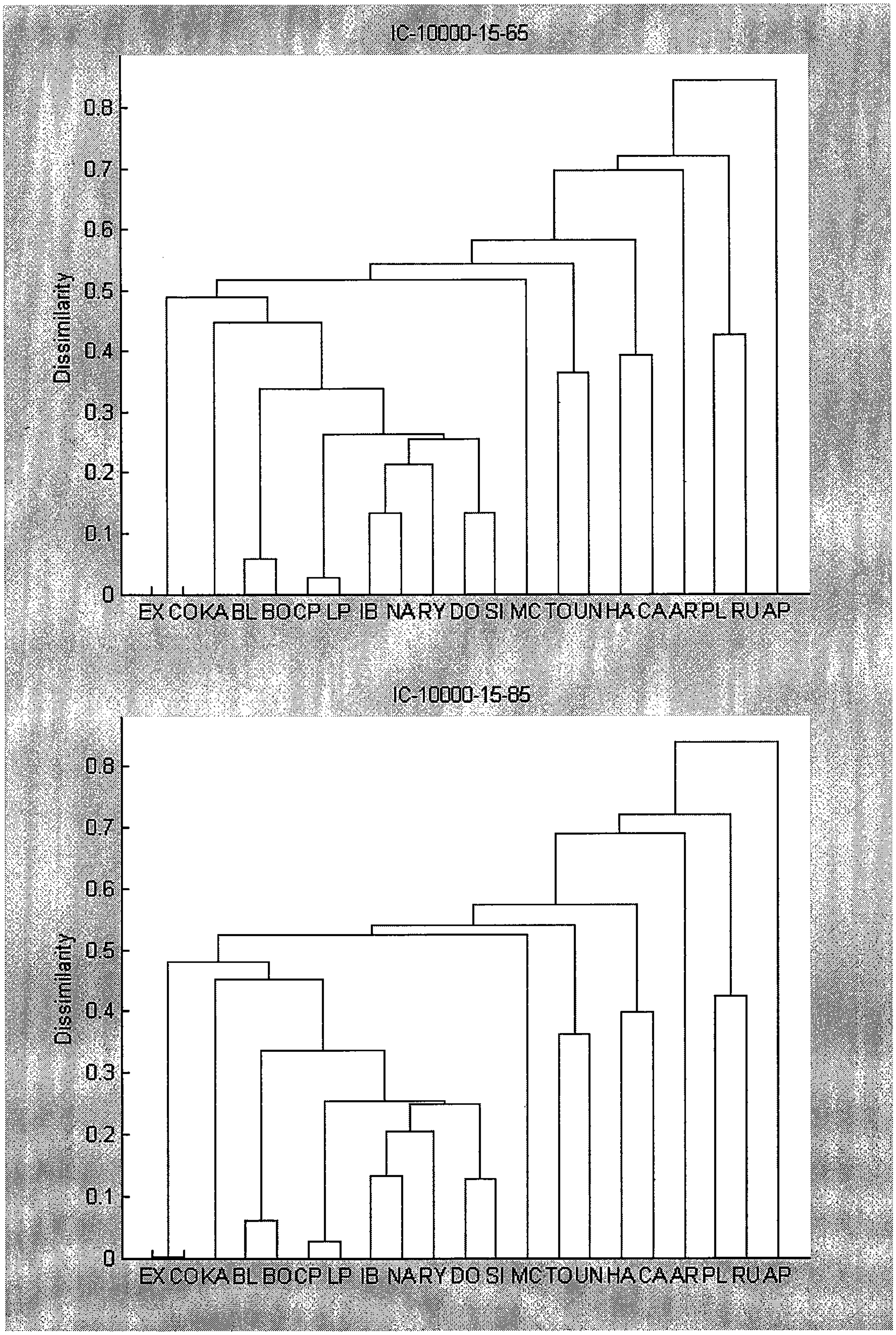
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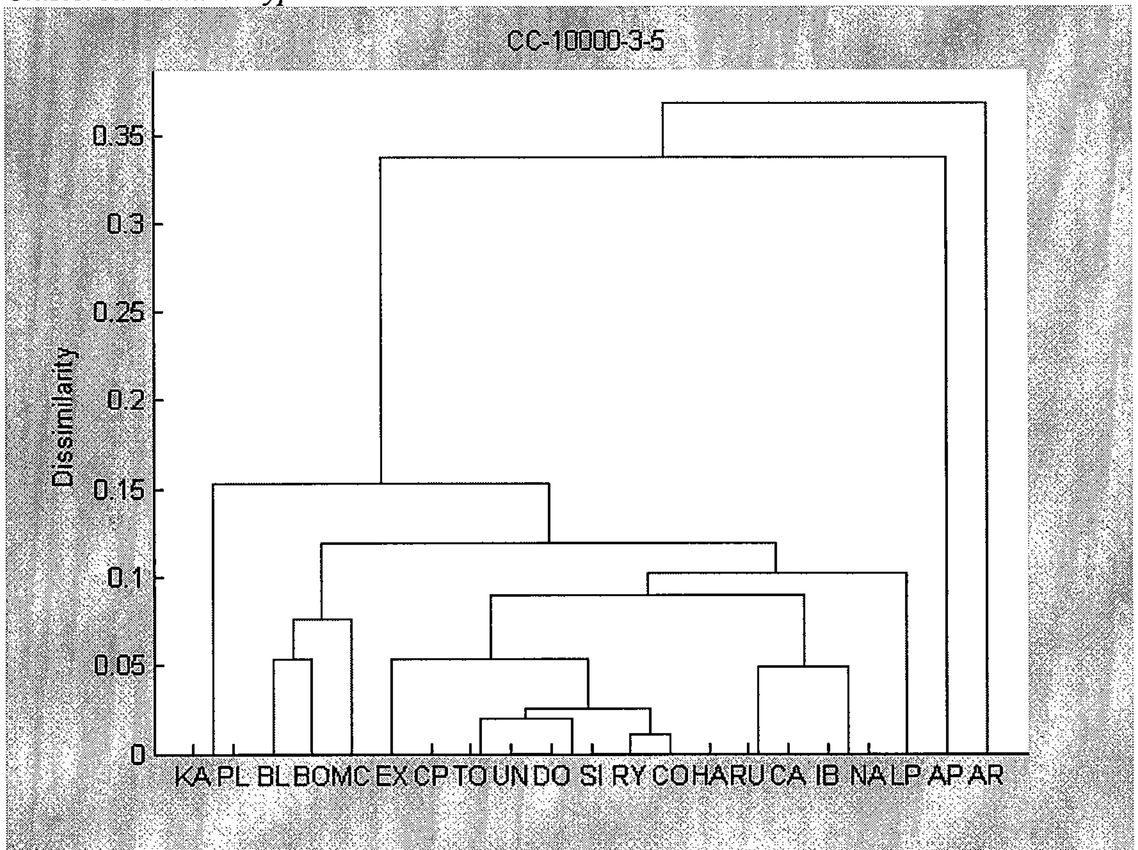
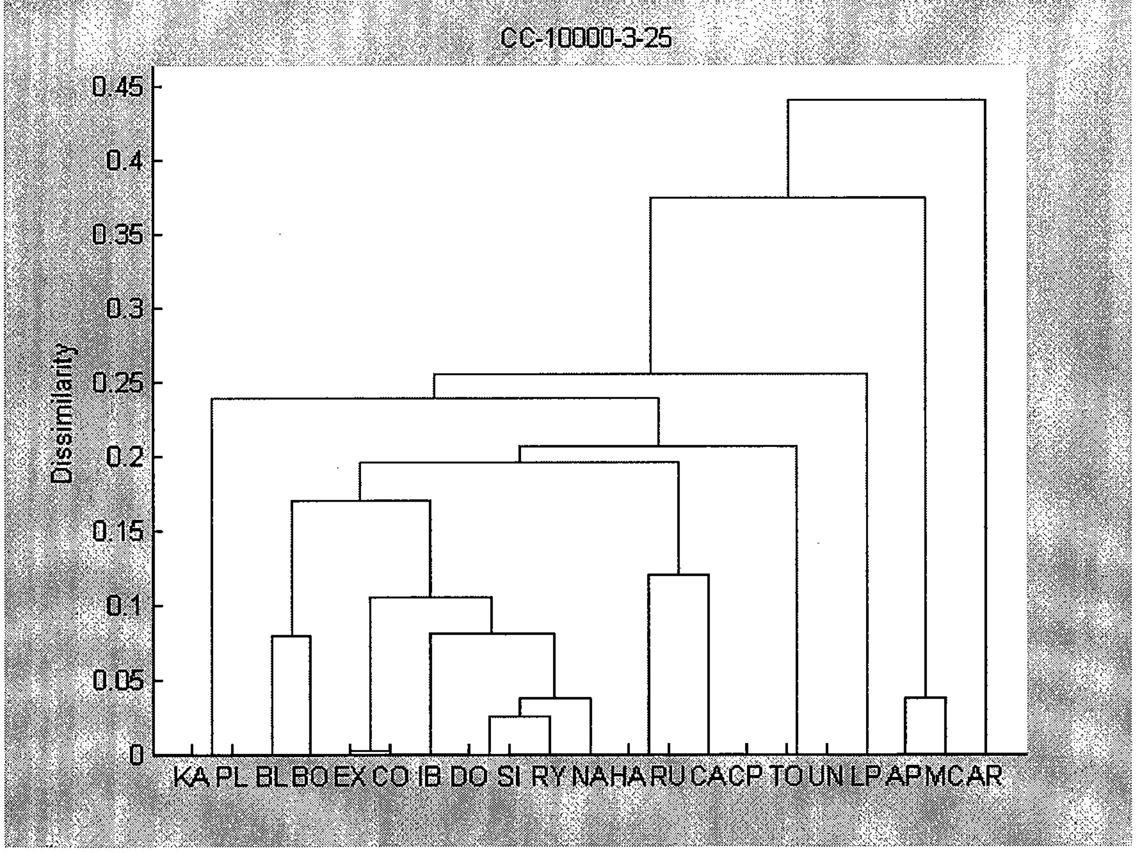
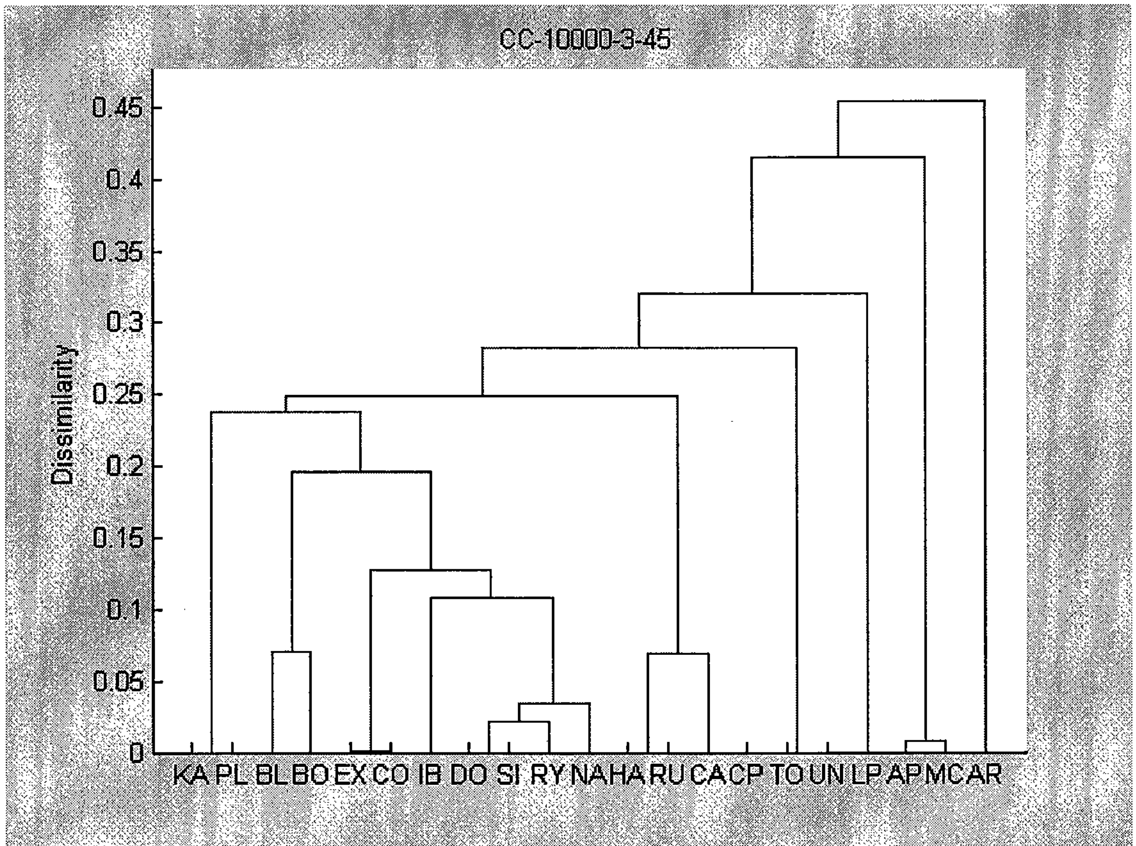
Clustered Culture Hypothesis – 3 alternatives



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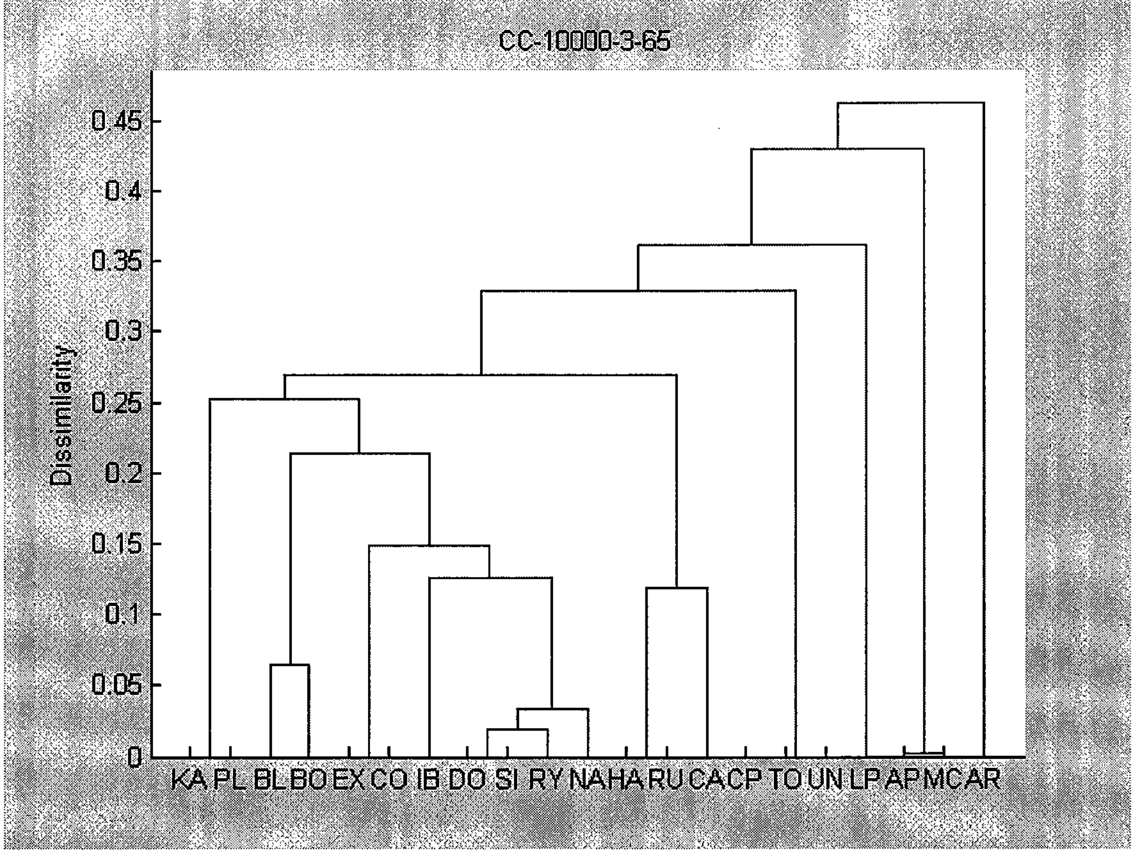
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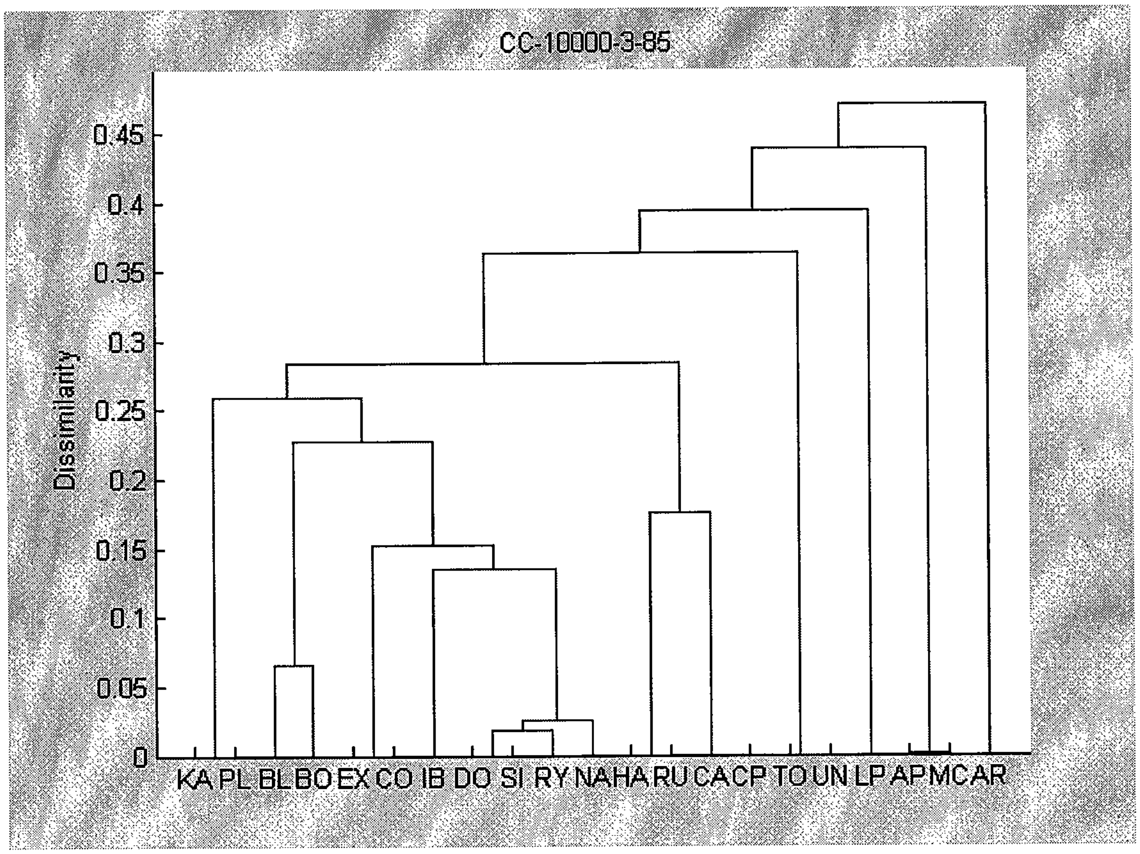

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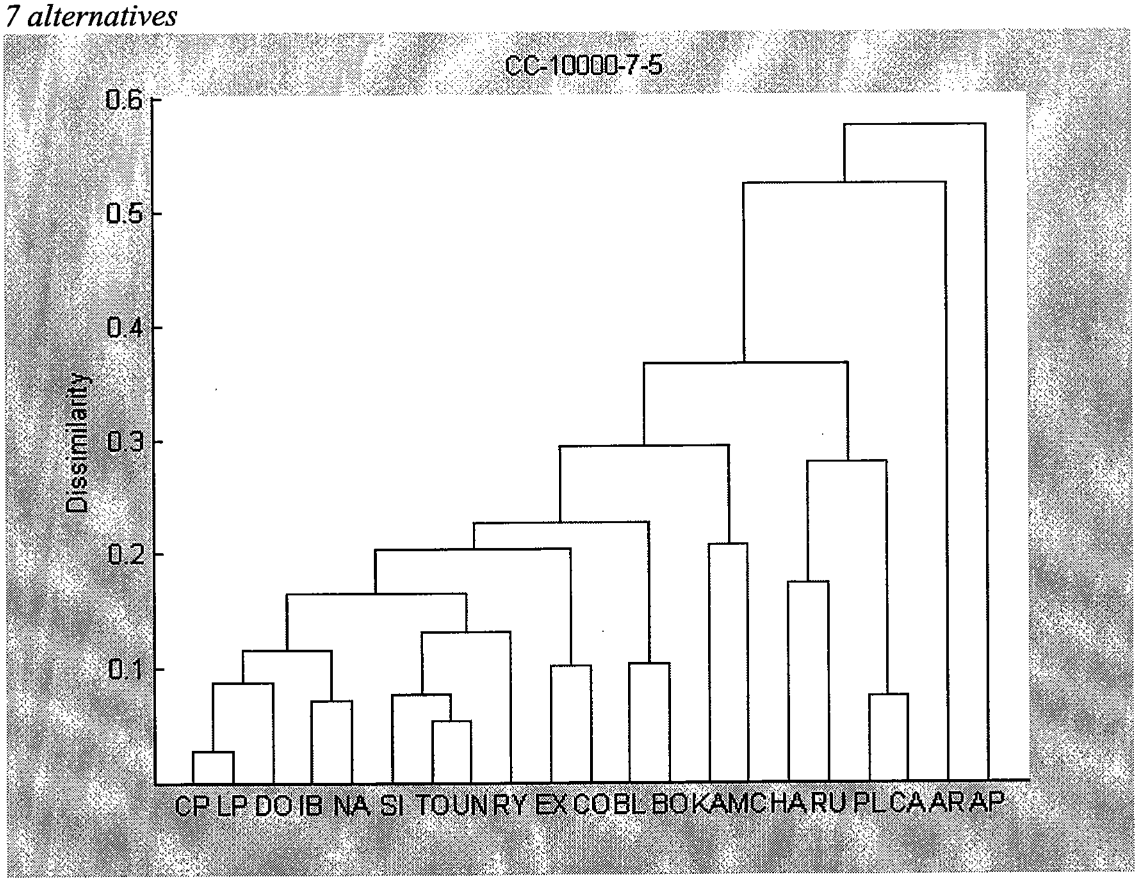

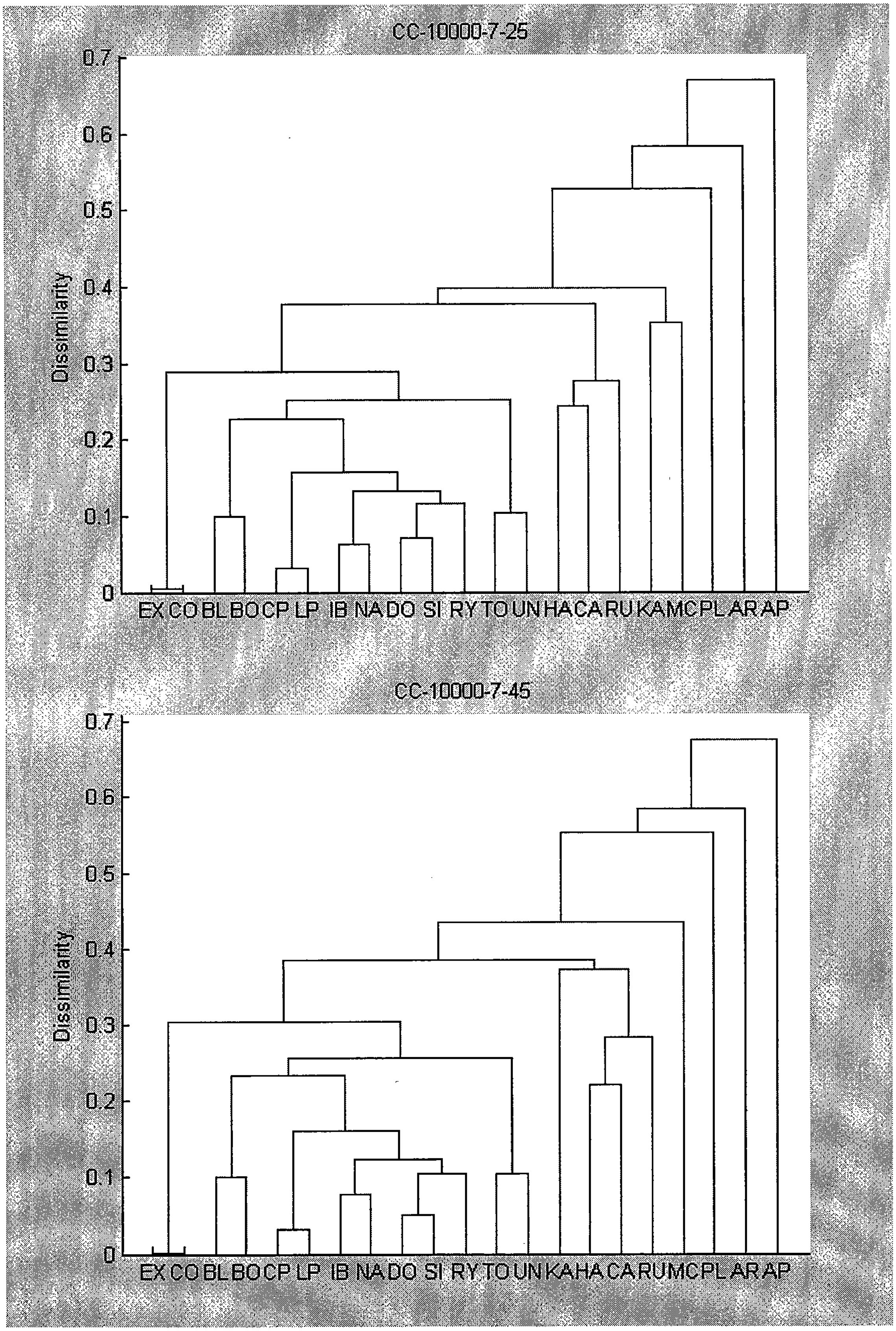
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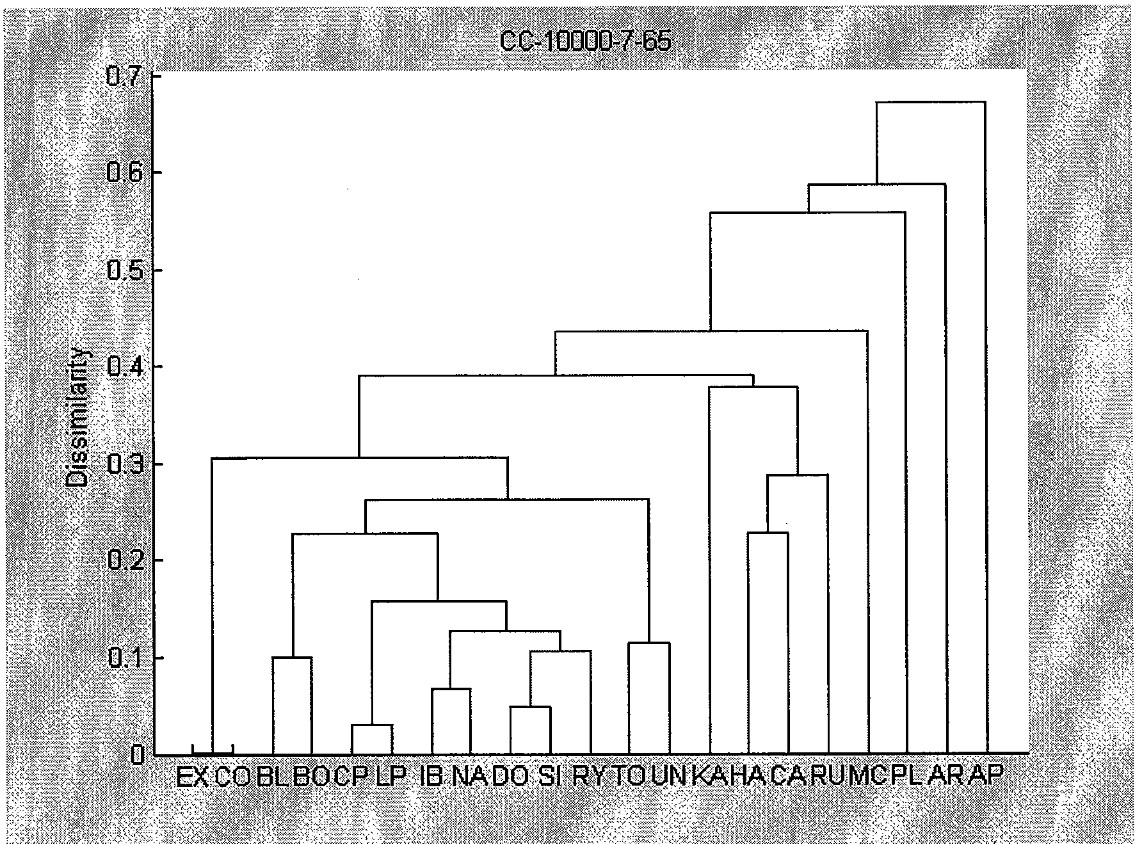
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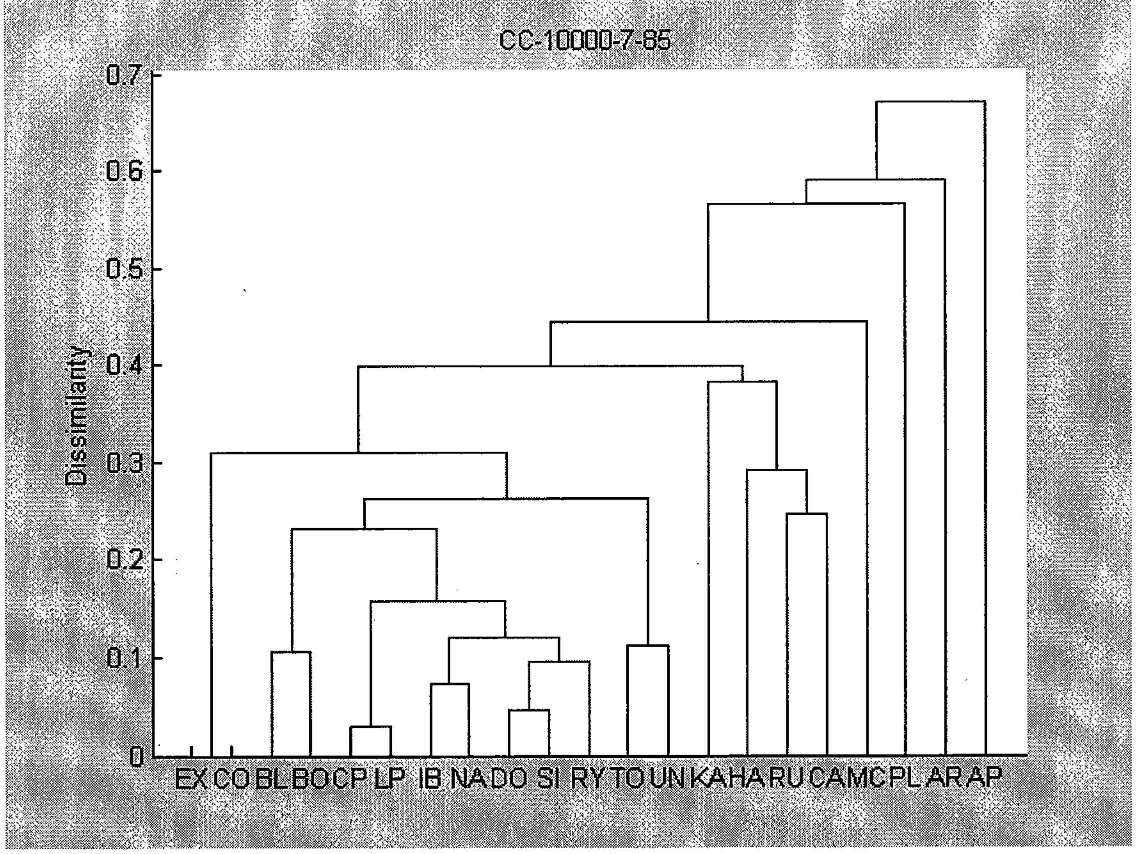
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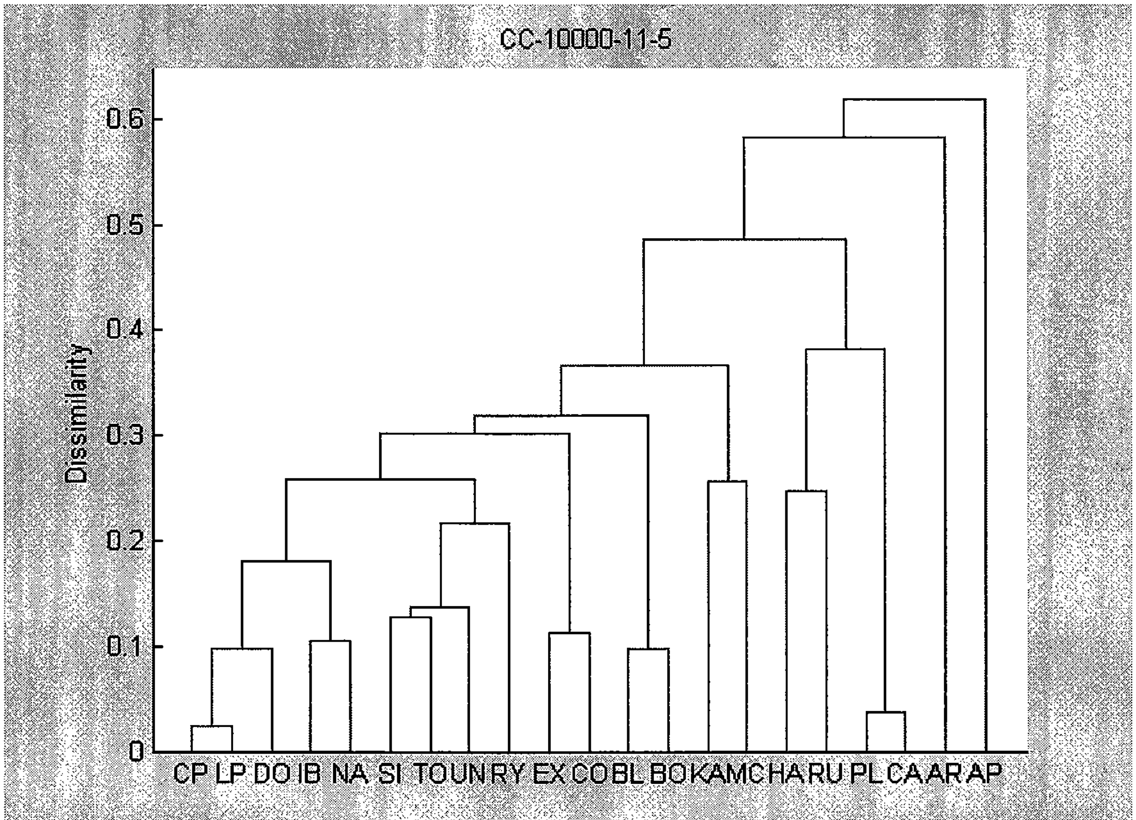
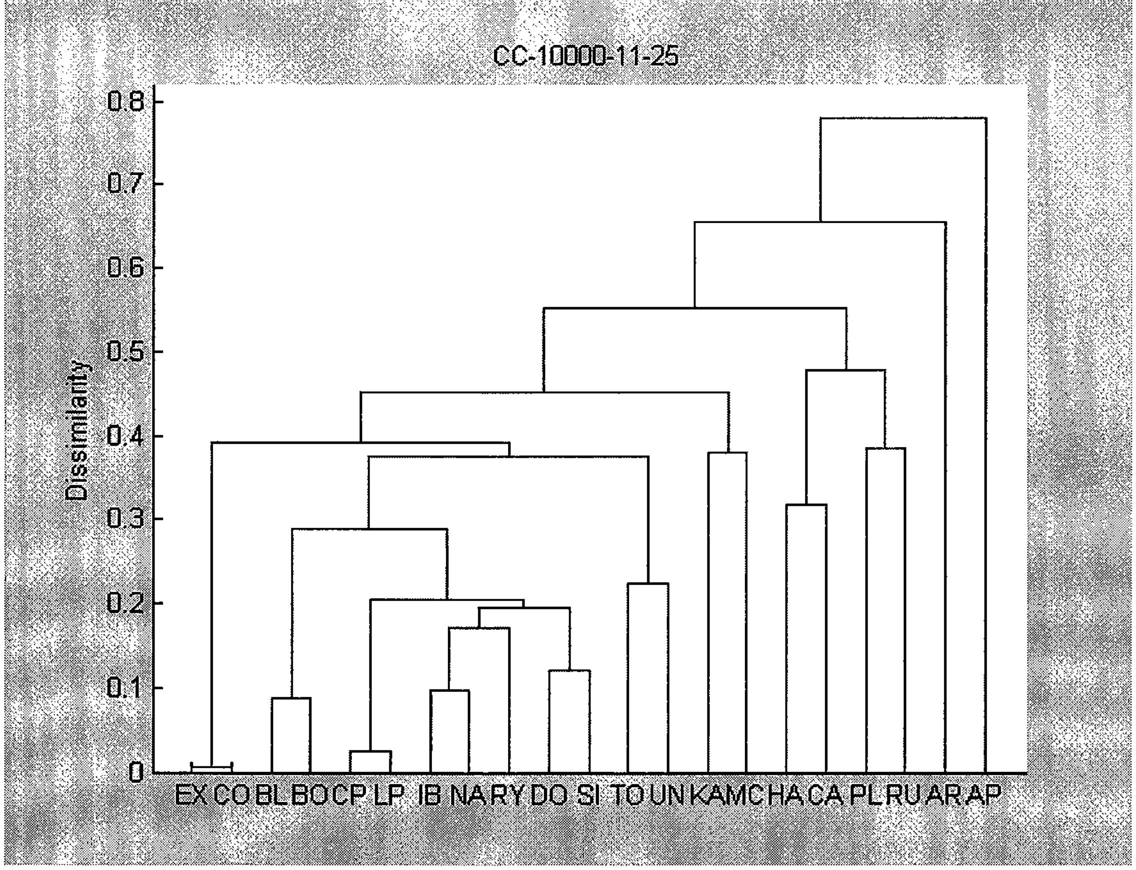
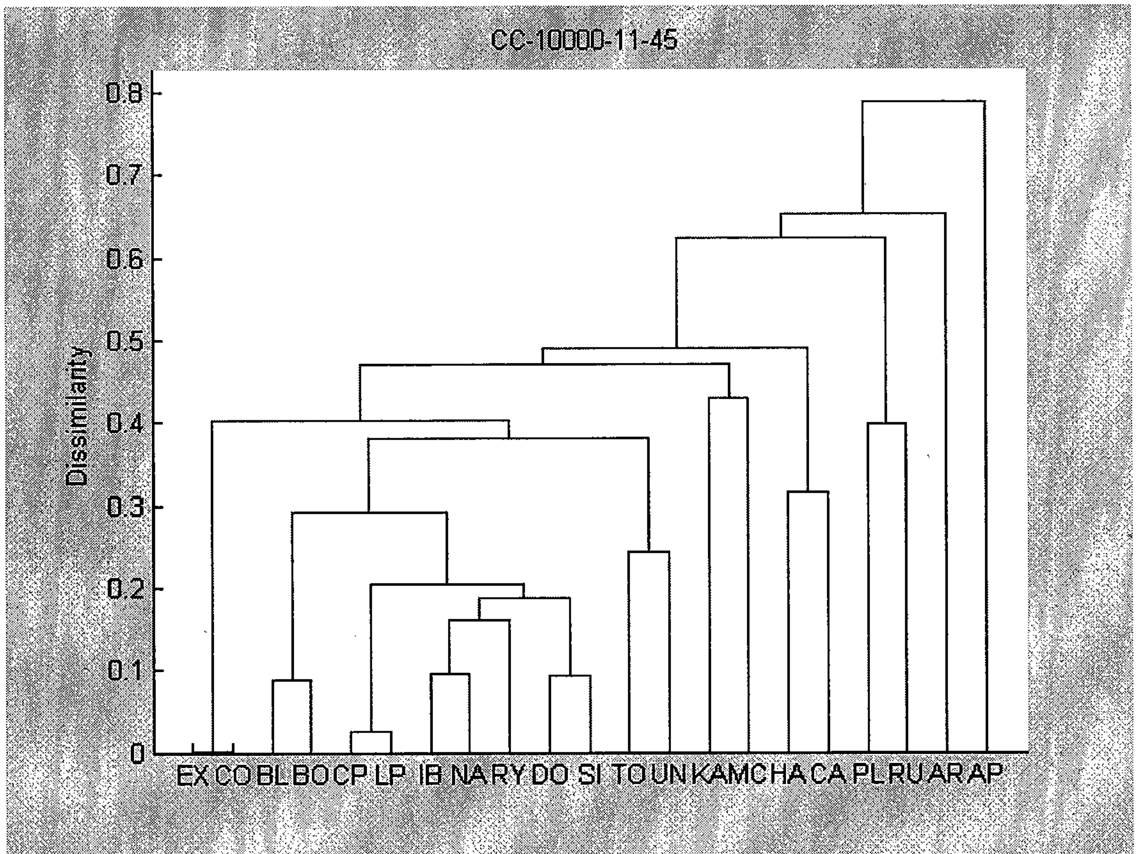
EX CO BL BO CP LP IB NA DO SI RY TO UN KA HA RU CA MC PL AR AP

11 alternatives



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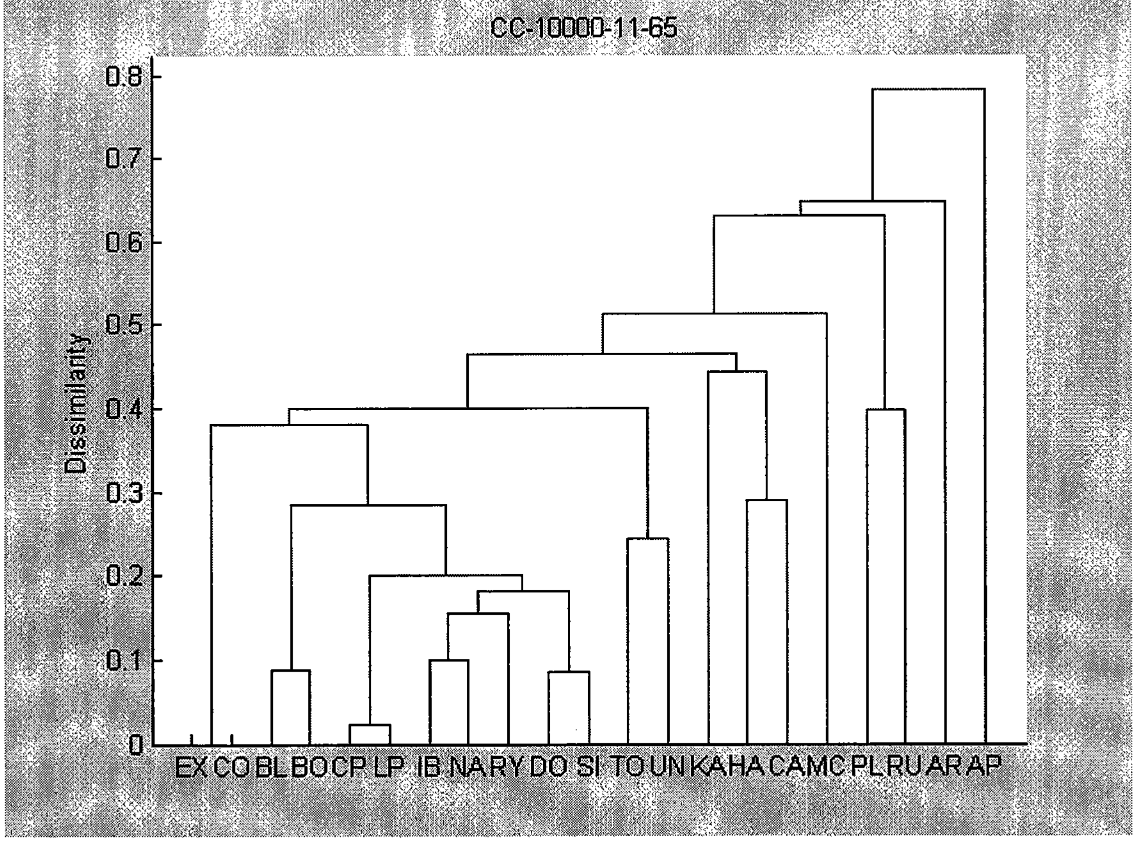
0.3
0.2
0.1
0
EX CO BL BO CP LP IB NA RY DO SI TO UN KA MC HA CA PL RU AR AP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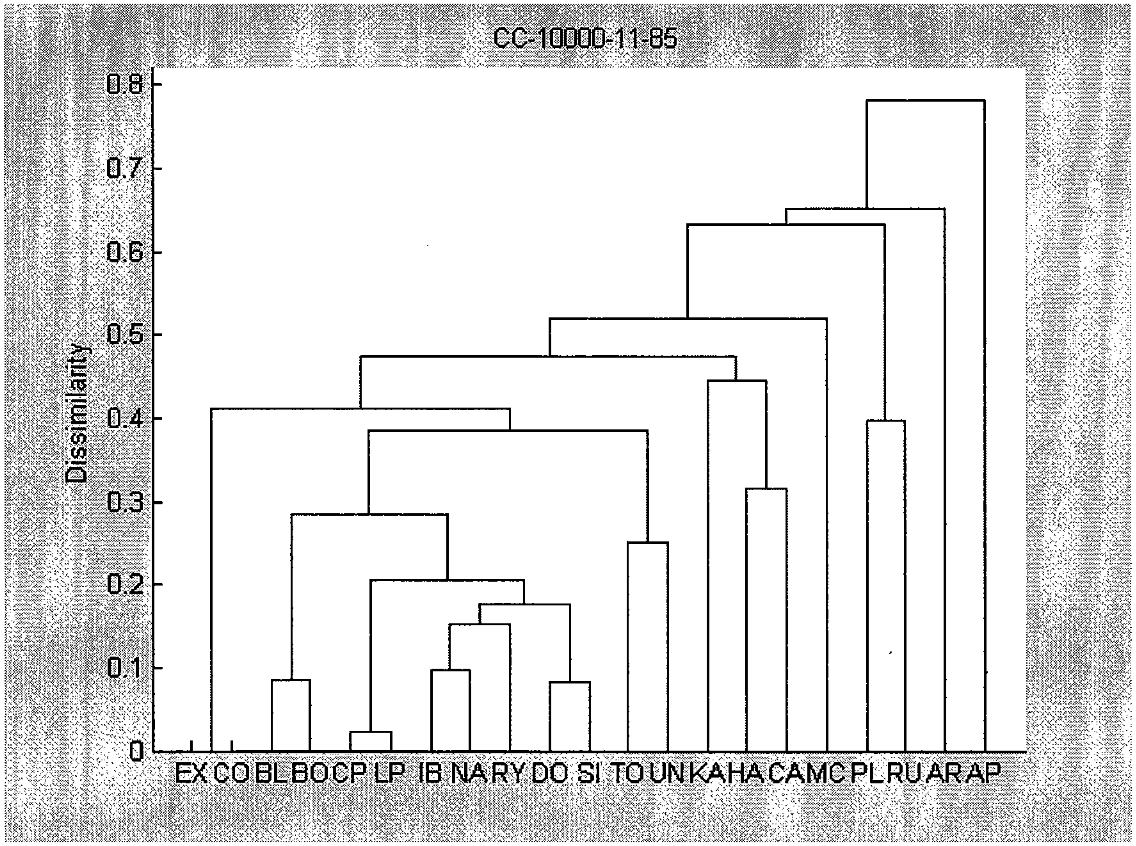
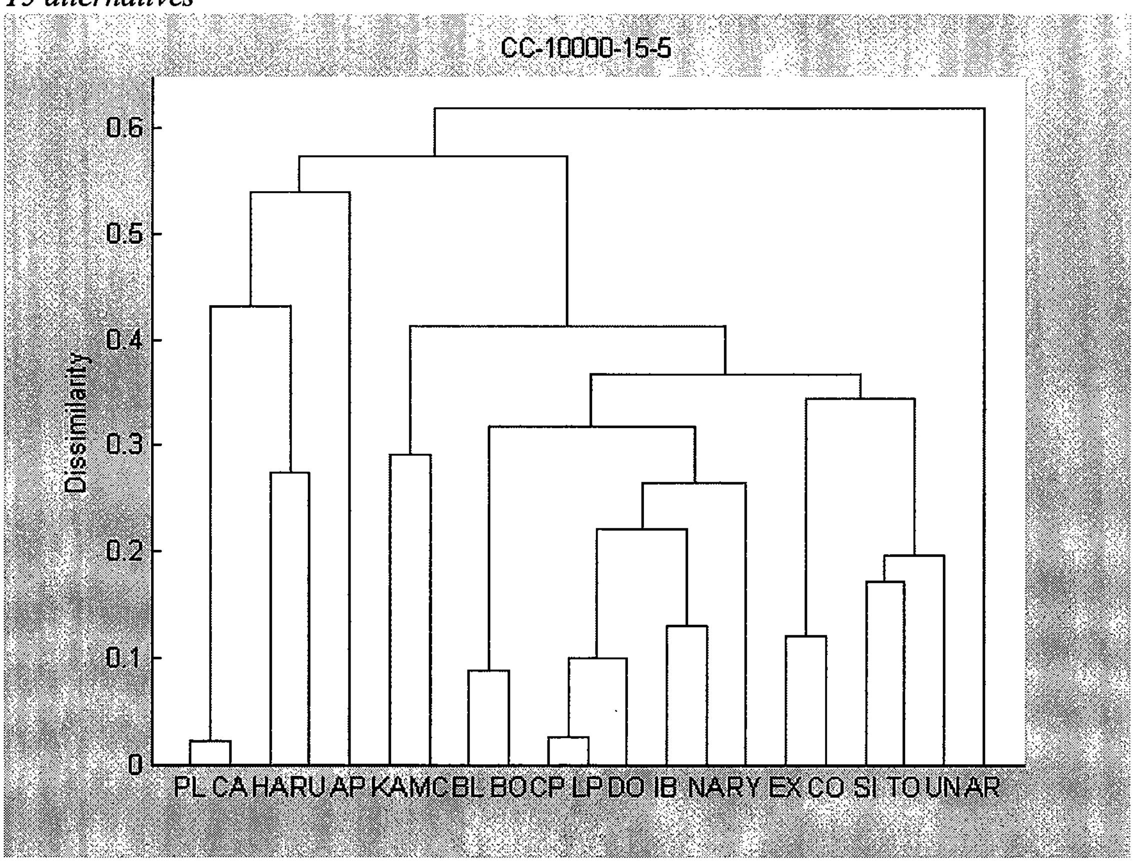
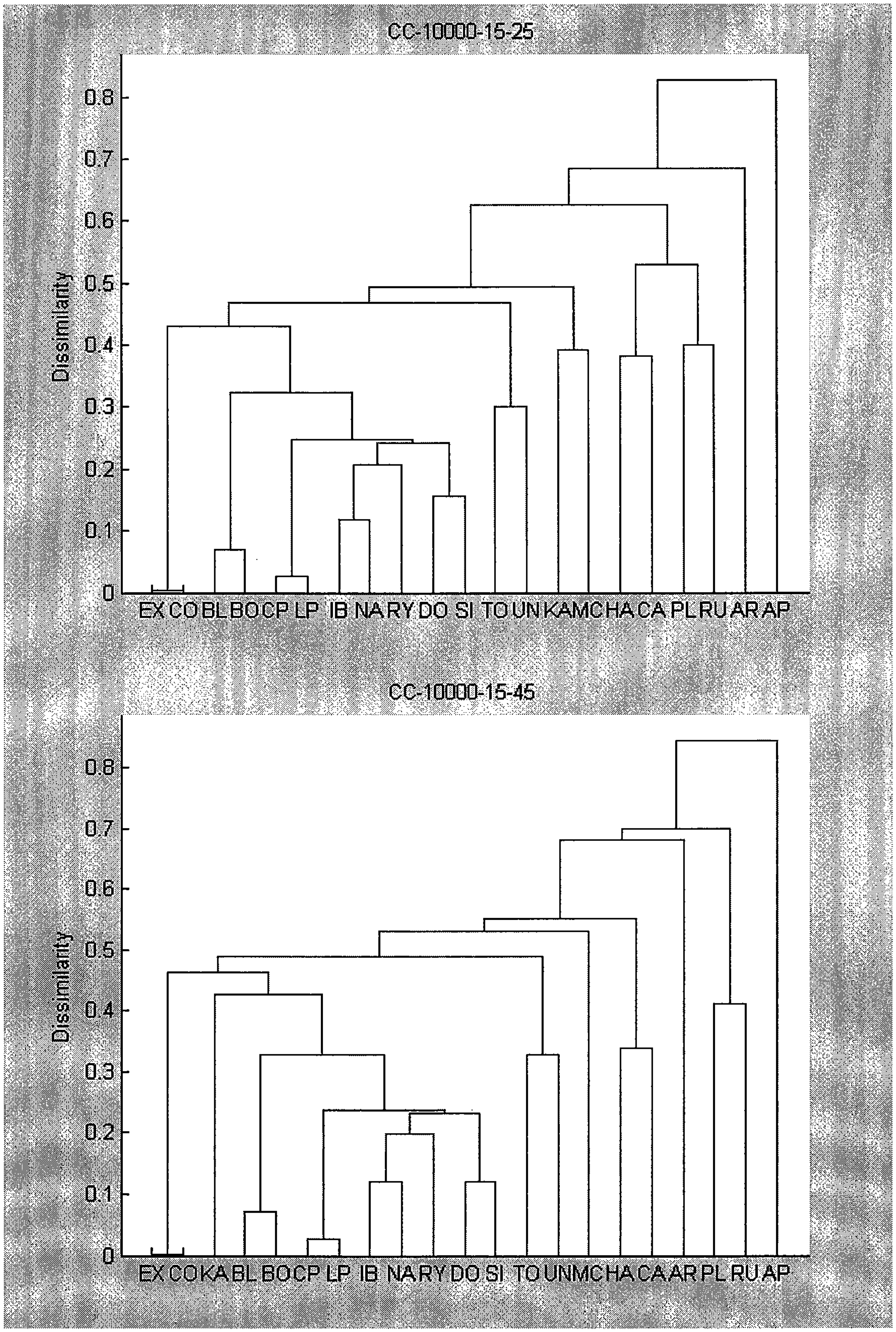
EX CO BL BO CP LP IB NA RY DO SI TO UN KA HA CA MC PL RU AR AP



15 alternatives

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EX CO BL BO CP LP IB NA RY DO SI TO UN KAM CHA CA PL RU AR AP
CC-10000-15-45
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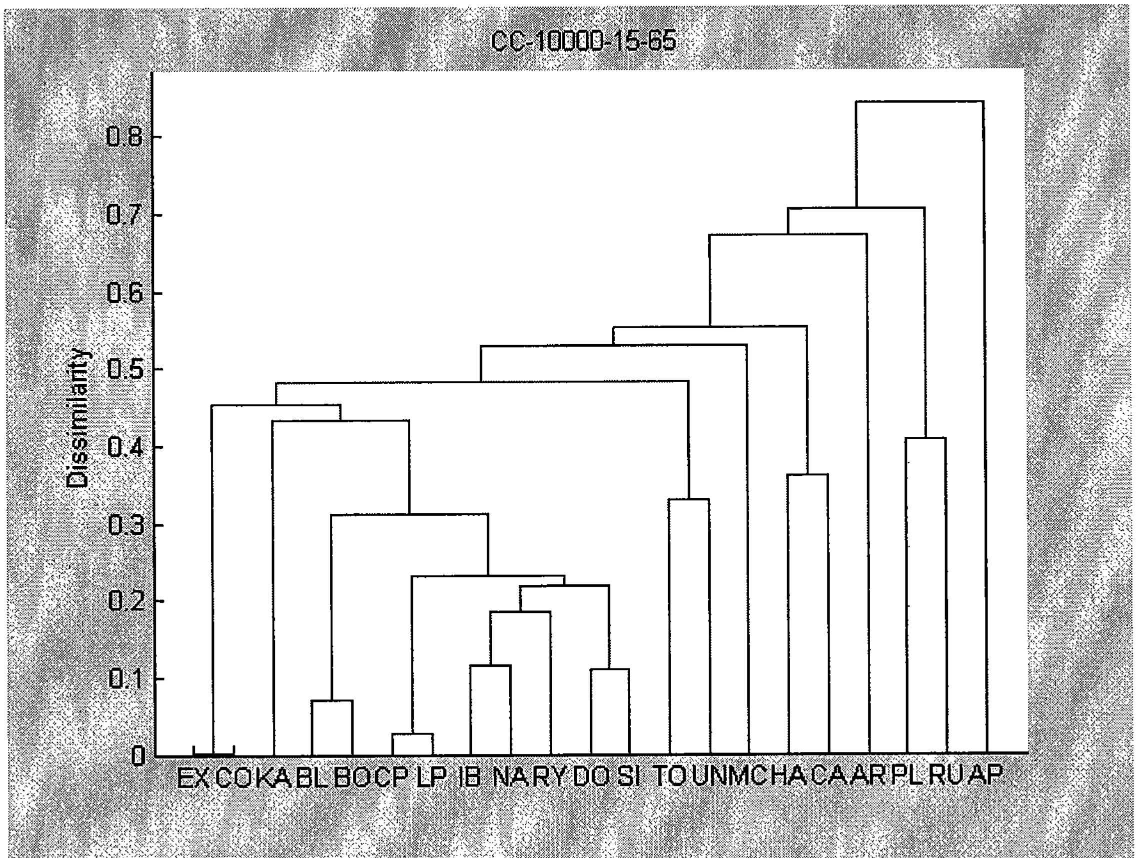
0.5
0.6
0.7
0.8
EX CO KA BL BO CP LP IB NA RY DO SI TO UN M CHA CA AR PL RU AP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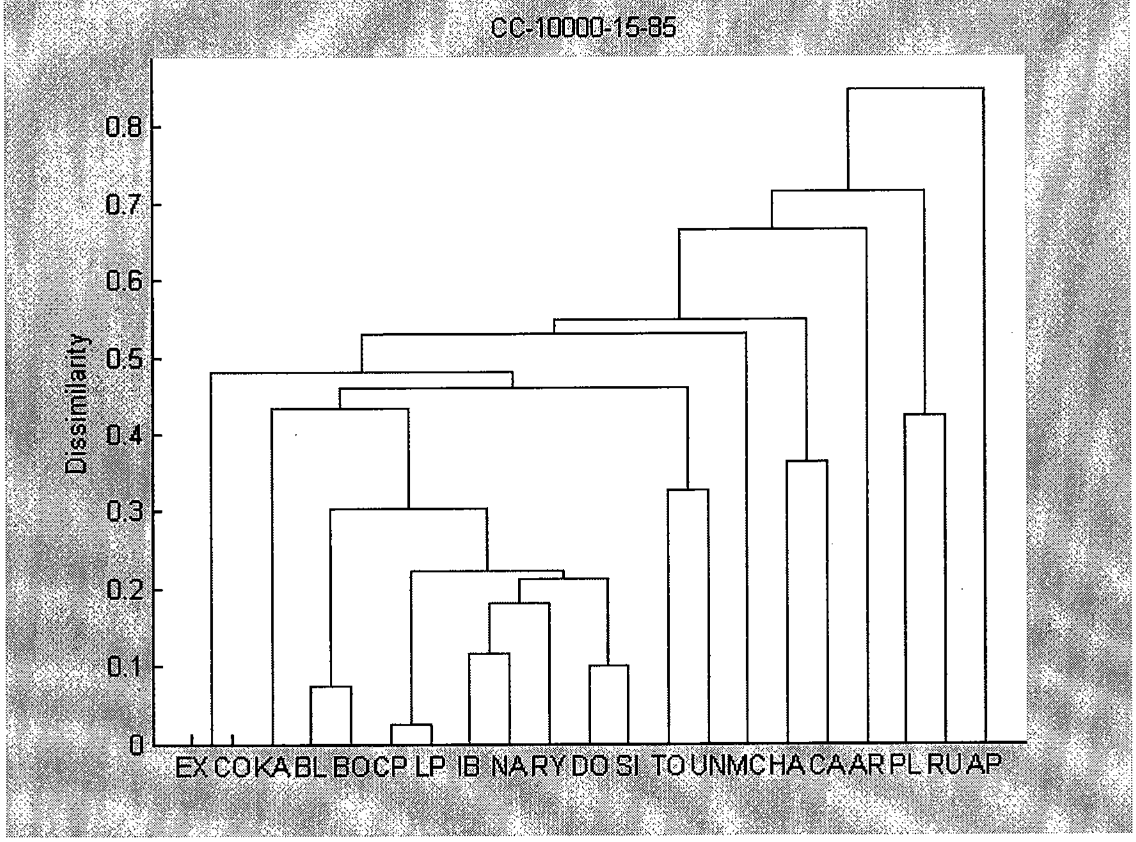
EX CO KA BL BO CP LP IB NA RY DO SI TO UN MC HA CA AR PL RU AP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0.2
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EX CO KA BL BO CP LP IB NA RY DO SI TO UN MC HA CA AR PL RU AP

Percentage of Condorcet-winning Profiles for each Profile Type

IC hypothesis

		# Voters				
		5	**25**	**45**	**65**	**85**
	3	0.94	0.91	0.91	0.92	0.91
	7	0.71	0.65	0.64	0.64	0.64
# Alternatives	**11**	0.58	0.50	0.49	0.48	0.48
	15	0.48	0.40	0.40	0.39	0.40

CC hypothesis

		# Voters				
		5	**25**	**45**	**65**	**85**
	3	0.86	0.65	0.55	0.48	0.44
	7	0.70	0.65	0.64	0.65	0.65
# Alternatives	**11**	0.58	0.52	0.52	0.52	0.52
	15	0.50	0.43	0.44	0.45	0.46

Sum Squared Error between Similarity Matrices: IC vs CC

		# Voters				
		5	**25**	**45**	**65**	**85**
	3	0.29	1.80	3.86	5.57	6.49
	7	0.02	0.00	0.01	0.01	0.01
# Alternatives	**11**	0.01	0.01	0.03	0.09	0.06
	15	0.02	0.05	0.06	0.18	0.16

IC hypothesis: Eigenvalues for each profile size

	3x5	3x25	3x45	3x65	3x85	7x5	7x25	7x45	7x65	7x85	11x5	11x25	11x45	11x65	11x85	15x5	15x25	15x45	15x65	15x85
1	0.39	0.53	0.52	0.53	0.54	0.70	0.71	0.72	0.73	0.74	0.94	0.87	0.88	0.88	0.88	1.15	0.98	0.98	0.98	0.98
2	0.28	0.43	0.43	0.46	0.47	0.51	0.58	0.58	0.59	0.58	0.50	0.63	0.64	0.65	0.65	0.53	0.66	0.68	0.69	0.68
3	0.16	0.25	0.25	0.25	0.26	0.32	0.38	0.38	0.39	0.38	0.45	0.46	0.47	0.48	0.48	0.50	0.52	0.51	0.52	0.52
4	0.12	0.12	0.14	0.14	0.13	0.26	0.32	0.32	0.33	0.32	0.29	0.42	0.42	0.43	0.43	0.33	0.48	0.48	0.48	0.48
5	0.05	0.10	0.10	0.09	0.10	0.21	0.31	0.32	0.32	0.32	0.27	0.36	0.38	0.38	0.39	0.31	0.40	0.42	0.43	0.43
6	0.05	0.07	0.09	0.09	0.09	0.20	0.25	0.26	0.27	0.27	0.25	0.34	0.35	0.35	0.36	0.30	0.37	0.37	0.38	0.38
7	0.04	0.05	0.07	0.06	0.07	0.17	0.22	0.24	0.24	0.24	0.24	0.29	0.30	0.32	0.32	0.28	0.33	0.36	0.36	0.36
8	0.03	0.04	0.04	0.03	0.04	0.16	0.19	0.19	0.19	0.19	0.23	0.24	0.25	0.25	0.25	0.24	0.28	0.28	0.28	0.28
9	0.02	0.04	0.02	0.03	0.04	0.09	0.15	0.16	0.16	0.16	0.13	0.20	0.20	0.21	0.21	0.17	0.23	0.22	0.24	0.23
10	0.01	0.02	0.02	0.02	0.02	0.08	0.14	0.15	0.16	0.16	0.11	0.17	0.19	0.20	0.19	0.14	0.19	0.20	0.21	0.21
11	0.01	0.01	0.01	0.01	0.01	0.08	0.12	0.13	0.14	0.14	0.11	0.16	0.18	0.18	0.18	0.13	0.18	0.19	0.20	0.20
12	0.00	0.01	0.01	0.01	0.01	0.06	0.11	0.10	0.10	0.11	0.10	0.16	0.15	0.15	0.16	0.12	0.18	0.18	0.19	0.19
13	0.00	0.01	0.00	0.00	0.01	0.04	0.09	0.09	0.09	0.09	0.07	0.14	0.14	0.14	0.14	0.09	0.17	0.17	0.18	0.18
14	0.00	0.00	0.00	0.00	0.00	0.04	0.06	0.06	0.05	0.06	0.06	0.11	0.12	0.13	0.13	0.08	0.15	0.16	0.17	0.17
15	0.00	0.00	0.00	0.00	0.00	0.04	0.05	0.05	0.05	0.05	0.05	0.09	0.09	0.09	0.09	0.06	0.11	0.11	0.11	0.11
16	0.00	0.00	0.00	0.00	0.00	0.03	0.04	0.04	0.03	0.03	0.05	0.05	0.05	0.05	0.05	0.06	0.06	0.06	0.06	0.06
17	0.00	0.00	0.00	0.00	0.00	0.03	0.03	0.03	0.03	0.03	0.05	0.05	0.04	0.04	0.04	0.05	0.06	0.06	0.06	0.06
18	0.00	0.00	0.00	0.00	0.00	0.03	0.03	0.03	0.02	0.02	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03
19	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.01	0.01	0.01	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
20	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
21	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

IC hypothesis: Sum squared error between similarity matrices of every pair of profile sizes

	3x5	3x25	3x45	3x65	3x85	7x5	7x25	7x45	7x65	7x85	11x5	11x25	11x45	11x65	11x85	15x5	15x25	15x45	15x65	15x85
3x5	0.00	1.20	1.27	1.40	1.62	9.06	16.13	17.15	17.71	17.67	18.82	30.20	32.36	33.63	33.74	27.94	41.23	43.10	44.82	44.34
3x25	1.20	0.00	0.03	0.03	0.04	5.69	10.98	11.73	12.19	12.14	13.44	23.07	24.85	25.90	26.02	21.16	32.80	34.41	35.97	35.48
3x45	1.27	0.03	0.00	0.01	0.05	5.97	11.14	11.85	12.31	12.26	13.71	23.26	25.00	26.03	26.16	21.41	32.98	34.57	36.12	35.63
3x65	1.40	0.03	0.01	0.00	0.02	5.81	10.91	11.61	12.06	12.01	13.47	22.95	24.68	25.70	25.82	21.12	32.62	34.19	35.74	35.25
3x85	1.62	0.04	0.05	0.02	0.00	5.33	10.25	10.94	11.38	11.33	12.70	21.97	23.67	24.67	24.79	20.16	31.45	33.00	34.52	34.04
7x5	9.06	5.69	5.97	5.81	5.33	0.00	1.62	2.11	2.31	2.28	1.99	7.11	8.35	9.05	9.12	5.83	12.90	14.11	15.16	14.90
7x25	16.13	10.98	11.14	10.91	10.25	1.62	0.00	0.06	0.08	0.09	1.21	2.36	3.00	3.42	3.45	3.35	6.22	6.93	7.68	7.47
7x45	17.15	11.73	11.85	11.61	10.94	2.11	0.06	0.00	0.01	0.02	1.38	2.04	2.57	2.93	2.97	3.29	5.66	6.28	6.99	6.77
7x65	17.71	12.19	12.31	12.06	11.38	2.31	0.08	0.01	0.00	0.01	1.43	1.87	2.37	2.72	2.75	3.23	5.37	5.96	6.66	6.44
7x85	17.67	12.14	12.26	12.01	11.33	2.28	0.09	0.02	0.01	0.00	1.41	1.89	2.38	2.73	2.75	3.21	5.39	5.98	6.66	6.45
11x5	18.82	13.44	13.71	13.47	12.70	1.99	1.21	1.38	1.43	1.41	0.00	2.65	3.43	3.82	3.90	1.03	5.85	6.78	7.49	7.34
11x25	30.20	23.07	23.26	22.95	21.97	7.11	2.36	2.04	1.87	1.89	2.65	0.00	0.08	0.16	0.18	1.95	0.94	1.24	1.58	1.50
11x45	32.36	24.85	25.00	24.68	23.67	8.35	3.00	2.57	2.37	2.38	3.43	0.08	0.00	0.03	0.03	2.40	0.64	0.83	1.10	1.02
11x65	33.63	25.90	26.03	25.70	24.67	9.05	3.42	2.93	2.72	2.73	3.82	0.16	0.03	0.00	0.01	2.57	0.50	0.64	0.88	0.80
11x85	33.74	26.02	26.16	25.82	24.79	9.12	3.45	2.97	2.75	2.75	3.90	0.18	0.03	0.01	0.00	2.66	0.51	0.63	0.87	0.79
15x5	27.94	21.16	21.41	21.12	20.16	5.83	3.35	3.29	3.23	3.21	1.03	1.95	2.40	2.57	2.66	0.00	3.31	4.05	4.51	4.45
15x25	41.23	32.80	32.98	32.62	31.45	12.90	6.22	5.66	5.37	5.39	5.85	0.94	0.64	0.50	0.51	3.31	0.00	0.06	0.13	0.13
15x45	43.10	34.41	34.57	34.19	33.00	14.11	6.93	6.28	5.96	5.98	6.78	1.24	0.83	0.64	0.63	4.05	0.06	0.00	0.03	0.02
15x65	44.82	35.97	36.12	35.74	34.52	15.16	7.68	6.99	6.66	6.66	7.49	1.58	1.10	0.88	0.87	4.51	0.13	0.03	0.00	0.01
15x85	44.34	35.48	35.63	35.25	34.04	14.90	7.47	6.77	6.44	6.45	7.34	1.50	1.02	0.80	0.79	4.45	0.13	0.02	0.01	0.00

CC hypothesis: Eigenvalues for each profile size

	3x5	3x25	3x45	3x65	3x85	7x5	7x25	7x45	7x65	7x85	11x5	11x25	11x45	11x65	11x85	15x5	15x25	15x45	15x65	15x85
1	0.44	0.64	0.73	0.75	0.76	0.70	0.71	0.72	0.74	0.76	0.95	0.87	0.89	0.88	0.89	1.14	0.97	0.97	0.98	1.00
2	0.30	0.42	0.51	0.61	0.69	0.53	0.57	0.59	0.59	0.60	0.51	0.63	0.64	0.64	0.65	0.52	0.65	0.67	0.67	0.68
3	0.21	0.34	0.37	0.38	0.40	0.33	0.38	0.39	0.38	0.38	0.46	0.46	0.47	0.47	0.46	0.50	0.50	0.51	0.51	0.50
4	0.16	0.26	0.33	0.34	0.36	0.26	0.32	0.33	0.33	0.33	0.29	0.41	0.42	0.41	0.42	0.33	0.46	0.47	0.46	0.46
5	0.09	0.22	0.25	0.26	0.26	0.22	0.31	0.31	0.32	0.32	0.27	0.37	0.36	0.37	0.37	0.30	0.39	0.41	0.40	0.40
6	0.06	0.15	0.19	0.21	0.23	0.20	0.25	0.26	0.26	0.26	0.26	0.34	0.34	0.34	0.34	0.29	0.37	0.37	0.36	0.36
7	0.05	0.13	0.15	0.17	0.18	0.18	0.23	0.23	0.24	0.24	0.24	0.28	0.30	0.31	0.30	0.27	0.32	0.35	0.35	0.34
8	0.04	0.10	0.11	0.13	0.13	0.16	0.19	0.19	0.19	0.19	0.24	0.24	0.24	0.24	0.25	0.23	0.28	0.28	0.27	0.27
9	0.04	0.05	0.05	0.06	0.07	0.09	0.15	0.16	0.16	0.16	0.14	0.19	0.19	0.19	0.20	0.17	0.22	0.21	0.21	0.21
10	0.02	0.04	0.04	0.05	0.06	0.08	0.14	0.15	0.16	0.16	0.11	0.17	0.19	0.19	0.19	0.13	0.19	0.19	0.20	0.21
11	0.01	0.03	0.03	0.02	0.03	0.08	0.13	0.13	0.14	0.14	0.11	0.16	0.17	0.17	0.17	0.13	0.18	0.19	0.19	0.19
12	0.01	0.02	0.02	0.02	0.01	0.07	0.11	0.10	0.10	0.11	0.10	0.15	0.14	0.14	0.15	0.12	0.17	0.17	0.17	0.17
13	0.00	0.02	0.01	0.01	0.01	0.05	0.09	0.09	0.09	0.09	0.07	0.13	0.14	0.13	0.13	0.09	0.17	0.16	0.16	0.16
14	0.00	0.01	0.00	0.00	0.00	0.04	0.06	0.05	0.06	0.05	0.06	0.10	0.11	0.12	0.12	0.08	0.14	0.15	0.15	0.15
15	0.00	0.00	0.00	0.00	0.00	0.04	0.05	0.05	0.05	0.05	0.05	0.09	0.08	0.08	0.08	0.06	0.11	0.10	0.10	0.09
16	0.00	0.00	0.00	0.00	0.00	0.03	0.04	0.04	0.04	0.04	0.05	0.05	0.05	0.05	0.05	0.06	0.06	0.06	0.05	0.05
17	0.00	0.00	0.00	0.00	0.00	0.03	0.03	0.04	0.03	0.03	0.05	0.05	0.04	0.04	0.04	0.05	0.06	0.05	0.05	0.05
18	0.00	0.00	0.00	0.00	0.00	0.03	0.03	0.02	0.02	0.02	0.04	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03
19	0.00	0.00	0.00	0.00	0.00	0.02	0.02	0.02	0.01	0.01	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
20	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
21	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

CC hypothesis: Sum squared error between similarity matrices of every pair of profile sizes

	3x5	3x25	3x45	3x65	3x85	7x5	7x25	7x45	7x65	7x85	11x5	11x25	11x45	11x65	11x85	15x5	15x25	15x45	15x65	15x85
3x5	0.00	2.86	5.30	7.24	8.82	7.57	13.53	14.60	14.92	15.47	16.41	25.90	27.44	27.31	28.02	23.07	34.79	36.53	36.19	36.60
3x25	2.86	0.00	0.45	1.13	1.82	3.41	6.43	7.08	7.26	7.59	8.56	14.96	16.02	15.89	16.37	13.13	21.53	22.88	22.65	23.03
3x45	5.30	0.45	0.00	0.19	0.54	3.32	5.23	5.72	5.86	6.12	7.06	12.20	13.10	12.97	13.39	10.81	17.84	19.05	18.86	19.24
3x65	7.24	1.13	0.19	0.00	0.10	3.68	4.92	5.30	5.41	5.63	6.52	10.90	11.70	11.58	11.94	9.75	15.95	17.06	16.91	17.28
3x85	8.82	1.82	0.54	0.10	0.00	4.13	4.94	5.26	5.35	5.54	6.35	10.25	10.98	10.86	11.19	9.23	14.89	15.95	15.81	16.19
7x5	7.57	3.41	3.32	3.68	4.13	0.00	1.43	1.89	2.04	2.17	1.91	6.33	7.17	7.22	7.56	4.77	10.97	12.12	11.93	12.20
7x25	13.53	6.43	5.23	4.92	4.94	1.43	0.00	0.04	0.07	0.11	1.30	2.15	2.58	2.56	2.77	2.97	5.31	5.95	5.80	5.95
7x45	14.60	7.08	5.72	5.30	5.26	1.89	0.04	0.00	0.01	0.03	1.45	1.81	2.17	2.12	2.31	2.94	4.78	5.32	5.17	5.29
7x65	14.92	7.26	5.86	5.41	5.35	2.04	0.07	0.01	0.00	0.01	1.51	1.72	2.05	2.00	2.19	2.94	4.62	5.14	4.99	5.10
7x85	15.47	7.59	6.12	5.63	5.54	2.17	0.11	0.03	0.01	0.00	1.45	1.57	1.89	1.84	2.01	2.78	4.37	4.89	4.72	4.83
11x5	16.41	8.56	7.06	6.52	6.35	1.91	1.30	1.45	1.51	1.45	0.00	2.45	2.98	3.11	3.28	0.66	4.86	5.78	5.71	5.95
11x25	25.90	14.96	12.20	10.90	10.25	6.33	2.15	1.81	1.72	1.57	2.45	0.00	0.04	0.08	0.10	1.98	0.72	0.97	0.92	1.00
11x45	27.44	16.02	13.10	11.70	10.98	7.17	2.58	2.17	2.05	1.89	2.98	0.04	0.00	0.02	0.02	2.34	0.55	0.71	0.65	0.71
11x65	27.31	15.89	12.97	11.58	10.86	7.22	2.56	2.12	2.00	1.84	3.11	0.08	0.02	0.00	0.01	2.51	0.62	0.75	0.68	0.73
11x85	28.02	16.37	13.39	11.94	11.19	7.56	2.77	2.31	2.19	2.01	3.28	0.10	0.02	0.01	0.00	2.58	0.54	0.65	0.59	0.62
15x5	23.07	13.13	10.81	9.75	9.23	4.77	2.97	2.94	2.94	2.78	0.66	1.98	2.34	2.51	2.58	0.00	3.11	3.89	3.90	4.13
15x25	34.79	21.53	17.84	15.95	14.89	10.97	5.31	4.78	4.62	4.37	4.86	0.72	0.55	0.62	0.54	3.11	0.00	0.07	0.08	0.15
15x45	36.53	22.88	19.05	17.06	15.95	12.12	5.95	5.32	5.14	4.89	5.78	0.97	0.71	0.75	0.65	3.89	0.07	0.00	0.02	0.04
15x65	36.19	22.65	18.86	16.91	15.81	11.93	5.80	5.17	4.99	4.72	5.71	0.92	0.65	0.68	0.59	3.90	0.08	0.02	0.00	0.02
15x85	36.60	23.03	19.24	17.28	16.19	12.20	5.95	5.29	5.10	4.83	5.95	1.00	0.71	0.73	0.62	4.13	0.15	0.04	0.02	0.00

Similarity Matrix: IC-3-5

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.60	0.61	0.72	0.76	0.75	0.70	0.66	0.70	0.71	0.78	0.70	0.69	0.60	0.66	0.70	0.70	0.70	0.72	0.72	0.66
KA	0.60	1.00	0.66	0.85	0.83	0.80	0.86	0.86	0.84	0.82	0.82	0.86	0.85	1.00	0.86	0.86	0.86	0.86	0.85	0.84	0.86
AR	0.61	0.66	1.00	0.65	0.66	0.65	0.65	0.64	0.64	0.63	0.64	0.65	0.65	0.66	0.64	0.65	0.65	0.65	0.65	0.64	0.64
BL	0.72	0.85	0.65	1.00	0.95	0.94	0.99	0.93	0.97	0.95	0.93	0.99	0.98	0.85	0.93	0.99	0.99	0.99	0.98	0.97	0.93
BO	0.76	0.83	0.66	0.95	1.00	0.91	0.94	0.89	0.92	0.91	0.92	0.94	0.93	0.83	0.89	0.94	0.94	0.94	0.94	0.93	0.89
EX	0.75	0.80	0.65	0.94	0.91	1.00	0.94	0.89	0.94	0.92	0.90	0.94	0.93	0.80	0.89	0.94	0.94	0.94	0.95	0.96	0.89
CP	0.70	0.86	0.65	0.99	0.94	0.94	1.00	0.94	0.98	0.95	0.92	1.00	0.99	0.86	0.94	1.00	1.00	1.00	0.99	0.98	0.94
HA	0.66	0.86	0.64	0.93	0.89	0.89	0.94	1.00	0.95	0.93	0.88	0.95	0.95	0.86	1.00	0.95	0.94	0.94	0.93	0.92	1.00
IB	0.70	0.84	0.64	0.97	0.92	0.94	0.98	0.95	1.00	0.96	0.92	0.98	0.99	0.84	0.95	0.98	0.98	0.98	0.99	0.98	0.95
LP	0.71	0.82	0.63	0.95	0.91	0.92	0.95	0.93	0.96	1.00	0.92	0.95	0.95	0.82	0.93	0.95	0.95	0.95	0.96	0.96	0.93
MC	0.78	0.82	0.64	0.93	0.92	0.90	0.92	0.88	0.92	0.92	1.00	0.92	0.91	0.82	0.88	0.92	0.92	0.92	0.93	0.94	0.88
DO	0.70	0.86	0.65	0.99	0.94	0.94	1.00	0.95	0.98	0.95	0.92	1.00	0.99	0.86	0.95	1.00	1.00	1.00	0.99	0.98	0.95
NA	0.69	0.85	0.65	0.98	0.93	0.93	0.99	0.95	0.99	0.95	0.91	0.99	1.00	0.85	0.95	0.99	0.99	0.99	0.98	0.97	0.95
PL	0.60	1.00	0.66	0.85	0.83	0.80	0.86	0.86	0.84	0.82	0.82	0.86	0.85	1.00	0.86	0.86	0.86	0.86	0.85	0.84	0.86
RU	0.66	0.86	0.64	0.93	0.89	0.89	0.94	1.00	0.95	0.93	0.88	0.95	0.95	0.86	1.00	0.95	0.94	0.94	0.93	0.92	1.00
SI	0.70	0.86	0.65	0.99	0.94	0.94	1.00	0.95	0.98	0.95	0.92	1.00	0.99	0.86	0.95	1.00	1.00	1.00	0.99	0.98	0.95
TO	0.70	0.86	0.65	0.99	0.94	0.94	1.00	0.94	0.98	0.95	0.92	1.00	0.99	0.86	0.94	1.00	1.00	1.00	0.99	0.98	0.94
UN	0.70	0.86	0.65	0.99	0.94	0.94	1.00	0.94	0.98	0.95	0.92	1.00	0.99	0.86	0.94	1.00	1.00	1.00	0.99	0.98	0.94
RY	0.72	0.85	0.65	0.98	0.94	0.95	0.99	0.93	0.99	0.96	0.93	0.99	0.98	0.85	0.93	0.99	0.99	0.99	1.00	0.99	0.93
CO	0.72	0.84	0.64	0.97	0.93	0.96	0.98	0.92	0.98	0.96	0.94	0.98	0.97	0.84	0.92	0.98	0.98	0.98	0.99	1.00	0.92
CA	0.66	0.86	0.64	0.93	0.89	0.89	0.94	1.00	0.95	0.93	0.88	0.95	0.95	0.86	1.00	0.95	0.94	0.94	0.93	0.92	1.00

Similarity Matrix: IC-3-25

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.55	0.56	0.71	0.74	0.73	0.70	0.65	0.69	0.69	0.97	0.70	0.70	0.55	0.65	0.70	0.70	0.70	0.70	0.73	0.60
KA	0.55	1.00	0.57	0.78	0.79	0.72	0.78	0.80	0.77	0.76	0.57	0.78	0.77	1.00	0.80	0.78	0.78	0.78	0.78	0.72	0.88
AR	0.56	0.57	1.00	0.59	0.60	0.59	0.59	0.58	0.59	0.59	0.57	0.59	0.59	0.57	0.58	0.59	0.59	0.59	0.59	0.59	0.58
BL	0.71	0.78	0.59	1.00	0.92	0.91	0.96	0.92	0.94	0.94	0.74	0.97	0.95	0.78	0.92	0.97	0.96	0.96	0.97	0.92	0.88
BO	0.74	0.79	0.60	0.92	1.00	0.85	0.88	0.85	0.86	0.86	0.77	0.89	0.87	0.79	0.85	0.89	0.88	0.88	0.89	0.85	0.83
EX	0.73	0.72	0.59	0.91	0.85	1.00	0.91	0.87	0.93	0.91	0.75	0.92	0.93	0.72	0.87	0.92	0.91	0.91	0.92	1.00	0.81
CP	0.70	0.78	0.59	0.96	0.88	0.91	1.00	0.92	0.95	0.94	0.72	0.97	0.95	0.78	0.92	0.97	1.00	1.00	0.96	0.91	0.87
HA	0.65	0.80	0.58	0.92	0.85	0.87	0.92	1.00	0.93	0.91	0.68	0.93	0.93	0.80	1.00	0.93	0.92	0.92	0.93	0.87	0.92
IB	0.69	0.77	0.59	0.94	0.86	0.93	0.95	0.93	1.00	0.94	0.72	0.97	0.99	0.77	0.93	0.97	0.95	0.95	0.97	0.93	0.88
LP	0.69	0.76	0.59	0.94	0.86	0.91	0.94	0.91	0.94	1.00	0.72	0.94	0.94	0.76	0.91	0.94	0.94	0.94	0.94	0.91	0.86
MC	0.97	0.57	0.57	0.74	0.77	0.75	0.72	0.68	0.72	0.72	1.00	0.73	0.72	0.57	0.68	0.73	0.72	0.72	0.73	0.76	0.63
DO	0.70	0.78	0.59	0.97	0.89	0.92	0.97	0.93	0.97	0.94	0.73	1.00	0.98	0.78	0.93	1.00	0.97	0.97	0.98	0.93	0.88
NA	0.70	0.77	0.59	0.95	0.87	0.93	0.95	0.93	0.99	0.94	0.72	0.98	1.00	0.77	0.93	0.98	0.95	0.95	0.97	0.93	0.88
PL	0.55	1.00	0.57	0.78	0.79	0.72	0.78	0.80	0.77	0.76	0.57	0.78	0.77	1.00	0.80	0.78	0.78	0.78	0.78	0.72	0.88
RU	0.65	0.80	0.58	0.92	0.85	0.87	0.92	1.00	0.93	0.91	0.68	0.93	0.93	0.80	1.00	0.93	0.92	0.92	0.93	0.87	0.92
SI	0.70	0.78	0.59	0.97	0.89	0.92	0.97	0.93	0.97	0.94	0.73	1.00	0.98	0.78	0.93	1.00	0.97	0.97	0.98	0.93	0.88
TO	0.70	0.78	0.59	0.96	0.88	0.91	1.00	0.92	0.95	0.94	0.72	0.97	0.95	0.78	0.92	0.97	1.00	1.00	0.96	0.91	0.87
UN	0.70	0.78	0.59	0.96	0.88	0.91	1.00	0.92	0.95	0.94	0.72	0.97	0.95	0.78	0.92	0.97	1.00	1.00	0.96	0.91	0.87
RY	0.70	0.78	0.59	0.97	0.89	0.92	0.96	0.93	0.97	0.94	0.73	0.98	0.97	0.78	0.93	0.98	0.96	0.96	1.00	0.93	0.88
CO	0.73	0.72	0.59	0.92	0.85	1.00	0.91	0.87	0.93	0.91	0.76	0.93	0.93	0.72	0.87	0.93	0.91	0.91	0.93	1.00	0.82
CA	0.60	0.88	0.58	0.88	0.83	0.81	0.87	0.92	0.88	0.86	0.63	0.88	0.88	0.88	0.92	0.88	0.87	0.87	0.88	0.82	1.00

Similarity Matrix: IC-3-45

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.55	0.56	0.72	0.75	0.74	0.71	0.67	0.70	0.71	1.00	0.72	0.71	0.55	0.67	0.72	0.71	0.71	0.72	0.74	0.65
KA	0.55	1.00	0.57	0.77	0.78	0.72	0.77	0.79	0.76	0.75	0.56	0.77	0.77	1.00	0.79	0.77	0.77	0.77	0.77	0.72	0.82
AR	0.56	0.57	1.00	0.60	0.61	0.59	0.59	0.59	0.59	0.59	0.56	0.60	0.59	0.57	0.59	0.60	0.59	0.59	0.60	0.59	0.59
BL	0.72	0.77	0.60	1.00	0.92	0.91	0.95	0.91	0.94	0.94	0.73	0.97	0.95	0.77	0.91	0.97	0.95	0.95	0.97	0.92	0.90
BO	0.75	0.78	0.61	0.92	1.00	0.85	0.87	0.84	0.86	0.86	0.76	0.89	0.88	0.78	0.84	0.89	0.87	0.87	0.89	0.85	0.84
EX	0.74	0.72	0.59	0.91	0.85	1.00	0.91	0.87	0.93	0.91	0.74	0.92	0.92	0.72	0.87	0.92	0.91	0.91	0.93	1.00	0.85
CP	0.71	0.77	0.59	0.95	0.87	0.91	1.00	0.92	0.94	0.94	0.71	0.96	0.95	0.77	0.92	0.96	1.00	1.00	0.95	0.91	0.90
HA	0.67	0.79	0.59	0.91	0.84	0.87	0.92	1.00	0.93	0.91	0.67	0.92	0.93	0.79	1.00	0.92	0.92	0.92	0.92	0.87	0.96
IB	0.70	0.76	0.59	0.94	0.86	0.93	0.94	0.93	1.00	0.94	0.71	0.97	0.99	0.76	0.93	0.97	0.94	0.94	0.97	0.93	0.91
LP	0.71	0.75	0.59	0.94	0.86	0.91	0.94	0.91	0.94	1.00	0.71	0.94	0.94	0.75	0.91	0.94	0.94	0.94	0.94	0.91	0.89
MC	1.00	0.56	0.56	0.73	0.76	0.74	0.71	0.67	0.71	0.71	1.00	0.72	0.71	0.56	0.67	0.72	0.71	0.71	0.72	0.74	0.65
DO	0.72	0.77	0.60	0.97	0.89	0.92	0.96	0.92	0.97	0.94	0.72	1.00	0.98	0.77	0.92	1.00	0.96	0.96	0.99	0.92	0.91
NA	0.71	0.77	0.59	0.95	0.88	0.92	0.95	0.93	0.99	0.94	0.71	0.98	1.00	0.77	0.93	0.98	0.95	0.95	0.98	0.93	0.91
PL	0.55	1.00	0.57	0.77	0.78	0.72	0.77	0.79	0.76	0.75	0.56	0.77	0.77	1.00	0.79	0.77	0.77	0.77	0.77	0.72	0.82
RU	0.67	0.79	0.59	0.91	0.84	0.87	0.92	1.00	0.93	0.91	0.67	0.92	0.93	0.79	1.00	0.92	0.92	0.92	0.92	0.87	0.96
SI	0.72	0.77	0.60	0.97	0.89	0.92	0.96	0.92	0.97	0.94	0.72	1.00	0.98	0.77	0.92	1.00	0.96	0.96	0.99	0.92	0.91
TO	0.71	0.77	0.59	0.95	0.87	0.91	1.00	0.92	0.94	0.94	0.71	0.96	0.95	0.77	0.92	0.96	1.00	1.00	0.95	0.91	0.90
UN	0.71	0.77	0.59	0.95	0.87	0.91	1.00	0.92	0.94	0.94	0.71	0.96	0.95	0.77	0.92	0.96	1.00	1.00	0.95	0.91	0.90
RY	0.72	0.77	0.60	0.97	0.89	0.93	0.95	0.92	0.97	0.94	0.72	0.99	0.98	0.77	0.92	0.99	0.95	0.95	1.00	0.93	0.91
CO	0.74	0.72	0.59	0.92	0.85	1.00	0.91	0.87	0.93	0.91	0.74	0.92	0.93	0.72	0.87	0.92	0.91	0.91	0.93	1.00	0.85
CA	0.65	0.82	0.59	0.90	0.84	0.85	0.90	0.96	0.91	0.89	0.65	0.91	0.91	0.82	0.96	0.91	0.90	0.90	0.91	0.85	1.00

Similarity Matrix: IC-3-65

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.54	0.55	0.73	0.75	0.74	0.71	0.66	0.71	0.71	1.00	0.72	0.72	0.54	0.66	0.72	0.71	0.71	0.72	0.74	0.63
KA	0.54	1.00	0.56	0.77	0.78	0.71	0.76	0.79	0.75	0.75	0.54	0.76	0.76	1.00	0.79	0.76	0.76	0.76	0.76	0.71	0.83
AR	0.55	0.56	1.00	0.58	0.59	0.57	0.58	0.57	0.58	0.57	0.55	0.58	0.58	0.56	0.57	0.58	0.58	0.58	0.58	0.57	0.57
BL	0.73	0.77	0.58	1.00	0.91	0.92	0.95	0.91	0.95	0.95	0.73	0.97	0.96	0.77	0.91	0.97	0.95	0.95	0.97	0.92	0.89
BO	0.75	0.78	0.59	0.91	1.00	0.85	0.86	0.84	0.86	0.86	0.75	0.89	0.88	0.78	0.84	0.89	0.86	0.86	0.89	0.85	0.84
EX	0.74	0.71	0.57	0.92	0.85	1.00	0.92	0.87	0.93	0.92	0.74	0.93	0.93	0.71	0.87	0.93	0.92	0.92	0.93	1.00	0.84
CP	0.71	0.76	0.58	0.95	0.86	0.92	1.00	0.91	0.95	0.95	0.71	0.96	0.95	0.76	0.91	0.96	1.00	1.00	0.95	0.92	0.88
HA	0.66	0.79	0.57	0.91	0.84	0.87	0.91	1.00	0.93	0.91	0.66	0.92	0.93	0.79	1.00	0.92	0.91	0.91	0.92	0.87	0.95
IB	0.71	0.75	0.58	0.95	0.86	0.93	0.95	0.93	1.00	0.95	0.71	0.98	0.99	0.75	0.93	0.98	0.95	0.95	0.98	0.93	0.90
LP	0.71	0.75	0.57	0.95	0.86	0.92	0.95	0.91	0.95	1.00	0.71	0.95	0.95	0.75	0.91	0.95	0.95	0.95	0.95	0.92	0.88
MC	1.00	0.54	0.55	0.73	0.75	0.74	0.71	0.66	0.71	0.71	1.00	0.72	0.72	0.54	0.66	0.72	0.71	0.71	0.72	0.74	0.63
DO	0.72	0.76	0.58	0.97	0.89	0.93	0.96	0.92	0.98	0.95	0.72	1.00	0.99	0.76	0.92	1.00	0.96	0.96	0.99	0.93	0.89
NA	0.72	0.76	0.58	0.96	0.88	0.93	0.95	0.93	0.99	0.95	0.72	0.99	1.00	0.76	0.93	0.99	0.95	0.95	0.98	0.93	0.90
PL	0.54	1.00	0.56	0.77	0.78	0.71	0.76	0.79	0.75	0.75	0.54	0.76	0.76	1.00	0.79	0.76	0.76	0.76	0.76	0.71	0.83
RU	0.66	0.79	0.57	0.91	0.84	0.87	0.91	1.00	0.93	0.91	0.66	0.92	0.93	0.79	1.00	0.92	0.91	0.91	0.92	0.87	0.95
SI	0.72	0.76	0.58	0.97	0.89	0.93	0.96	0.92	0.98	0.95	0.72	1.00	0.99	0.76	0.92	1.00	0.96	0.96	0.99	0.93	0.89
TO	0.71	0.76	0.58	0.95	0.86	0.92	1.00	0.91	0.95	0.95	0.71	0.96	0.95	0.76	0.91	0.96	1.00	1.00	0.95	0.92	0.88
UN	0.71	0.76	0.58	0.95	0.86	0.92	1.00	0.91	0.95	0.95	0.71	0.96	0.95	0.76	0.91	0.96	1.00	1.00	0.95	0.92	0.88
RY	0.72	0.76	0.58	0.97	0.89	0.93	0.95	0.92	0.98	0.95	0.72	0.99	0.98	0.76	0.92	0.99	0.95	0.95	1.00	0.93	0.89
CO	0.74	0.71	0.57	0.92	0.85	1.00	0.92	0.87	0.93	0.92	0.74	0.93	0.93	0.71	0.87	0.93	0.92	0.92	0.93	1.00	0.84
CA	0.63	0.83	0.57	0.89	0.84	0.84	0.88	0.95	0.90	0.88	0.63	0.89	0.90	0.83	0.95	0.89	0.88	0.88	0.89	0.84	1.00

Similarity Matrix: IC-3-85

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.53	0.54	0.72	0.75	0.73	0.70	0.65	0.70	0.70	1.00	0.71	0.71	0.53	0.65	0.71	0.70	0.70	0.71	0.73	0.61
KA	0.53	1.00	0.56	0.76	0.77	0.70	0.75	0.78	0.75	0.74	0.54	0.76	0.75	1.00	0.78	0.76	0.75	0.75	0.75	0.70	0.86
AR	0.54	0.56	1.00	0.59	0.59	0.58	0.58	0.58	0.58	0.58	0.54	0.59	0.58	0.56	0.58	0.59	0.58	0.58	0.58	0.58	0.57
BL	0.72	0.76	0.59	1.00	0.91	0.91	0.95	0.91	0.94	0.94	0.72	0.97	0.96	0.76	0.91	0.97	0.95	0.95	0.97	0.91	0.87
BO	0.75	0.77	0.59	0.91	1.00	0.84	0.86	0.83	0.85	0.85	0.75	0.88	0.87	0.77	0.83	0.88	0.86	0.86	0.88	0.84	0.82
EX	0.73	0.70	0.58	0.91	0.84	1.00	0.91	0.86	0.93	0.91	0.73	0.92	0.93	0.70	0.86	0.92	0.91	0.91	0.92	1.00	0.81
CP	0.70	0.75	0.58	0.95	0.86	0.91	1.00	0.91	0.94	0.94	0.70	0.95	0.94	0.75	0.91	0.95	1.00	1.00	0.95	0.91	0.86
HA	0.65	0.78	0.58	0.91	0.83	0.86	0.91	1.00	0.93	0.90	0.65	0.92	0.92	0.78	1.00	0.92	0.91	0.91	0.92	0.86	0.92
IB	0.70	0.75	0.58	0.94	0.85	0.93	0.94	0.93	1.00	0.94	0.70	0.97	0.98	0.75	0.93	0.97	0.94	0.94	0.97	0.93	0.87
LP	0.70	0.74	0.58	0.94	0.85	0.91	0.94	0.90	0.94	1.00	0.70	0.94	0.94	0.74	0.90	0.94	0.94	0.94	0.94	0.91	0.86
MC	1.00	0.54	0.54	0.72	0.75	0.73	0.70	0.65	0.70	0.70	1.00	0.71	0.71	0.54	0.65	0.71	0.70	0.70	0.71	0.73	0.61
DO	0.71	0.76	0.59	0.97	0.88	0.92	0.95	0.92	0.97	0.94	0.71	1.00	0.99	0.76	0.92	1.00	0.95	0.95	0.99	0.92	0.87
NA	0.71	0.75	0.58	0.96	0.87	0.93	0.94	0.92	0.98	0.94	0.71	0.99	1.00	0.75	0.92	0.99	0.94	0.94	0.98	0.93	0.87
PL	0.53	1.00	0.56	0.76	0.77	0.70	0.75	0.78	0.75	0.74	0.54	0.76	0.75	1.00	0.78	0.76	0.75	0.75	0.75	0.70	0.86
RU	0.65	0.78	0.58	0.91	0.83	0.86	0.91	1.00	0.93	0.90	0.65	0.92	0.92	0.78	1.00	0.92	0.91	0.91	0.92	0.86	0.92
SI	0.71	0.76	0.59	0.97	0.88	0.92	0.95	0.92	0.97	0.94	0.71	1.00	0.99	0.76	0.92	1.00	0.95	0.95	0.99	0.92	0.87
TO	0.70	0.75	0.58	0.95	0.86	0.91	1.00	0.91	0.94	0.94	0.70	0.95	0.94	0.75	0.91	0.95	1.00	1.00	0.95	0.91	0.86
UN	0.70	0.75	0.58	0.95	0.86	0.91	1.00	0.91	0.94	0.94	0.70	0.95	0.94	0.75	0.91	0.95	1.00	1.00	0.95	0.91	0.86
RY	0.71	0.75	0.58	0.97	0.88	0.92	0.95	0.92	0.97	0.94	0.71	0.99	0.98	0.75	0.92	0.99	0.95	0.95	1.00	0.92	0.87
CO	0.73	0.70	0.58	0.91	0.84	1.00	0.91	0.86	0.93	0.91	0.73	0.92	0.93	0.70	0.86	0.92	0.91	0.91	0.92	1.00	0.81
CA	0.61	0.86	0.57	0.87	0.82	0.81	0.86	0.92	0.87	0.86	0.61	0.87	0.87	0.86	0.92	0.87	0.86	0.86	0.87	0.81	1.00

Similarity Matrix: IC-7-5

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.40	0.45	0.44	0.47	0.49	0.42	0.39	0.43	0.40	0.40	0.45	0.42	0.40	0.43	0.47	0.47	0.46	0.45	0.45	0.38
KA	0.40	1.00	0.50	0.76	0.74	0.65	0.75	0.70	0.72	0.74	0.80	0.77	0.74	0.63	0.68	0.74	0.73	0.72	0.73	0.70	0.64
AR	0.45	0.50	1.00	0.50	0.51	0.49	0.48	0.46	0.48	0.47	0.48	0.50	0.48	0.43	0.46	0.51	0.51	0.50	0.50	0.49	0.42
BL	0.44	0.76	0.50	1.00	0.90	0.75	0.86	0.73	0.82	0.85	0.72	0.89	0.83	0.54	0.68	0.82	0.83	0.81	0.84	0.83	0.58
BO	0.47	0.74	0.51	0.90	1.00	0.71	0.75	0.64	0.72	0.75	0.69	0.78	0.72	0.50	0.62	0.72	0.72	0.70	0.74	0.74	0.52
EX	0.49	0.65	0.49	0.75	0.71	1.00	0.76	0.64	0.77	0.75	0.63	0.78	0.76	0.49	0.62	0.76	0.78	0.75	0.80	0.90	0.51
CP	0.42	0.75	0.48	0.86	0.75	0.76	1.00	0.77	0.89	0.97	0.71	0.93	0.92	0.56	0.71	0.83	0.84	0.82	0.85	0.85	0.60
HA	0.39	0.70	0.46	0.73	0.64	0.64	0.77	1.00	0.77	0.76	0.62	0.76	0.78	0.64	0.82	0.76	0.76	0.75	0.74	0.71	0.71
IB	0.43	0.72	0.48	0.82	0.72	0.77	0.89	0.77	1.00	0.87	0.69	0.88	0.93	0.56	0.72	0.87	0.87	0.85	0.88	0.86	0.61
LP	0.40	0.74	0.47	0.85	0.75	0.75	0.97	0.76	0.87	1.00	0.71	0.91	0.90	0.55	0.70	0.81	0.81	0.79	0.83	0.84	0.60
MC	0.40	0.80	0.48	0.72	0.69	0.63	0.71	0.62	0.69	0.71	1.00	0.73	0.70	0.50	0.58	0.69	0.70	0.67	0.70	0.68	0.50
DO	0.45	0.77	0.50	0.89	0.78	0.78	0.93	0.76	0.88	0.91	0.73	1.00	0.90	0.57	0.71	0.88	0.89	0.86	0.87	0.85	0.60
NA	0.42	0.74	0.48	0.83	0.72	0.76	0.92	0.78	0.93	0.90	0.70	0.90	1.00	0.57	0.72	0.86	0.86	0.83	0.85	0.84	0.61
PL	0.40	0.63	0.43	0.54	0.50	0.49	0.56	0.64	0.56	0.55	0.50	0.57	0.57	1.00	0.72	0.61	0.58	0.61	0.57	0.54	0.93
RU	0.43	0.68	0.46	0.68	0.62	0.62	0.71	0.82	0.72	0.70	0.58	0.71	0.72	0.72	1.00	0.72	0.73	0.73	0.72	0.68	0.79
SI	0.47	0.74	0.51	0.82	0.72	0.76	0.83	0.76	0.87	0.81	0.69	0.88	0.86	0.61	0.72	1.00	0.93	0.93	0.88	0.83	0.63
TO	0.47	0.73	0.51	0.83	0.72	0.78	0.84	0.76	0.87	0.81	0.70	0.89	0.86	0.58	0.73	0.93	1.00	0.95	0.89	0.85	0.61
UN	0.46	0.72	0.50	0.81	0.70	0.75	0.82	0.75	0.85	0.79	0.67	0.86	0.83	0.61	0.73	0.93	0.95	1.00	0.87	0.83	0.63
RY	0.45	0.73	0.50	0.84	0.74	0.80	0.85	0.74	0.88	0.83	0.70	0.87	0.85	0.57	0.72	0.88	0.89	0.87	1.00	0.87	0.60
CO	0.45	0.70	0.49	0.83	0.74	0.90	0.85	0.71	0.86	0.84	0.68	0.85	0.84	0.54	0.68	0.83	0.85	0.83	0.87	1.00	0.57
CA	0.38	0.64	0.42	0.58	0.52	0.51	0.60	0.71	0.61	0.60	0.50	0.60	0.61	0.93	0.79	0.63	0.61	0.63	0.60	0.57	1.00

Similarity Matrix: IC-7-25

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.27	0.31	0.37	0.39	0.38	0.35	0.29	0.33	0.34	0.29	0.35	0.34	0.22	0.28	0.35	0.35	0.33	0.34	0.38	0.26
KA	0.27	1.00	0.42	0.69	0.70	0.54	0.65	0.65	0.63	0.65	0.65	0.67	0.64	0.59	0.62	0.66	0.62	0.59	0.66	0.55	0.65
AR	0.31	0.42	1.00	0.45	0.46	0.41	0.43	0.40	0.42	0.43	0.42	0.44	0.42	0.33	0.38	0.43	0.43	0.41	0.43	0.41	0.38
BL	0.37	0.69	0.45	1.00	0.90	0.72	0.83	0.68	0.79	0.82	0.64	0.86	0.80	0.46	0.61	0.83	0.76	0.73	0.82	0.72	0.61
BO	0.39	0.70	0.46	0.90	1.00	0.67	0.73	0.61	0.69	0.72	0.67	0.76	0.70	0.46	0.57	0.73	0.66	0.63	0.73	0.67	0.57
EX	0.38	0.54	0.41	0.72	0.67	1.00	0.73	0.57	0.73	0.73	0.55	0.74	0.73	0.38	0.51	0.72	0.69	0.65	0.74	1.00	0.51
CP	0.35	0.65	0.43	0.83	0.73	0.73	1.00	0.71	0.85	0.97	0.60	0.87	0.87	0.46	0.62	0.81	0.79	0.75	0.84	0.73	0.63
HA	0.29	0.65	0.40	0.68	0.61	0.57	0.71	1.00	0.72	0.71	0.51	0.70	0.72	0.52	0.71	0.69	0.68	0.65	0.71	0.57	0.76
IB	0.33	0.63	0.42	0.79	0.69	0.73	0.85	0.72	1.00	0.85	0.58	0.86	0.94	0.45	0.62	0.85	0.78	0.74	0.88	0.73	0.63
LP	0.34	0.65	0.43	0.82	0.72	0.73	0.97	0.71	0.85	1.00	0.60	0.85	0.87	0.45	0.62	0.80	0.76	0.73	0.84	0.73	0.63
MC	0.29	0.65	0.42	0.64	0.67	0.55	0.60	0.51	0.58	0.60	1.00	0.62	0.59	0.36	0.45	0.61	0.57	0.54	0.60	0.56	0.47
DO	0.35	0.67	0.44	0.86	0.76	0.74	0.87	0.70	0.86	0.85	0.62	1.00	0.88	0.47	0.62	0.93	0.80	0.76	0.89	0.74	0.63
NA	0.34	0.64	0.42	0.80	0.70	0.73	0.87	0.72	0.94	0.87	0.59	0.88	1.00	0.45	0.62	0.86	0.78	0.74	0.89	0.74	0.64
PL	0.22	0.59	0.33	0.46	0.46	0.38	0.46	0.52	0.45	0.45	0.36	0.47	0.45	1.00	0.65	0.47	0.46	0.45	0.46	0.38	0.58
RU	0.28	0.62	0.38	0.61	0.57	0.51	0.62	0.71	0.62	0.62	0.45	0.62	0.62	0.65	1.00	0.61	0.61	0.59	0.62	0.51	0.73
SI	0.35	0.66	0.43	0.83	0.73	0.72	0.81	0.69	0.85	0.80	0.61	0.93	0.86	0.47	0.61	1.00	0.82	0.78	0.88	0.72	0.62
TO	0.35	0.62	0.43	0.76	0.66	0.69	0.79	0.68	0.78	0.76	0.57	0.80	0.78	0.46	0.61	0.82	1.00	0.90	0.79	0.69	0.59
UN	0.33	0.59	0.41	0.73	0.63	0.65	0.75	0.65	0.74	0.73	0.54	0.76	0.74	0.45	0.59	0.78	0.90	1.00	0.75	0.66	0.57
RY	0.34	0.66	0.43	0.82	0.73	0.74	0.84	0.71	0.88	0.84	0.60	0.89	0.89	0.46	0.62	0.88	0.79	0.75	1.00	0.74	0.63
CO	0.38	0.55	0.41	0.72	0.67	1.00	0.73	0.57	0.73	0.73	0.56	0.74	0.74	0.38	0.51	0.72	0.69	0.66	0.74	1.00	0.51
CA	0.26	0.65	0.38	0.61	0.57	0.51	0.63	0.76	0.63	0.63	0.47	0.63	0.64	0.58	0.73	0.62	0.59	0.57	0.63	0.51	1.00

Similarity Matrix: IC-7-45

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.27	0.31	0.39	0.41	0.40	0.36	0.29	0.35	0.36	0.30	0.37	0.35	0.21	0.28	0.37	0.36	0.34	0.36	0.40	0.27
KA	0.27	1.00	0.41	0.68	0.69	0.51	0.63	0.63	0.61	0.63	0.61	0.65	0.63	0.57	0.61	0.64	0.59	0.56	0.64	0.51	0.64
AR	0.31	0.41	1.00	0.45	0.46	0.40	0.42	0.39	0.41	0.42	0.41	0.43	0.42	0.33	0.37	0.43	0.42	0.40	0.43	0.40	0.38
BL	0.39	0.68	0.45	1.00	0.90	0.70	0.82	0.68	0.78	0.82	0.64	0.86	0.80	0.44	0.59	0.83	0.75	0.72	0.83	0.70	0.63
BO	0.41	0.69	0.46	0.90	1.00	0.65	0.72	0.62	0.68	0.72	0.66	0.76	0.70	0.44	0.56	0.73	0.65	0.62	0.73	0.65	0.59
EX	0.40	0.51	0.40	0.70	0.65	1.00	0.72	0.56	0.72	0.72	0.53	0.72	0.73	0.35	0.49	0.71	0.67	0.64	0.72	1.00	0.52
CP	0.36	0.63	0.42	0.82	0.72	0.72	1.00	0.71	0.84	0.97	0.59	0.86	0.87	0.43	0.61	0.81	0.78	0.74	0.84	0.72	0.65
HA	0.29	0.63	0.39	0.68	0.62	0.56	0.71	1.00	0.71	0.71	0.50	0.71	0.72	0.49	0.68	0.69	0.66	0.63	0.70	0.56	0.78
IB	0.35	0.61	0.41	0.78	0.68	0.72	0.84	0.71	1.00	0.84	0.57	0.86	0.93	0.42	0.60	0.85	0.76	0.73	0.88	0.72	0.65
LP	0.36	0.63	0.42	0.82	0.72	0.72	0.97	0.71	0.84	1.00	0.58	0.85	0.87	0.43	0.60	0.81	0.76	0.72	0.84	0.72	0.65
MC	0.30	0.61	0.41	0.64	0.66	0.53	0.59	0.50	0.57	0.58	1.00	0.61	0.58	0.34	0.43	0.60	0.56	0.52	0.60	0.53	0.47
DO	0.37	0.65	0.43	0.86	0.76	0.72	0.86	0.71	0.86	0.85	0.61	1.00	0.89	0.44	0.60	0.94	0.78	0.74	0.90	0.72	0.65
NA	0.35	0.63	0.42	0.80	0.70	0.73	0.87	0.72	0.93	0.87	0.58	0.89	1.00	0.43	0.61	0.86	0.76	0.72	0.90	0.73	0.66
PL	0.21	0.57	0.33	0.44	0.44	0.35	0.43	0.49	0.42	0.43	0.34	0.44	0.43	1.00	0.62	0.44	0.43	0.42	0.43	0.36	0.55
RU	0.28	0.61	0.37	0.59	0.56	0.49	0.61	0.68	0.60	0.60	0.43	0.60	0.61	0.62	1.00	0.59	0.57	0.55	0.60	0.49	0.75
SI	0.37	0.64	0.43	0.83	0.73	0.71	0.81	0.69	0.85	0.81	0.60	0.94	0.86	0.44	0.59	1.00	0.79	0.75	0.89	0.71	0.64
TO	0.36	0.59	0.42	0.75	0.65	0.67	0.78	0.66	0.76	0.76	0.56	0.78	0.76	0.43	0.57	0.79	1.00	0.89	0.77	0.67	0.61
UN	0.34	0.56	0.40	0.72	0.62	0.64	0.74	0.63	0.73	0.72	0.52	0.74	0.72	0.42	0.55	0.75	0.89	1.00	0.73	0.64	0.58
RY	0.36	0.64	0.43	0.83	0.73	0.72	0.84	0.70	0.88	0.84	0.60	0.90	0.90	0.43	0.60	0.89	0.77	0.73	1.00	0.72	0.65
CO	0.40	0.51	0.40	0.70	0.65	1.00	0.72	0.56	0.72	0.72	0.53	0.72	0.73	0.36	0.49	0.71	0.67	0.64	0.72	1.00	0.52
CA	0.27	0.64	0.38	0.63	0.59	0.52	0.65	0.78	0.65	0.65	0.47	0.65	0.66	0.55	0.75	0.64	0.61	0.58	0.65	0.52	1.00

Similarity Matrix: IC-7-65

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.25	0.30	0.38	0.39	0.39	0.35	0.29	0.34	0.35	0.30	0.36	0.35	0.21	0.26	0.35	0.35	0.33	0.35	0.39	0.26
KA	0.25	1.00	0.42	0.67	0.69	0.50	0.62	0.63	0.60	0.62	0.58	0.64	0.61	0.56	0.61	0.63	0.59	0.56	0.62	0.50	0.64
AR	0.30	0.42	1.00	0.44	0.46	0.40	0.42	0.39	0.41	0.42	0.41	0.43	0.41	0.32	0.37	0.43	0.41	0.39	0.42	0.40	0.37
BL	0.38	0.67	0.44	1.00	0.90	0.70	0.82	0.68	0.78	0.81	0.64	0.86	0.80	0.44	0.58	0.83	0.75	0.72	0.82	0.70	0.63
BO	0.39	0.69	0.46	0.90	1.00	0.64	0.72	0.61	0.68	0.72	0.67	0.76	0.71	0.44	0.55	0.74	0.65	0.62	0.73	0.64	0.59
EX	0.39	0.50	0.40	0.70	0.64	1.00	0.72	0.56	0.72	0.72	0.54	0.71	0.72	0.35	0.48	0.70	0.66	0.63	0.72	1.00	0.51
CP	0.35	0.62	0.42	0.82	0.72	0.72	1.00	0.70	0.85	0.97	0.59	0.86	0.87	0.43	0.60	0.82	0.78	0.74	0.84	0.72	0.65
HA	0.29	0.63	0.39	0.68	0.61	0.56	0.70	1.00	0.71	0.70	0.50	0.70	0.71	0.48	0.68	0.69	0.66	0.63	0.70	0.56	0.77
IB	0.34	0.60	0.41	0.78	0.68	0.72	0.85	0.71	1.00	0.84	0.56	0.86	0.93	0.42	0.59	0.85	0.76	0.72	0.88	0.72	0.65
LP	0.35	0.62	0.42	0.81	0.72	0.72	0.97	0.70	0.84	1.00	0.58	0.85	0.87	0.42	0.60	0.81	0.75	0.72	0.84	0.72	0.65
MC	0.30	0.58	0.41	0.64	0.67	0.54	0.59	0.50	0.56	0.58	1.00	0.61	0.58	0.32	0.42	0.60	0.55	0.52	0.59	0.54	0.46
DO	0.36	0.64	0.43	0.86	0.76	0.71	0.86	0.70	0.86	0.85	0.61	1.00	0.88	0.43	0.60	0.95	0.77	0.73	0.90	0.71	0.65
NA	0.35	0.61	0.41	0.80	0.71	0.72	0.87	0.71	0.93	0.87	0.58	0.88	1.00	0.42	0.60	0.87	0.75	0.72	0.90	0.72	0.65
PL	0.21	0.56	0.32	0.44	0.44	0.35	0.43	0.48	0.42	0.42	0.32	0.43	0.42	1.00	0.62	0.43	0.42	0.41	0.43	0.35	0.54
RU	0.26	0.61	0.37	0.58	0.55	0.48	0.60	0.68	0.59	0.60	0.42	0.60	0.60	0.62	1.00	0.59	0.58	0.55	0.59	0.48	0.76
SI	0.35	0.63	0.43	0.83	0.74	0.70	0.82	0.69	0.85	0.81	0.60	0.95	0.87	0.43	0.59	1.00	0.78	0.74	0.90	0.70	0.64
TO	0.35	0.59	0.41	0.75	0.65	0.66	0.78	0.66	0.76	0.75	0.55	0.77	0.75	0.42	0.58	0.78	1.00	0.89	0.76	0.66	0.60
UN	0.33	0.56	0.39	0.72	0.62	0.63	0.74	0.63	0.72	0.72	0.52	0.73	0.72	0.41	0.55	0.74	0.89	1.00	0.73	0.63	0.58
RY	0.35	0.62	0.42	0.82	0.73	0.72	0.84	0.70	0.88	0.84	0.59	0.90	0.90	0.43	0.59	0.90	0.76	0.73	1.00	0.72	0.65
CO	0.39	0.50	0.40	0.70	0.64	1.00	0.72	0.56	0.72	0.72	0.54	0.71	0.72	0.35	0.48	0.70	0.66	0.63	0.72	1.00	0.51
CA	0.26	0.64	0.37	0.63	0.59	0.51	0.65	0.77	0.65	0.65	0.46	0.65	0.65	0.54	0.76	0.64	0.60	0.58	0.65	0.51	1.00

Similarity Matrix: IC-7-85

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.26	0.30	0.38	0.40	0.41	0.36	0.29	0.35	0.36	0.31	0.37	0.35	0.20	0.27	0.36	0.35	0.33	0.36	0.41	0.27
KA	0.26	1.00	0.42	0.67	0.69	0.51	0.62	0.63	0.60	0.62	0.57	0.64	0.61	0.56	0.61	0.63	0.59	0.55	0.63	0.51	0.64
AR	0.30	0.42	1.00	0.44	0.45	0.40	0.42	0.39	0.41	0.42	0.41	0.43	0.42	0.31	0.37	0.43	0.41	0.39	0.42	0.40	0.38
BL	0.38	0.67	0.44	1.00	0.91	0.70	0.82	0.68	0.78	0.82	0.65	0.85	0.80	0.44	0.59	0.83	0.75	0.71	0.82	0.70	0.62
BO	0.40	0.69	0.45	0.91	1.00	0.65	0.72	0.63	0.68	0.72	0.67	0.76	0.71	0.44	0.56	0.73	0.66	0.62	0.73	0.65	0.58
EX	0.41	0.51	0.40	0.70	0.65	1.00	0.72	0.56	0.72	0.72	0.54	0.72	0.73	0.35	0.48	0.71	0.66	0.63	0.72	1.00	0.50
CP	0.36	0.62	0.42	0.82	0.72	0.72	1.00	0.71	0.84	0.97	0.59	0.85	0.87	0.42	0.60	0.82	0.78	0.73	0.84	0.72	0.63
HA	0.29	0.63	0.39	0.68	0.63	0.56	0.71	1.00	0.71	0.71	0.50	0.70	0.72	0.48	0.67	0.70	0.67	0.63	0.71	0.56	0.75
IB	0.35	0.60	0.41	0.78	0.68	0.72	0.84	0.71	1.00	0.84	0.57	0.86	0.93	0.42	0.59	0.86	0.76	0.72	0.88	0.72	0.63
LP	0.36	0.62	0.42	0.82	0.72	0.72	0.97	0.71	0.84	1.00	0.59	0.85	0.86	0.42	0.60	0.81	0.75	0.71	0.83	0.72	0.63
MC	0.31	0.57	0.41	0.65	0.67	0.54	0.59	0.50	0.57	0.59	1.00	0.61	0.58	0.32	0.42	0.60	0.56	0.52	0.59	0.54	0.47
DO	0.37	0.64	0.43	0.85	0.76	0.72	0.85	0.70	0.86	0.85	0.61	1.00	0.89	0.43	0.60	0.95	0.77	0.72	0.90	0.72	0.64
NA	0.35	0.61	0.42	0.80	0.71	0.73	0.87	0.72	0.93	0.86	0.58	0.89	1.00	0.42	0.60	0.87	0.76	0.71	0.90	0.73	0.64
PL	0.20	0.56	0.31	0.44	0.44	0.35	0.42	0.48	0.42	0.42	0.32	0.43	0.42	1.00	0.62	0.43	0.42	0.40	0.42	0.35	0.54
RU	0.27	0.61	0.37	0.59	0.56	0.48	0.60	0.67	0.59	0.60	0.42	0.60	0.60	0.62	1.00	0.59	0.57	0.54	0.59	0.48	0.75
SI	0.36	0.63	0.43	0.83	0.73	0.71	0.82	0.70	0.86	0.81	0.60	0.95	0.87	0.43	0.59	1.00	0.78	0.73	0.90	0.71	0.63
TO	0.35	0.59	0.41	0.75	0.66	0.66	0.78	0.67	0.76	0.75	0.56	0.77	0.76	0.42	0.57	0.78	1.00	0.88	0.76	0.66	0.59
UN	0.33	0.55	0.39	0.71	0.62	0.63	0.73	0.63	0.72	0.71	0.52	0.72	0.71	0.40	0.54	0.73	0.88	1.00	0.72	0.63	0.56
RY	0.36	0.63	0.42	0.82	0.73	0.72	0.84	0.71	0.88	0.83	0.59	0.90	0.90	0.42	0.59	0.90	0.76	0.72	1.00	0.72	0.63
CO	0.41	0.51	0.40	0.70	0.65	1.00	0.72	0.56	0.72	0.72	0.54	0.72	0.73	0.35	0.48	0.71	0.66	0.63	0.72	1.00	0.50
CA	0.27	0.64	0.38	0.62	0.58	0.50	0.63	0.75	0.63	0.63	0.47	0.64	0.64	0.54	0.75	0.63	0.59	0.56	0.63	0.50	1.00

Similarity Matrix: IC-11-5

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.33	0.40	0.32	0.33	0.45	0.31	0.34	0.34	0.30	0.31	0.35	0.33	0.47	0.44	0.45	0.44	0.47	0.38	0.41	0.45
KA	0.33	1.00	0.43	0.72	0.71	0.56	0.70	0.60	0.65	0.70	0.75	0.72	0.67	0.46	0.56	0.65	0.65	0.61	0.67	0.62	0.47
AR	0.40	0.43	1.00	0.44	0.45	0.45	0.43	0.39	0.42	0.42	0.40	0.45	0.42	0.36	0.40	0.46	0.45	0.44	0.44	0.45	0.35
BL	0.32	0.72	0.44	1.00	0.91	0.62	0.80	0.60	0.72	0.79	0.62	0.82	0.74	0.40	0.55	0.70	0.71	0.67	0.74	0.71	0.41
BO	0.33	0.71	0.45	0.91	1.00	0.59	0.71	0.54	0.63	0.70	0.60	0.73	0.64	0.37	0.50	0.61	0.62	0.58	0.66	0.63	0.38
EX	0.45	0.56	0.45	0.62	0.59	1.00	0.63	0.52	0.66	0.63	0.51	0.66	0.64	0.41	0.54	0.67	0.69	0.64	0.71	0.88	0.41
CP	0.31	0.70	0.43	0.80	0.71	0.63	1.00	0.65	0.81	0.98	0.64	0.91	0.84	0.42	0.58	0.72	0.73	0.68	0.77	0.73	0.44
HA	0.34	0.60	0.39	0.60	0.54	0.52	0.65	1.00	0.66	0.65	0.50	0.65	0.67	0.54	0.75	0.64	0.65	0.63	0.63	0.59	0.58
IB	0.34	0.65	0.42	0.72	0.63	0.66	0.81	0.66	1.00	0.81	0.60	0.80	0.90	0.44	0.61	0.79	0.79	0.73	0.80	0.76	0.46
LP	0.30	0.70	0.42	0.79	0.70	0.63	0.98	0.65	0.81	1.00	0.64	0.89	0.84	0.42	0.58	0.71	0.71	0.67	0.76	0.72	0.44
MC	0.31	0.75	0.40	0.62	0.60	0.51	0.64	0.50	0.60	0.64	1.00	0.65	0.61	0.37	0.46	0.59	0.59	0.55	0.60	0.57	0.37
DO	0.35	0.72	0.45	0.82	0.73	0.66	0.91	0.65	0.80	0.89	0.65	1.00	0.83	0.43	0.60	0.77	0.79	0.72	0.79	0.76	0.45
NA	0.33	0.67	0.42	0.74	0.64	0.64	0.84	0.67	0.90	0.84	0.61	0.83	1.00	0.44	0.60	0.77	0.77	0.71	0.77	0.74	0.46
PL	0.47	0.46	0.36	0.40	0.37	0.41	0.42	0.54	0.44	0.42	0.37	0.43	0.44	1.00	0.67	0.52	0.49	0.57	0.46	0.44	0.96
RU	0.44	0.56	0.40	0.55	0.50	0.54	0.58	0.75	0.61	0.58	0.46	0.60	0.60	0.67	1.00	0.63	0.64	0.65	0.62	0.59	0.70
SI	0.45	0.65	0.46	0.70	0.61	0.67	0.72	0.64	0.79	0.71	0.59	0.77	0.77	0.52	0.63	1.00	0.88	0.86	0.79	0.75	0.53
TO	0.44	0.65	0.45	0.71	0.62	0.69	0.73	0.65	0.79	0.71	0.59	0.79	0.77	0.49	0.64	0.88	1.00	0.87	0.80	0.78	0.50
UN	0.47	0.61	0.44	0.67	0.58	0.64	0.68	0.63	0.73	0.67	0.55	0.72	0.71	0.57	0.65	0.86	0.87	1.00	0.75	0.72	0.58
RY	0.38	0.67	0.44	0.74	0.66	0.71	0.77	0.63	0.80	0.76	0.60	0.79	0.77	0.46	0.62	0.79	0.80	0.75	1.00	0.79	0.47
CO	0.41	0.62	0.45	0.71	0.63	0.88	0.73	0.59	0.76	0.72	0.57	0.76	0.74	0.44	0.59	0.75	0.78	0.72	0.79	1.00	0.45
CA	0.45	0.47	0.35	0.41	0.38	0.41	0.44	0.58	0.46	0.44	0.37	0.45	0.46	0.96	0.70	0.53	0.50	0.58	0.47	0.45	1.00

Similarity Matrix: IC-11-25

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.17	0.21	0.25	0.26	0.26	0.23	0.18	0.22	0.23	0.19	0.24	0.22	0.14	0.17	0.24	0.25	0.23	0.23	0.26	0.16
KA	0.17	1.00	0.37	0.65	0.66	0.45	0.61	0.55	0.56	0.60	0.62	0.63	0.57	0.43	0.50	0.60	0.53	0.48	0.60	0.46	0.53
AR	0.21	0.37	1.00	0.40	0.41	0.34	0.38	0.33	0.36	0.37	0.36	0.38	0.36	0.24	0.29	0.38	0.36	0.33	0.38	0.34	0.30
BL	0.25	0.65	0.40	1.00	0.92	0.61	0.77	0.54	0.69	0.76	0.60	0.80	0.71	0.34	0.45	0.74	0.65	0.58	0.74	0.62	0.48
BO	0.26	0.66	0.41	0.92	1.00	0.58	0.69	0.50	0.61	0.68	0.62	0.72	0.63	0.33	0.43	0.67	0.57	0.51	0.67	0.59	0.46
EX	0.26	0.45	0.34	0.61	0.58	1.00	0.63	0.43	0.61	0.63	0.46	0.63	0.62	0.26	0.35	0.61	0.55	0.49	0.63	0.99	0.37
CP	0.23	0.61	0.38	0.77	0.69	0.63	1.00	0.58	0.78	0.97	0.55	0.83	0.81	0.34	0.46	0.74	0.66	0.59	0.78	0.63	0.50
HA	0.18	0.55	0.33	0.54	0.50	0.43	0.58	1.00	0.59	0.58	0.42	0.58	0.59	0.42	0.57	0.56	0.54	0.49	0.58	0.43	0.67
IB	0.22	0.56	0.36	0.69	0.61	0.61	0.78	0.59	1.00	0.79	0.51	0.79	0.91	0.33	0.46	0.77	0.66	0.58	0.82	0.61	0.51
LP	0.23	0.60	0.37	0.76	0.68	0.63	0.97	0.58	0.79	1.00	0.55	0.83	0.81	0.33	0.46	0.73	0.65	0.58	0.78	0.63	0.50
MC	0.19	0.62	0.36	0.60	0.62	0.46	0.55	0.42	0.51	0.55	1.00	0.57	0.52	0.26	0.35	0.54	0.49	0.43	0.54	0.46	0.37
DO	0.24	0.63	0.38	0.80	0.72	0.63	0.83	0.58	0.79	0.83	0.57	1.00	0.82	0.35	0.47	0.88	0.68	0.60	0.83	0.63	0.51
NA	0.22	0.57	0.36	0.71	0.63	0.62	0.81	0.59	0.91	0.81	0.52	0.82	1.00	0.33	0.46	0.78	0.66	0.58	0.83	0.62	0.51
PL	0.14	0.43	0.24	0.34	0.33	0.26	0.34	0.42	0.33	0.33	0.26	0.35	0.33	1.00	0.62	0.35	0.35	0.35	0.34	0.26	0.47
RU	0.17	0.50	0.29	0.45	0.43	0.35	0.46	0.57	0.46	0.46	0.35	0.47	0.46	0.62	1.00	0.46	0.45	0.42	0.47	0.35	0.62
SI	0.24	0.60	0.38	0.74	0.67	0.61	0.74	0.56	0.77	0.73	0.54	0.88	0.78	0.35	0.46	1.00	0.71	0.63	0.81	0.61	0.49
TO	0.25	0.53	0.36	0.65	0.57	0.55	0.66	0.54	0.66	0.65	0.49	0.68	0.66	0.35	0.45	0.71	1.00	0.77	0.68	0.56	0.46
UN	0.23	0.48	0.33	0.58	0.51	0.49	0.59	0.49	0.58	0.58	0.43	0.60	0.58	0.35	0.42	0.63	0.77	1.00	0.60	0.49	0.42
RY	0.23	0.60	0.38	0.74	0.67	0.63	0.78	0.58	0.82	0.78	0.54	0.83	0.83	0.34	0.47	0.81	0.68	0.60	1.00	0.63	0.50
CO	0.26	0.46	0.34	0.62	0.59	0.99	0.63	0.43	0.61	0.63	0.46	0.63	0.62	0.26	0.35	0.61	0.56	0.49	0.63	1.00	0.37
CA	0.16	0.53	0.30	0.48	0.46	0.37	0.50	0.67	0.51	0.50	0.37	0.51	0.51	0.47	0.62	0.49	0.46	0.42	0.50	0.37	1.00

Similarity Matrix: IC-11-45

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.17	0.20	0.25	0.26	0.26	0.22	0.18	0.22	0.22	0.18	0.23	0.22	0.13	0.17	0.23	0.23	0.21	0.23	0.26	0.16
KA	0.17	1.00	0.36	0.63	0.64	0.42	0.58	0.54	0.54	0.58	0.57	0.60	0.55	0.41	0.48	0.58	0.50	0.44	0.58	0.42	0.53
AR	0.20	0.36	1.00	0.40	0.41	0.33	0.37	0.32	0.35	0.37	0.34	0.38	0.36	0.23	0.28	0.37	0.35	0.30	0.36	0.33	0.30
BL	0.25	0.63	0.40	1.00	0.92	0.60	0.77	0.55	0.69	0.76	0.58	0.79	0.71	0.32	0.43	0.75	0.63	0.56	0.74	0.60	0.50
BO	0.26	0.64	0.41	0.92	1.00	0.57	0.69	0.51	0.61	0.69	0.59	0.71	0.63	0.32	0.42	0.67	0.55	0.48	0.66	0.57	0.48
EX	0.26	0.42	0.33	0.60	0.57	1.00	0.62	0.42	0.61	0.62	0.43	0.61	0.62	0.23	0.33	0.59	0.53	0.47	0.61	1.00	0.37
CP	0.22	0.58	0.37	0.77	0.69	0.62	1.00	0.58	0.78	0.97	0.52	0.82	0.81	0.31	0.44	0.75	0.64	0.57	0.78	0.62	0.53
HA	0.18	0.54	0.32	0.55	0.51	0.42	0.58	1.00	0.58	0.58	0.40	0.58	0.59	0.38	0.54	0.57	0.53	0.47	0.58	0.42	0.68
IB	0.22	0.54	0.35	0.69	0.61	0.61	0.78	0.58	1.00	0.79	0.48	0.78	0.89	0.30	0.43	0.77	0.63	0.56	0.81	0.61	0.51
LP	0.22	0.58	0.37	0.76	0.69	0.62	0.97	0.58	0.79	1.00	0.52	0.82	0.82	0.31	0.44	0.74	0.63	0.56	0.78	0.62	0.52
MC	0.18	0.57	0.34	0.58	0.59	0.43	0.52	0.40	0.48	0.52	1.00	0.54	0.50	0.23	0.31	0.53	0.46	0.40	0.51	0.43	0.36
DO	0.23	0.60	0.38	0.79	0.71	0.61	0.82	0.58	0.78	0.82	0.54	1.00	0.81	0.32	0.44	0.90	0.65	0.57	0.83	0.62	0.52
NA	0.22	0.55	0.36	0.71	0.63	0.62	0.81	0.59	0.89	0.82	0.50	0.81	1.00	0.31	0.44	0.79	0.63	0.56	0.84	0.62	0.52
PL	0.13	0.41	0.23	0.32	0.32	0.23	0.31	0.38	0.30	0.31	0.23	0.32	0.31	1.00	0.60	0.32	0.32	0.30	0.31	0.23	0.44
RU	0.17	0.48	0.28	0.43	0.42	0.33	0.44	0.54	0.43	0.44	0.31	0.44	0.44	0.60	1.00	0.43	0.42	0.38	0.44	0.33	0.61
SI	0.23	0.58	0.37	0.75	0.67	0.59	0.75	0.57	0.77	0.74	0.53	0.90	0.79	0.32	0.43	1.00	0.68	0.59	0.81	0.59	0.51
TO	0.23	0.50	0.35	0.63	0.55	0.53	0.64	0.53	0.63	0.63	0.46	0.65	0.63	0.32	0.42	0.68	1.00	0.75	0.64	0.53	0.46
UN	0.21	0.44	0.30	0.56	0.48	0.47	0.57	0.47	0.56	0.56	0.40	0.57	0.56	0.30	0.38	0.59	0.75	1.00	0.56	0.47	0.41
RY	0.23	0.58	0.36	0.74	0.66	0.61	0.78	0.58	0.81	0.78	0.51	0.83	0.84	0.31	0.44	0.81	0.64	0.56	1.00	0.61	0.51
CO	0.26	0.42	0.33	0.60	0.57	1.00	0.62	0.42	0.61	0.62	0.43	0.62	0.62	0.23	0.33	0.59	0.53	0.47	0.61	1.00	0.37
CA	0.16	0.53	0.30	0.50	0.48	0.37	0.53	0.68	0.51	0.52	0.36	0.52	0.52	0.44	0.61	0.51	0.46	0.41	0.51	0.37	1.00

Similarity Matrix: IC-11-65

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.17	0.20	0.26	0.27	0.28	0.24	0.18	0.22	0.24	0.19	0.24	0.23	0.13	0.16	0.24	0.23	0.21	0.23	0.28	0.17
KA	0.17	1.00	0.36	0.63	0.64	0.40	0.57	0.54	0.53	0.56	0.55	0.58	0.54	0.40	0.47	0.56	0.49	0.43	0.56	0.40	0.53
AR	0.20	0.36	1.00	0.40	0.41	0.33	0.37	0.31	0.34	0.36	0.35	0.37	0.35	0.22	0.27	0.37	0.34	0.29	0.35	0.33	0.29
BL	0.26	0.63	0.40	1.00	0.92	0.59	0.76	0.54	0.68	0.75	0.57	0.78	0.70	0.31	0.43	0.74	0.62	0.55	0.72	0.59	0.50
BO	0.27	0.64	0.41	0.92	1.00	0.55	0.68	0.50	0.60	0.68	0.60	0.70	0.62	0.31	0.41	0.66	0.54	0.47	0.65	0.55	0.47
EX	0.28	0.40	0.33	0.59	0.55	1.00	0.61	0.40	0.59	0.61	0.42	0.61	0.60	0.22	0.32	0.59	0.52	0.45	0.60	1.00	0.36
CP	0.24	0.57	0.37	0.76	0.68	0.61	1.00	0.58	0.77	0.98	0.52	0.81	0.80	0.30	0.44	0.74	0.64	0.56	0.77	0.61	0.52
HA	0.18	0.54	0.31	0.54	0.50	0.40	0.58	1.00	0.57	0.58	0.40	0.57	0.58	0.37	0.53	0.55	0.52	0.45	0.57	0.40	0.69
IB	0.22	0.53	0.34	0.68	0.60	0.59	0.77	0.57	1.00	0.77	0.47	0.79	0.89	0.29	0.43	0.77	0.63	0.55	0.81	0.59	0.51
LP	0.24	0.56	0.36	0.75	0.68	0.61	0.98	0.58	0.77	1.00	0.51	0.81	0.81	0.30	0.44	0.74	0.63	0.55	0.77	0.61	0.52
MC	0.19	0.55	0.35	0.57	0.60	0.42	0.52	0.40	0.47	0.51	1.00	0.53	0.48	0.22	0.31	0.51	0.45	0.39	0.50	0.42	0.36
DO	0.24	0.58	0.37	0.78	0.70	0.61	0.81	0.57	0.79	0.81	0.53	1.00	0.81	0.30	0.44	0.90	0.64	0.56	0.83	0.61	0.52
NA	0.23	0.54	0.35	0.70	0.62	0.60	0.80	0.58	0.89	0.81	0.48	0.81	1.00	0.30	0.43	0.79	0.63	0.55	0.85	0.60	0.52
PL	0.13	0.40	0.22	0.31	0.31	0.22	0.30	0.37	0.29	0.30	0.22	0.30	0.30	1.00	0.59	0.30	0.29	0.28	0.30	0.22	0.42
RU	0.16	0.47	0.27	0.43	0.41	0.32	0.44	0.53	0.43	0.44	0.31	0.44	0.43	0.59	1.00	0.43	0.41	0.37	0.43	0.32	0.57
SI	0.24	0.56	0.37	0.74	0.66	0.59	0.74	0.55	0.77	0.74	0.51	0.90	0.79	0.30	0.43	1.00	0.66	0.57	0.82	0.59	0.50
TO	0.23	0.49	0.34	0.62	0.54	0.52	0.64	0.52	0.63	0.63	0.45	0.64	0.63	0.29	0.41	0.66	1.00	0.74	0.63	0.52	0.46
UN	0.21	0.43	0.29	0.55	0.47	0.45	0.56	0.45	0.55	0.55	0.39	0.56	0.55	0.28	0.37	0.57	0.74	1.00	0.55	0.45	0.40
RY	0.23	0.56	0.35	0.72	0.65	0.60	0.77	0.57	0.81	0.77	0.50	0.83	0.85	0.30	0.43	0.82	0.63	0.55	1.00	0.60	0.51
CO	0.28	0.40	0.33	0.59	0.55	1.00	0.61	0.40	0.59	0.61	0.42	0.61	0.60	0.22	0.32	0.59	0.52	0.45	0.60	1.00	0.36
CA	0.17	0.53	0.29	0.50	0.47	0.36	0.52	0.69	0.51	0.52	0.36	0.52	0.52	0.42	0.57	0.50	0.46	0.40	0.51	0.36	1.00

Similarity Matrix: IC-11-85

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.16	0.20	0.25	0.26	0.27	0.23	0.18	0.22	0.23	0.18	0.23	0.22	0.13	0.16	0.23	0.23	0.20	0.23	0.27	0.16
KA	0.16	1.00	0.35	0.63	0.65	0.40	0.57	0.54	0.52	0.57	0.55	0.59	0.54	0.39	0.47	0.57	0.48	0.42	0.56	0.40	0.53
AR	0.20	0.35	1.00	0.38	0.40	0.32	0.36	0.31	0.33	0.36	0.33	0.36	0.34	0.22	0.27	0.36	0.33	0.28	0.35	0.32	0.29
BL	0.25	0.63	0.38	1.00	0.92	0.59	0.76	0.56	0.68	0.76	0.58	0.79	0.70	0.31	0.43	0.75	0.62	0.54	0.73	0.59	0.50
BO	0.26	0.65	0.40	0.92	1.00	0.55	0.69	0.52	0.60	0.68	0.60	0.71	0.63	0.30	0.42	0.67	0.54	0.47	0.66	0.55	0.48
EX	0.27	0.40	0.32	0.59	0.55	1.00	0.61	0.41	0.59	0.60	0.42	0.60	0.60	0.23	0.32	0.59	0.52	0.45	0.59	1.00	0.36
CP	0.23	0.57	0.36	0.76	0.69	0.61	1.00	0.59	0.78	0.97	0.52	0.82	0.80	0.30	0.45	0.75	0.63	0.55	0.77	0.61	0.52
HA	0.18	0.54	0.31	0.56	0.52	0.41	0.59	1.00	0.59	0.59	0.40	0.59	0.60	0.36	0.52	0.57	0.52	0.45	0.59	0.41	0.67
IB	0.22	0.52	0.33	0.68	0.60	0.59	0.78	0.59	1.00	0.79	0.48	0.79	0.89	0.29	0.42	0.77	0.63	0.55	0.82	0.59	0.51
LP	0.23	0.57	0.36	0.76	0.68	0.60	0.97	0.59	0.79	1.00	0.51	0.81	0.81	0.30	0.44	0.75	0.62	0.55	0.78	0.60	0.52
MC	0.18	0.55	0.33	0.58	0.60	0.42	0.52	0.40	0.48	0.51	1.00	0.53	0.49	0.21	0.30	0.52	0.45	0.38	0.50	0.42	0.36
DO	0.23	0.59	0.36	0.79	0.71	0.60	0.82	0.59	0.79	0.81	0.53	1.00	0.81	0.31	0.44	0.91	0.64	0.55	0.83	0.60	0.52
NA	0.22	0.54	0.34	0.70	0.63	0.60	0.80	0.60	0.89	0.81	0.49	0.81	1.00	0.30	0.43	0.79	0.63	0.55	0.85	0.60	0.51
PL	0.13	0.39	0.22	0.31	0.30	0.23	0.30	0.36	0.29	0.30	0.21	0.31	0.30	1.00	0.59	0.30	0.30	0.27	0.30	0.23	0.42
RU	0.16	0.47	0.27	0.43	0.42	0.32	0.45	0.52	0.42	0.44	0.30	0.44	0.43	0.59	1.00	0.42	0.40	0.36	0.43	0.32	0.57
SI	0.23	0.57	0.36	0.75	0.67	0.59	0.75	0.57	0.77	0.75	0.52	0.91	0.79	0.30	0.42	1.00	0.65	0.56	0.82	0.59	0.50
TO	0.23	0.48	0.33	0.62	0.54	0.52	0.63	0.52	0.63	0.62	0.45	0.64	0.63	0.30	0.40	0.65	1.00	0.72	0.63	0.52	0.45
UN	0.20	0.42	0.28	0.54	0.47	0.45	0.55	0.45	0.55	0.55	0.38	0.55	0.55	0.27	0.36	0.56	0.72	1.00	0.55	0.45	0.39
RY	0.23	0.56	0.35	0.73	0.66	0.59	0.77	0.59	0.82	0.78	0.50	0.83	0.85	0.30	0.43	0.82	0.63	0.55	1.00	0.59	0.51
CO	0.27	0.40	0.32	0.59	0.55	1.00	0.61	0.41	0.59	0.60	0.42	0.60	0.60	0.23	0.32	0.59	0.52	0.45	0.59	1.00	0.36
CA	0.16	0.53	0.29	0.50	0.48	0.36	0.52	0.67	0.51	0.52	0.36	0.52	0.51	0.42	0.57	0.50	0.45	0.39	0.51	0.36	1.00

Similarity Matrix: IC-15-5

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.26	0.34	0.25	0.25	0.45	0.25	0.32	0.28	0.24	0.23	0.28	0.27	0.55	0.43	0.45	0.43	0.52	0.34	0.40	0.54
KA	0.26	1.00	0.39	0.70	0.69	0.50	0.69	0.51	0.60	0.68	0.70	0.70	0.62	0.35	0.47	0.57	0.58	0.53	0.62	0.56	0.36
AR	0.34	0.39	1.00	0.40	0.41	0.41	0.38	0.32	0.36	0.37	0.35	0.40	0.36	0.31	0.34	0.40	0.40	0.38	0.39	0.41	0.30
BL	0.25	0.70	0.40	1.00	0.91	0.54	0.76	0.51	0.66	0.75	0.56	0.78	0.67	0.31	0.46	0.61	0.63	0.57	0.67	0.62	0.32
BO	0.25	0.69	0.41	0.91	1.00	0.51	0.67	0.45	0.57	0.66	0.53	0.70	0.58	0.28	0.42	0.52	0.54	0.48	0.60	0.56	0.29
EX	0.45	0.50	0.41	0.54	0.51	1.00	0.55	0.43	0.57	0.54	0.44	0.58	0.54	0.38	0.49	0.62	0.66	0.57	0.64	0.88	0.37
CP	0.25	0.69	0.38	0.76	0.67	0.55	1.00	0.56	0.76	0.97	0.59	0.90	0.80	0.33	0.50	0.63	0.64	0.58	0.72	0.64	0.34
HA	0.32	0.51	0.32	0.51	0.45	0.43	0.56	1.00	0.57	0.56	0.41	0.56	0.58	0.48	0.71	0.55	0.55	0.54	0.54	0.50	0.50
IB	0.28	0.60	0.36	0.66	0.57	0.57	0.76	0.57	1.00	0.77	0.54	0.75	0.87	0.36	0.52	0.71	0.71	0.63	0.75	0.67	0.37
LP	0.24	0.68	0.37	0.75	0.66	0.54	0.97	0.56	0.77	1.00	0.59	0.88	0.81	0.33	0.50	0.62	0.63	0.58	0.72	0.63	0.34
MC	0.23	0.70	0.35	0.56	0.53	0.44	0.59	0.41	0.54	0.59	1.00	0.60	0.55	0.29	0.38	0.51	0.51	0.45	0.54	0.50	0.29
DO	0.28	0.70	0.40	0.78	0.70	0.58	0.90	0.56	0.75	0.88	0.60	1.00	0.77	0.35	0.51	0.68	0.71	0.62	0.73	0.68	0.36
NA	0.27	0.62	0.36	0.67	0.58	0.54	0.80	0.58	0.87	0.81	0.55	0.77	1.00	0.35	0.51	0.68	0.68	0.61	0.71	0.63	0.36
PL	0.55	0.35	0.31	0.31	0.28	0.38	0.33	0.48	0.36	0.33	0.29	0.35	0.35	1.00	0.63	0.47	0.44	0.58	0.39	0.39	0.98
RU	0.43	0.47	0.34	0.46	0.42	0.49	0.50	0.71	0.52	0.50	0.38	0.51	0.51	0.63	1.00	0.56	0.57	0.59	0.54	0.53	0.65
SI	0.45	0.57	0.40	0.61	0.52	0.62	0.63	0.55	0.71	0.62	0.51	0.68	0.68	0.47	0.56	1.00	0.83	0.80	0.72	0.68	0.47
TO	0.43	0.58	0.40	0.63	0.54	0.66	0.64	0.55	0.71	0.63	0.51	0.71	0.68	0.44	0.57	0.83	1.00	0.79	0.74	0.73	0.44
UN	0.52	0.53	0.38	0.57	0.48	0.57	0.58	0.54	0.63	0.58	0.45	0.62	0.61	0.58	0.59	0.80	0.79	1.00	0.66	0.64	0.58
RY	0.34	0.62	0.39	0.67	0.60	0.64	0.72	0.54	0.75	0.72	0.54	0.73	0.71	0.39	0.54	0.72	0.74	0.66	1.00	0.72	0.40
CO	0.40	0.56	0.41	0.62	0.56	0.88	0.64	0.50	0.67	0.63	0.50	0.68	0.63	0.39	0.53	0.68	0.73	0.64	0.72	1.00	0.38
CA	0.54	0.36	0.30	0.32	0.29	0.37	0.34	0.50	0.37	0.34	0.29	0.36	0.36	0.98	0.65	0.47	0.44	0.58	0.40	0.38	1.00

Similarity Matrix: IC-15-25

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.14	0.16	0.19	0.20	0.20	0.17	0.14	0.16	0.17	0.15	0.18	0.16	0.13	0.14	0.19	0.22	0.20	0.17	0.20	0.12
KA	0.14	1.00	0.33	0.63	0.63	0.39	0.59	0.50	0.52	0.58	0.61	0.60	0.54	0.34	0.41	0.56	0.47	0.39	0.56	0.39	0.47
AR	0.16	0.33	1.00	0.37	0.38	0.31	0.34	0.28	0.31	0.34	0.31	0.35	0.32	0.19	0.24	0.34	0.32	0.26	0.33	0.31	0.24
BL	0.19	0.63	0.37	1.00	0.94	0.54	0.73	0.47	0.62	0.73	0.56	0.75	0.65	0.26	0.36	0.68	0.56	0.47	0.68	0.55	0.41
BO	0.20	0.63	0.38	0.94	1.00	0.53	0.67	0.44	0.56	0.66	0.57	0.69	0.58	0.25	0.34	0.62	0.49	0.41	0.62	0.53	0.39
EX	0.20	0.39	0.31	0.54	0.53	1.00	0.56	0.35	0.54	0.56	0.38	0.55	0.54	0.19	0.27	0.53	0.47	0.38	0.55	0.99	0.29
CP	0.17	0.59	0.34	0.73	0.67	0.56	1.00	0.51	0.73	0.97	0.51	0.81	0.76	0.26	0.38	0.68	0.56	0.47	0.73	0.56	0.44
HA	0.14	0.50	0.28	0.47	0.44	0.35	0.51	1.00	0.51	0.52	0.37	0.51	0.52	0.35	0.50	0.49	0.46	0.39	0.51	0.35	0.61
IB	0.16	0.52	0.31	0.62	0.56	0.54	0.73	0.51	1.00	0.74	0.45	0.74	0.88	0.25	0.36	0.71	0.57	0.47	0.77	0.54	0.42
LP	0.17	0.58	0.34	0.73	0.66	0.56	0.97	0.52	0.74	1.00	0.50	0.80	0.77	0.26	0.38	0.68	0.56	0.47	0.74	0.56	0.44
MC	0.15	0.61	0.31	0.56	0.57	0.38	0.51	0.37	0.45	0.50	1.00	0.52	0.47	0.20	0.27	0.49	0.43	0.34	0.49	0.38	0.32
DO	0.18	0.60	0.35	0.75	0.69	0.55	0.81	0.51	0.74	0.80	0.52	1.00	0.77	0.27	0.38	0.84	0.59	0.48	0.78	0.56	0.43
NA	0.16	0.54	0.32	0.65	0.58	0.54	0.76	0.52	0.88	0.77	0.47	0.77	1.00	0.26	0.37	0.72	0.56	0.47	0.79	0.55	0.43
PL	0.13	0.34	0.19	0.26	0.25	0.19	0.26	0.35	0.25	0.26	0.20	0.27	0.26	1.00	0.60	0.27	0.28	0.29	0.26	0.19	0.43
RU	0.14	0.41	0.24	0.36	0.34	0.27	0.38	0.50	0.36	0.38	0.27	0.38	0.37	0.60	1.00	0.37	0.37	0.33	0.37	0.27	0.56
SI	0.19	0.56	0.34	0.68	0.62	0.53	0.68	0.49	0.71	0.68	0.49	0.84	0.72	0.27	0.37	1.00	0.63	0.52	0.75	0.53	0.42
TO	0.22	0.47	0.32	0.56	0.49	0.47	0.56	0.46	0.57	0.56	0.43	0.59	0.56	0.28	0.37	0.63	1.00	0.67	0.59	0.47	0.38
UN	0.20	0.39	0.26	0.47	0.41	0.38	0.47	0.39	0.47	0.47	0.34	0.48	0.47	0.29	0.33	0.52	0.67	1.00	0.48	0.38	0.32
RY	0.17	0.56	0.33	0.68	0.62	0.55	0.73	0.51	0.77	0.74	0.49	0.78	0.79	0.26	0.37	0.75	0.59	0.48	1.00	0.56	0.42
CO	0.20	0.39	0.31	0.55	0.53	0.99	0.56	0.35	0.54	0.56	0.38	0.56	0.55	0.19	0.27	0.53	0.47	0.38	0.56	1.00	0.29
CA	0.12	0.47	0.24	0.41	0.39	0.29	0.44	0.61	0.42	0.44	0.32	0.43	0.43	0.43	0.56	0.42	0.38	0.32	0.42	0.29	1.00

Similarity Matrix: IC-15-45

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.12	0.16	0.18	0.19	0.20	0.17	0.13	0.16	0.17	0.13	0.17	0.16	0.10	0.12	0.18	0.19	0.16	0.17	0.20	0.12
KA	0.12	1.00	0.32	0.61	0.62	0.37	0.56	0.50	0.50	0.56	0.56	0.57	0.52	0.33	0.40	0.54	0.44	0.37	0.54	0.37	0.47
AR	0.16	0.32	1.00	0.35	0.37	0.29	0.33	0.26	0.30	0.32	0.31	0.33	0.31	0.18	0.22	0.32	0.29	0.24	0.32	0.29	0.24
BL	0.18	0.61	0.35	1.00	0.94	0.54	0.73	0.49	0.62	0.73	0.55	0.76	0.65	0.25	0.35	0.70	0.55	0.46	0.68	0.54	0.43
BO	0.19	0.62	0.37	0.94	1.00	0.51	0.67	0.46	0.56	0.66	0.56	0.69	0.59	0.25	0.34	0.63	0.48	0.40	0.62	0.51	0.41
EX	0.20	0.37	0.29	0.54	0.51	1.00	0.56	0.35	0.53	0.56	0.37	0.55	0.54	0.17	0.25	0.53	0.45	0.37	0.55	1.00	0.30
CP	0.17	0.56	0.33	0.73	0.67	0.56	1.00	0.52	0.73	0.97	0.49	0.81	0.77	0.24	0.36	0.70	0.55	0.46	0.74	0.56	0.45
HA	0.13	0.50	0.26	0.49	0.46	0.35	0.52	1.00	0.51	0.51	0.36	0.51	0.51	0.32	0.46	0.49	0.44	0.37	0.51	0.35	0.64
IB	0.16	0.50	0.30	0.62	0.56	0.53	0.73	0.51	1.00	0.74	0.43	0.73	0.87	0.23	0.34	0.71	0.55	0.46	0.77	0.53	0.43
LP	0.17	0.56	0.32	0.73	0.66	0.56	0.97	0.51	0.74	1.00	0.49	0.80	0.78	0.24	0.36	0.70	0.55	0.46	0.74	0.56	0.45
MC	0.13	0.56	0.31	0.55	0.56	0.37	0.49	0.36	0.43	0.49	1.00	0.50	0.46	0.19	0.26	0.49	0.41	0.33	0.47	0.37	0.32
DO	0.17	0.57	0.33	0.76	0.69	0.55	0.81	0.51	0.73	0.80	0.50	1.00	0.77	0.24	0.35	0.86	0.57	0.47	0.78	0.55	0.45
NA	0.16	0.52	0.31	0.65	0.59	0.54	0.77	0.51	0.87	0.78	0.46	0.77	1.00	0.24	0.35	0.74	0.55	0.46	0.81	0.55	0.44
PL	0.10	0.33	0.18	0.25	0.25	0.17	0.24	0.32	0.23	0.24	0.19	0.24	0.24	1.00	0.58	0.24	0.24	0.24	0.24	0.17	0.38
RU	0.12	0.40	0.22	0.35	0.34	0.25	0.36	0.46	0.34	0.36	0.26	0.35	0.35	0.58	1.00	0.34	0.33	0.29	0.35	0.25	0.51
SI	0.18	0.54	0.32	0.70	0.63	0.53	0.70	0.49	0.71	0.70	0.49	0.86	0.74	0.24	0.34	1.00	0.60	0.49	0.77	0.53	0.43
TO	0.19	0.44	0.29	0.55	0.48	0.45	0.55	0.44	0.55	0.55	0.41	0.57	0.55	0.24	0.33	0.60	1.00	0.66	0.57	0.45	0.38
UN	0.16	0.37	0.24	0.46	0.40	0.37	0.46	0.37	0.46	0.46	0.33	0.47	0.46	0.24	0.29	0.49	0.66	1.00	0.47	0.37	0.32
RY	0.17	0.54	0.32	0.68	0.62	0.55	0.74	0.51	0.77	0.74	0.47	0.78	0.81	0.24	0.35	0.77	0.57	0.47	1.00	0.55	0.43
CO	0.20	0.37	0.29	0.54	0.51	1.00	0.56	0.35	0.53	0.56	0.37	0.55	0.55	0.17	0.25	0.53	0.45	0.37	0.55	1.00	0.30
CA	0.12	0.47	0.24	0.43	0.41	0.30	0.45	0.64	0.43	0.45	0.32	0.45	0.44	0.38	0.51	0.43	0.38	0.32	0.43	0.30	1.00

Similarity Matrix: IC-15-65

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.12	0.14	0.19	0.19	0.21	0.17	0.12	0.15	0.17	0.13	0.17	0.16	0.09	0.11	0.17	0.17	0.15	0.16	0.21	0.11
KA	0.12	1.00	0.32	0.61	0.62	0.36	0.56	0.49	0.49	0.55	0.54	0.57	0.52	0.31	0.39	0.54	0.43	0.35	0.52	0.36	0.47
AR	0.14	0.32	1.00	0.36	0.36	0.28	0.33	0.26	0.30	0.32	0.30	0.33	0.31	0.17	0.22	0.32	0.28	0.23	0.31	0.28	0.25
BL	0.19	0.61	0.36	1.00	0.94	0.53	0.73	0.47	0.62	0.72	0.56	0.75	0.65	0.23	0.34	0.70	0.53	0.44	0.67	0.53	0.42
BO	0.19	0.62	0.36	0.94	1.00	0.50	0.67	0.45	0.56	0.66	0.57	0.69	0.59	0.23	0.33	0.64	0.47	0.38	0.62	0.50	0.41
EX	0.21	0.36	0.28	0.53	0.50	1.00	0.55	0.33	0.52	0.55	0.37	0.53	0.54	0.16	0.24	0.52	0.44	0.35	0.53	1.00	0.29
CP	0.17	0.56	0.33	0.73	0.67	0.55	1.00	0.51	0.72	0.97	0.49	0.79	0.75	0.23	0.35	0.69	0.54	0.45	0.72	0.55	0.44
HA	0.12	0.49	0.26	0.47	0.45	0.33	0.51	1.00	0.50	0.51	0.35	0.50	0.50	0.31	0.43	0.48	0.42	0.34	0.50	0.33	0.61
IB	0.15	0.49	0.30	0.62	0.56	0.52	0.72	0.50	1.00	0.73	0.44	0.73	0.87	0.22	0.33	0.71	0.54	0.44	0.77	0.52	0.42
LP	0.17	0.55	0.32	0.72	0.66	0.55	0.97	0.51	0.73	1.00	0.49	0.78	0.76	0.24	0.35	0.69	0.54	0.44	0.72	0.55	0.44
MC	0.13	0.54	0.30	0.56	0.57	0.37	0.49	0.35	0.44	0.49	1.00	0.51	0.46	0.17	0.24	0.49	0.39	0.32	0.47	0.37	0.31
DO	0.17	0.57	0.33	0.75	0.69	0.53	0.79	0.50	0.73	0.78	0.51	1.00	0.76	0.24	0.35	0.87	0.55	0.45	0.77	0.53	0.44
NA	0.16	0.52	0.31	0.65	0.59	0.54	0.75	0.50	0.87	0.76	0.46	0.76	1.00	0.23	0.34	0.73	0.54	0.45	0.80	0.54	0.44
PL	0.09	0.31	0.17	0.23	0.23	0.16	0.23	0.31	0.22	0.24	0.17	0.24	0.23	1.00	0.57	0.23	0.23	0.22	0.23	0.16	0.36
RU	0.11	0.39	0.22	0.34	0.33	0.24	0.35	0.43	0.33	0.35	0.24	0.35	0.34	0.57	1.00	0.34	0.32	0.27	0.34	0.24	0.50
SI	0.17	0.54	0.32	0.70	0.64	0.52	0.69	0.48	0.71	0.69	0.49	0.87	0.73	0.23	0.34	1.00	0.57	0.46	0.76	0.52	0.42
TO	0.17	0.43	0.28	0.53	0.47	0.44	0.54	0.42	0.54	0.54	0.39	0.55	0.54	0.23	0.32	0.57	1.00	0.64	0.55	0.44	0.36
UN	0.15	0.35	0.23	0.44	0.38	0.35	0.45	0.34	0.44	0.44	0.32	0.45	0.45	0.22	0.27	0.46	0.64	1.00	0.45	0.35	0.30
RY	0.16	0.52	0.31	0.67	0.62	0.53	0.72	0.50	0.77	0.72	0.47	0.77	0.80	0.23	0.34	0.76	0.55	0.45	1.00	0.53	0.43
CO	0.21	0.36	0.28	0.53	0.50	1.00	0.55	0.33	0.52	0.55	0.37	0.53	0.54	0.16	0.24	0.52	0.44	0.35	0.53	1.00	0.29
CA	0.11	0.47	0.25	0.42	0.41	0.29	0.44	0.61	0.42	0.44	0.31	0.44	0.44	0.36	0.50	0.42	0.36	0.30	0.43	0.29	1.00

Similarity Matrix: IC-15-85

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.12	0.15	0.19	0.19	0.21	0.17	0.13	0.17	0.17	0.13	0.18	0.17	0.10	0.12	0.18	0.18	0.15	0.17	0.21	0.12
KA	0.12	1.00	0.33	0.61	0.62	0.36	0.55	0.49	0.48	0.54	0.52	0.56	0.51	0.31	0.38	0.53	0.43	0.35	0.53	0.36	0.47
AR	0.15	0.33	1.00	0.36	0.37	0.29	0.33	0.27	0.30	0.33	0.31	0.34	0.31	0.17	0.21	0.33	0.29	0.23	0.32	0.29	0.25
BL	0.19	0.61	0.36	1.00	0.94	0.53	0.73	0.48	0.62	0.72	0.55	0.75	0.66	0.24	0.34	0.70	0.54	0.45	0.68	0.53	0.43
BO	0.19	0.62	0.37	0.94	1.00	0.51	0.67	0.46	0.56	0.66	0.56	0.69	0.59	0.23	0.33	0.64	0.48	0.39	0.62	0.51	0.41
EX	0.21	0.36	0.29	0.53	0.51	1.00	0.55	0.34	0.53	0.55	0.37	0.55	0.54	0.17	0.24	0.52	0.44	0.36	0.54	1.00	0.29
CP	0.17	0.55	0.33	0.73	0.67	0.55	1.00	0.52	0.72	0.97	0.49	0.79	0.76	0.23	0.34	0.70	0.54	0.45	0.74	0.55	0.44
HA	0.13	0.49	0.27	0.48	0.46	0.34	0.52	1.00	0.51	0.52	0.34	0.51	0.52	0.31	0.43	0.50	0.43	0.36	0.51	0.34	0.60
IB	0.17	0.48	0.30	0.62	0.56	0.53	0.72	0.51	1.00	0.73	0.44	0.74	0.87	0.23	0.33	0.72	0.55	0.45	0.78	0.53	0.43
LP	0.17	0.54	0.33	0.72	0.66	0.55	0.97	0.52	0.73	1.00	0.49	0.79	0.77	0.23	0.35	0.70	0.54	0.45	0.74	0.55	0.44
MC	0.13	0.52	0.31	0.55	0.56	0.37	0.49	0.34	0.44	0.49	1.00	0.50	0.45	0.17	0.23	0.48	0.39	0.31	0.47	0.37	0.30
DO	0.18	0.56	0.34	0.75	0.69	0.55	0.79	0.51	0.74	0.79	0.50	1.00	0.77	0.24	0.34	0.87	0.56	0.45	0.78	0.55	0.44
NA	0.17	0.51	0.31	0.66	0.59	0.54	0.76	0.52	0.87	0.77	0.45	0.77	1.00	0.23	0.34	0.74	0.55	0.45	0.82	0.54	0.44
PL	0.10	0.31	0.17	0.24	0.23	0.17	0.23	0.31	0.23	0.23	0.17	0.24	0.23	1.00	0.58	0.24	0.23	0.22	0.24	0.17	0.35
RU	0.12	0.38	0.21	0.34	0.33	0.24	0.34	0.43	0.33	0.35	0.23	0.34	0.34	0.58	1.00	0.33	0.31	0.26	0.34	0.24	0.47
SI	0.18	0.53	0.33	0.70	0.64	0.52	0.70	0.50	0.72	0.70	0.48	0.87	0.74	0.24	0.33	1.00	0.58	0.47	0.77	0.53	0.43
TO	0.18	0.43	0.29	0.54	0.48	0.44	0.54	0.43	0.55	0.54	0.39	0.56	0.55	0.23	0.31	0.58	1.00	0.64	0.55	0.44	0.36
UN	0.15	0.35	0.23	0.45	0.39	0.36	0.45	0.36	0.45	0.45	0.31	0.45	0.45	0.22	0.26	0.47	0.64	1.00	0.45	0.36	0.30
RY	0.17	0.53	0.32	0.68	0.62	0.54	0.74	0.51	0.78	0.74	0.47	0.78	0.82	0.24	0.34	0.77	0.55	0.45	1.00	0.54	0.44
CO	0.21	0.36	0.29	0.53	0.51	1.00	0.55	0.34	0.53	0.55	0.37	0.55	0.54	0.17	0.24	0.53	0.44	0.36	0.54	1.00	0.29
CA	0.12	0.47	0.25	0.43	0.41	0.29	0.44	0.60	0.43	0.44	0.30	0.44	0.44	0.35	0.47	0.43	0.36	0.30	0.44	0.29	1.00

Similarity Matrix: CC-3-5

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.58	0.60	0.73	0.78	0.72	0.67	0.60	0.63	0.66	0.78	0.67	0.63	0.58	0.60	0.67	0.67	0.67	0.69	0.70	0.60
KA	0.58	1.00	0.65	0.83	0.79	0.83	0.87	0.85	0.85	0.80	0.80	0.89	0.85	1.00	0.85	0.89	0.87	0.87	0.87	0.86	0.85
AR	0.60	0.65	1.00	0.64	0.65	0.64	0.64	0.61	0.62	0.61	0.63	0.64	0.62	0.65	0.61	0.64	0.64	0.64	0.64	0.63	0.61
BL	0.73	0.83	0.64	1.00	0.95	0.92	0.94	0.85	0.90	0.91	0.94	0.94	0.90	0.83	0.85	0.94	0.94	0.94	0.96	0.95	0.85
BO	0.78	0.79	0.65	0.95	1.00	0.88	0.89	0.80	0.85	0.85	0.91	0.89	0.85	0.79	0.80	0.89	0.89	0.89	0.91	0.90	0.80
EX	0.72	0.83	0.64	0.92	0.88	1.00	0.94	0.85	0.90	0.87	0.88	0.94	0.90	0.83	0.85	0.94	0.94	0.94	0.96	0.97	0.85
CP	0.67	0.87	0.64	0.94	0.89	0.94	1.00	0.89	0.94	0.90	0.88	0.98	0.94	0.87	0.89	0.98	1.00	1.00	0.98	0.97	0.89
HA	0.60	0.85	0.61	0.85	0.80	0.85	0.89	1.00	0.95	0.89	0.82	0.91	0.95	0.85	1.00	0.91	0.89	0.89	0.89	0.88	1.00
IB	0.63	0.85	0.62	0.90	0.85	0.90	0.94	0.95	1.00	0.90	0.84	0.96	1.00	0.85	0.95	0.96	0.94	0.94	0.94	0.93	0.95
LP	0.66	0.80	0.61	0.91	0.85	0.87	0.90	0.89	0.90	1.00	0.88	0.90	0.90	0.80	0.89	0.90	0.90	0.90	0.90	0.91	0.89
MC	0.78	0.80	0.63	0.94	0.91	0.88	0.88	0.82	0.84	0.88	1.00	0.88	0.84	0.80	0.82	0.88	0.88	0.88	0.90	0.91	0.82
DO	0.67	0.89	0.64	0.94	0.89	0.94	0.98	0.91	0.96	0.90	0.88	1.00	0.96	0.89	0.91	1.00	0.98	0.98	0.98	0.97	0.91
NA	0.63	0.85	0.62	0.90	0.85	0.90	0.94	0.95	1.00	0.90	0.84	0.96	1.00	0.85	0.95	0.96	0.94	0.94	0.94	0.93	0.95
PL	0.58	1.00	0.65	0.83	0.79	0.83	0.87	0.85	0.85	0.80	0.80	0.89	0.85	1.00	0.85	0.89	0.87	0.87	0.87	0.86	0.85
RU	0.60	0.85	0.61	0.85	0.80	0.85	0.89	1.00	0.95	0.89	0.82	0.91	0.95	0.85	1.00	0.91	0.89	0.89	0.89	0.88	1.00
SI	0.67	0.89	0.64	0.94	0.89	0.94	0.98	0.91	0.96	0.90	0.88	1.00	0.96	0.89	0.91	1.00	0.98	0.98	0.98	0.97	0.91
TO	0.67	0.87	0.64	0.94	0.89	0.94	1.00	0.89	0.94	0.90	0.88	0.98	0.94	0.87	0.89	0.98	1.00	1.00	0.98	0.97	0.89
UN	0.67	0.87	0.64	0.94	0.89	0.94	1.00	0.89	0.94	0.90	0.88	0.98	0.94	0.87	0.89	0.98	1.00	1.00	0.98	0.97	0.89
RY	0.69	0.87	0.64	0.96	0.91	0.96	0.98	0.89	0.94	0.90	0.90	0.98	0.94	0.87	0.89	0.98	0.98	0.98	1.00	0.99	0.89
CO	0.70	0.86	0.63	0.95	0.90	0.97	0.97	0.88	0.93	0.91	0.91	0.97	0.93	0.86	0.88	0.97	0.97	0.97	0.99	1.00	0.88
CA	0.60	0.85	0.61	0.85	0.80	0.85	0.89	1.00	0.95	0.89	0.82	0.91	0.95	0.85	1.00	0.91	0.89	0.89	0.89	0.88	1.00

Similarity Matrix: CC-3-25

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.54	0.55	0.71	0.75	0.66	0.61	0.51	0.57	0.58	0.96	0.64	0.62	0.54	0.51	0.64	0.61	0.61	0.65	0.66	0.52
KA	0.54	1.00	0.57	0.78	0.77	0.73	0.70	0.74	0.75	0.66	0.58	0.80	0.79	1.00	0.74	0.80	0.70	0.70	0.80	0.73	0.86
AR	0.55	0.57	1.00	0.59	0.60	0.56	0.55	0.53	0.54	0.52	0.57	0.57	0.56	0.57	0.53	0.57	0.55	0.55	0.58	0.57	0.55
BL	0.71	0.78	0.59	1.00	0.92	0.85	0.80	0.75	0.81	0.77	0.75	0.90	0.87	0.78	0.75	0.90	0.80	0.80	0.91	0.85	0.79
BO	0.75	0.77	0.60	0.92	1.00	0.78	0.72	0.68	0.73	0.69	0.78	0.82	0.79	0.77	0.68	0.82	0.72	0.72	0.83	0.78	0.74
EX	0.66	0.73	0.56	0.85	0.78	1.00	0.80	0.77	0.88	0.75	0.69	0.90	0.90	0.73	0.77	0.90	0.80	0.80	0.90	1.00	0.77
CP	0.61	0.70	0.55	0.80	0.72	0.80	1.00	0.79	0.80	0.77	0.65	0.83	0.80	0.70	0.79	0.83	1.00	1.00	0.82	0.80	0.74
HA	0.51	0.74	0.53	0.75	0.68	0.77	0.79	1.00	0.89	0.75	0.54	0.83	0.85	0.74	1.00	0.83	0.79	0.79	0.82	0.78	0.88
IB	0.57	0.75	0.54	0.81	0.73	0.88	0.80	0.89	1.00	0.77	0.61	0.92	0.95	0.75	0.89	0.92	0.80	0.80	0.90	0.88	0.87
LP	0.58	0.66	0.52	0.77	0.69	0.75	0.77	0.75	0.77	1.00	0.61	0.77	0.77	0.66	0.75	0.77	0.77	0.77	0.77	0.75	0.73
MC	0.96	0.58	0.57	0.75	0.78	0.69	0.65	0.54	0.61	0.61	1.00	0.68	0.66	0.58	0.54	0.68	0.65	0.65	0.69	0.70	0.56
DO	0.64	0.80	0.57	0.90	0.82	0.90	0.83	0.83	0.92	0.77	0.68	1.00	0.97	0.80	0.83	1.00	0.83	0.83	0.97	0.90	0.85
NA	0.62	0.79	0.56	0.87	0.79	0.90	0.80	0.85	0.95	0.77	0.66	0.97	1.00	0.79	0.85	0.97	0.80	0.80	0.95	0.90	0.86
PL	0.54	1.00	0.57	0.78	0.77	0.73	0.70	0.74	0.75	0.66	0.58	0.80	0.79	1.00	0.74	0.80	0.70	0.70	0.80	0.73	0.86
RU	0.51	0.74	0.53	0.75	0.68	0.77	0.79	1.00	0.89	0.75	0.54	0.83	0.85	0.74	1.00	0.83	0.79	0.79	0.82	0.78	0.88
SI	0.64	0.80	0.57	0.90	0.82	0.90	0.83	0.83	0.92	0.77	0.68	1.00	0.97	0.80	0.83	1.00	0.83	0.83	0.97	0.90	0.85
TO	0.61	0.70	0.55	0.80	0.72	0.80	1.00	0.79	0.80	0.77	0.65	0.83	0.80	0.70	0.79	0.83	1.00	1.00	0.82	0.80	0.74
UN	0.61	0.70	0.55	0.80	0.72	0.80	1.00	0.79	0.80	0.77	0.65	0.83	0.80	0.70	0.79	0.83	1.00	1.00	0.82	0.80	0.74
RY	0.65	0.80	0.58	0.91	0.83	0.90	0.82	0.82	0.90	0.77	0.69	0.97	0.95	0.80	0.82	0.97	0.82	0.82	1.00	0.90	0.84
CO	0.66	0.73	0.57	0.85	0.78	1.00	0.80	0.78	0.88	0.75	0.70	0.90	0.90	0.73	0.78	0.90	0.80	0.80	0.90	1.00	0.77
CA	0.52	0.86	0.55	0.79	0.74	0.77	0.74	0.88	0.87	0.73	0.56	0.85	0.86	0.86	0.88	0.85	0.74	0.74	0.84	0.77	1.00

Similarity Matrix: CC-3-45

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.53	0.55	0.71	0.75	0.63	0.57	0.46	0.53	0.54	0.99	0.63	0.61	0.53	0.46	0.63	0.57	0.57	0.63	0.63	0.48
KA	0.53	1.00	0.56	0.77	0.77	0.71	0.66	0.70	0.72	0.60	0.54	0.80	0.78	1.00	0.70	0.80	0.66	0.66	0.80	0.71	0.76
AR	0.55	0.56	1.00	0.58	0.60	0.55	0.53	0.50	0.52	0.49	0.55	0.57	0.56	0.56	0.50	0.57	0.53	0.53	0.57	0.55	0.52
BL	0.71	0.77	0.58	1.00	0.93	0.81	0.74	0.68	0.76	0.70	0.72	0.88	0.85	0.77	0.68	0.88	0.74	0.74	0.89	0.81	0.72
BO	0.75	0.77	0.60	0.93	1.00	0.75	0.67	0.62	0.69	0.63	0.76	0.81	0.78	0.77	0.62	0.81	0.67	0.67	0.82	0.75	0.67
EX	0.63	0.71	0.55	0.81	0.75	1.00	0.73	0.72	0.85	0.69	0.64	0.88	0.88	0.71	0.72	0.88	0.73	0.73	0.88	1.00	0.74
CP	0.57	0.66	0.53	0.74	0.67	0.73	1.00	0.71	0.73	0.70	0.58	0.76	0.73	0.66	0.71	0.76	1.00	1.00	0.75	0.73	0.71
HA	0.46	0.70	0.50	0.68	0.62	0.72	0.71	1.00	0.86	0.69	0.46	0.78	0.80	0.70	1.00	0.78	0.71	0.71	0.77	0.72	0.93
IB	0.53	0.72	0.52	0.76	0.69	0.85	0.73	0.86	1.00	0.70	0.54	0.89	0.92	0.72	0.86	0.89	0.73	0.73	0.87	0.85	0.87
LP	0.54	0.60	0.49	0.70	0.63	0.69	0.70	0.69	0.70	1.00	0.54	0.70	0.70	0.60	0.69	0.70	0.70	0.70	0.70	0.69	0.68
MC	0.99	0.54	0.55	0.72	0.76	0.64	0.58	0.46	0.54	0.54	1.00	0.63	0.61	0.54	0.46	0.63	0.58	0.58	0.64	0.64	0.48
DO	0.63	0.80	0.57	0.88	0.81	0.88	0.76	0.78	0.89	0.70	0.63	1.00	0.97	0.80	0.78	1.00	0.76	0.76	0.98	0.88	0.82
NA	0.61	0.78	0.56	0.85	0.78	0.88	0.73	0.80	0.92	0.70	0.61	0.97	1.00	0.78	0.80	0.97	0.73	0.73	0.96	0.88	0.83
PL	0.53	1.00	0.56	0.77	0.77	0.71	0.66	0.70	0.72	0.60	0.54	0.80	0.78	1.00	0.70	0.80	0.66	0.66	0.80	0.71	0.76
RU	0.46	0.70	0.50	0.68	0.62	0.72	0.71	1.00	0.86	0.69	0.46	0.78	0.80	0.70	1.00	0.78	0.71	0.71	0.77	0.72	0.93
SI	0.63	0.80	0.57	0.88	0.81	0.88	0.76	0.78	0.89	0.70	0.63	1.00	0.97	0.80	0.78	1.00	0.76	0.76	0.98	0.88	0.82
TO	0.57	0.66	0.53	0.74	0.67	0.73	1.00	0.71	0.73	0.70	0.58	0.76	0.73	0.66	0.71	0.76	1.00	1.00	0.75	0.73	0.71
UN	0.57	0.66	0.53	0.74	0.67	0.73	1.00	0.71	0.73	0.70	0.58	0.76	0.73	0.66	0.71	0.76	1.00	1.00	0.75	0.73	0.71
RY	0.63	0.80	0.57	0.89	0.82	0.88	0.75	0.77	0.87	0.70	0.64	0.98	0.96	0.80	0.77	0.98	0.75	0.75	1.00	0.88	0.81
CO	0.63	0.71	0.55	0.81	0.75	1.00	0.73	0.72	0.85	0.69	0.64	0.88	0.88	0.71	0.72	0.88	0.73	0.73	0.88	1.00	0.74
CA	0.48	0.76	0.52	0.72	0.67	0.74	0.71	0.93	0.87	0.68	0.48	0.82	0.83	0.76	0.93	0.82	0.71	0.71	0.81	0.74	1.00

Similarity Matrix: CC-3-65

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.53	0.55	0.72	0.75	0.62	0.54	0.43	0.52	0.52	1.00	0.62	0.60	0.53	0.43	0.62	0.54	0.54	0.63	0.62	0.47
KA	0.53	1.00	0.56	0.76	0.77	0.68	0.61	0.67	0.71	0.57	0.53	0.79	0.77	1.00	0.67	0.79	0.61	0.61	0.78	0.68	0.79
AR	0.55	0.56	1.00	0.59	0.60	0.55	0.51	0.47	0.52	0.48	0.55	0.57	0.56	0.56	0.47	0.57	0.51	0.51	0.57	0.55	0.51
BL	0.72	0.76	0.59	1.00	0.94	0.78	0.70	0.64	0.73	0.65	0.72	0.86	0.83	0.76	0.64	0.86	0.70	0.70	0.87	0.78	0.72
BO	0.75	0.77	0.60	0.94	1.00	0.73	0.63	0.59	0.67	0.59	0.75	0.80	0.77	0.77	0.59	0.80	0.63	0.63	0.81	0.73	0.67
EX	0.62	0.68	0.55	0.78	0.73	1.00	0.68	0.68	0.83	0.64	0.63	0.86	0.86	0.68	0.68	0.86	0.68	0.68	0.85	1.00	0.72
CP	0.54	0.61	0.51	0.70	0.63	0.68	1.00	0.67	0.68	0.65	0.54	0.70	0.68	0.61	0.67	0.70	1.00	1.00	0.70	0.68	0.65
HA	0.43	0.67	0.47	0.64	0.59	0.68	0.67	1.00	0.84	0.64	0.44	0.75	0.77	0.67	1.00	0.75	0.67	0.67	0.75	0.68	0.88
IB	0.52	0.71	0.52	0.73	0.67	0.83	0.68	0.84	1.00	0.66	0.52	0.87	0.90	0.71	0.84	0.87	0.68	0.68	0.86	0.83	0.85
LP	0.52	0.57	0.48	0.65	0.59	0.64	0.65	0.64	0.66	1.00	0.52	0.66	0.66	0.57	0.64	0.66	0.65	0.65	0.66	0.64	0.63
MC	1.00	0.53	0.55	0.72	0.75	0.63	0.54	0.44	0.52	0.52	1.00	0.62	0.60	0.53	0.44	0.62	0.54	0.54	0.63	0.63	0.48
DO	0.62	0.79	0.57	0.86	0.80	0.86	0.70	0.75	0.87	0.66	0.62	1.00	0.97	0.79	0.75	1.00	0.70	0.70	0.98	0.86	0.82
NA	0.60	0.77	0.56	0.83	0.77	0.86	0.68	0.77	0.90	0.66	0.60	0.97	1.00	0.77	0.77	0.97	0.68	0.68	0.96	0.86	0.83
PL	0.53	1.00	0.56	0.76	0.77	0.68	0.61	0.67	0.71	0.57	0.53	0.79	0.77	1.00	0.67	0.79	0.61	0.61	0.78	0.68	0.79
RU	0.43	0.67	0.47	0.64	0.59	0.68	0.67	1.00	0.84	0.64	0.44	0.75	0.77	0.67	1.00	0.75	0.67	0.67	0.75	0.68	0.88
SI	0.62	0.79	0.57	0.86	0.80	0.86	0.70	0.75	0.87	0.66	0.62	1.00	0.97	0.79	0.75	1.00	0.70	0.70	0.98	0.86	0.82
TO	0.54	0.61	0.51	0.70	0.63	0.68	1.00	0.67	0.68	0.65	0.54	0.70	0.68	0.61	0.67	0.70	1.00	1.00	0.70	0.68	0.65
UN	0.54	0.61	0.51	0.70	0.63	0.68	1.00	0.67	0.68	0.65	0.54	0.70	0.68	0.61	0.67	0.70	1.00	1.00	0.70	0.68	0.65
RY	0.63	0.78	0.57	0.87	0.81	0.85	0.70	0.75	0.86	0.66	0.63	0.98	0.96	0.78	0.75	0.98	0.70	0.70	1.00	0.85	0.81
CO	0.62	0.68	0.55	0.78	0.73	1.00	0.68	0.68	0.83	0.64	0.63	0.86	0.86	0.68	0.68	0.86	0.68	0.68	0.85	1.00	0.72
CA	0.47	0.79	0.51	0.72	0.67	0.72	0.65	0.88	0.85	0.63	0.48	0.82	0.83	0.79	0.88	0.82	0.65	0.65	0.81	0.72	1.00

Similarity Matrix: CC-3-85

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.53	0.55	0.72	0.75	0.61	0.52	0.42	0.51	0.50	1.00	0.62	0.60	0.53	0.42	0.62	0.52	0.52	0.62	0.61	0.47
KA	0.53	1.00	0.55	0.76	0.77	0.67	0.58	0.64	0.69	0.54	0.53	0.78	0.77	1.00	0.64	0.78	0.58	0.58	0.78	0.67	0.82
AR	0.55	0.55	1.00	0.59	0.59	0.54	0.49	0.47	0.51	0.46	0.55	0.56	0.55	0.55	0.47	0.56	0.49	0.49	0.56	0.54	0.52
BL	0.72	0.76	0.59	1.00	0.93	0.76	0.65	0.61	0.71	0.62	0.72	0.85	0.83	0.76	0.61	0.85	0.65	0.65	0.86	0.76	0.72
BO	0.75	0.77	0.59	0.93	1.00	0.71	0.59	0.56	0.64	0.56	0.75	0.78	0.76	0.77	0.56	0.78	0.59	0.59	0.79	0.71	0.68
EX	0.61	0.67	0.54	0.76	0.71	1.00	0.65	0.67	0.83	0.61	0.62	0.85	0.86	0.67	0.67	0.85	0.65	0.65	0.85	1.00	0.71
CP	0.52	0.58	0.49	0.65	0.59	0.65	1.00	0.64	0.66	0.63	0.53	0.67	0.65	0.58	0.64	0.67	1.00	1.00	0.67	0.65	0.62
HA	0.42	0.64	0.47	0.61	0.56	0.67	0.64	1.00	0.83	0.62	0.42	0.73	0.74	0.64	1.00	0.73	0.64	0.64	0.73	0.67	0.82
IB	0.51	0.69	0.51	0.71	0.64	0.83	0.66	0.83	1.00	0.62	0.51	0.86	0.88	0.69	0.83	0.86	0.66	0.66	0.85	0.83	0.83
LP	0.50	0.54	0.46	0.62	0.56	0.61	0.63	0.62	0.62	1.00	0.50	0.63	0.63	0.54	0.62	0.63	0.63	0.63	0.63	0.61	0.59
MC	1.00	0.53	0.55	0.72	0.75	0.62	0.53	0.42	0.51	0.50	1.00	0.62	0.60	0.53	0.42	0.62	0.53	0.53	0.62	0.62	0.47
DO	0.62	0.78	0.56	0.85	0.78	0.85	0.67	0.73	0.86	0.63	0.62	1.00	0.98	0.78	0.73	1.00	0.67	0.67	0.98	0.85	0.81
NA	0.60	0.77	0.55	0.83	0.76	0.86	0.65	0.74	0.88	0.63	0.60	0.98	1.00	0.77	0.74	0.98	0.65	0.65	0.97	0.86	0.82
PL	0.53	1.00	0.55	0.76	0.77	0.67	0.58	0.64	0.69	0.54	0.53	0.78	0.77	1.00	0.64	0.78	0.58	0.58	0.78	0.67	0.82
RU	0.42	0.64	0.47	0.61	0.56	0.67	0.64	1.00	0.83	0.62	0.42	0.73	0.74	0.64	1.00	0.73	0.64	0.64	0.73	0.67	0.82
SI	0.62	0.78	0.56	0.85	0.78	0.85	0.67	0.73	0.86	0.63	0.62	1.00	0.98	0.78	0.73	1.00	0.67	0.67	0.98	0.85	0.81
TO	0.52	0.58	0.49	0.65	0.59	0.65	1.00	0.64	0.66	0.63	0.53	0.67	0.65	0.58	0.64	0.67	1.00	1.00	0.67	0.65	0.62
UN	0.52	0.58	0.49	0.65	0.59	0.65	1.00	0.64	0.66	0.63	0.53	0.67	0.65	0.58	0.64	0.67	1.00	1.00	0.67	0.65	0.62
RY	0.62	0.78	0.56	0.86	0.79	0.85	0.67	0.73	0.85	0.63	0.62	0.98	0.97	0.78	0.73	0.98	0.67	0.67	1.00	0.85	0.81
CO	0.61	0.67	0.54	0.76	0.71	1.00	0.65	0.67	0.83	0.61	0.62	0.85	0.86	0.67	0.67	0.85	0.65	0.65	0.85	1.00	0.71
CA	0.47	0.82	0.52	0.72	0.68	0.71	0.62	0.82	0.83	0.59	0.47	0.81	0.82	0.82	0.82	0.81	0.62	0.62	0.81	0.71	1.00

Similarity Matrix: CC-7-5

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.40	0.45	0.43	0.46	0.48	0.41	0.38	0.42	0.40	0.39	0.44	0.41	0.39	0.42	0.46	0.46	0.45	0.45	0.44	0.37
KA	0.40	1.00	0.49	0.76	0.74	0.64	0.74	0.70	0.71	0.74	0.79	0.76	0.73	0.63	0.68	0.73	0.72	0.71	0.72	0.70	0.63
AR	0.45	0.49	1.00	0.49	0.51	0.49	0.47	0.45	0.47	0.46	0.47	0.50	0.47	0.44	0.45	0.50	0.50	0.49	0.49	0.48	0.42
BL	0.43	0.76	0.49	1.00	0.90	0.74	0.85	0.72	0.81	0.85	0.72	0.89	0.82	0.54	0.67	0.81	0.82	0.80	0.83	0.82	0.58
BO	0.46	0.74	0.51	0.90	1.00	0.70	0.75	0.63	0.70	0.75	0.69	0.78	0.72	0.50	0.61	0.70	0.72	0.69	0.74	0.73	0.52
EX	0.48	0.64	0.49	0.74	0.70	1.00	0.75	0.62	0.75	0.74	0.63	0.77	0.74	0.48	0.61	0.74	0.76	0.74	0.79	0.90	0.50
CP	0.41	0.74	0.47	0.85	0.75	0.75	1.00	0.76	0.87	0.97	0.71	0.92	0.91	0.55	0.70	0.82	0.82	0.81	0.83	0.84	0.60
HA	0.38	0.70	0.45	0.72	0.63	0.62	0.76	1.00	0.77	0.75	0.61	0.75	0.78	0.64	0.83	0.75	0.75	0.74	0.73	0.70	0.71
IB	0.42	0.71	0.47	0.81	0.70	0.75	0.87	0.77	1.00	0.86	0.68	0.87	0.93	0.56	0.72	0.87	0.86	0.84	0.87	0.85	0.61
LP	0.40	0.74	0.46	0.85	0.75	0.74	0.97	0.75	0.86	1.00	0.70	0.90	0.90	0.54	0.69	0.79	0.80	0.78	0.81	0.83	0.59
MC	0.39	0.79	0.47	0.72	0.69	0.63	0.71	0.61	0.68	0.70	1.00	0.72	0.69	0.49	0.57	0.69	0.69	0.67	0.69	0.68	0.49
DO	0.44	0.76	0.50	0.89	0.78	0.77	0.92	0.75	0.87	0.90	0.72	1.00	0.89	0.57	0.70	0.87	0.88	0.85	0.86	0.85	0.60
NA	0.41	0.73	0.47	0.82	0.72	0.74	0.91	0.78	0.93	0.90	0.69	0.89	1.00	0.56	0.71	0.84	0.84	0.82	0.83	0.83	0.61
PL	0.39	0.63	0.44	0.54	0.50	0.48	0.55	0.64	0.56	0.54	0.49	0.57	0.56	1.00	0.73	0.61	0.58	0.61	0.57	0.53	0.92
RU	0.42	0.68	0.45	0.67	0.61	0.61	0.70	0.83	0.72	0.69	0.57	0.70	0.71	0.73	1.00	0.72	0.72	0.72	0.71	0.67	0.80
SI	0.46	0.73	0.50	0.81	0.70	0.74	0.82	0.75	0.87	0.79	0.69	0.87	0.84	0.61	0.72	1.00	0.92	0.92	0.87	0.82	0.63
TO	0.46	0.72	0.50	0.82	0.72	0.76	0.82	0.75	0.86	0.80	0.69	0.88	0.84	0.58	0.72	0.92	1.00	0.95	0.88	0.84	0.61
UN	0.45	0.71	0.49	0.80	0.69	0.74	0.81	0.74	0.84	0.78	0.67	0.85	0.82	0.61	0.72	0.92	0.95	1.00	0.86	0.82	0.63
RY	0.45	0.72	0.49	0.83	0.74	0.79	0.83	0.73	0.87	0.81	0.69	0.86	0.83	0.57	0.71	0.87	0.88	0.86	1.00	0.86	0.60
CO	0.44	0.70	0.48	0.82	0.73	0.90	0.84	0.70	0.85	0.83	0.68	0.85	0.83	0.53	0.67	0.82	0.84	0.82	0.86	1.00	0.56
CA	0.37	0.63	0.42	0.58	0.52	0.50	0.60	0.71	0.61	0.59	0.49	0.60	0.61	0.92	0.80	0.63	0.61	0.63	0.60	0.56	1.00

Similarity Matrix: CC-7-25

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.27	0.30	0.38	0.40	0.38	0.34	0.29	0.34	0.34	0.30	0.36	0.34	0.23	0.28	0.36	0.35	0.34	0.35	0.38	0.26
KA	0.27	1.00	0.42	0.68	0.70	0.54	0.65	0.64	0.62	0.65	0.65	0.66	0.64	0.58	0.62	0.65	0.61	0.58	0.65	0.54	0.64
AR	0.30	0.42	1.00	0.45	0.46	0.40	0.43	0.40	0.42	0.42	0.42	0.44	0.43	0.35	0.38	0.44	0.43	0.41	0.43	0.41	0.38
BL	0.38	0.68	0.45	1.00	0.90	0.72	0.83	0.68	0.79	0.82	0.65	0.86	0.80	0.46	0.61	0.83	0.77	0.73	0.83	0.72	0.62
BO	0.40	0.70	0.46	0.90	1.00	0.66	0.73	0.62	0.69	0.72	0.67	0.76	0.70	0.46	0.57	0.73	0.67	0.63	0.73	0.67	0.57
EX	0.38	0.54	0.40	0.72	0.66	1.00	0.73	0.57	0.73	0.73	0.55	0.73	0.73	0.38	0.51	0.71	0.68	0.65	0.73	0.99	0.51
CP	0.34	0.65	0.43	0.83	0.73	0.73	1.00	0.71	0.85	0.97	0.60	0.86	0.87	0.46	0.63	0.81	0.79	0.75	0.84	0.73	0.64
HA	0.29	0.64	0.40	0.68	0.62	0.57	0.71	1.00	0.71	0.71	0.52	0.70	0.72	0.52	0.71	0.69	0.68	0.65	0.70	0.58	0.76
IB	0.34	0.62	0.42	0.79	0.69	0.73	0.85	0.71	1.00	0.84	0.58	0.86	0.94	0.45	0.62	0.84	0.77	0.73	0.88	0.74	0.63
LP	0.34	0.65	0.42	0.82	0.72	0.73	0.97	0.71	0.84	1.00	0.60	0.85	0.87	0.45	0.62	0.80	0.76	0.72	0.83	0.73	0.63
MC	0.30	0.65	0.42	0.65	0.67	0.55	0.60	0.52	0.58	0.60	1.00	0.62	0.59	0.36	0.45	0.61	0.58	0.54	0.61	0.55	0.47
DO	0.36	0.66	0.44	0.86	0.76	0.73	0.86	0.70	0.86	0.85	0.62	1.00	0.88	0.47	0.62	0.93	0.80	0.76	0.89	0.73	0.63
NA	0.34	0.64	0.43	0.80	0.70	0.73	0.87	0.72	0.94	0.87	0.59	0.88	1.00	0.46	0.63	0.85	0.77	0.73	0.89	0.74	0.64
PL	0.23	0.58	0.35	0.46	0.46	0.38	0.46	0.52	0.45	0.45	0.36	0.47	0.46	1.00	0.64	0.47	0.46	0.46	0.46	0.38	0.58
RU	0.28	0.62	0.38	0.61	0.57	0.51	0.63	0.71	0.62	0.62	0.45	0.62	0.63	0.64	1.00	0.61	0.61	0.59	0.62	0.52	0.74
SI	0.36	0.65	0.44	0.83	0.73	0.71	0.81	0.69	0.84	0.80	0.61	0.93	0.85	0.47	0.61	1.00	0.82	0.78	0.87	0.72	0.62
TO	0.35	0.61	0.43	0.77	0.67	0.68	0.79	0.68	0.77	0.76	0.58	0.80	0.77	0.46	0.61	0.82	1.00	0.90	0.78	0.68	0.60
UN	0.34	0.58	0.41	0.73	0.63	0.65	0.75	0.65	0.73	0.72	0.54	0.76	0.73	0.46	0.59	0.78	0.90	1.00	0.74	0.65	0.58
RY	0.35	0.65	0.43	0.83	0.73	0.73	0.84	0.70	0.88	0.83	0.61	0.89	0.89	0.46	0.62	0.87	0.78	0.74	1.00	0.74	0.63
CO	0.38	0.54	0.41	0.72	0.67	0.99	0.73	0.58	0.74	0.73	0.55	0.73	0.74	0.38	0.52	0.72	0.68	0.65	0.74	1.00	0.52
CA	0.26	0.64	0.38	0.62	0.57	0.51	0.64	0.76	0.63	0.63	0.47	0.63	0.64	0.58	0.74	0.62	0.60	0.58	0.63	0.52	1.00

Similarity Matrix: CC-7-45

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.25	0.30	0.37	0.39	0.39	0.35	0.28	0.33	0.34	0.29	0.36	0.34	0.21	0.26	0.35	0.34	0.32	0.35	0.39	0.26
KA	0.25	1.00	0.42	0.67	0.69	0.52	0.63	0.63	0.61	0.63	0.61	0.65	0.62	0.57	0.61	0.64	0.60	0.57	0.63	0.52	0.63
AR	0.30	0.42	1.00	0.45	0.47	0.40	0.43	0.40	0.42	0.42	0.42	0.44	0.43	0.33	0.37	0.44	0.43	0.41	0.43	0.40	0.38
BL	0.37	0.67	0.45	1.00	0.90	0.70	0.82	0.67	0.78	0.81	0.64	0.85	0.80	0.45	0.59	0.83	0.76	0.73	0.82	0.70	0.63
BO	0.39	0.69	0.47	0.90	1.00	0.65	0.72	0.61	0.68	0.71	0.67	0.75	0.70	0.44	0.55	0.73	0.66	0.63	0.72	0.65	0.58
EX	0.39	0.52	0.40	0.70	0.65	1.00	0.71	0.55	0.72	0.71	0.54	0.72	0.72	0.36	0.48	0.71	0.67	0.63	0.72	1.00	0.51
CP	0.35	0.63	0.43	0.82	0.72	0.71	1.00	0.70	0.84	0.97	0.59	0.85	0.86	0.43	0.61	0.82	0.79	0.75	0.84	0.71	0.65
HA	0.28	0.63	0.40	0.67	0.61	0.55	0.70	1.00	0.71	0.70	0.50	0.70	0.71	0.49	0.69	0.69	0.67	0.64	0.70	0.55	0.78
IB	0.33	0.61	0.42	0.78	0.68	0.72	0.84	0.71	1.00	0.84	0.57	0.86	0.92	0.42	0.60	0.85	0.76	0.73	0.88	0.72	0.65
LP	0.34	0.63	0.42	0.81	0.71	0.71	0.97	0.70	0.84	1.00	0.59	0.84	0.86	0.43	0.61	0.81	0.76	0.73	0.84	0.71	0.65
MC	0.29	0.61	0.42	0.64	0.67	0.54	0.59	0.50	0.57	0.59	1.00	0.61	0.58	0.33	0.42	0.60	0.56	0.53	0.60	0.54	0.47
DO	0.36	0.65	0.44	0.85	0.75	0.72	0.85	0.70	0.86	0.84	0.61	1.00	0.89	0.44	0.60	0.95	0.79	0.75	0.90	0.72	0.65
NA	0.34	0.62	0.43	0.80	0.70	0.72	0.86	0.71	0.92	0.86	0.58	0.89	1.00	0.43	0.60	0.87	0.77	0.73	0.90	0.72	0.65
PL	0.21	0.57	0.33	0.45	0.44	0.36	0.43	0.49	0.42	0.43	0.33	0.44	0.43	1.00	0.63	0.44	0.43	0.42	0.43	0.36	0.55
RU	0.26	0.61	0.37	0.59	0.55	0.48	0.61	0.69	0.60	0.61	0.42	0.60	0.60	0.63	1.00	0.60	0.58	0.56	0.60	0.48	0.75
SI	0.35	0.64	0.44	0.83	0.73	0.71	0.82	0.69	0.85	0.81	0.60	0.95	0.87	0.44	0.60	1.00	0.80	0.76	0.89	0.71	0.64
TO	0.34	0.60	0.43	0.76	0.66	0.67	0.79	0.67	0.76	0.76	0.56	0.79	0.77	0.43	0.58	0.80	1.00	0.90	0.78	0.67	0.61
UN	0.32	0.57	0.41	0.73	0.63	0.63	0.75	0.64	0.73	0.73	0.53	0.75	0.73	0.42	0.56	0.76	0.90	1.00	0.74	0.63	0.59
RY	0.35	0.63	0.43	0.82	0.72	0.72	0.84	0.70	0.88	0.84	0.60	0.90	0.90	0.43	0.60	0.89	0.78	0.74	1.00	0.72	0.64
CO	0.39	0.52	0.40	0.70	0.65	1.00	0.71	0.55	0.72	0.71	0.54	0.72	0.72	0.36	0.48	0.71	0.67	0.63	0.72	1.00	0.51
CA	0.26	0.63	0.38	0.63	0.58	0.51	0.65	0.78	0.65	0.65	0.47	0.65	0.65	0.55	0.75	0.64	0.61	0.59	0.64	0.51	1.00

Similarity Matrix: CC-7-65

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.25	0.30	0.38	0.40	0.39	0.35	0.29	0.34	0.35	0.29	0.36	0.35	0.21	0.26	0.36	0.35	0.33	0.35	0.39	0.26
KA	0.25	1.00	0.41	0.66	0.68	0.50	0.62	0.62	0.59	0.61	0.59	0.64	0.61	0.57	0.61	0.63	0.58	0.55	0.62	0.50	0.64
AR	0.30	0.41	1.00	0.45	0.46	0.41	0.43	0.40	0.42	0.43	0.41	0.44	0.42	0.33	0.37	0.44	0.42	0.40	0.43	0.41	0.39
BL	0.38	0.66	0.45	1.00	0.90	0.70	0.82	0.68	0.78	0.82	0.64	0.86	0.80	0.44	0.58	0.84	0.76	0.72	0.82	0.70	0.63
BO	0.40	0.68	0.46	0.90	1.00	0.65	0.72	0.62	0.69	0.72	0.67	0.76	0.70	0.44	0.55	0.74	0.66	0.62	0.73	0.65	0.59
EX	0.39	0.50	0.41	0.70	0.65	1.00	0.71	0.56	0.71	0.71	0.54	0.72	0.72	0.35	0.48	0.71	0.66	0.63	0.71	1.00	0.51
CP	0.35	0.62	0.43	0.82	0.72	0.71	1.00	0.70	0.84	0.97	0.59	0.85	0.87	0.43	0.60	0.82	0.79	0.74	0.84	0.71	0.64
HA	0.29	0.62	0.40	0.68	0.62	0.56	0.70	1.00	0.71	0.70	0.50	0.70	0.71	0.48	0.67	0.69	0.66	0.63	0.70	0.56	0.77
IB	0.34	0.59	0.42	0.78	0.69	0.71	0.84	0.71	1.00	0.84	0.56	0.86	0.93	0.42	0.59	0.85	0.76	0.73	0.88	0.71	0.65
LP	0.35	0.61	0.43	0.82	0.72	0.71	0.97	0.70	0.84	1.00	0.59	0.84	0.86	0.42	0.60	0.81	0.76	0.72	0.84	0.71	0.64
MC	0.29	0.59	0.41	0.64	0.67	0.54	0.59	0.50	0.56	0.59	1.00	0.61	0.58	0.33	0.42	0.60	0.55	0.52	0.59	0.54	0.46
DO	0.36	0.64	0.44	0.86	0.76	0.72	0.85	0.70	0.86	0.84	0.61	1.00	0.88	0.44	0.60	0.95	0.78	0.74	0.90	0.72	0.65
NA	0.35	0.61	0.42	0.80	0.70	0.72	0.87	0.71	0.93	0.86	0.58	0.88	1.00	0.42	0.59	0.87	0.76	0.72	0.90	0.72	0.65
PL	0.21	0.57	0.33	0.44	0.44	0.35	0.43	0.48	0.42	0.42	0.33	0.44	0.42	1.00	0.63	0.43	0.42	0.41	0.43	0.35	0.55
RU	0.26	0.61	0.37	0.58	0.55	0.48	0.60	0.67	0.59	0.60	0.42	0.60	0.59	0.63	1.00	0.59	0.57	0.54	0.59	0.48	0.75
SI	0.36	0.63	0.44	0.84	0.74	0.71	0.82	0.69	0.85	0.81	0.60	0.95	0.87	0.43	0.59	1.00	0.79	0.75	0.89	0.71	0.63
TO	0.35	0.58	0.42	0.76	0.66	0.66	0.79	0.66	0.76	0.76	0.55	0.78	0.76	0.42	0.57	0.79	1.00	0.89	0.77	0.66	0.59
UN	0.33	0.55	0.40	0.72	0.62	0.63	0.74	0.63	0.73	0.72	0.52	0.74	0.72	0.41	0.54	0.75	0.89	1.00	0.73	0.63	0.57
RY	0.35	0.62	0.43	0.82	0.73	0.71	0.84	0.70	0.88	0.84	0.59	0.90	0.90	0.43	0.59	0.89	0.77	0.73	1.00	0.71	0.64
CO	0.39	0.50	0.41	0.70	0.65	1.00	0.71	0.56	0.71	0.71	0.54	0.72	0.72	0.35	0.48	0.71	0.66	0.63	0.71	1.00	0.51
CA	0.26	0.64	0.39	0.63	0.59	0.51	0.64	0.77	0.65	0.64	0.46	0.65	0.65	0.55	0.75	0.63	0.59	0.57	0.64	0.51	1.00

Similarity Matrix: CC-7-85

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.25	0.30	0.38	0.39	0.40	0.35	0.29	0.35	0.35	0.30	0.36	0.35	0.20	0.27	0.36	0.35	0.33	0.35	0.40	0.26
KA	0.25	1.00	0.41	0.66	0.68	0.49	0.61	0.62	0.59	0.61	0.56	0.63	0.61	0.56	0.60	0.62	0.58	0.55	0.62	0.49	0.63
AR	0.30	0.41	1.00	0.45	0.46	0.40	0.42	0.39	0.41	0.42	0.41	0.44	0.42	0.31	0.37	0.43	0.42	0.40	0.43	0.40	0.38
BL	0.38	0.66	0.45	1.00	0.89	0.69	0.82	0.68	0.78	0.82	0.64	0.86	0.81	0.43	0.58	0.84	0.76	0.72	0.83	0.69	0.61
BO	0.39	0.68	0.46	0.89	1.00	0.64	0.72	0.61	0.68	0.71	0.67	0.75	0.70	0.43	0.55	0.73	0.66	0.62	0.72	0.64	0.57
EX	0.40	0.49	0.40	0.69	0.64	1.00	0.71	0.55	0.71	0.71	0.54	0.71	0.72	0.34	0.47	0.70	0.66	0.62	0.71	1.00	0.49
CP	0.35	0.61	0.42	0.82	0.72	0.71	1.00	0.71	0.85	0.97	0.58	0.85	0.87	0.42	0.59	0.82	0.78	0.74	0.84	0.71	0.62
HA	0.29	0.62	0.39	0.68	0.61	0.55	0.71	1.00	0.71	0.70	0.49	0.70	0.71	0.48	0.67	0.69	0.66	0.63	0.70	0.55	0.75
IB	0.35	0.59	0.41	0.78	0.68	0.71	0.85	0.71	1.00	0.84	0.56	0.86	0.93	0.41	0.58	0.86	0.76	0.72	0.88	0.71	0.62
LP	0.35	0.61	0.42	0.82	0.71	0.71	0.97	0.70	0.84	1.00	0.58	0.84	0.86	0.42	0.59	0.81	0.75	0.72	0.84	0.71	0.62
MC	0.30	0.56	0.41	0.64	0.67	0.54	0.58	0.49	0.56	0.58	1.00	0.60	0.57	0.31	0.41	0.60	0.55	0.52	0.59	0.54	0.45
DO	0.36	0.63	0.44	0.86	0.75	0.71	0.85	0.70	0.86	0.84	0.60	1.00	0.89	0.43	0.59	0.95	0.77	0.73	0.91	0.71	0.62
NA	0.35	0.61	0.42	0.81	0.70	0.72	0.87	0.71	0.93	0.86	0.57	0.89	1.00	0.42	0.59	0.88	0.76	0.73	0.91	0.72	0.63
PL	0.20	0.56	0.31	0.43	0.43	0.34	0.42	0.48	0.41	0.42	0.31	0.43	0.42	1.00	0.63	0.42	0.41	0.40	0.42	0.34	0.55
RU	0.27	0.60	0.37	0.58	0.55	0.47	0.59	0.67	0.58	0.59	0.41	0.59	0.59	0.63	1.00	0.58	0.57	0.54	0.59	0.47	0.75
SI	0.36	0.62	0.43	0.84	0.73	0.70	0.82	0.69	0.86	0.81	0.60	0.95	0.88	0.42	0.58	1.00	0.78	0.74	0.90	0.70	0.61
TO	0.35	0.58	0.42	0.76	0.66	0.66	0.78	0.66	0.76	0.75	0.55	0.77	0.76	0.41	0.57	0.78	1.00	0.89	0.77	0.66	0.58
UN	0.33	0.55	0.40	0.72	0.62	0.62	0.74	0.63	0.72	0.72	0.52	0.73	0.73	0.40	0.54	0.74	0.89	1.00	0.73	0.62	0.56
RY	0.35	0.62	0.43	0.83	0.72	0.71	0.84	0.70	0.88	0.84	0.59	0.91	0.91	0.42	0.59	0.90	0.77	0.73	1.00	0.71	0.62
CO	0.40	0.49	0.40	0.69	0.64	1.00	0.71	0.55	0.71	0.71	0.54	0.71	0.72	0.34	0.47	0.70	0.66	0.62	0.71	1.00	0.49
CA	0.26	0.63	0.38	0.61	0.57	0.49	0.62	0.75	0.62	0.62	0.45	0.62	0.63	0.55	0.75	0.61	0.58	0.56	0.62	0.49	1.00

Similarity Matrix: CC-11-5

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.32	0.40	0.32	0.32	0.45	0.31	0.34	0.35	0.30	0.30	0.35	0.33	0.48	0.43	0.45	0.44	0.47	0.39	0.41	0.46
KA	0.32	1.00	0.43	0.72	0.71	0.56	0.72	0.59	0.66	0.71	0.74	0.74	0.68	0.45	0.56	0.65	0.65	0.61	0.66	0.63	0.46
AR	0.40	0.43	1.00	0.44	0.45	0.44	0.41	0.38	0.41	0.41	0.40	0.44	0.41	0.35	0.39	0.45	0.45	0.43	0.43	0.44	0.35
BL	0.32	0.72	0.44	1.00	0.90	0.62	0.79	0.59	0.72	0.79	0.62	0.82	0.73	0.39	0.54	0.69	0.71	0.66	0.73	0.70	0.41
BO	0.32	0.71	0.45	0.90	1.00	0.58	0.70	0.53	0.62	0.69	0.59	0.72	0.63	0.36	0.49	0.60	0.61	0.57	0.64	0.62	0.37
EX	0.45	0.56	0.44	0.62	0.58	1.00	0.63	0.50	0.65	0.62	0.52	0.66	0.63	0.40	0.53	0.67	0.70	0.64	0.70	0.89	0.39
CP	0.31	0.72	0.41	0.79	0.70	0.63	1.00	0.65	0.81	0.98	0.64	0.91	0.84	0.42	0.58	0.71	0.72	0.68	0.76	0.72	0.44
HA	0.34	0.59	0.38	0.59	0.53	0.50	0.65	1.00	0.66	0.64	0.49	0.64	0.66	0.54	0.75	0.63	0.63	0.62	0.62	0.58	0.57
IB	0.35	0.66	0.41	0.72	0.62	0.65	0.81	0.66	1.00	0.81	0.60	0.80	0.89	0.44	0.61	0.79	0.79	0.73	0.80	0.75	0.46
LP	0.30	0.71	0.41	0.79	0.69	0.62	0.98	0.64	0.81	1.00	0.64	0.89	0.84	0.41	0.57	0.70	0.71	0.67	0.75	0.72	0.44
MC	0.30	0.74	0.40	0.62	0.59	0.52	0.64	0.49	0.60	0.64	1.00	0.65	0.62	0.36	0.45	0.58	0.59	0.54	0.60	0.57	0.36
DO	0.35	0.74	0.44	0.82	0.72	0.66	0.91	0.64	0.80	0.89	0.65	1.00	0.83	0.43	0.59	0.76	0.78	0.71	0.79	0.75	0.45
NA	0.33	0.68	0.41	0.73	0.63	0.63	0.84	0.66	0.89	0.84	0.62	0.83	1.00	0.44	0.59	0.76	0.77	0.71	0.77	0.73	0.46
PL	0.48	0.45	0.35	0.39	0.36	0.40	0.42	0.54	0.44	0.41	0.36	0.43	0.44	1.00	0.67	0.51	0.48	0.56	0.46	0.43	0.96
RU	0.43	0.56	0.39	0.54	0.49	0.53	0.58	0.75	0.61	0.57	0.45	0.59	0.59	0.67	1.00	0.62	0.63	0.63	0.61	0.58	0.70
SI	0.45	0.65	0.45	0.69	0.60	0.67	0.71	0.63	0.79	0.70	0.58	0.76	0.76	0.51	0.62	1.00	0.87	0.86	0.79	0.74	0.52
TO	0.44	0.65	0.45	0.71	0.61	0.70	0.72	0.63	0.79	0.71	0.59	0.78	0.77	0.48	0.63	0.87	1.00	0.86	0.81	0.78	0.49
UN	0.47	0.61	0.43	0.66	0.57	0.64	0.68	0.62	0.73	0.67	0.54	0.71	0.71	0.56	0.63	0.86	0.86	1.00	0.75	0.71	0.56
RY	0.39	0.66	0.43	0.73	0.64	0.70	0.76	0.62	0.80	0.75	0.60	0.79	0.77	0.46	0.61	0.79	0.81	0.75	1.00	0.78	0.47
CO	0.41	0.63	0.44	0.70	0.62	0.89	0.72	0.58	0.75	0.72	0.57	0.75	0.73	0.43	0.58	0.74	0.78	0.71	0.78	1.00	0.43
CA	0.46	0.46	0.35	0.41	0.37	0.39	0.44	0.57	0.46	0.44	0.36	0.45	0.46	0.96	0.70	0.52	0.49	0.56	0.47	0.43	1.00

Similarity Matrix: CC-11-25

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.18	0.21	0.25	0.26	0.26	0.23	0.19	0.22	0.23	0.19	0.24	0.22	0.14	0.17	0.24	0.25	0.23	0.23	0.26	0.17
KA	0.18	1.00	0.36	0.65	0.66	0.46	0.61	0.56	0.56	0.60	0.62	0.63	0.58	0.44	0.49	0.60	0.53	0.47	0.60	0.46	0.54
AR	0.21	0.36	1.00	0.39	0.40	0.34	0.37	0.33	0.35	0.36	0.35	0.37	0.35	0.24	0.29	0.37	0.36	0.32	0.36	0.34	0.29
BL	0.25	0.65	0.39	1.00	0.91	0.62	0.78	0.56	0.70	0.77	0.60	0.80	0.72	0.33	0.45	0.75	0.65	0.59	0.75	0.62	0.50
BO	0.26	0.66	0.40	0.91	1.00	0.58	0.69	0.52	0.61	0.69	0.61	0.72	0.64	0.33	0.42	0.67	0.57	0.50	0.66	0.59	0.47
EX	0.26	0.46	0.34	0.62	0.58	1.00	0.64	0.45	0.62	0.64	0.46	0.64	0.63	0.26	0.36	0.61	0.56	0.50	0.63	0.99	0.38
CP	0.23	0.61	0.37	0.78	0.69	0.64	1.00	0.60	0.78	0.98	0.55	0.84	0.82	0.33	0.47	0.74	0.66	0.59	0.79	0.64	0.52
HA	0.19	0.56	0.33	0.56	0.52	0.45	0.60	1.00	0.60	0.60	0.43	0.60	0.61	0.42	0.57	0.59	0.56	0.50	0.60	0.45	0.68
IB	0.22	0.56	0.35	0.70	0.61	0.62	0.78	0.60	1.00	0.79	0.51	0.80	0.90	0.33	0.46	0.78	0.67	0.60	0.82	0.63	0.51
LP	0.23	0.60	0.36	0.77	0.69	0.64	0.98	0.60	0.79	1.00	0.55	0.83	0.82	0.33	0.47	0.74	0.65	0.59	0.79	0.64	0.52
MC	0.19	0.62	0.35	0.60	0.61	0.46	0.55	0.43	0.51	0.55	1.00	0.57	0.53	0.26	0.34	0.55	0.50	0.43	0.54	0.46	0.39
DO	0.24	0.63	0.37	0.80	0.72	0.64	0.84	0.60	0.80	0.83	0.57	1.00	0.82	0.34	0.47	0.88	0.69	0.60	0.83	0.64	0.52
NA	0.22	0.58	0.35	0.72	0.64	0.63	0.82	0.61	0.90	0.82	0.53	0.82	1.00	0.33	0.47	0.79	0.66	0.59	0.84	0.63	0.52
PL	0.14	0.44	0.24	0.33	0.33	0.26	0.33	0.42	0.33	0.33	0.26	0.34	0.33	1.00	0.62	0.34	0.34	0.35	0.34	0.26	0.48
RU	0.17	0.49	0.29	0.45	0.42	0.36	0.47	0.57	0.46	0.47	0.34	0.47	0.47	0.62	1.00	0.46	0.45	0.42	0.47	0.36	0.62
SI	0.24	0.60	0.37	0.75	0.67	0.61	0.74	0.59	0.78	0.74	0.55	0.88	0.79	0.34	0.46	1.00	0.72	0.64	0.81	0.62	0.51
TO	0.25	0.53	0.36	0.65	0.57	0.56	0.66	0.56	0.67	0.65	0.50	0.69	0.66	0.34	0.45	0.72	1.00	0.78	0.68	0.57	0.47
UN	0.23	0.47	0.32	0.59	0.50	0.50	0.59	0.50	0.60	0.59	0.43	0.60	0.59	0.35	0.42	0.64	0.78	1.00	0.60	0.50	0.43
RY	0.23	0.60	0.36	0.75	0.66	0.63	0.79	0.60	0.82	0.79	0.54	0.83	0.84	0.34	0.47	0.81	0.68	0.60	1.00	0.63	0.51
CO	0.26	0.46	0.34	0.62	0.59	0.99	0.64	0.45	0.63	0.64	0.46	0.64	0.63	0.26	0.36	0.62	0.57	0.50	0.63	1.00	0.39
CA	0.17	0.54	0.29	0.50	0.47	0.38	0.52	0.68	0.51	0.52	0.39	0.52	0.52	0.48	0.62	0.51	0.47	0.43	0.51	0.39	1.00

Similarity Matrix: CC-11-45

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.17	0.20	0.25	0.26	0.26	0.23	0.18	0.22	0.23	0.18	0.23	0.22	0.13	0.16	0.23	0.24	0.21	0.23	0.26	0.16
KA	0.17	1.00	0.36	0.64	0.65	0.43	0.59	0.55	0.55	0.59	0.57	0.60	0.56	0.42	0.48	0.58	0.52	0.46	0.58	0.43	0.54
AR	0.20	0.36	1.00	0.40	0.41	0.34	0.37	0.33	0.35	0.37	0.35	0.38	0.36	0.23	0.28	0.38	0.35	0.31	0.37	0.34	0.30
BL	0.25	0.64	0.40	1.00	0.91	0.61	0.77	0.56	0.70	0.77	0.59	0.80	0.72	0.31	0.43	0.76	0.65	0.58	0.75	0.61	0.50
BO	0.26	0.65	0.41	0.91	1.00	0.57	0.68	0.51	0.61	0.68	0.61	0.71	0.63	0.31	0.41	0.67	0.57	0.49	0.66	0.57	0.47
EX	0.26	0.43	0.34	0.61	0.57	1.00	0.63	0.43	0.61	0.63	0.45	0.62	0.63	0.24	0.34	0.61	0.55	0.48	0.63	1.00	0.38
CP	0.23	0.59	0.37	0.77	0.68	0.63	1.00	0.60	0.79	0.97	0.53	0.83	0.82	0.32	0.46	0.76	0.67	0.59	0.79	0.63	0.52
HA	0.18	0.55	0.33	0.56	0.51	0.43	0.60	1.00	0.60	0.60	0.41	0.60	0.60	0.39	0.55	0.58	0.54	0.48	0.60	0.43	0.69
IB	0.22	0.55	0.35	0.70	0.61	0.61	0.79	0.60	1.00	0.79	0.49	0.80	0.91	0.30	0.44	0.78	0.66	0.59	0.83	0.61	0.51
LP	0.23	0.59	0.37	0.77	0.68	0.63	0.97	0.60	0.79	1.00	0.53	0.82	0.82	0.31	0.45	0.76	0.66	0.58	0.79	0.63	0.52
MC	0.18	0.57	0.35	0.59	0.61	0.45	0.53	0.41	0.49	0.53	1.00	0.54	0.50	0.23	0.31	0.53	0.47	0.41	0.52	0.45	0.36
DO	0.23	0.60	0.38	0.80	0.71	0.62	0.83	0.60	0.80	0.82	0.54	1.00	0.83	0.32	0.45	0.91	0.68	0.60	0.84	0.62	0.52
NA	0.22	0.56	0.36	0.72	0.63	0.63	0.82	0.60	0.91	0.82	0.50	0.83	1.00	0.31	0.44	0.80	0.66	0.58	0.85	0.63	0.52
PL	0.13	0.42	0.23	0.31	0.31	0.24	0.32	0.39	0.30	0.31	0.23	0.32	0.31	1.00	0.60	0.32	0.31	0.31	0.31	0.24	0.46
RU	0.16	0.48	0.28	0.43	0.41	0.34	0.46	0.55	0.44	0.45	0.31	0.45	0.44	0.60	1.00	0.44	0.43	0.39	0.44	0.34	0.63
SI	0.23	0.58	0.38	0.76	0.67	0.61	0.76	0.58	0.78	0.76	0.53	0.91	0.80	0.32	0.44	1.00	0.70	0.62	0.83	0.61	0.51
TO	0.24	0.52	0.35	0.65	0.57	0.55	0.67	0.54	0.66	0.66	0.47	0.68	0.66	0.31	0.43	0.70	1.00	0.76	0.67	0.55	0.47
UN	0.21	0.46	0.31	0.58	0.49	0.48	0.59	0.48	0.59	0.58	0.41	0.60	0.58	0.31	0.39	0.62	0.76	1.00	0.59	0.48	0.42
RY	0.23	0.58	0.37	0.75	0.66	0.63	0.79	0.60	0.83	0.79	0.52	0.84	0.85	0.31	0.44	0.83	0.67	0.59	1.00	0.63	0.51
CO	0.26	0.43	0.34	0.61	0.57	1.00	0.63	0.43	0.61	0.63	0.45	0.62	0.63	0.24	0.34	0.61	0.55	0.48	0.63	1.00	0.38
CA	0.16	0.54	0.30	0.50	0.47	0.38	0.52	0.69	0.51	0.52	0.36	0.52	0.52	0.46	0.63	0.51	0.47	0.42	0.51	0.38	1.00

Similarity Matrix: CC-11-65

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.17	0.20	0.25	0.26	0.28	0.24	0.19	0.23	0.24	0.18	0.24	0.23	0.13	0.16	0.24	0.23	0.21	0.23	0.28	0.17
KA	0.17	1.00	0.37	0.64	0.65	0.42	0.58	0.56	0.54	0.58	0.55	0.60	0.56	0.41	0.48	0.58	0.51	0.45	0.58	0.42	0.55
AR	0.20	0.37	1.00	0.40	0.42	0.35	0.38	0.33	0.36	0.38	0.36	0.39	0.37	0.23	0.28	0.39	0.36	0.31	0.38	0.35	0.31
BL	0.25	0.64	0.40	1.00	0.91	0.61	0.78	0.57	0.70	0.77	0.58	0.80	0.73	0.31	0.43	0.77	0.65	0.58	0.75	0.61	0.52
BO	0.26	0.65	0.42	0.91	1.00	0.57	0.69	0.53	0.62	0.69	0.60	0.71	0.64	0.31	0.41	0.68	0.56	0.50	0.67	0.57	0.49
EX	0.28	0.42	0.35	0.61	0.57	1.00	0.63	0.44	0.62	0.63	0.43	0.63	0.63	0.24	0.33	0.62	0.55	0.49	0.63	1.00	0.40
CP	0.24	0.58	0.38	0.78	0.69	0.63	1.00	0.61	0.79	0.98	0.52	0.83	0.82	0.31	0.44	0.77	0.67	0.59	0.79	0.63	0.54
HA	0.19	0.56	0.33	0.57	0.53	0.44	0.61	1.00	0.61	0.61	0.40	0.60	0.61	0.39	0.53	0.59	0.54	0.49	0.60	0.44	0.71
IB	0.23	0.54	0.36	0.70	0.62	0.62	0.79	0.61	1.00	0.79	0.48	0.80	0.90	0.31	0.43	0.79	0.66	0.59	0.83	0.62	0.53
LP	0.24	0.58	0.38	0.77	0.69	0.63	0.98	0.61	0.79	1.00	0.51	0.82	0.82	0.31	0.44	0.76	0.65	0.58	0.79	0.63	0.54
MC	0.18	0.55	0.36	0.58	0.60	0.43	0.52	0.40	0.48	0.51	1.00	0.53	0.49	0.22	0.30	0.52	0.47	0.40	0.51	0.43	0.37
DO	0.24	0.60	0.39	0.80	0.71	0.63	0.83	0.60	0.80	0.82	0.53	1.00	0.83	0.32	0.44	0.92	0.67	0.59	0.85	0.63	0.54
NA	0.23	0.56	0.37	0.73	0.64	0.63	0.82	0.61	0.90	0.82	0.49	0.83	1.00	0.31	0.44	0.81	0.66	0.59	0.86	0.63	0.54
PL	0.13	0.41	0.23	0.31	0.31	0.24	0.31	0.39	0.31	0.31	0.22	0.32	0.31	1.00	0.60	0.32	0.30	0.29	0.32	0.24	0.44
RU	0.16	0.48	0.28	0.43	0.41	0.33	0.44	0.53	0.43	0.44	0.30	0.44	0.44	0.60	1.00	0.44	0.41	0.37	0.44	0.33	0.59
SI	0.24	0.58	0.39	0.77	0.68	0.62	0.77	0.59	0.79	0.76	0.52	0.92	0.81	0.32	0.44	1.00	0.69	0.61	0.84	0.62	0.53
TO	0.23	0.51	0.36	0.65	0.56	0.55	0.67	0.54	0.66	0.65	0.47	0.67	0.66	0.30	0.41	0.69	1.00	0.76	0.67	0.55	0.48
UN	0.21	0.45	0.31	0.58	0.50	0.49	0.59	0.49	0.59	0.58	0.40	0.59	0.59	0.29	0.37	0.61	0.76	1.00	0.59	0.49	0.43
RY	0.23	0.58	0.38	0.75	0.67	0.63	0.79	0.60	0.83	0.79	0.51	0.85	0.86	0.32	0.44	0.84	0.67	0.59	1.00	0.63	0.54
CO	0.28	0.42	0.35	0.61	0.57	1.00	0.63	0.44	0.62	0.63	0.43	0.63	0.63	0.24	0.33	0.62	0.55	0.49	0.63	1.00	0.40
CA	0.17	0.55	0.31	0.52	0.49	0.40	0.54	0.71	0.53	0.54	0.37	0.54	0.54	0.44	0.59	0.53	0.48	0.43	0.54	0.40	1.00

Similarity Matrix: CC-11-85

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.16	0.20	0.25	0.26	0.28	0.24	0.18	0.23	0.24	0.18	0.24	0.24	0.12	0.15	0.24	0.23	0.21	0.24	0.28	0.16
KA	0.16	1.00	0.37	0.64	0.65	0.42	0.58	0.55	0.54	0.58	0.53	0.59	0.55	0.42	0.49	0.57	0.50	0.44	0.57	0.42	0.56
AR	0.20	0.37	1.00	0.40	0.41	0.34	0.37	0.32	0.35	0.37	0.35	0.38	0.36	0.23	0.28	0.37	0.35	0.31	0.37	0.34	0.30
BL	0.25	0.64	0.40	1.00	0.91	0.61	0.78	0.57	0.71	0.77	0.57	0.80	0.73	0.31	0.44	0.77	0.65	0.58	0.76	0.61	0.51
BO	0.26	0.65	0.41	0.91	1.00	0.57	0.69	0.53	0.62	0.69	0.59	0.72	0.64	0.31	0.42	0.68	0.57	0.50	0.67	0.57	0.49
EX	0.28	0.42	0.34	0.61	0.57	1.00	0.62	0.42	0.61	0.62	0.43	0.62	0.62	0.23	0.32	0.60	0.54	0.47	0.61	1.00	0.38
CP	0.24	0.58	0.37	0.78	0.69	0.62	1.00	0.60	0.79	0.98	0.51	0.82	0.81	0.31	0.44	0.76	0.67	0.59	0.79	0.62	0.53
HA	0.18	0.55	0.32	0.57	0.53	0.42	0.60	1.00	0.60	0.60	0.40	0.60	0.61	0.38	0.53	0.58	0.54	0.48	0.59	0.42	0.69
IB	0.23	0.54	0.35	0.71	0.62	0.61	0.79	0.60	1.00	0.79	0.47	0.81	0.90	0.29	0.43	0.79	0.65	0.58	0.83	0.61	0.52
LP	0.24	0.58	0.37	0.77	0.69	0.62	0.98	0.60	0.79	1.00	0.51	0.82	0.82	0.30	0.44	0.76	0.65	0.58	0.79	0.62	0.53
MC	0.18	0.53	0.35	0.57	0.59	0.43	0.51	0.40	0.47	0.51	1.00	0.52	0.49	0.21	0.30	0.51	0.46	0.40	0.50	0.43	0.36
DO	0.24	0.59	0.38	0.80	0.72	0.62	0.82	0.60	0.81	0.82	0.52	1.00	0.83	0.31	0.44	0.92	0.67	0.59	0.85	0.62	0.53
NA	0.24	0.55	0.36	0.73	0.64	0.62	0.81	0.61	0.90	0.82	0.49	0.83	1.00	0.30	0.43	0.81	0.66	0.58	0.87	0.62	0.53
PL	0.12	0.42	0.23	0.31	0.31	0.23	0.31	0.38	0.29	0.30	0.21	0.31	0.30	1.00	0.60	0.31	0.30	0.29	0.31	0.23	0.44
RU	0.15	0.49	0.28	0.44	0.42	0.32	0.44	0.53	0.43	0.44	0.30	0.44	0.43	0.60	1.00	0.43	0.41	0.37	0.44	0.32	0.59
SI	0.24	0.57	0.37	0.77	0.68	0.60	0.76	0.58	0.79	0.76	0.51	0.92	0.81	0.31	0.43	1.00	0.69	0.60	0.84	0.60	0.52
TO	0.23	0.50	0.35	0.65	0.57	0.54	0.67	0.54	0.65	0.65	0.46	0.67	0.66	0.30	0.41	0.69	1.00	0.75	0.66	0.54	0.47
UN	0.21	0.44	0.31	0.58	0.50	0.47	0.59	0.48	0.58	0.58	0.40	0.59	0.58	0.29	0.37	0.60	0.75	1.00	0.59	0.47	0.42
RY	0.24	0.57	0.37	0.76	0.67	0.61	0.79	0.59	0.83	0.79	0.50	0.85	0.87	0.31	0.44	0.84	0.66	0.59	1.00	0.61	0.52
CO	0.28	0.42	0.34	0.61	0.57	1.00	0.62	0.42	0.61	0.62	0.43	0.62	0.62	0.23	0.32	0.60	0.54	0.47	0.61	1.00	0.38
CA	0.16	0.56	0.30	0.51	0.49	0.38	0.53	0.69	0.52	0.53	0.36	0.53	0.53	0.44	0.59	0.52	0.47	0.42	0.52	0.38	1.00

Similarity Matrix: CC-15-5

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.27	0.36	0.25	0.25	0.45	0.26	0.32	0.30	0.25	0.24	0.29	0.28	0.55	0.43	0.44	0.43	0.52	0.35	0.41	0.54
KA	0.27	1.00	0.40	0.71	0.70	0.51	0.69	0.51	0.61	0.69	0.71	0.71	0.63	0.36	0.48	0.59	0.59	0.53	0.62	0.57	0.36
AR	0.36	0.40	1.00	0.41	0.42	0.43	0.38	0.34	0.38	0.38	0.35	0.41	0.38	0.31	0.35	0.41	0.42	0.39	0.40	0.42	0.30
BL	0.25	0.71	0.41	1.00	0.91	0.55	0.77	0.52	0.67	0.76	0.58	0.79	0.68	0.31	0.47	0.63	0.64	0.58	0.69	0.62	0.32
BO	0.25	0.70	0.42	0.91	1.00	0.52	0.68	0.46	0.58	0.67	0.54	0.70	0.59	0.28	0.42	0.54	0.56	0.49	0.61	0.57	0.29
EX	0.45	0.51	0.43	0.55	0.52	1.00	0.55	0.45	0.59	0.55	0.45	0.59	0.56	0.38	0.49	0.62	0.66	0.58	0.65	0.88	0.37
CP	0.26	0.69	0.38	0.77	0.68	0.55	1.00	0.57	0.76	0.97	0.61	0.91	0.80	0.34	0.51	0.64	0.66	0.60	0.72	0.65	0.35
HA	0.32	0.51	0.34	0.52	0.46	0.45	0.57	1.00	0.58	0.57	0.43	0.57	0.59	0.48	0.73	0.57	0.57	0.56	0.55	0.51	0.51
IB	0.30	0.61	0.38	0.67	0.58	0.59	0.76	0.58	1.00	0.77	0.56	0.76	0.87	0.36	0.53	0.73	0.73	0.65	0.76	0.68	0.38
LP	0.25	0.69	0.38	0.76	0.67	0.55	0.97	0.57	0.77	1.00	0.61	0.89	0.81	0.34	0.51	0.64	0.65	0.59	0.72	0.65	0.35
MC	0.24	0.71	0.35	0.58	0.54	0.45	0.61	0.43	0.56	0.61	1.00	0.62	0.57	0.29	0.39	0.52	0.53	0.47	0.55	0.51	0.29
DO	0.29	0.71	0.41	0.79	0.70	0.59	0.91	0.57	0.76	0.89	0.62	1.00	0.78	0.35	0.52	0.69	0.71	0.63	0.74	0.68	0.36
NA	0.28	0.63	0.38	0.68	0.59	0.56	0.80	0.59	0.87	0.81	0.57	0.78	1.00	0.36	0.53	0.70	0.70	0.62	0.73	0.65	0.37
PL	0.55	0.36	0.31	0.31	0.28	0.38	0.34	0.48	0.36	0.34	0.29	0.35	0.36	1.00	0.63	0.47	0.44	0.57	0.39	0.39	0.98
RU	0.43	0.48	0.35	0.47	0.42	0.49	0.51	0.73	0.53	0.51	0.39	0.52	0.53	0.63	1.00	0.56	0.58	0.59	0.55	0.54	0.65
SI	0.44	0.59	0.41	0.63	0.54	0.62	0.64	0.57	0.73	0.64	0.52	0.69	0.70	0.47	0.56	1.00	0.83	0.81	0.73	0.69	0.47
TO	0.43	0.59	0.42	0.64	0.56	0.66	0.66	0.57	0.73	0.65	0.53	0.71	0.70	0.44	0.58	0.83	1.00	0.80	0.75	0.74	0.44
UN	0.52	0.53	0.39	0.58	0.49	0.58	0.60	0.56	0.65	0.59	0.47	0.63	0.62	0.57	0.59	0.81	0.80	1.00	0.67	0.65	0.57
RY	0.35	0.62	0.40	0.69	0.61	0.65	0.72	0.55	0.76	0.72	0.55	0.74	0.73	0.39	0.55	0.73	0.75	0.67	1.00	0.73	0.40
CO	0.41	0.57	0.42	0.62	0.57	0.88	0.65	0.51	0.68	0.65	0.51	0.68	0.65	0.39	0.54	0.69	0.74	0.65	0.73	1.00	0.39
CA	0.54	0.36	0.30	0.32	0.29	0.37	0.35	0.51	0.38	0.35	0.29	0.36	0.37	0.98	0.65	0.47	0.44	0.57	0.40	0.39	1.00

Similarity Matrix: CC-15-25

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.14	0.17	0.19	0.19	0.21	0.18	0.14	0.17	0.17	0.15	0.18	0.17	0.13	0.14	0.19	0.22	0.20	0.18	0.21	0.13
KA	0.14	1.00	0.34	0.63	0.64	0.41	0.60	0.50	0.53	0.59	0.61	0.61	0.55	0.34	0.42	0.57	0.48	0.41	0.57	0.42	0.47
AR	0.17	0.34	1.00	0.37	0.38	0.32	0.35	0.28	0.32	0.34	0.32	0.36	0.33	0.20	0.24	0.35	0.33	0.28	0.34	0.32	0.25
BL	0.19	0.63	0.37	1.00	0.93	0.57	0.75	0.49	0.65	0.75	0.55	0.77	0.67	0.27	0.37	0.70	0.58	0.50	0.69	0.57	0.42
BO	0.19	0.64	0.38	0.93	1.00	0.55	0.68	0.46	0.58	0.68	0.56	0.70	0.60	0.26	0.36	0.63	0.51	0.43	0.63	0.55	0.40
EX	0.21	0.41	0.32	0.57	0.55	1.00	0.58	0.37	0.55	0.58	0.40	0.58	0.56	0.20	0.28	0.56	0.50	0.42	0.57	1.00	0.31
CP	0.18	0.60	0.35	0.75	0.68	0.58	1.00	0.52	0.74	0.97	0.50	0.82	0.77	0.27	0.39	0.69	0.59	0.50	0.74	0.59	0.45
HA	0.14	0.50	0.28	0.49	0.46	0.37	0.52	1.00	0.53	0.52	0.37	0.53	0.53	0.37	0.51	0.51	0.47	0.41	0.53	0.37	0.62
IB	0.17	0.53	0.32	0.65	0.58	0.55	0.74	0.53	1.00	0.75	0.46	0.75	0.88	0.27	0.37	0.73	0.59	0.50	0.78	0.56	0.43
LP	0.17	0.59	0.34	0.75	0.68	0.58	0.97	0.52	0.75	1.00	0.50	0.81	0.78	0.27	0.39	0.69	0.58	0.50	0.75	0.59	0.45
MC	0.15	0.61	0.32	0.55	0.56	0.40	0.50	0.37	0.46	0.50	1.00	0.52	0.47	0.20	0.27	0.49	0.43	0.35	0.49	0.40	0.32
DO	0.18	0.61	0.36	0.77	0.70	0.58	0.82	0.53	0.75	0.81	0.52	1.00	0.77	0.28	0.39	0.84	0.61	0.51	0.78	0.59	0.44
NA	0.17	0.55	0.33	0.67	0.60	0.56	0.77	0.53	0.88	0.78	0.47	0.77	1.00	0.27	0.38	0.74	0.59	0.50	0.80	0.57	0.44
PL	0.13	0.34	0.20	0.27	0.26	0.20	0.27	0.37	0.27	0.27	0.20	0.28	0.27	1.00	0.60	0.28	0.29	0.30	0.28	0.20	0.44
RU	0.14	0.42	0.24	0.37	0.36	0.28	0.39	0.51	0.37	0.39	0.27	0.39	0.38	0.60	1.00	0.38	0.38	0.35	0.39	0.28	0.56
SI	0.19	0.57	0.35	0.70	0.63	0.56	0.69	0.51	0.73	0.69	0.49	0.84	0.74	0.28	0.38	1.00	0.66	0.55	0.76	0.56	0.42
TO	0.22	0.48	0.33	0.58	0.51	0.50	0.59	0.47	0.59	0.58	0.43	0.61	0.59	0.29	0.38	0.66	1.00	0.70	0.61	0.50	0.39
UN	0.20	0.41	0.28	0.50	0.43	0.42	0.50	0.41	0.50	0.50	0.35	0.51	0.50	0.30	0.35	0.55	0.70	1.00	0.51	0.42	0.34
RY	0.18	0.57	0.34	0.69	0.63	0.57	0.74	0.53	0.78	0.75	0.49	0.78	0.80	0.28	0.39	0.76	0.61	0.51	1.00	0.58	0.44
CO	0.21	0.42	0.32	0.57	0.55	1.00	0.59	0.37	0.56	0.59	0.40	0.59	0.57	0.20	0.28	0.56	0.50	0.42	0.58	1.00	0.31
CA	0.13	0.47	0.25	0.42	0.40	0.31	0.45	0.62	0.43	0.45	0.32	0.44	0.44	0.44	0.56	0.42	0.39	0.34	0.44	0.31	1.00

Similarity Matrix: CC-15-45

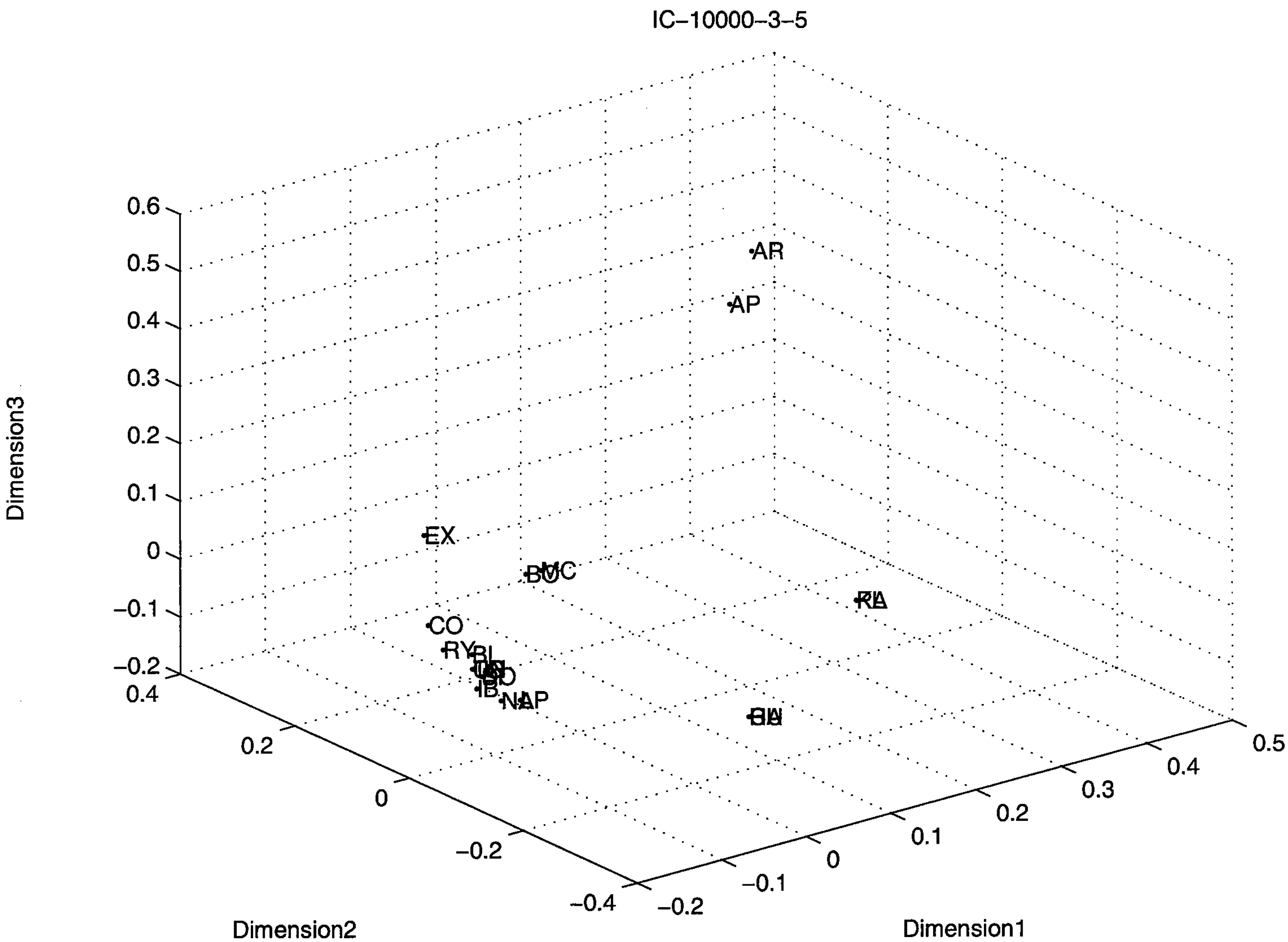
	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.12	0.15	0.18	0.18	0.20	0.16	0.13	0.16	0.16	0.13	0.17	0.16	0.10	0.12	0.17	0.19	0.16	0.16	0.20	0.12
KA	0.12	1.00	0.33	0.62	0.63	0.39	0.58	0.51	0.52	0.57	0.56	0.59	0.54	0.33	0.41	0.56	0.47	0.39	0.56	0.39	0.48
AR	0.15	0.33	1.00	0.37	0.37	0.31	0.34	0.27	0.32	0.34	0.31	0.34	0.33	0.18	0.23	0.34	0.32	0.26	0.34	0.31	0.25
BL	0.18	0.62	0.37	1.00	0.93	0.56	0.74	0.50	0.64	0.74	0.55	0.76	0.67	0.25	0.35	0.71	0.58	0.49	0.69	0.56	0.44
BO	0.18	0.63	0.37	0.93	1.00	0.53	0.67	0.46	0.57	0.67	0.56	0.69	0.60	0.25	0.34	0.64	0.50	0.42	0.63	0.53	0.42
EX	0.20	0.39	0.31	0.56	0.53	1.00	0.56	0.36	0.55	0.57	0.39	0.57	0.56	0.18	0.26	0.55	0.48	0.39	0.56	1.00	0.32
CP	0.16	0.58	0.34	0.74	0.67	0.56	1.00	0.54	0.75	0.97	0.49	0.81	0.78	0.25	0.37	0.72	0.59	0.50	0.75	0.56	0.47
HA	0.13	0.51	0.27	0.50	0.46	0.36	0.54	1.00	0.53	0.54	0.36	0.54	0.54	0.33	0.47	0.52	0.47	0.39	0.53	0.36	0.66
IB	0.16	0.52	0.32	0.64	0.57	0.55	0.75	0.53	1.00	0.75	0.45	0.75	0.88	0.24	0.35	0.74	0.59	0.50	0.79	0.55	0.46
LP	0.16	0.57	0.34	0.74	0.67	0.57	0.97	0.54	0.75	1.00	0.49	0.81	0.79	0.25	0.37	0.72	0.58	0.49	0.75	0.57	0.47
MC	0.13	0.56	0.31	0.55	0.56	0.39	0.49	0.36	0.45	0.49	1.00	0.51	0.46	0.18	0.25	0.49	0.41	0.33	0.48	0.39	0.32
DO	0.17	0.59	0.34	0.76	0.69	0.57	0.81	0.54	0.75	0.81	0.51	1.00	0.79	0.26	0.37	0.88	0.60	0.50	0.80	0.57	0.47
NA	0.16	0.54	0.33	0.67	0.60	0.56	0.78	0.54	0.88	0.79	0.46	0.79	1.00	0.24	0.36	0.76	0.59	0.50	0.82	0.56	0.47
PL	0.10	0.33	0.18	0.25	0.25	0.18	0.25	0.33	0.24	0.25	0.18	0.26	0.24	1.00	0.59	0.26	0.26	0.25	0.25	0.18	0.38
RU	0.12	0.41	0.23	0.35	0.34	0.26	0.37	0.47	0.35	0.37	0.25	0.37	0.36	0.59	1.00	0.36	0.35	0.31	0.36	0.26	0.52
SI	0.17	0.56	0.34	0.71	0.64	0.55	0.72	0.52	0.74	0.72	0.49	0.88	0.76	0.26	0.36	1.00	0.63	0.52	0.78	0.55	0.46
TO	0.19	0.47	0.32	0.58	0.50	0.48	0.59	0.47	0.59	0.58	0.41	0.60	0.59	0.26	0.35	0.63	1.00	0.67	0.60	0.48	0.41
UN	0.16	0.39	0.26	0.49	0.42	0.39	0.50	0.39	0.50	0.49	0.33	0.50	0.50	0.25	0.31	0.52	0.67	1.00	0.50	0.39	0.35
RY	0.16	0.56	0.34	0.69	0.63	0.56	0.75	0.53	0.79	0.75	0.48	0.80	0.82	0.25	0.36	0.78	0.60	0.50	1.00	0.56	0.46
CO	0.20	0.39	0.31	0.56	0.53	1.00	0.56	0.36	0.55	0.57	0.39	0.57	0.56	0.18	0.26	0.55	0.48	0.39	0.56	1.00	0.32
CA	0.12	0.48	0.25	0.44	0.42	0.32	0.47	0.66	0.46	0.47	0.32	0.47	0.47	0.38	0.52	0.46	0.41	0.35	0.46	0.32	1.00

Similarity Matrix: CC-15-65

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.12	0.15	0.18	0.19	0.20	0.17	0.13	0.16	0.17	0.13	0.17	0.17	0.10	0.12	0.17	0.18	0.16	0.17	0.20	0.12
KA	0.12	1.00	0.34	0.62	0.63	0.38	0.57	0.50	0.51	0.57	0.54	0.58	0.53	0.32	0.40	0.55	0.47	0.39	0.55	0.38	0.49
AR	0.15	0.34	1.00	0.38	0.39	0.32	0.35	0.27	0.32	0.35	0.32	0.36	0.34	0.17	0.22	0.35	0.32	0.26	0.34	0.32	0.25
BL	0.18	0.62	0.38	1.00	0.93	0.56	0.76	0.50	0.66	0.75	0.55	0.77	0.69	0.25	0.36	0.73	0.59	0.50	0.71	0.56	0.45
BO	0.19	0.63	0.39	0.93	1.00	0.53	0.68	0.47	0.59	0.68	0.57	0.70	0.62	0.25	0.34	0.66	0.51	0.43	0.64	0.53	0.43
EX	0.20	0.38	0.32	0.56	0.53	1.00	0.58	0.36	0.56	0.58	0.39	0.57	0.57	0.18	0.26	0.55	0.48	0.40	0.57	1.00	0.31
CP	0.17	0.57	0.35	0.76	0.68	0.58	1.00	0.53	0.75	0.97	0.50	0.81	0.78	0.25	0.36	0.73	0.61	0.51	0.76	0.58	0.47
HA	0.13	0.50	0.27	0.50	0.47	0.36	0.53	1.00	0.53	0.54	0.35	0.53	0.53	0.33	0.46	0.52	0.47	0.39	0.53	0.37	0.64
IB	0.16	0.51	0.32	0.66	0.59	0.56	0.75	0.53	1.00	0.76	0.45	0.76	0.89	0.24	0.35	0.75	0.59	0.50	0.80	0.56	0.45
LP	0.17	0.57	0.35	0.75	0.68	0.58	0.97	0.54	0.76	1.00	0.49	0.81	0.79	0.25	0.36	0.73	0.60	0.50	0.77	0.58	0.47
MC	0.13	0.54	0.32	0.55	0.57	0.39	0.50	0.35	0.45	0.49	1.00	0.51	0.47	0.17	0.24	0.49	0.41	0.34	0.48	0.39	0.32
DO	0.17	0.58	0.36	0.77	0.70	0.57	0.81	0.53	0.76	0.81	0.51	1.00	0.80	0.25	0.36	0.89	0.61	0.51	0.81	0.57	0.46
NA	0.17	0.53	0.34	0.69	0.62	0.57	0.78	0.53	0.89	0.79	0.47	0.80	1.00	0.24	0.36	0.77	0.59	0.50	0.83	0.57	0.46
PL	0.10	0.32	0.17	0.25	0.25	0.18	0.25	0.33	0.24	0.25	0.17	0.25	0.24	1.00	0.59	0.25	0.25	0.24	0.25	0.18	0.39
RU	0.12	0.40	0.22	0.36	0.34	0.26	0.36	0.46	0.35	0.36	0.24	0.36	0.36	0.59	1.00	0.36	0.34	0.30	0.36	0.26	0.52
SI	0.17	0.55	0.35	0.73	0.66	0.55	0.73	0.52	0.75	0.73	0.49	0.89	0.77	0.25	0.36	1.00	0.63	0.52	0.80	0.55	0.45
TO	0.18	0.47	0.32	0.59	0.51	0.48	0.61	0.47	0.59	0.60	0.41	0.61	0.59	0.25	0.34	0.63	1.00	0.67	0.61	0.48	0.40
UN	0.16	0.39	0.26	0.50	0.43	0.40	0.51	0.39	0.50	0.50	0.34	0.51	0.50	0.24	0.30	0.52	0.67	1.00	0.50	0.40	0.35
RY	0.17	0.55	0.34	0.71	0.64	0.57	0.76	0.53	0.80	0.77	0.48	0.81	0.83	0.25	0.36	0.80	0.61	0.50	1.00	0.57	0.46
CO	0.20	0.38	0.32	0.56	0.53	1.00	0.58	0.37	0.56	0.58	0.39	0.57	0.57	0.18	0.26	0.55	0.48	0.40	0.57	1.00	0.32
CA	0.12	0.49	0.25	0.45	0.43	0.31	0.47	0.64	0.45	0.47	0.32	0.46	0.46	0.39	0.52	0.45	0.40	0.35	0.46	0.32	1.00

Similarity Matrix: CC-15-85

	AP	KA	AR	BL	BO	EX	CP	HA	IB	LP	MC	DO	NA	PL	RU	SI	TO	UN	RY	CO	CA
AP	1.00	0.11	0.14	0.18	0.18	0.20	0.17	0.13	0.16	0.17	0.13	0.17	0.16	0.08	0.11	0.16	0.17	0.14	0.16	0.20	0.11
KA	0.11	1.00	0.35	0.61	0.63	0.37	0.57	0.51	0.51	0.56	0.52	0.58	0.53	0.32	0.39	0.56	0.47	0.39	0.55	0.37	0.49
AR	0.14	0.35	1.00	0.39	0.40	0.31	0.36	0.30	0.33	0.36	0.33	0.36	0.34	0.17	0.22	0.35	0.32	0.27	0.35	0.31	0.27
BL	0.18	0.61	0.39	1.00	0.93	0.55	0.76	0.51	0.67	0.75	0.55	0.79	0.69	0.24	0.35	0.74	0.60	0.51	0.72	0.55	0.46
BO	0.18	0.63	0.40	0.93	1.00	0.53	0.69	0.48	0.59	0.68	0.57	0.71	0.62	0.24	0.34	0.67	0.53	0.44	0.66	0.53	0.43
EX	0.20	0.37	0.31	0.55	0.53	1.00	0.57	0.36	0.55	0.57	0.38	0.56	0.56	0.17	0.25	0.54	0.47	0.40	0.55	1.00	0.31
CP	0.17	0.57	0.36	0.76	0.69	0.57	1.00	0.55	0.76	0.97	0.50	0.81	0.79	0.23	0.35	0.74	0.61	0.52	0.77	0.57	0.47
HA	0.13	0.51	0.30	0.51	0.48	0.36	0.55	1.00	0.54	0.55	0.36	0.55	0.54	0.32	0.45	0.53	0.47	0.40	0.54	0.36	0.64
IB	0.16	0.51	0.33	0.67	0.59	0.55	0.76	0.54	1.00	0.77	0.45	0.77	0.88	0.23	0.34	0.75	0.59	0.51	0.80	0.55	0.46
LP	0.17	0.56	0.36	0.75	0.68	0.57	0.97	0.55	0.77	1.00	0.49	0.81	0.80	0.23	0.35	0.74	0.60	0.51	0.78	0.57	0.47
MC	0.13	0.52	0.33	0.55	0.57	0.38	0.50	0.36	0.45	0.49	1.00	0.51	0.46	0.16	0.23	0.49	0.42	0.35	0.48	0.38	0.31
DO	0.17	0.58	0.36	0.79	0.71	0.56	0.81	0.55	0.77	0.81	0.51	1.00	0.80	0.24	0.35	0.90	0.62	0.52	0.82	0.56	0.47
NA	0.16	0.53	0.34	0.69	0.62	0.56	0.79	0.54	0.88	0.80	0.46	0.80	1.00	0.23	0.35	0.77	0.60	0.51	0.84	0.56	0.46
PL	0.08	0.32	0.17	0.24	0.24	0.17	0.23	0.32	0.23	0.23	0.16	0.24	0.23	1.00	0.58	0.23	0.23	0.22	0.23	0.17	0.37
RU	0.11	0.39	0.22	0.35	0.34	0.25	0.35	0.45	0.34	0.35	0.23	0.35	0.35	0.58	1.00	0.34	0.33	0.29	0.34	0.25	0.51
SI	0.16	0.56	0.35	0.74	0.67	0.54	0.74	0.53	0.75	0.74	0.49	0.90	0.77	0.23	0.34	1.00	0.63	0.53	0.81	0.54	0.45
TO	0.17	0.47	0.32	0.60	0.53	0.47	0.61	0.47	0.59	0.60	0.42	0.62	0.60	0.23	0.33	0.63	1.00	0.67	0.60	0.47	0.40
UN	0.14	0.39	0.27	0.51	0.44	0.40	0.52	0.40	0.51	0.51	0.35	0.52	0.51	0.22	0.29	0.53	0.67	1.00	0.51	0.40	0.35
RY	0.16	0.55	0.35	0.72	0.66	0.55	0.77	0.54	0.80	0.78	0.48	0.82	0.84	0.23	0.34	0.81	0.60	0.51	1.00	0.55	0.46
CO	0.20	0.37	0.31	0.55	0.53	1.00	0.57	0.36	0.55	0.57	0.38	0.56	0.56	0.17	0.25	0.54	0.47	0.40	0.55	1.00	0.31
CA	0.11	0.49	0.27	0.46	0.43	0.31	0.47	0.64	0.46	0.47	0.31	0.47	0.46	0.37	0.51	0.45	0.40	0.35	0.46	0.31	1.00


IC–10000–3–5
Dimension3
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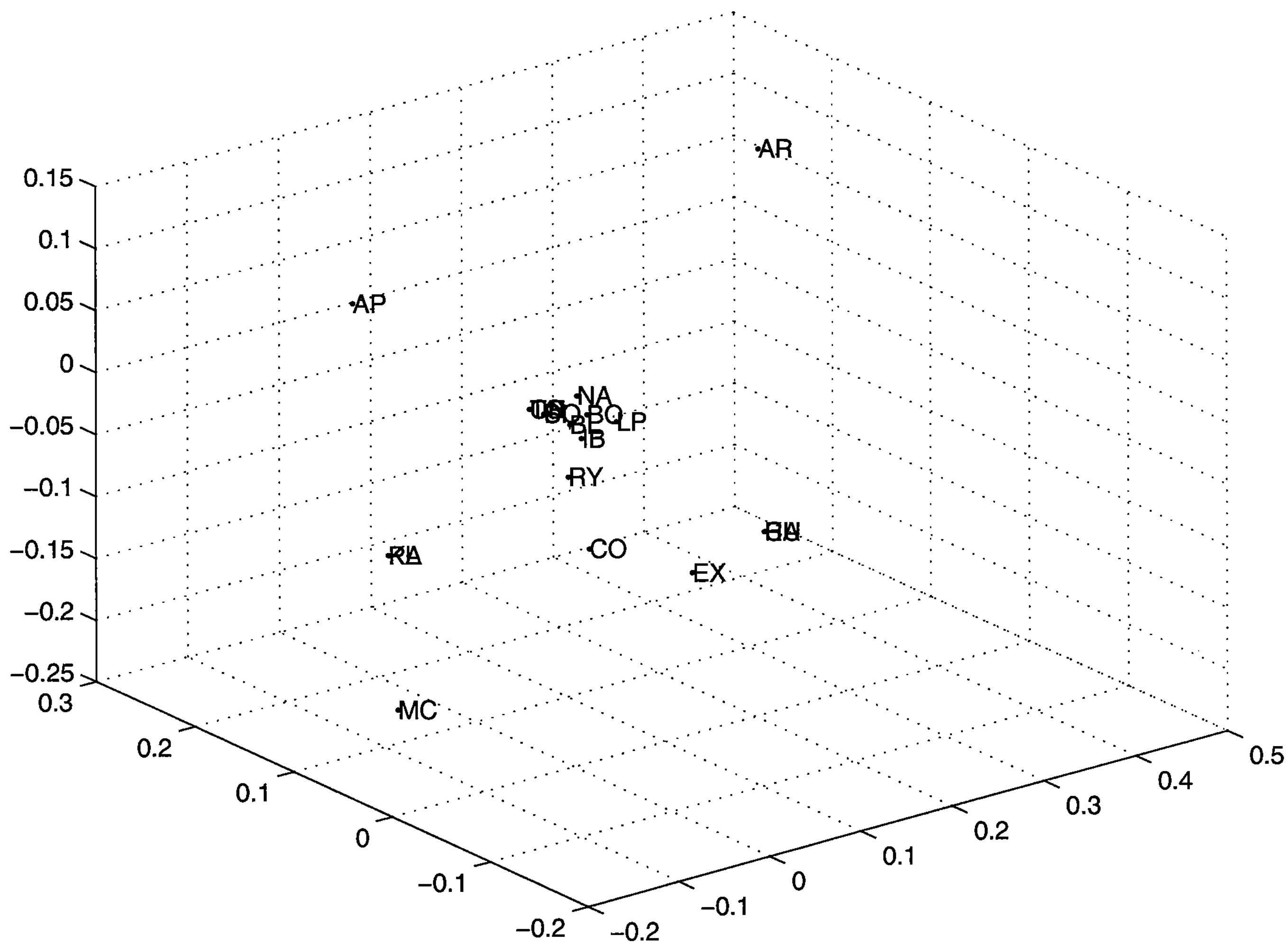
0.4
0.3
0.2
0.1
0
–0.1
–0.2
AR
AP
EX
MC
BO
CO
RY
BI
IB
NAP
FL
BA
0.4
0.2
0
–0.2
–0.4
Dimension2
–0.2
–0.1
0
0.1
0.2
0.3
0.4
0.5
Dimension1



AR
AP
NA
BQ
LP
IB
RY
CO
EX
MC
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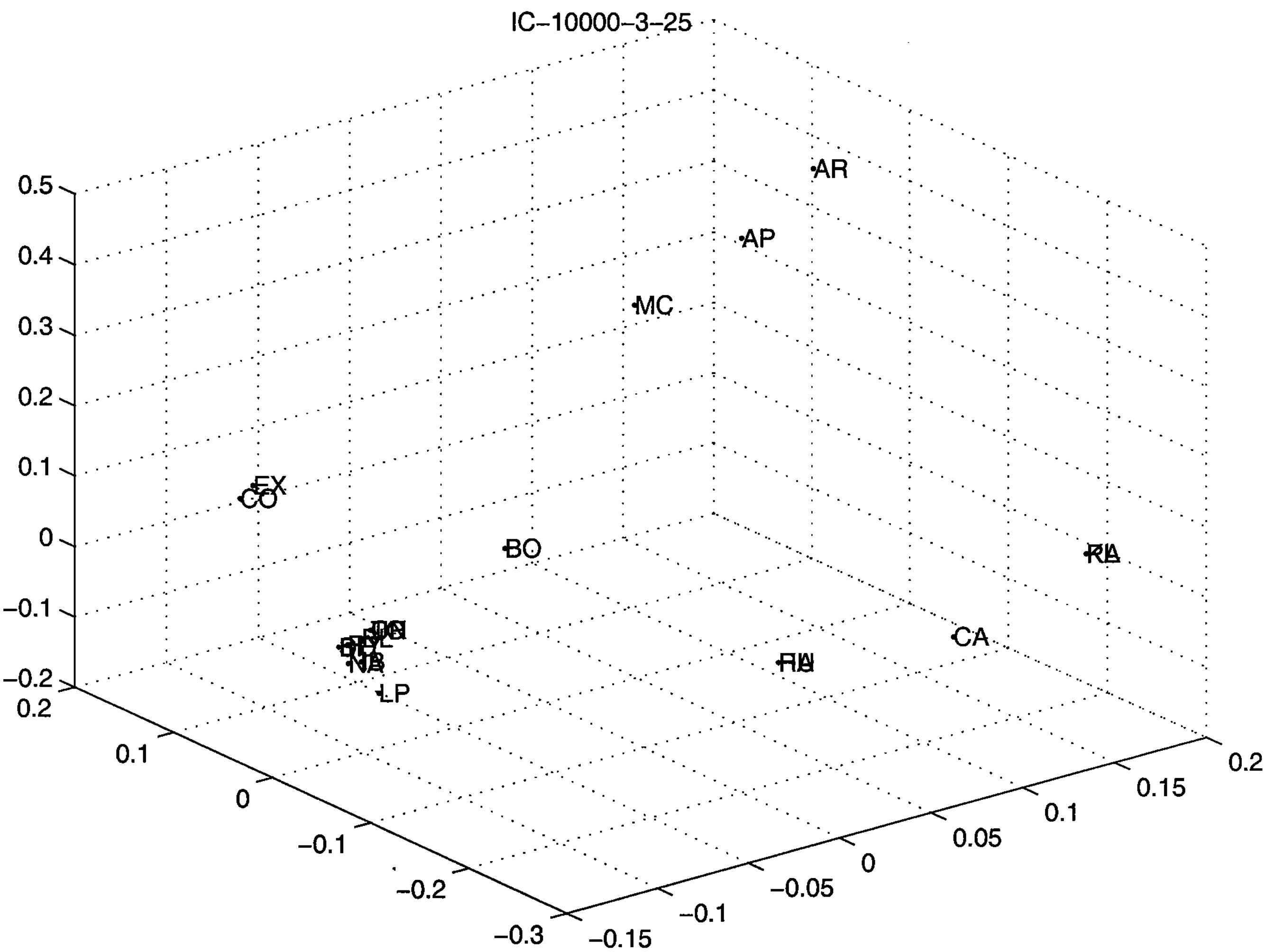
0.1
0.05
0
−0.05
−0.1
−0.15
−0.2
−0.25
0.3
0.2
0.1
0
−0.1
−0.2
−0.2
−0.1
0
0.1
0.2
0.3
0.4
0.5

Dimension5


IC–10000–3–25
AR
AP
MC
EX
CO
BO
LP
CA
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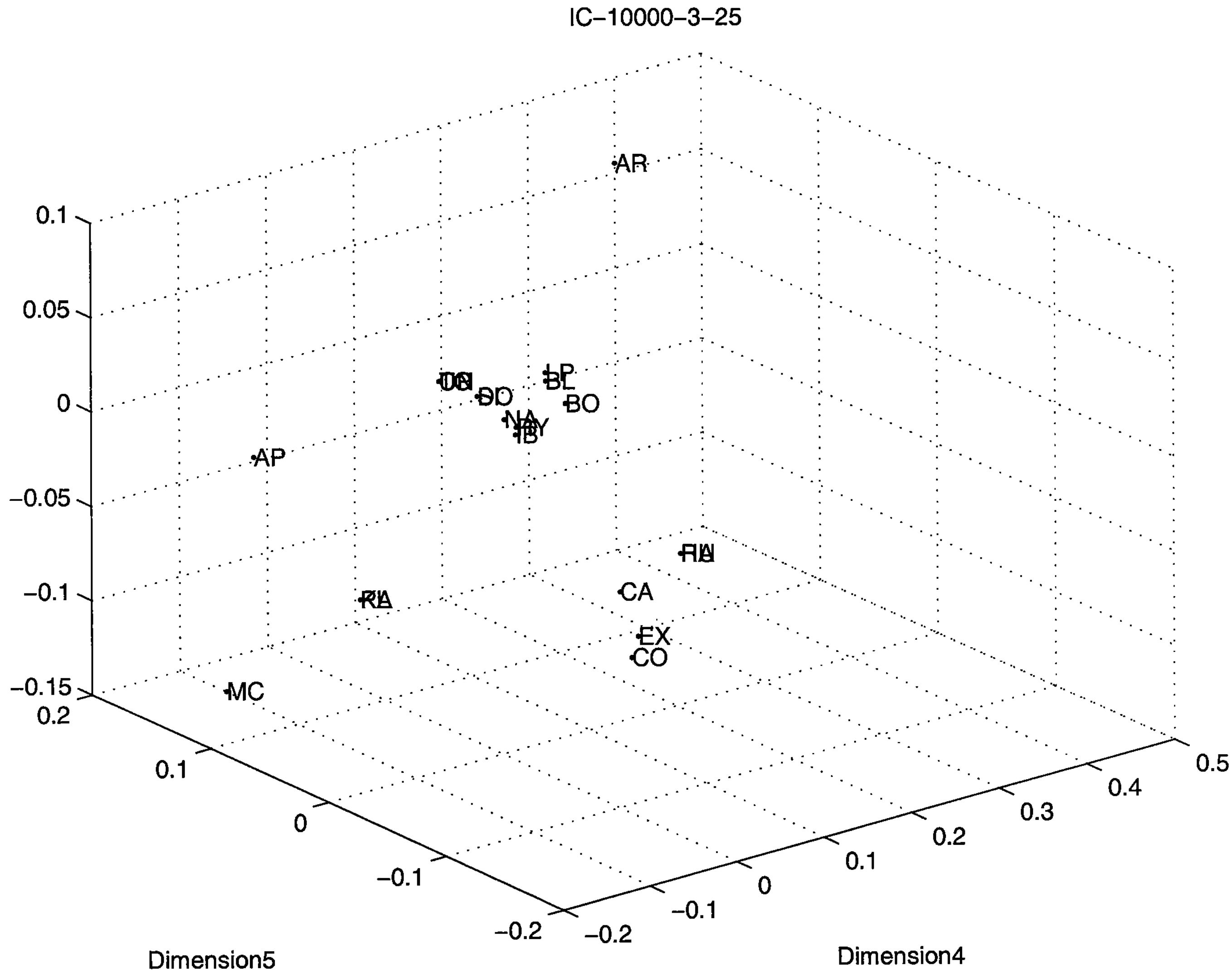
0.4
0.3
0.2
0.1
0
–0.1
–0.2
0.2
0.1
0
–0.1
–0.2
–0.3
–0.15
–0.1
–0.05
0
0.05
0.1
0.15
0.2



IC-10000-3-25
AR
LP
BL
BO
DD
NA
IB
AP
CA
EX
CO
MC
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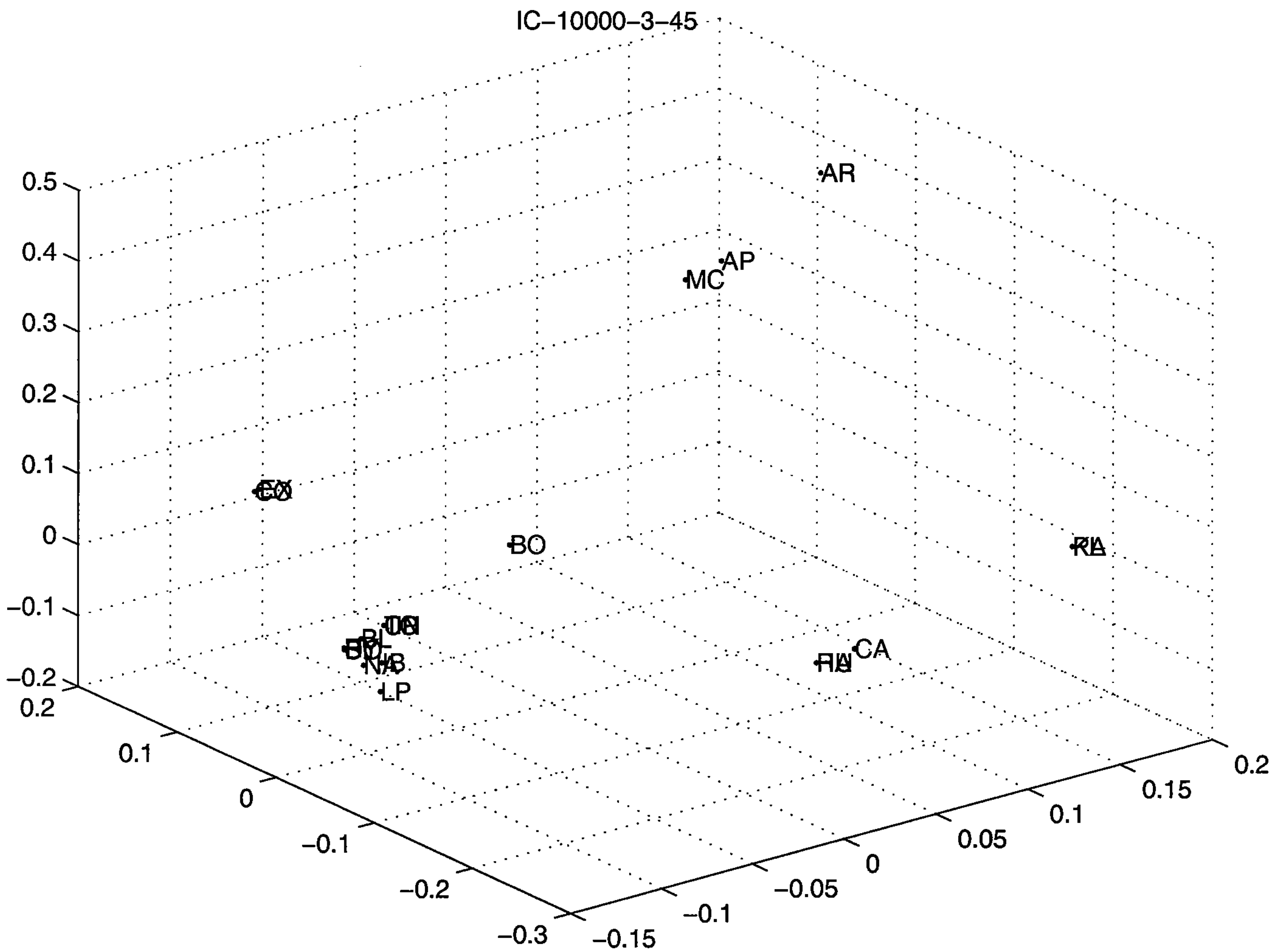
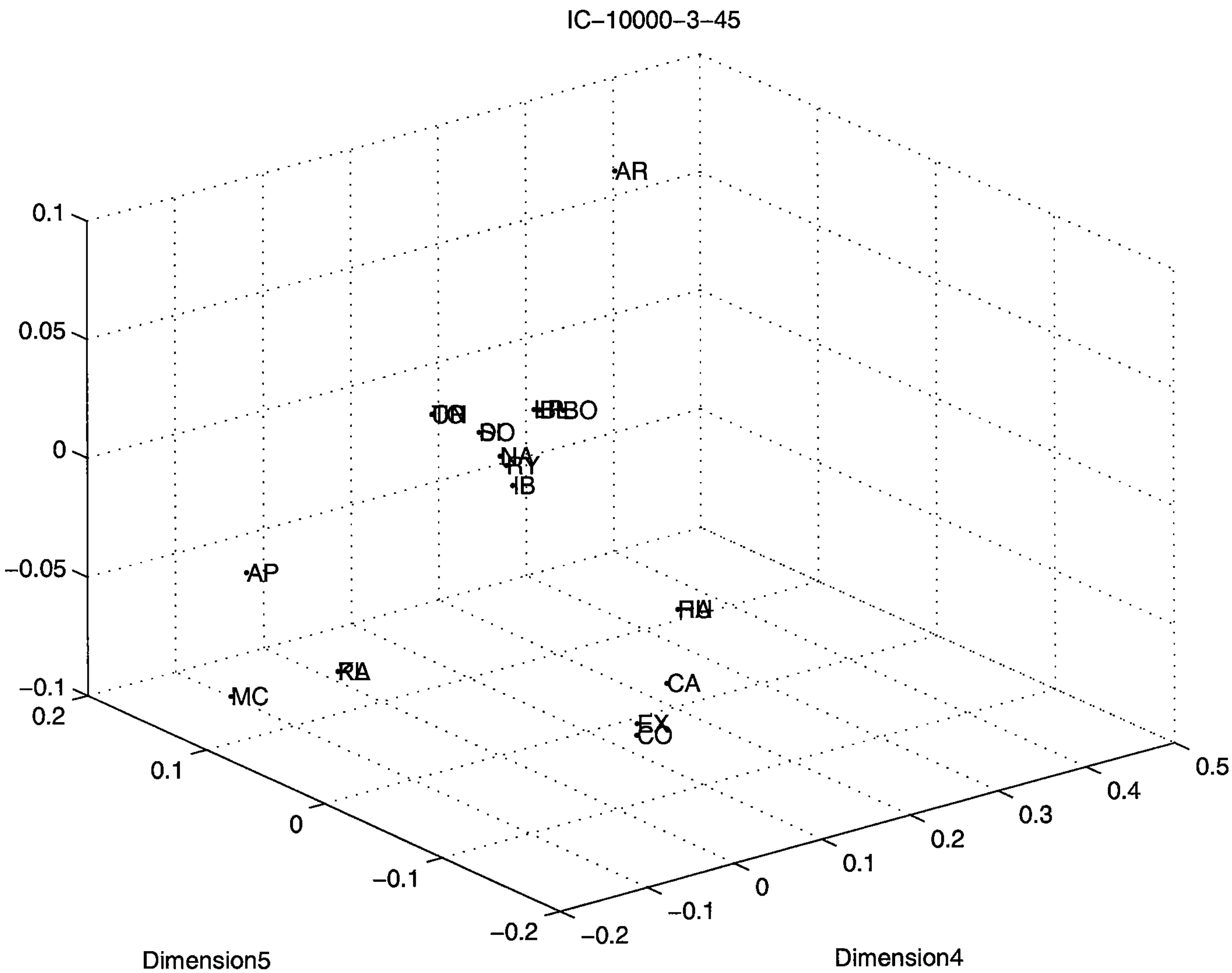
0.05
0
-0.05
-0.1
-0.15
0.2
0.1
0
-0.1
-0.2
-0.2
-0.1
0
0.1
0.2
0.3
0.4
0.5
Dimension5
Dimension4



IC–10000-3-45
AR
AP
MC
CO
BO
RL
CA
HA
LP
0.5
0.4
0.3
0.2
0.1
0
–0.1
–0.2
0.2
0.1
0
–0.1
–0.2
–0.3
–0.15
–0.1
–0.05
0
0.05
0.1
0.15
0.2


IC–10000–3–45
AR
BO
DO
NA
IB
AP
MC
CA
EX
CO
0.1
0.05
0
–0.05
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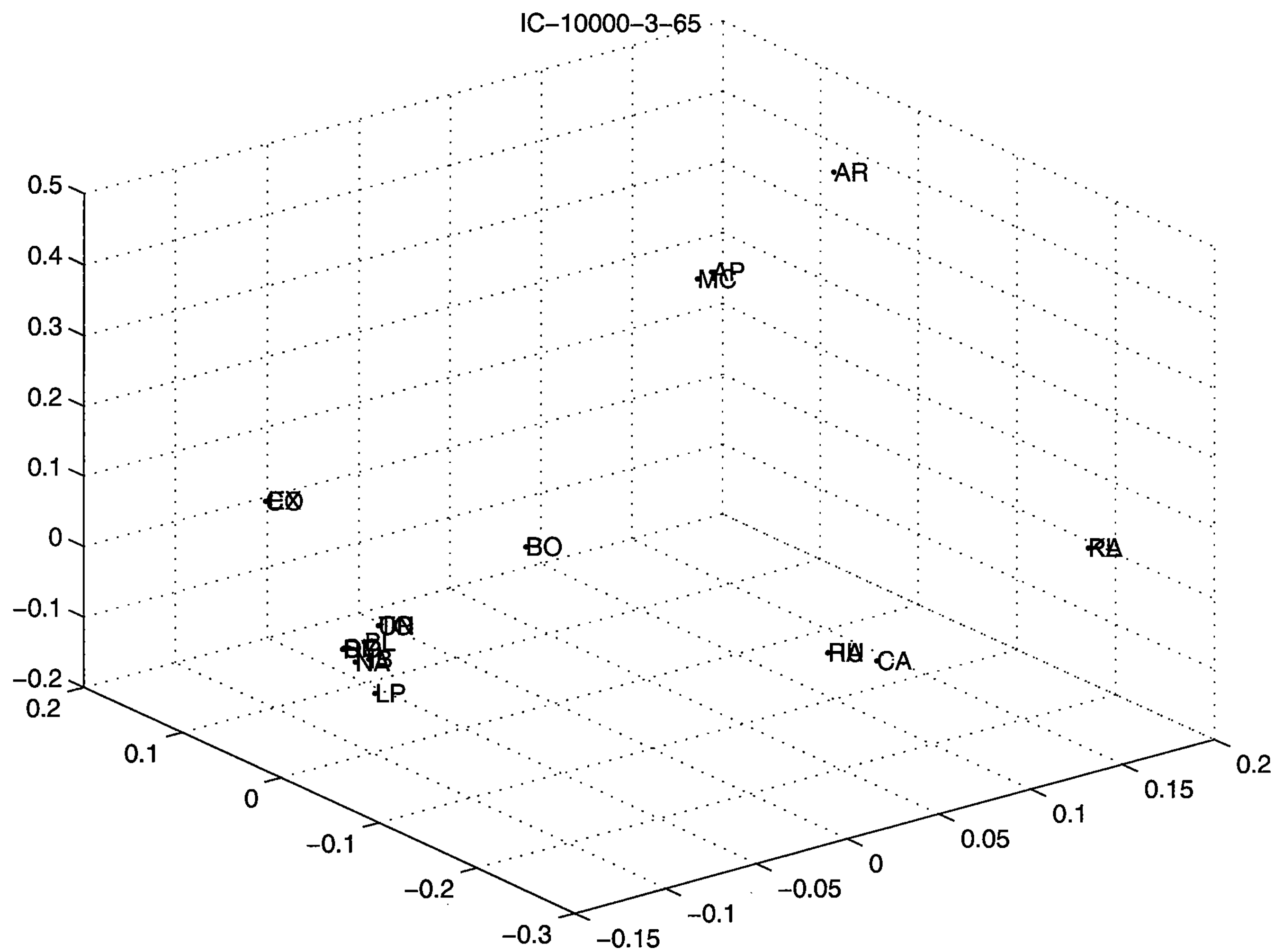
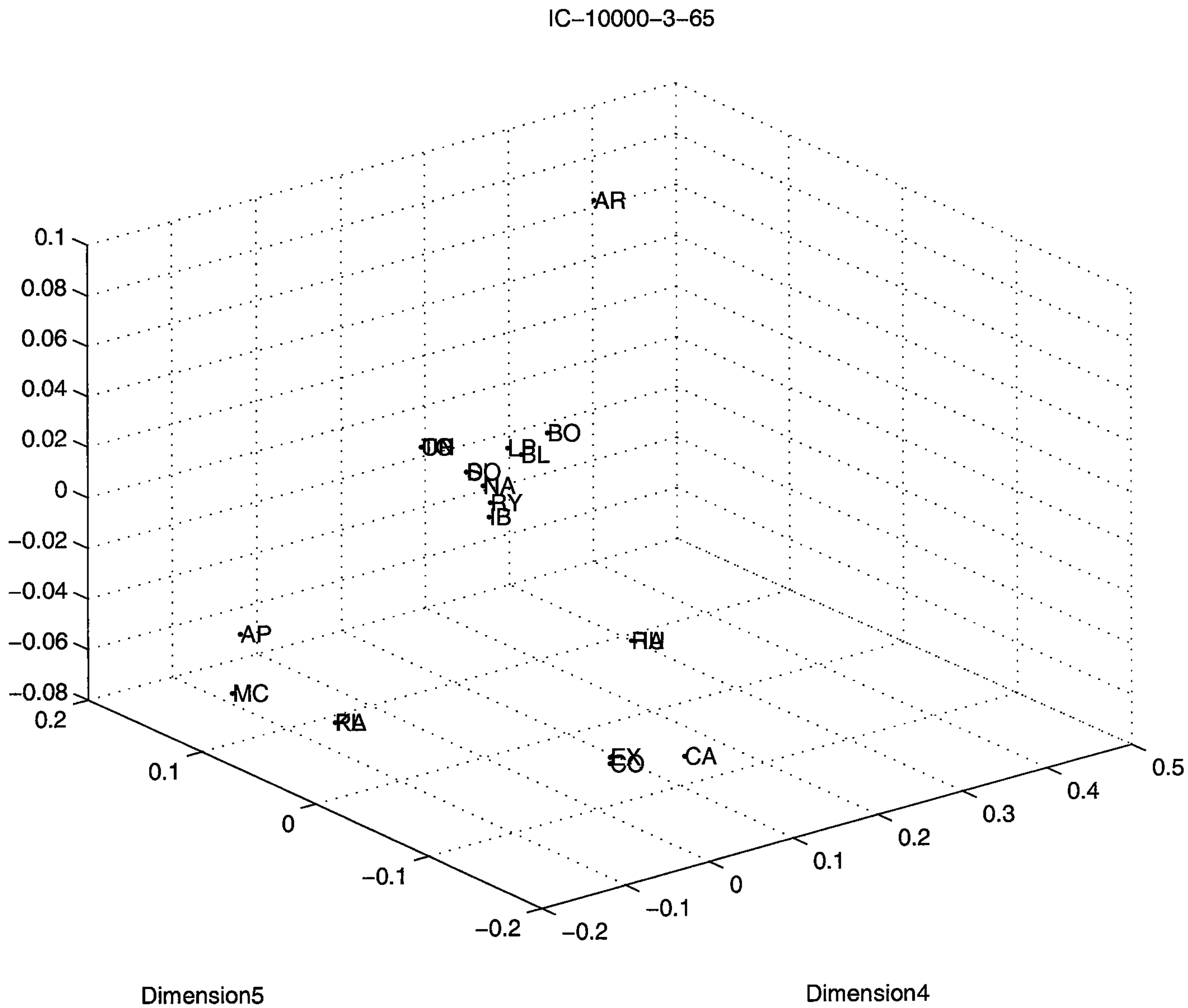
0.2
0.1
0
–0.1
–0.2
–0.2
–0.1
0
0.1
0.2
0.3
0.4
0.5
Dimension5
Dimension4



IC−10000−3−65
AR
AP
MC
CX
BO
RA
RU
CA
LP



IC-10000-3-65
AR
BO
LB
BL
DO
NA
RY
IB
AP
MC
EX
CO
CA
0.1
0.08
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0.04
0.02
0
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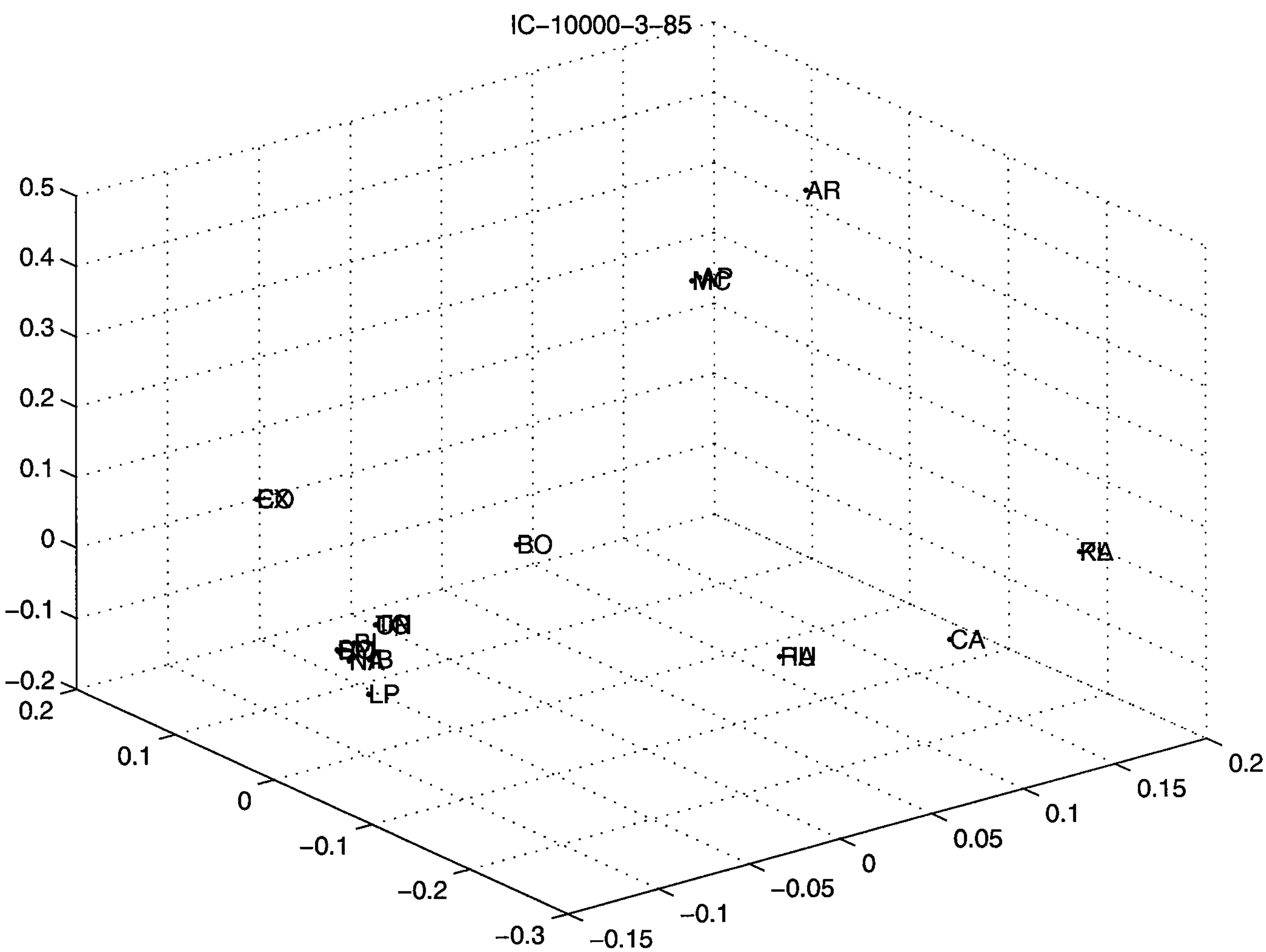
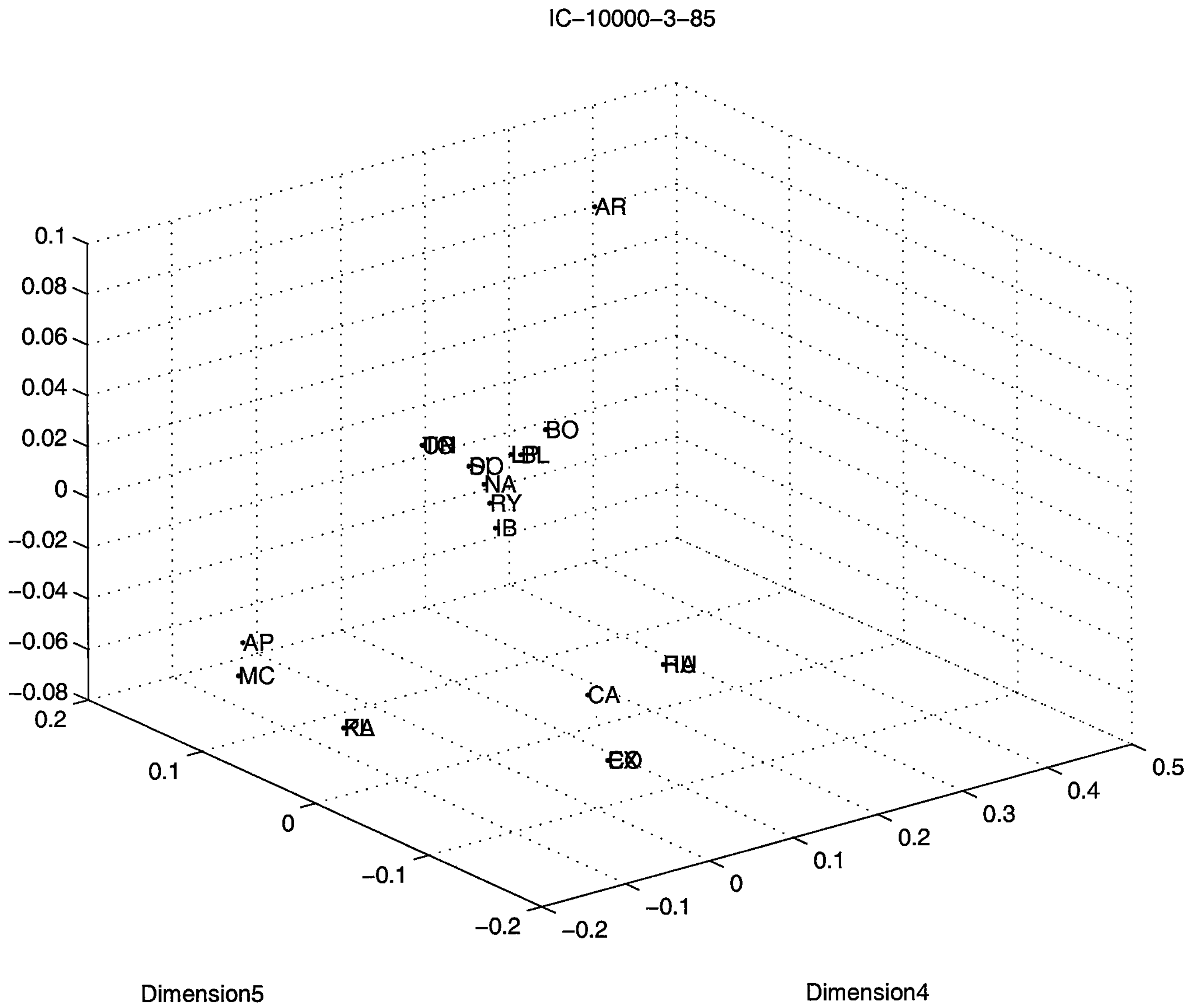
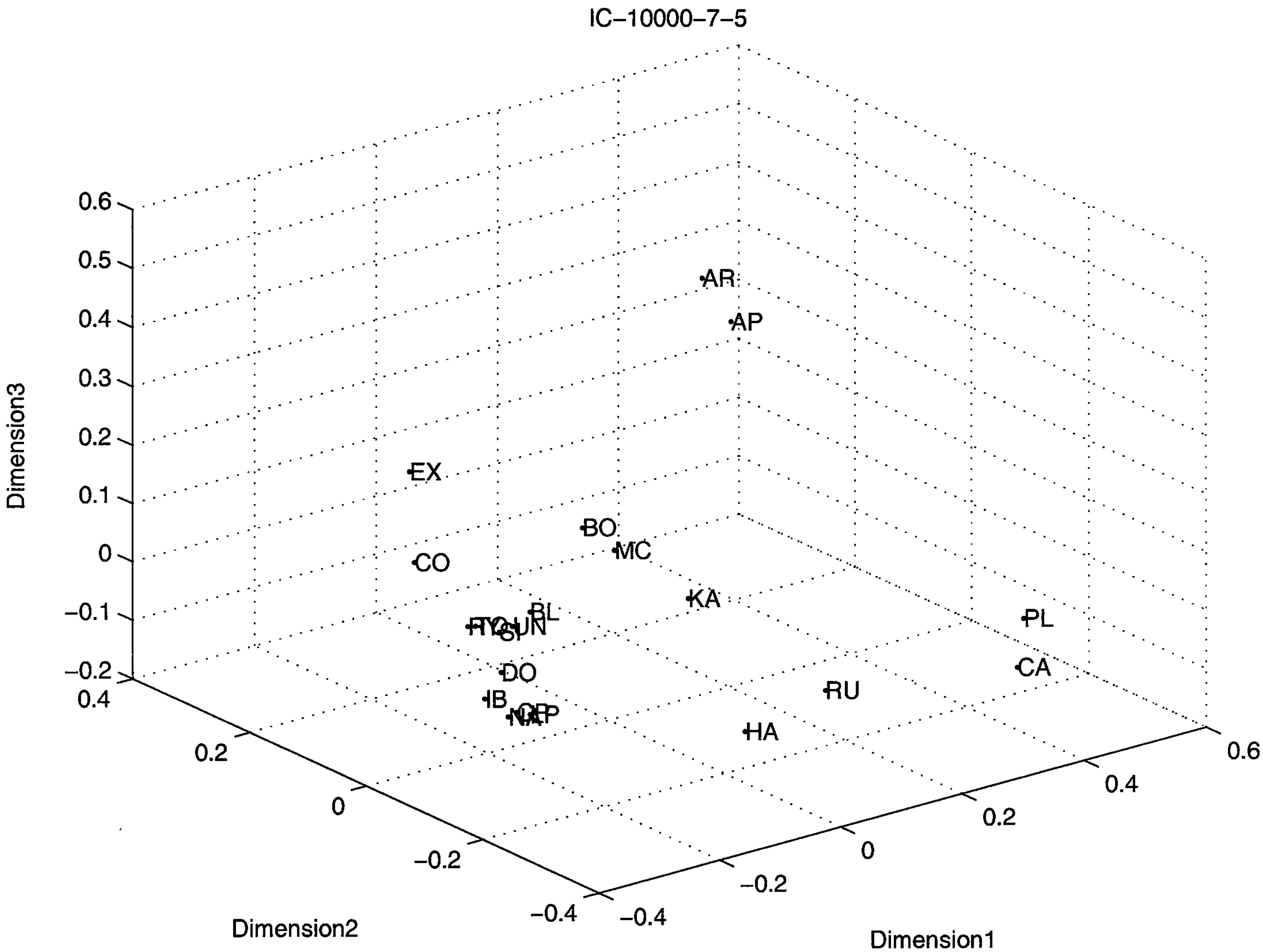
-0.08
0.2
0.1
0
-0.1
-0.2
-0.2
-0.1
0
0.1
0.2
0.3
0.4
0.5
Dimension5
Dimension4

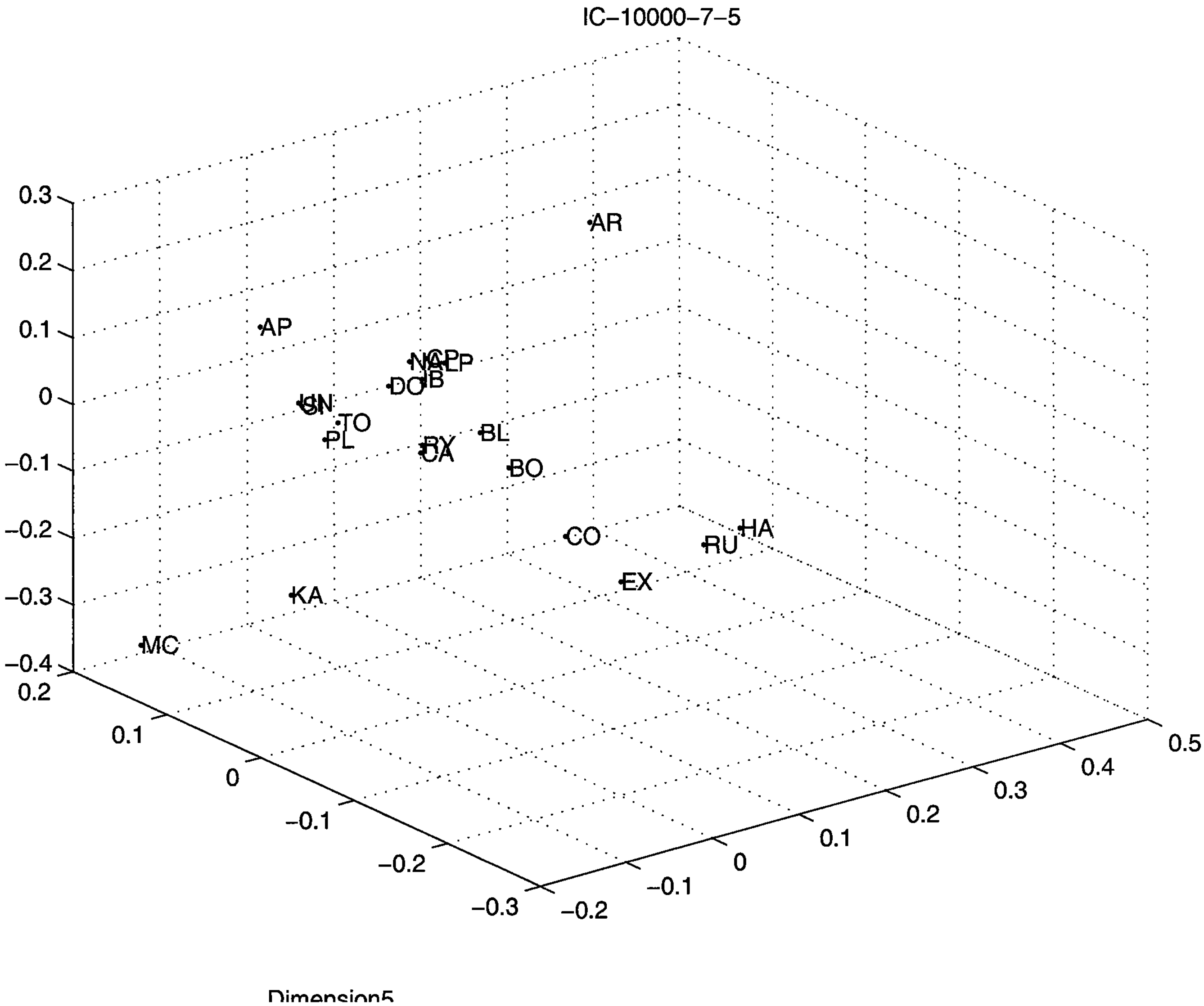


IC−10000−3−85
AR
MP
MC
CX
BO
RL
CA
RU
LP
0.5
0.4
0.3
0.2
0.1
0
−0.1
−0.2
0.2
0.1
0
−0.1
−0.2
−0.3
−0.15
−0.1
−0.05
0
0.05
0.1
0.15
0.2

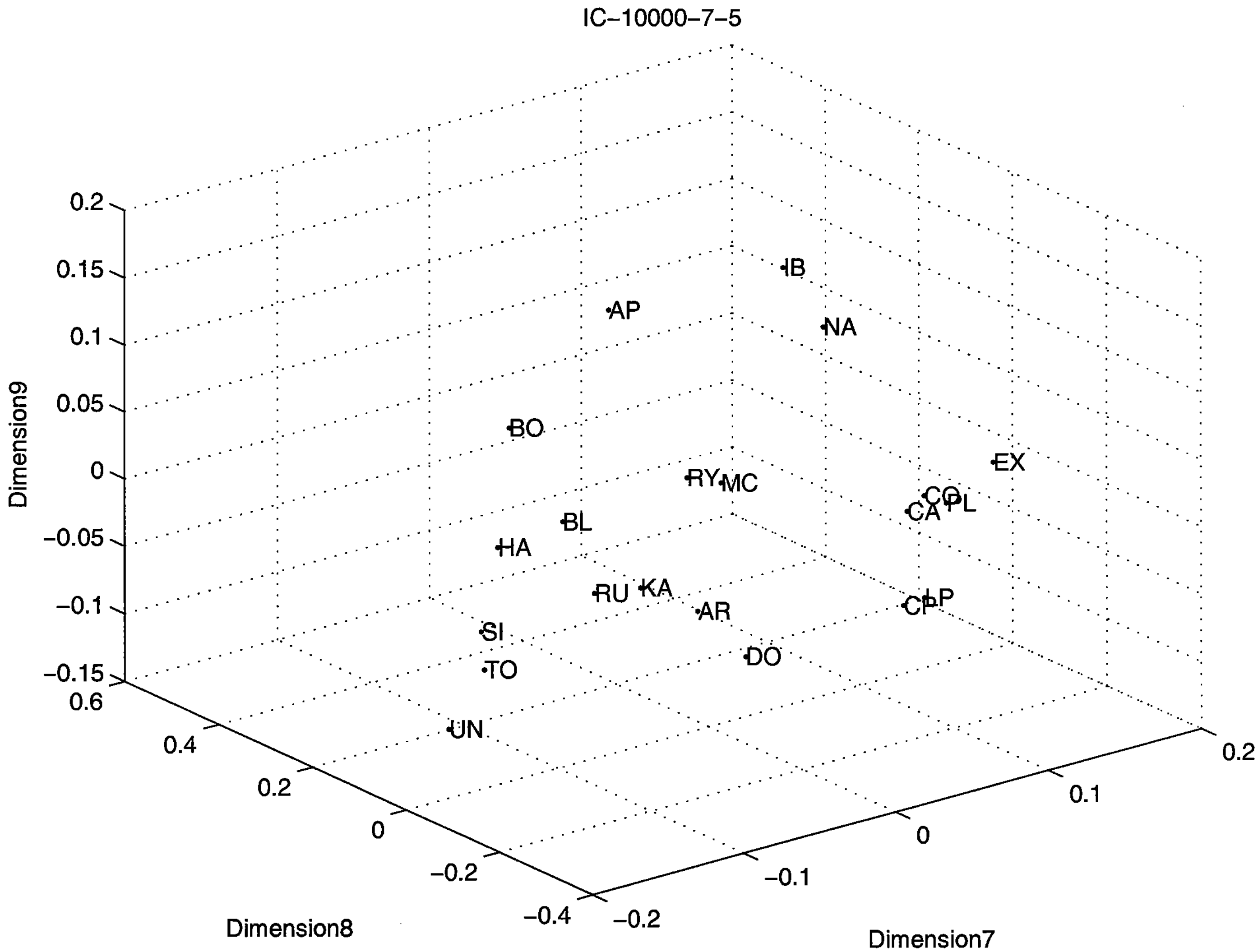

IC–10000–3–85
AR
BO
LBL
DO
NA
RY
IB
AP
MC
CA
Dimension5
Dimension4



IC−10000−7−5
Dimension3
Dimension2
Dimension1
0.6
0.5
0.4
0.3
0.2
0.1
0
−0.1
−0.2
0.4
0.2
0
−0.2
−0.4
−0.4
−0.2
0
0.2
0.4
0.6
AR
AP
EX
BO
MC
CO
KA
BL
PL
SI
UN
DO
CA
RU
IB
NA
HA



IC−10000−7−5
0.3
0.2
0.1
0
−0.1
−0.2
−0.3
−0.4
0.2
0.1
0
−0.1
−0.2
−0.3
−0.2
−0.1
0
0.1
0.2
0.3
0.4
0.5
AR
AP
LP
IB
DO
TO
PL
CA
BL
BO
CO
HA
RU
EX
KA
MC
Dimension5



IC–10000–7–5
Dimension9
0.2
0.15
0.1
0.05
0
−0.05
−0.1
−0.15
Dimension8
0.6
0.4
0.2
0
−0.2
−0.4
Dimension7
−0.2
−0.1
0
0.1
0.2
IB
AP
NA
BO
RY
MC
EX
CO
PL
CA
BL
HA
RU
KA
AR
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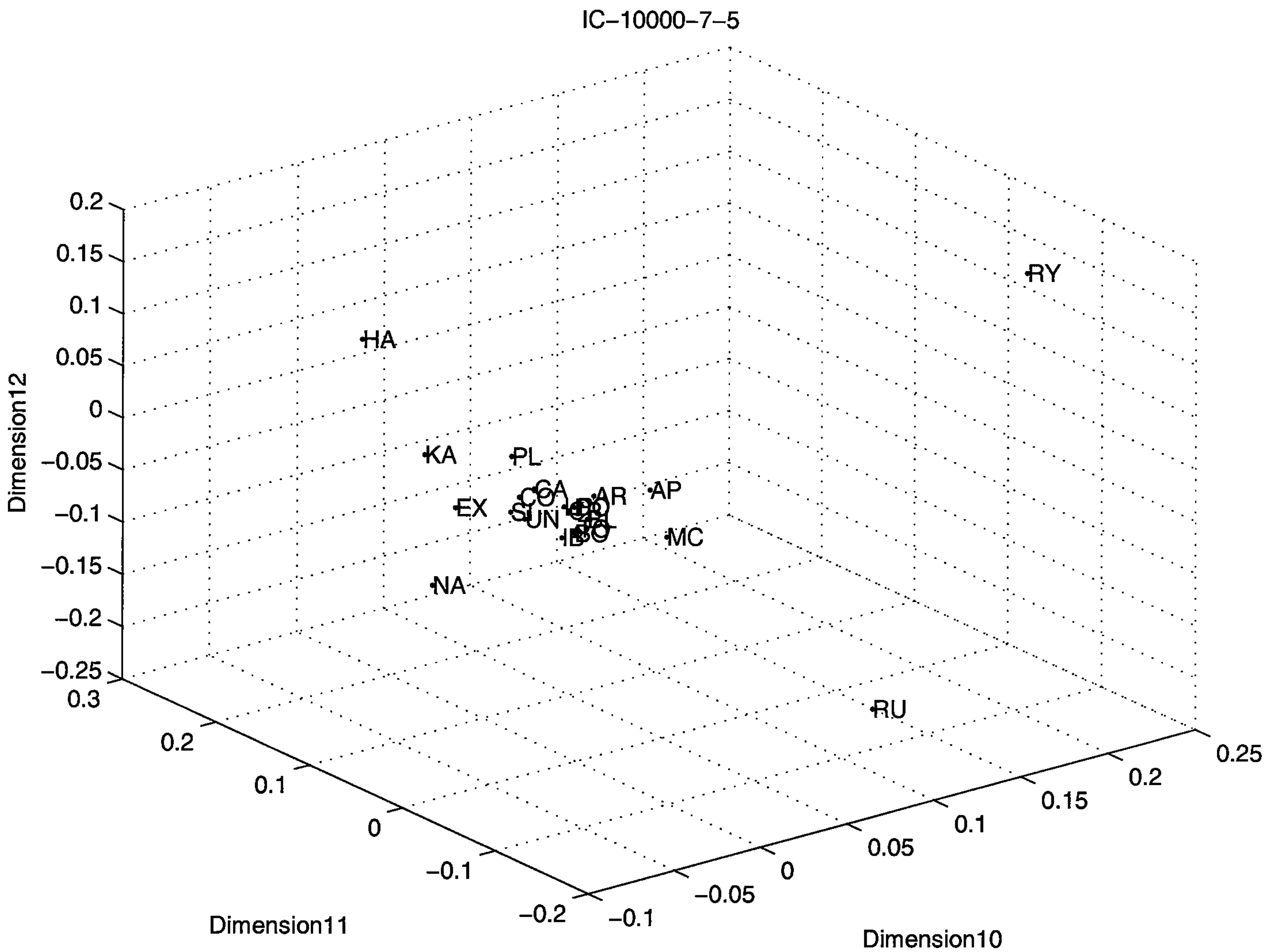
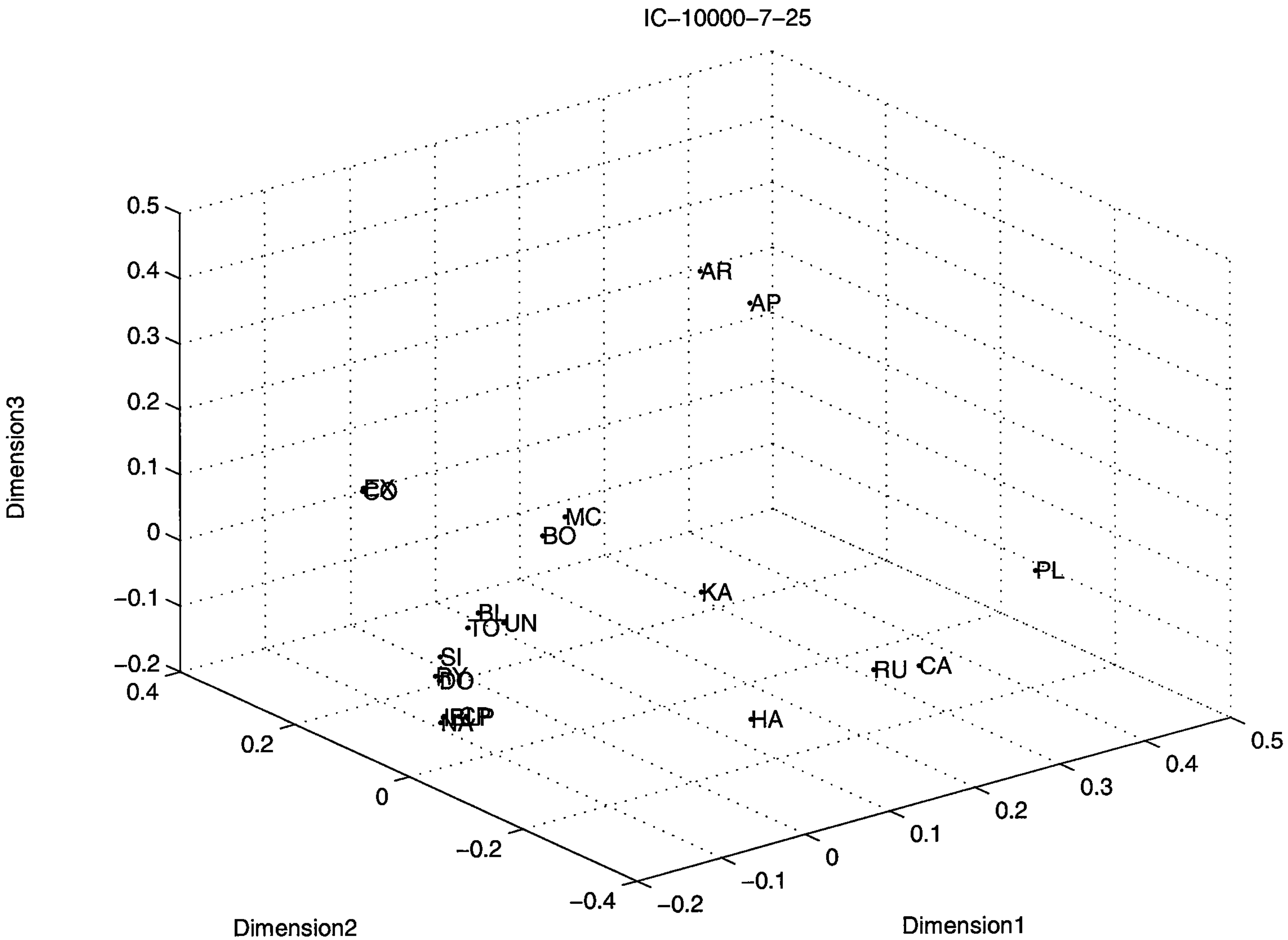
LP
SI
TO
DO
UN

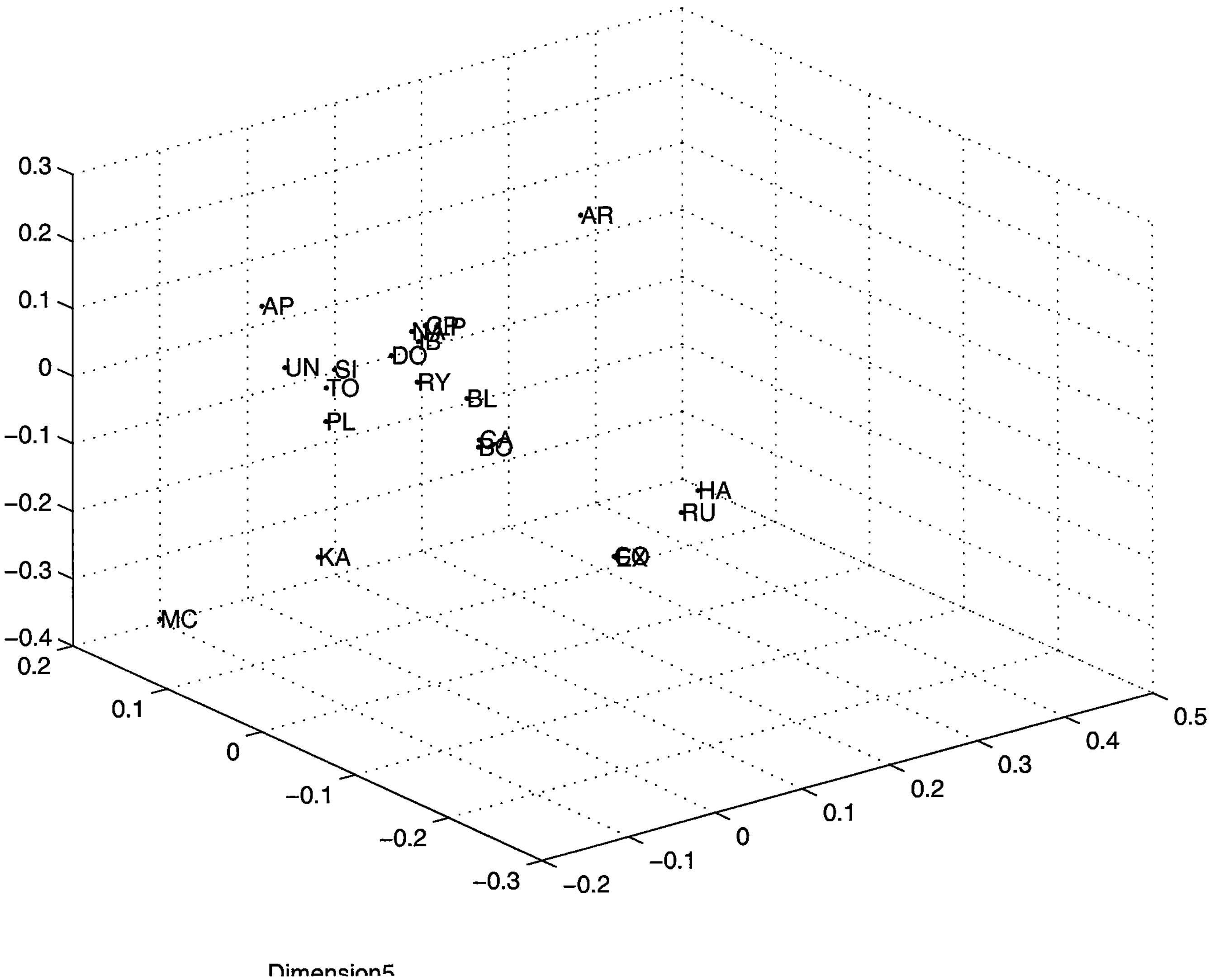


IC−10000−7−5
Dimension12
Dimension11
Dimension10
HA
KA
PL
CA
CO
EX
SU
UN
AR
AP
IB
MC
NA
RY
RU



IC−10000−7−25
Dimension3
Dimension2
Dimension1
AR
AP
EX
CO
MC
BO
PL
KA
BI
TO
UN
SI
RY
DO
IR
CL
P
NA
RU
CA
HA

IC–10000–7–25



AR
AP
CP
NA
LP
JB
DO
UN
SI
TO
RY
BL
PL
CA
BO
HA
RU
KA
CO
EX
MC
0.3
0.2
0.1
0
−0.1
−0.2
−0.3
−0.4
0.2
0.1
0
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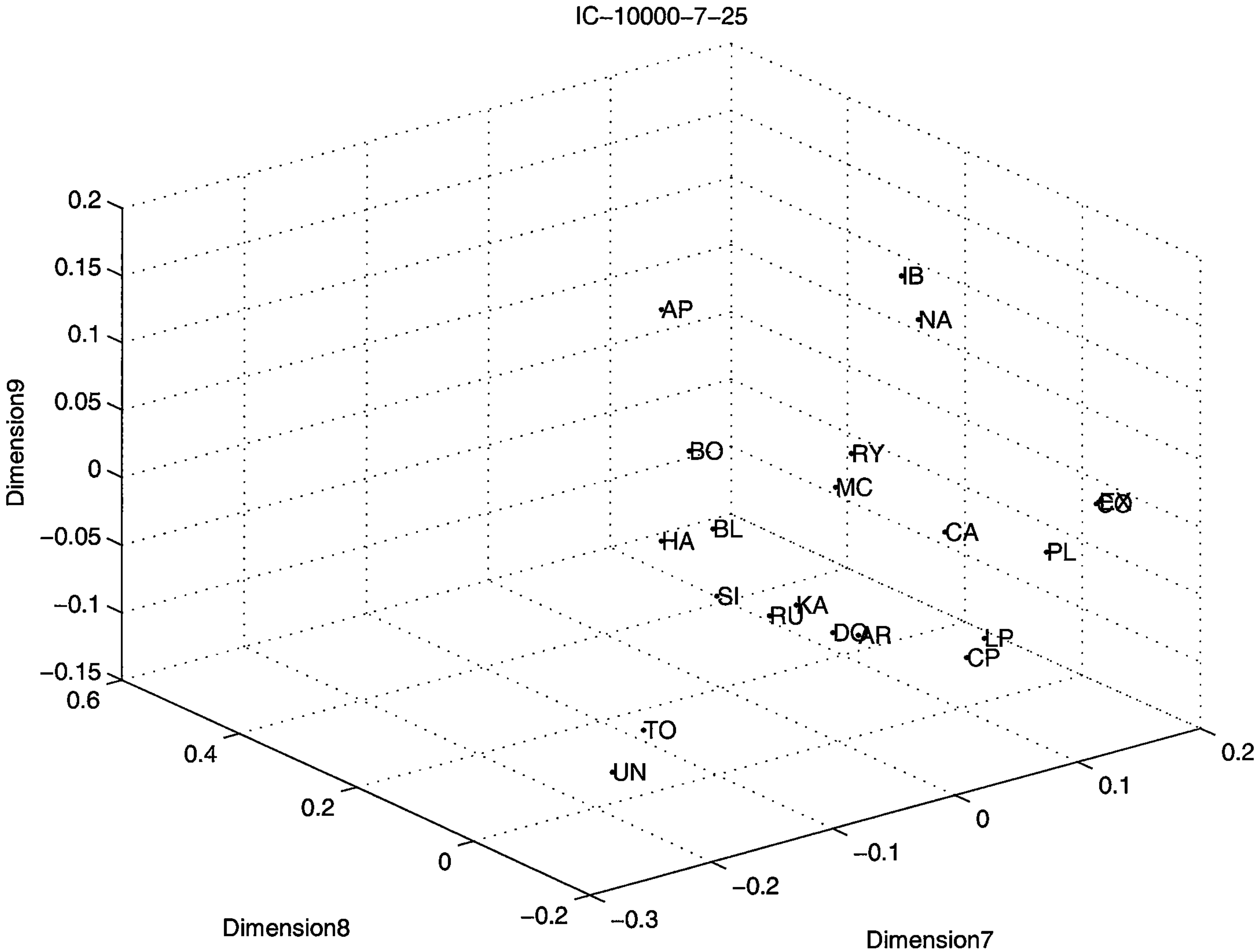

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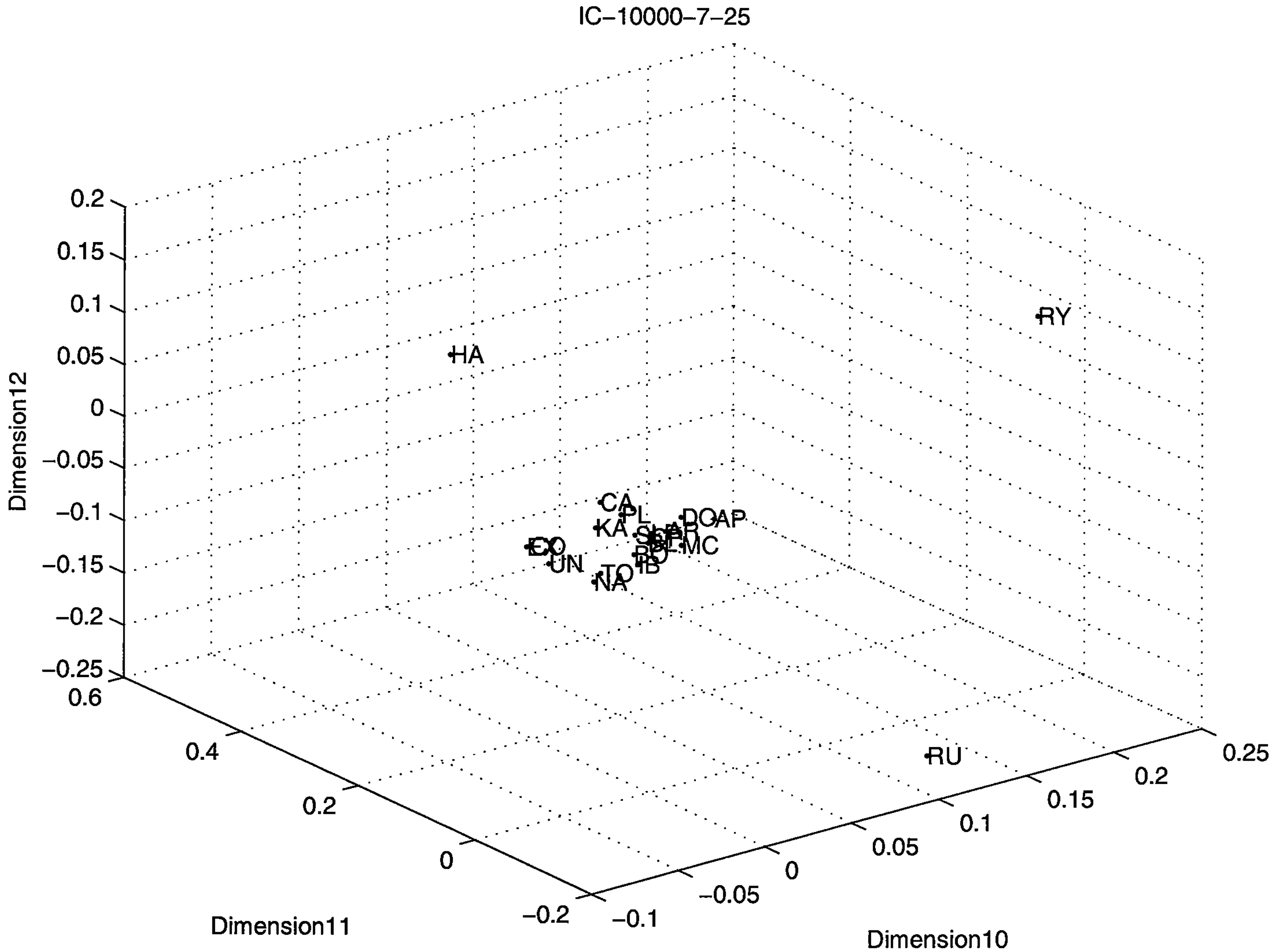

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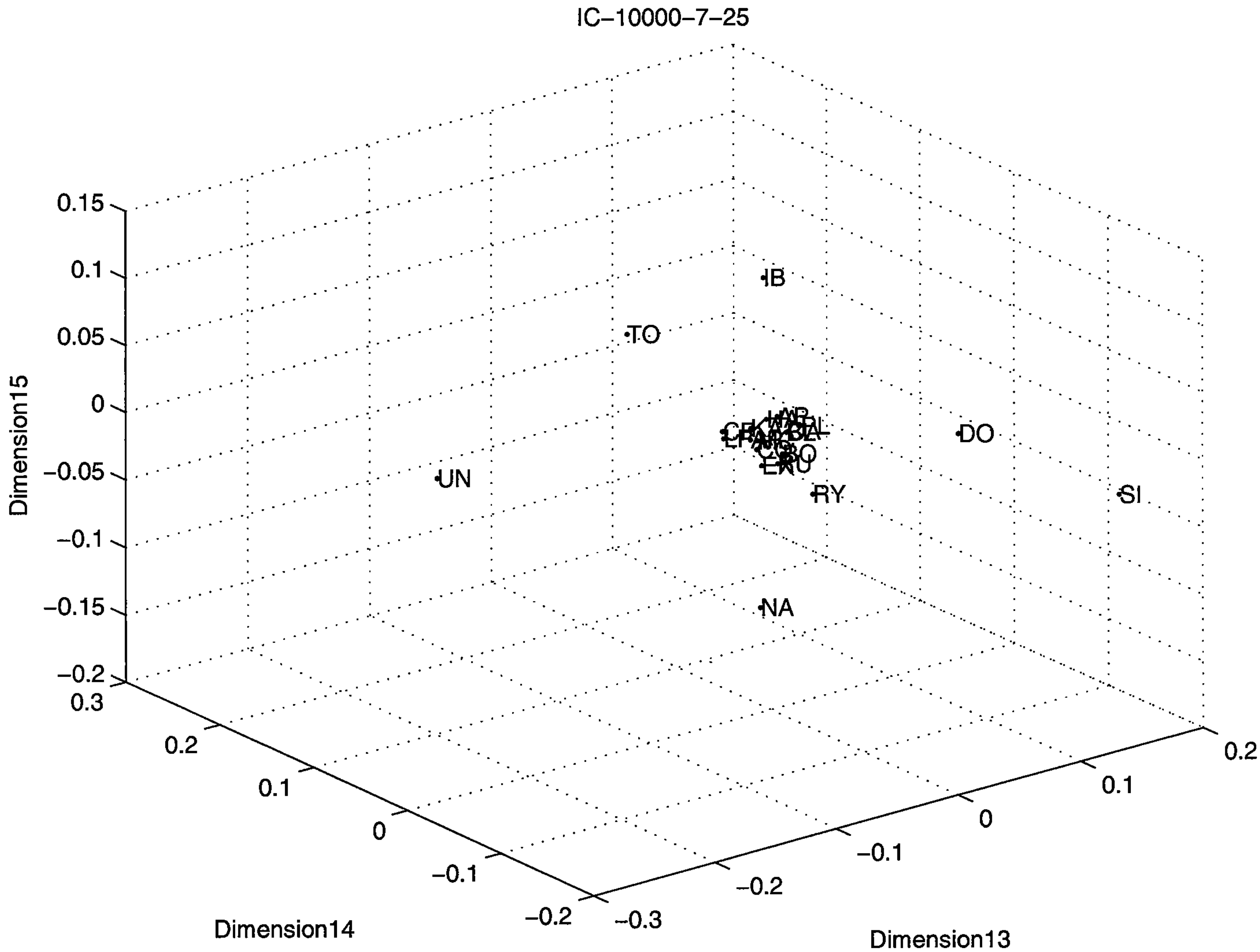

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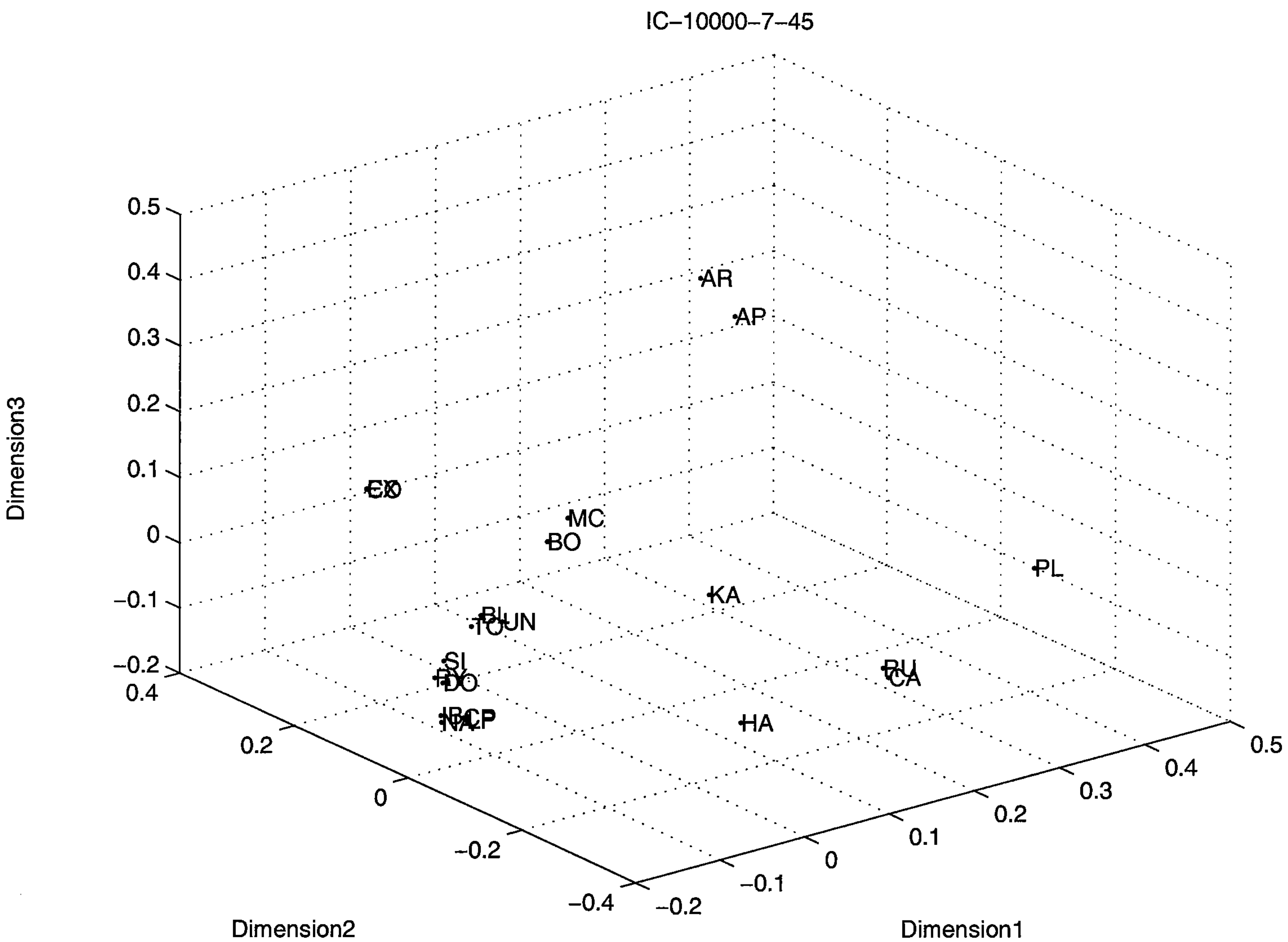

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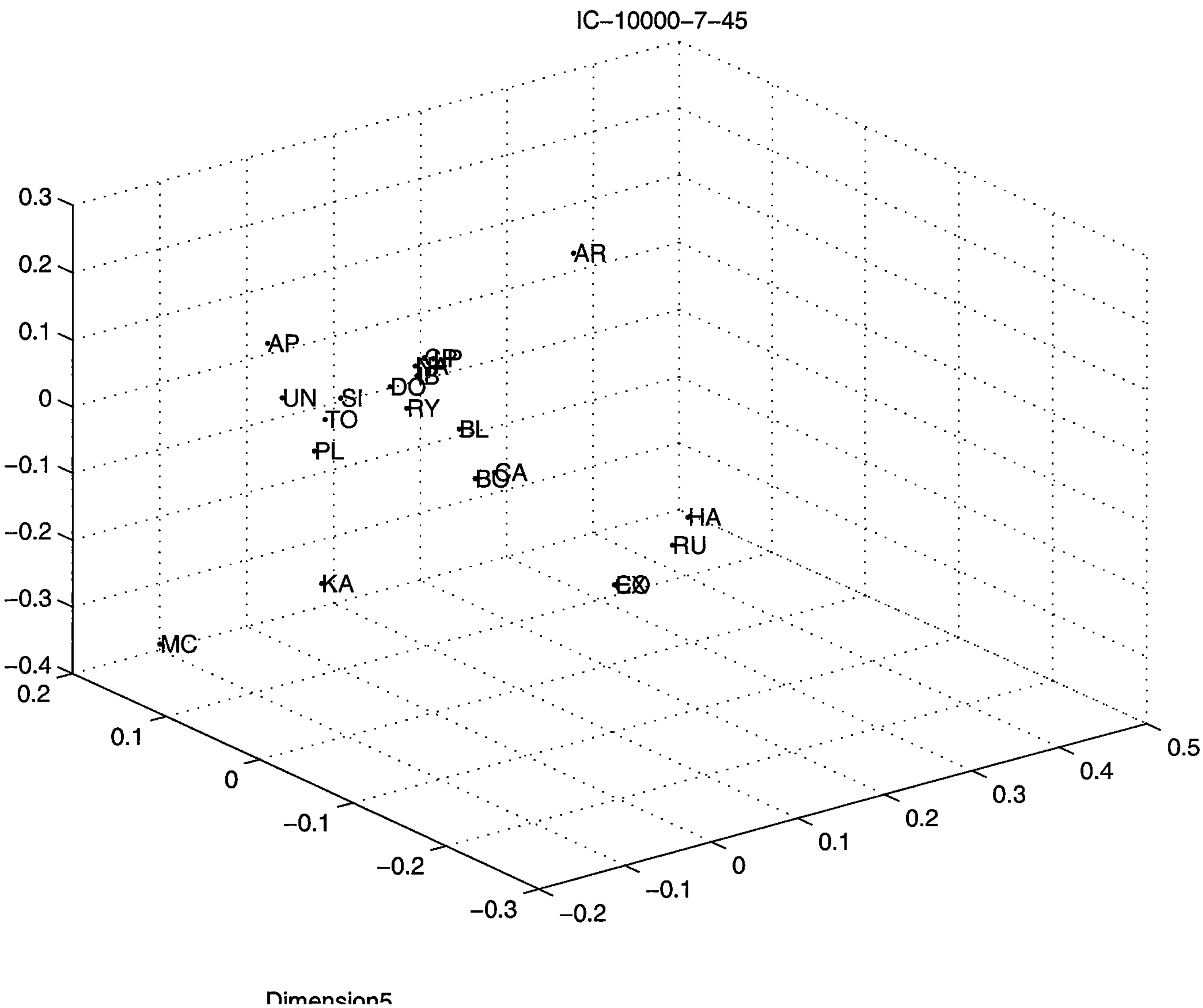
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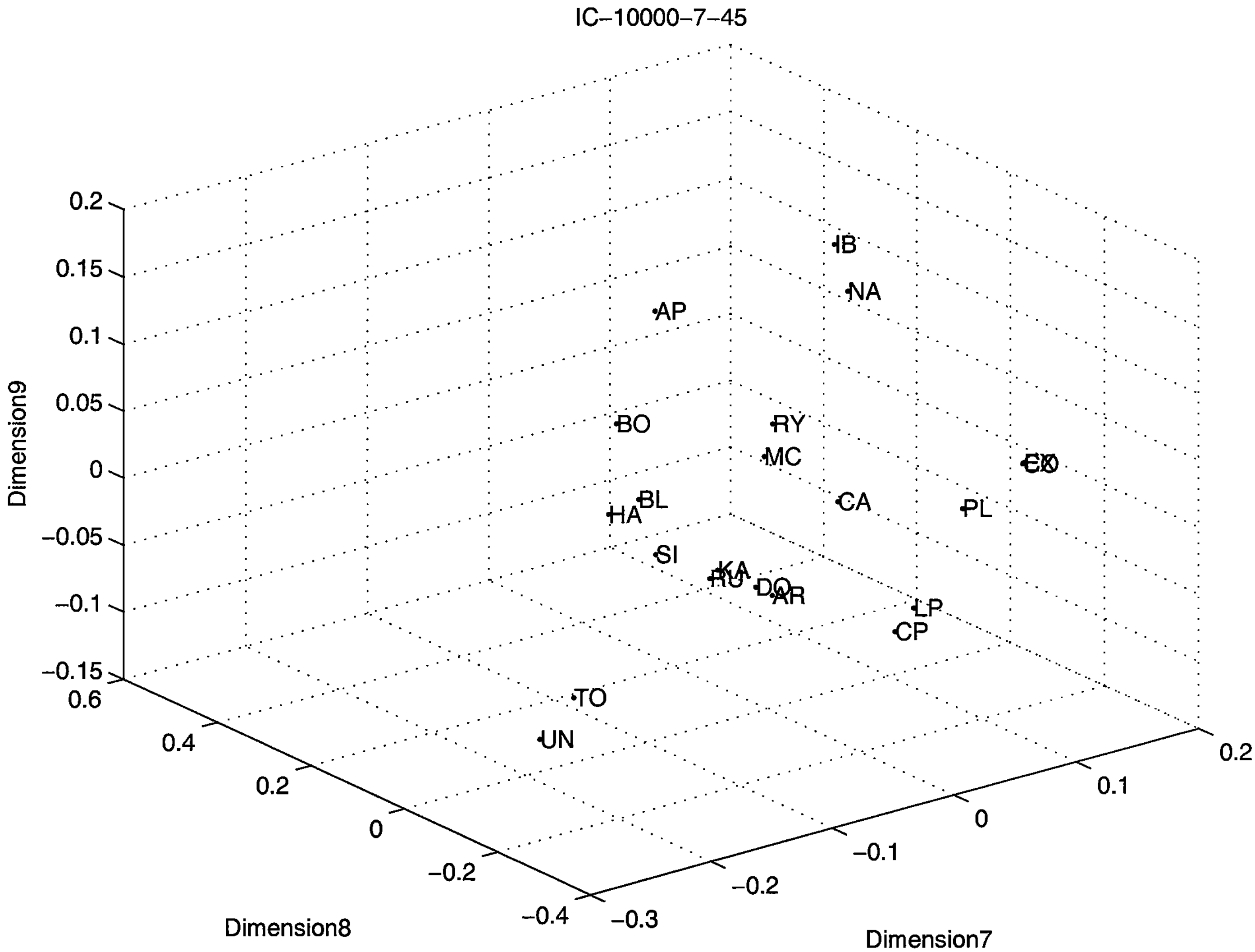
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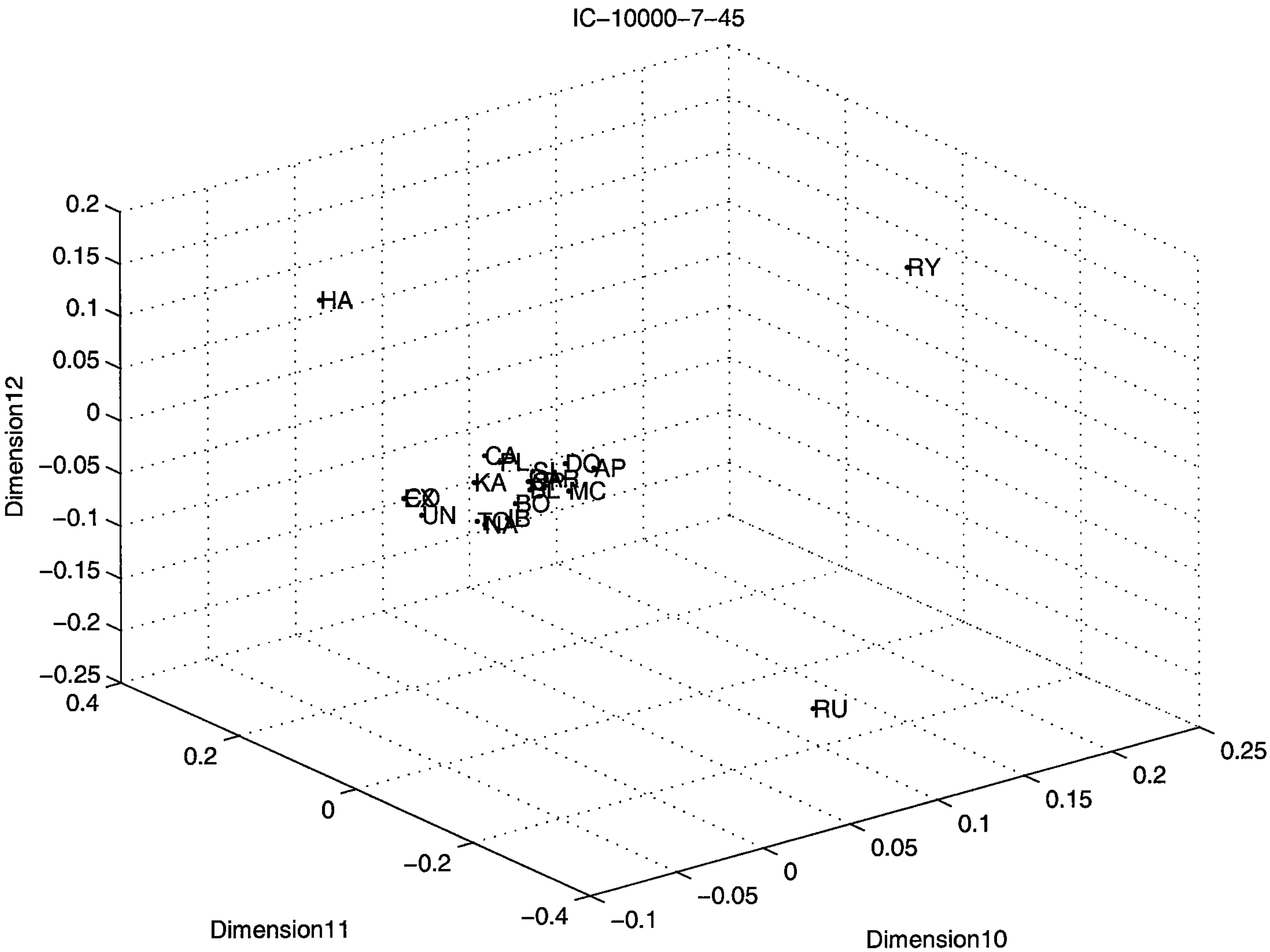
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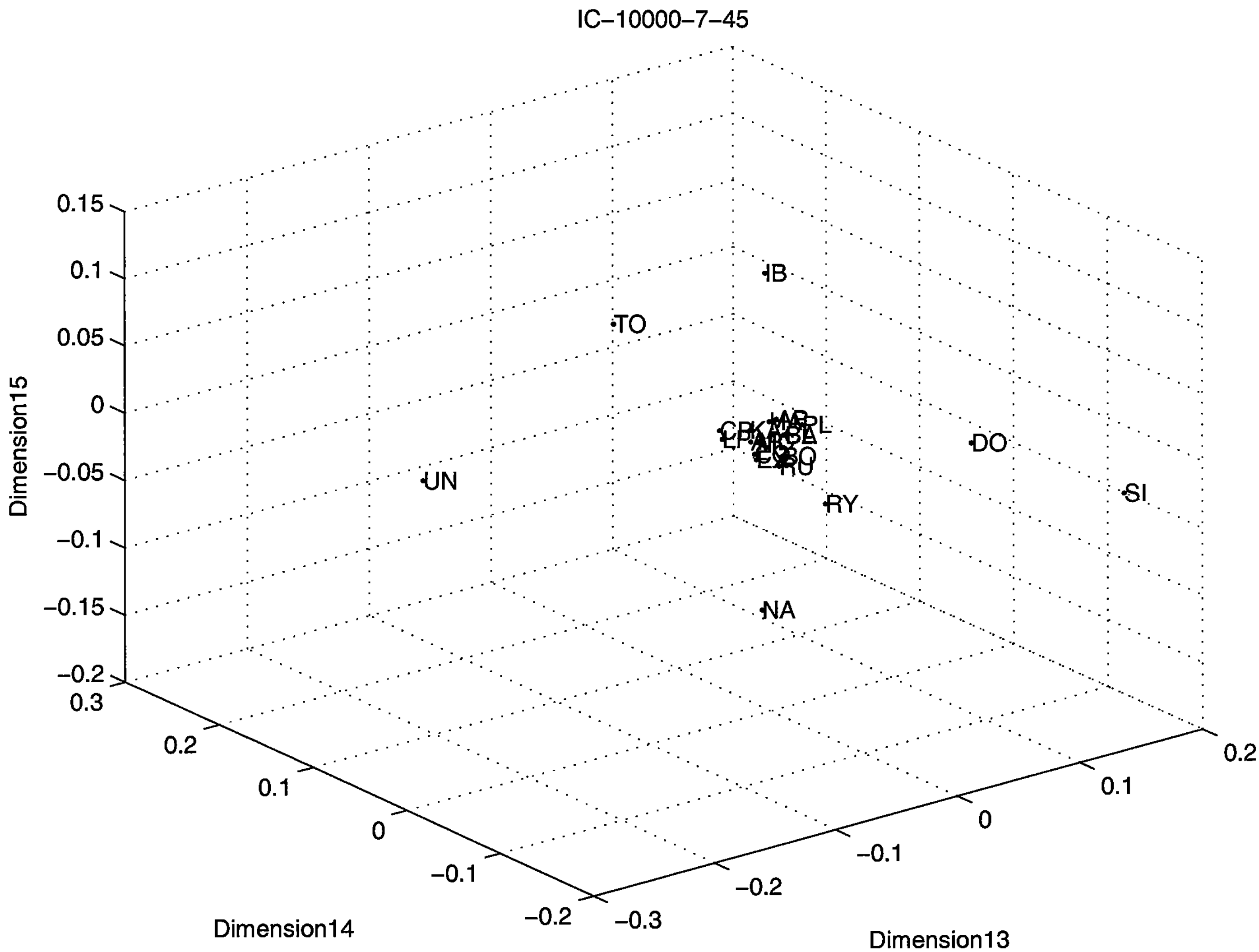
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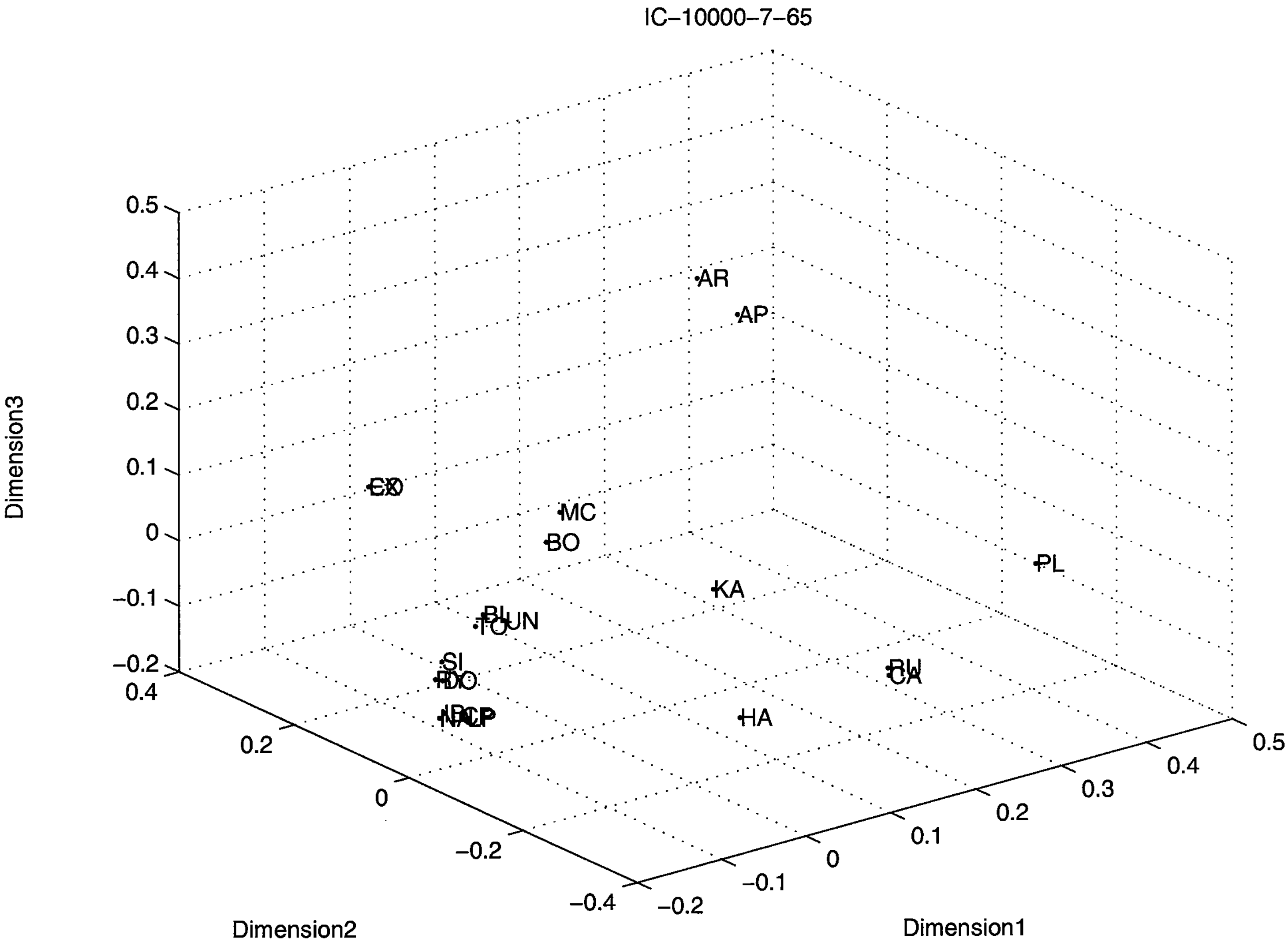
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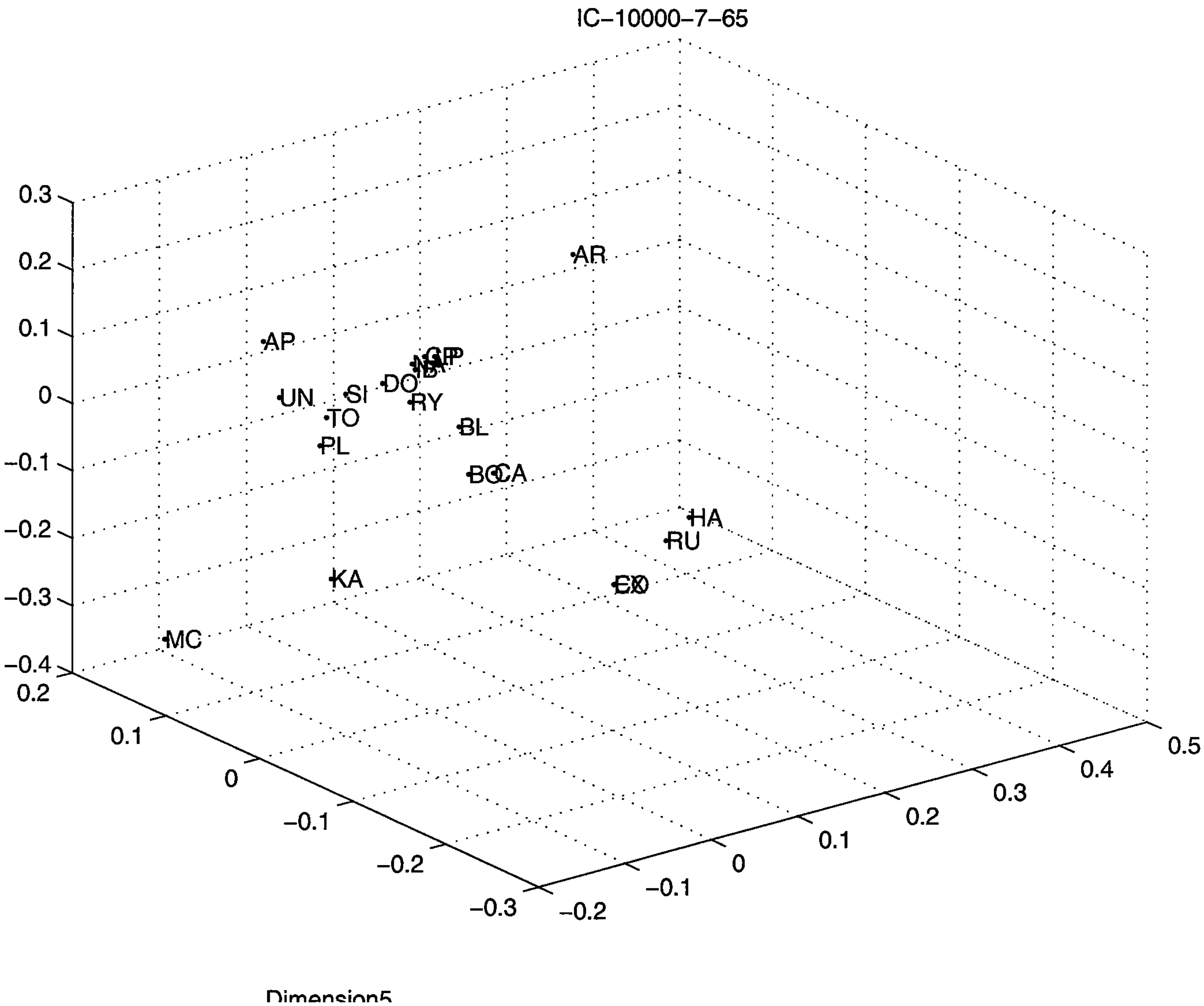
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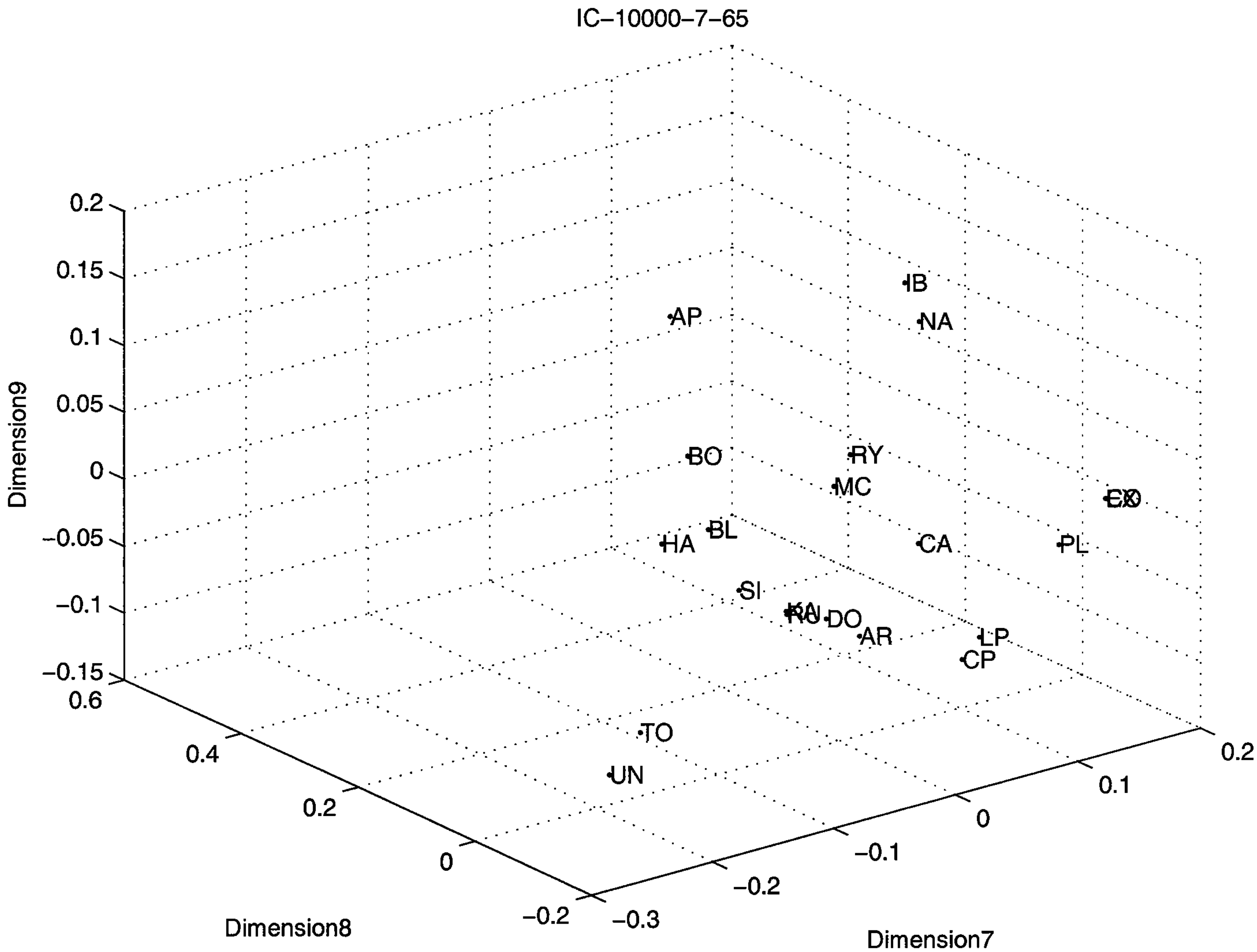

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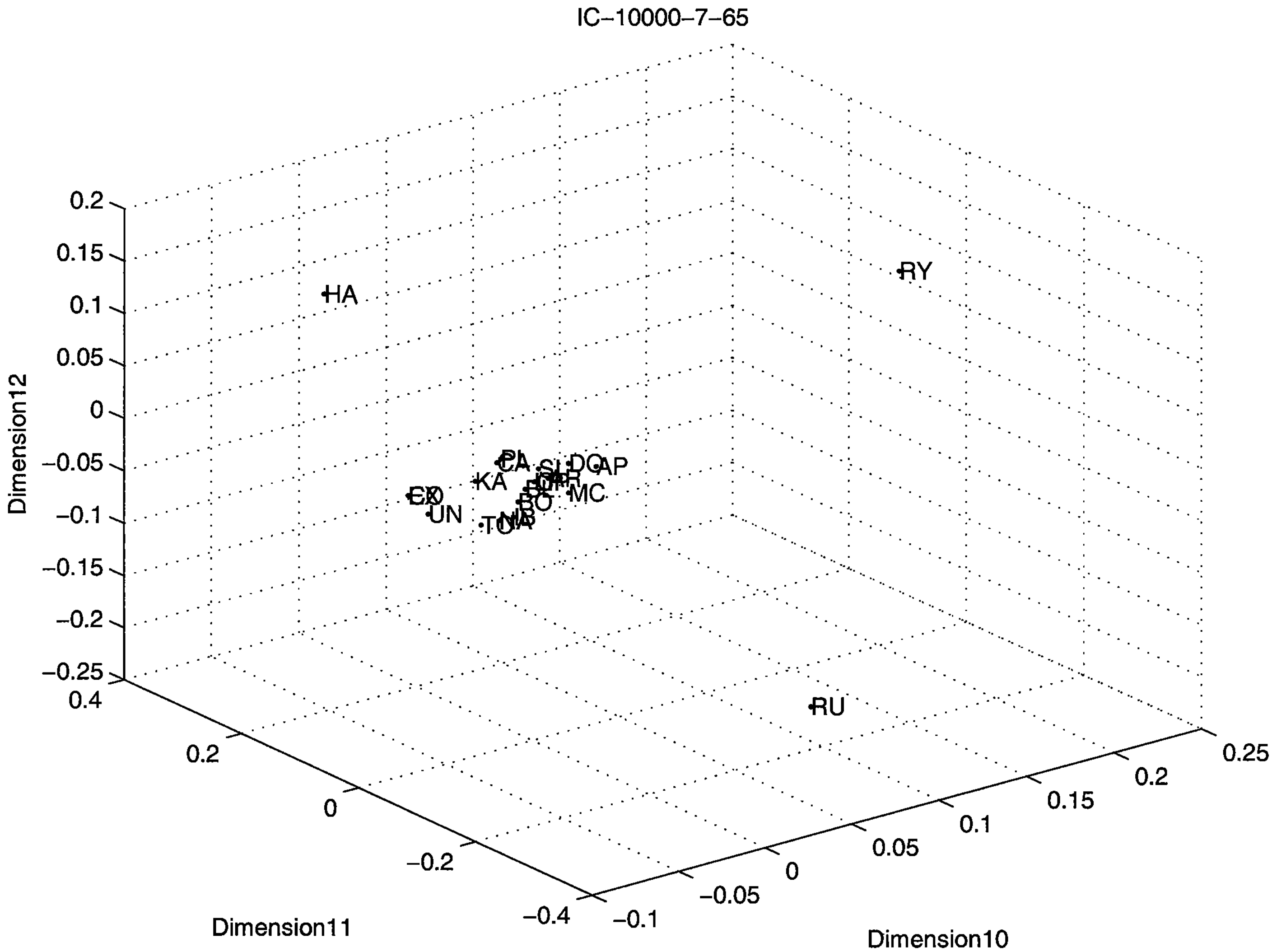

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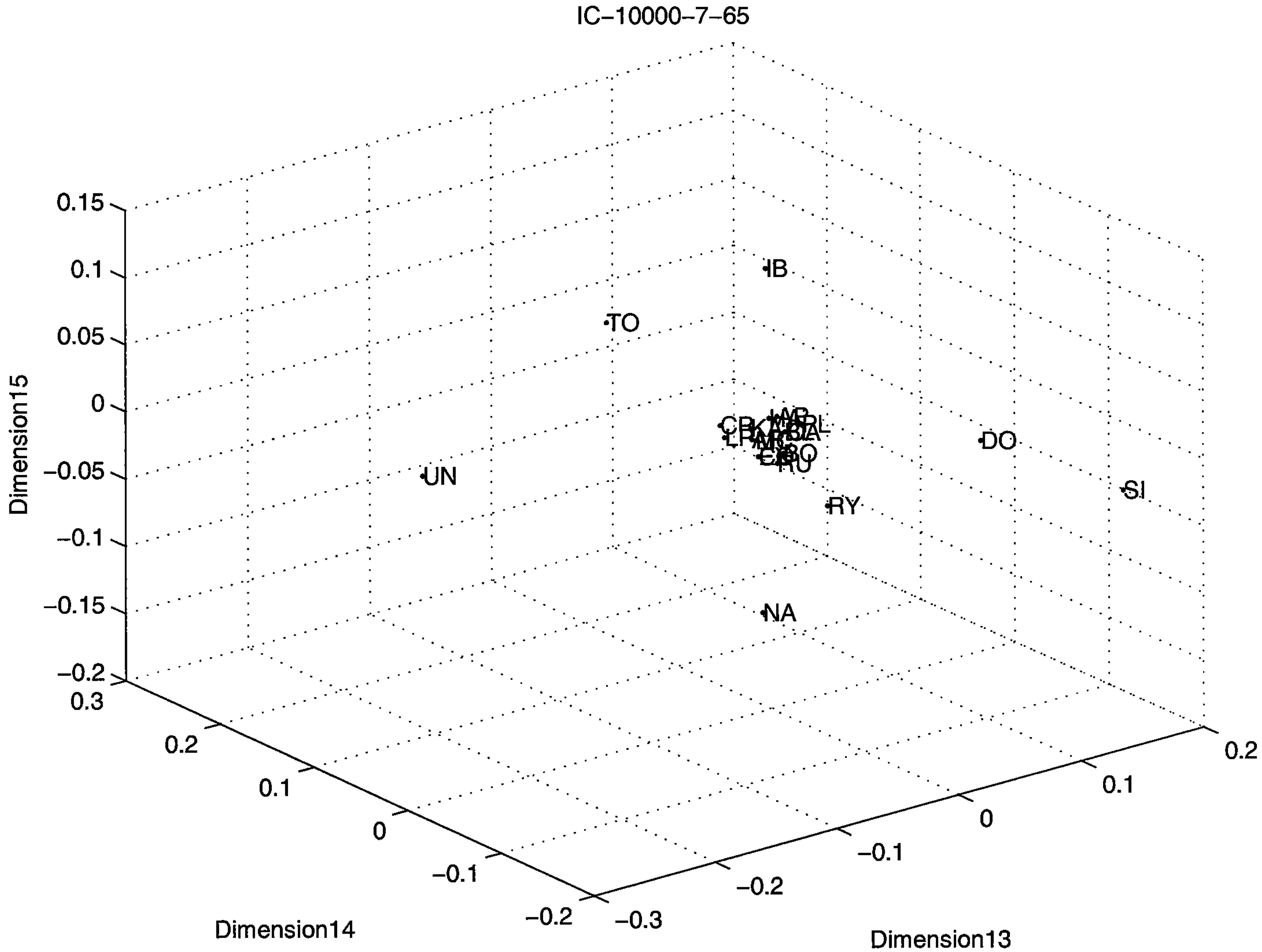

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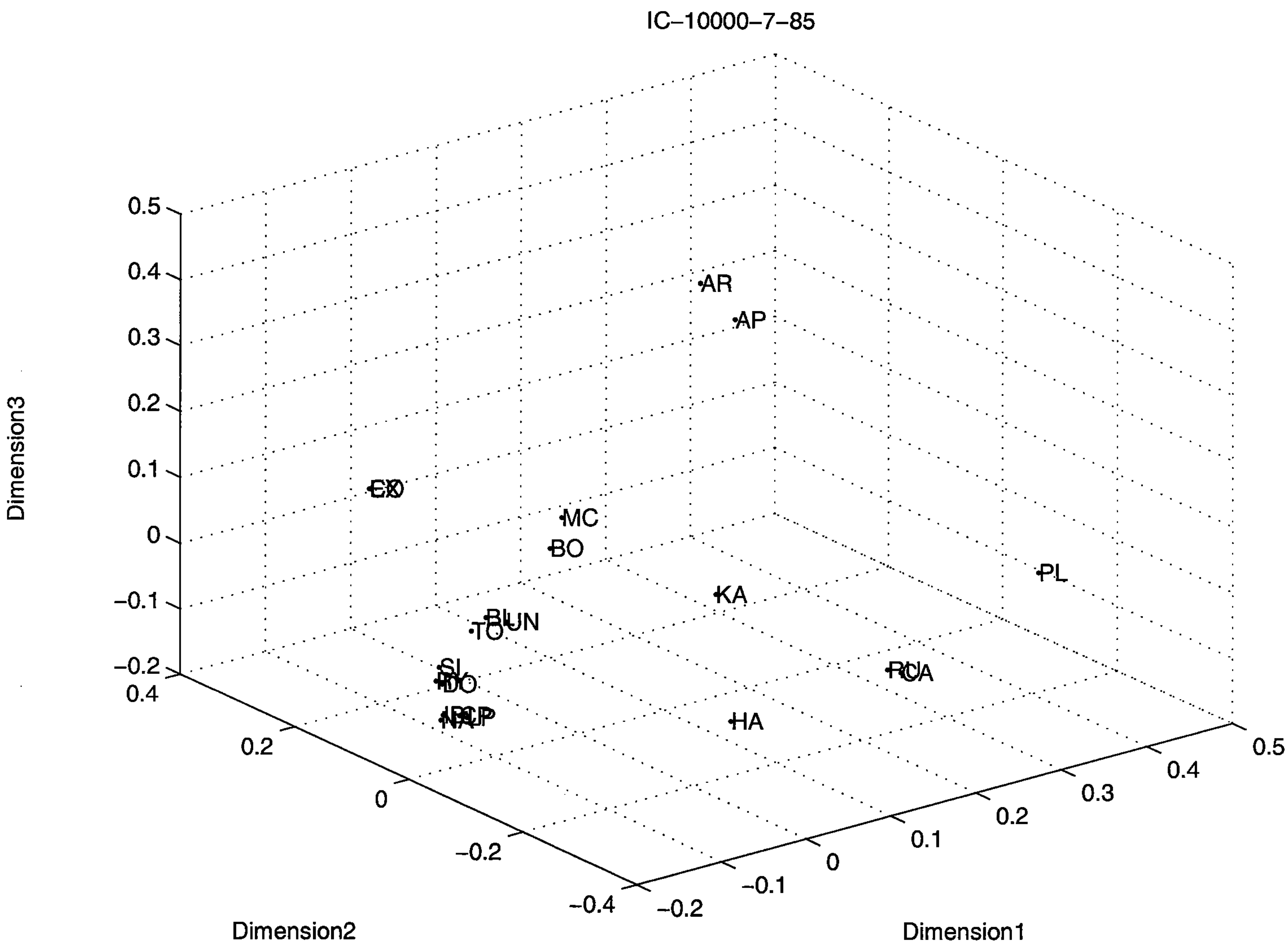
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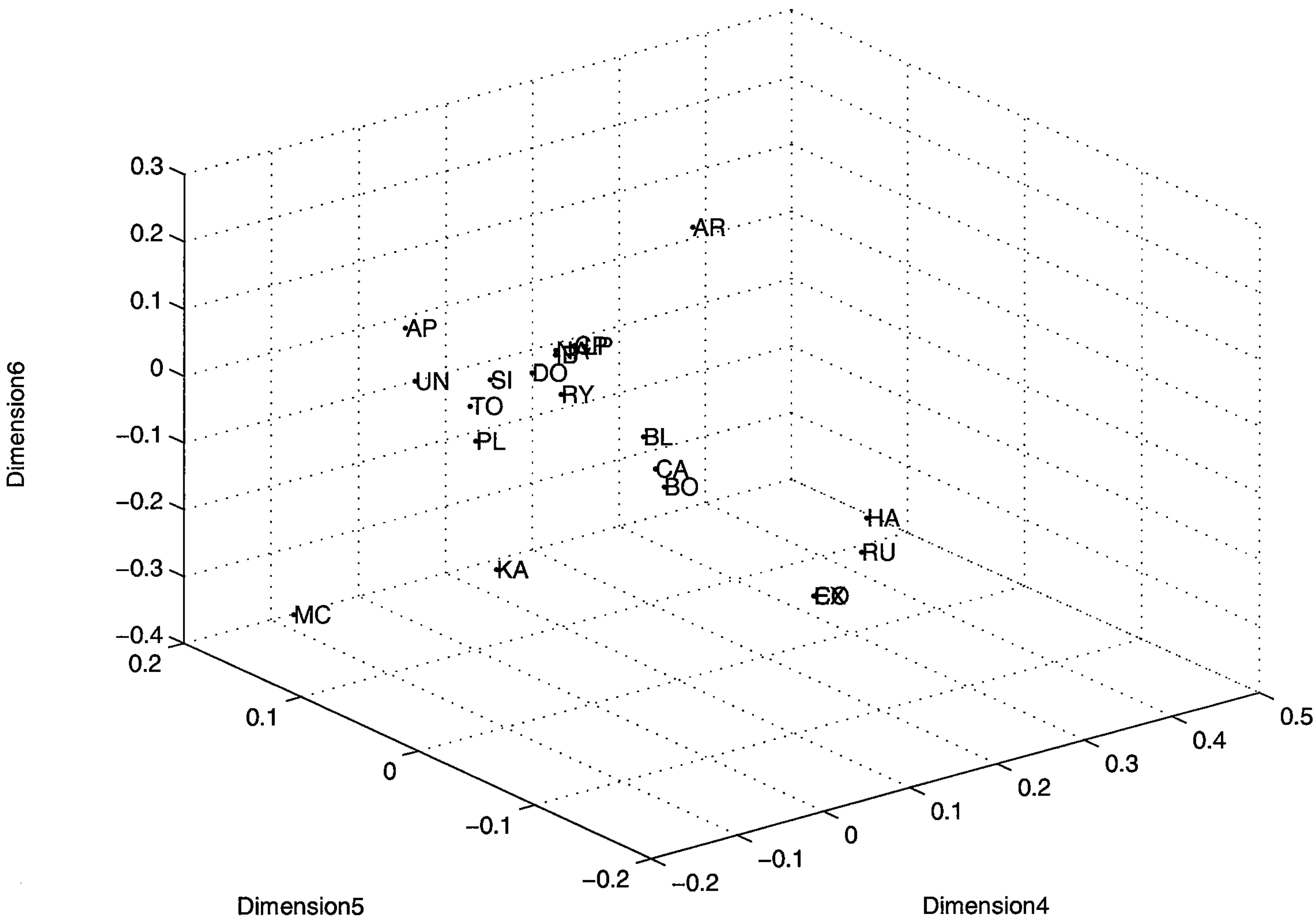

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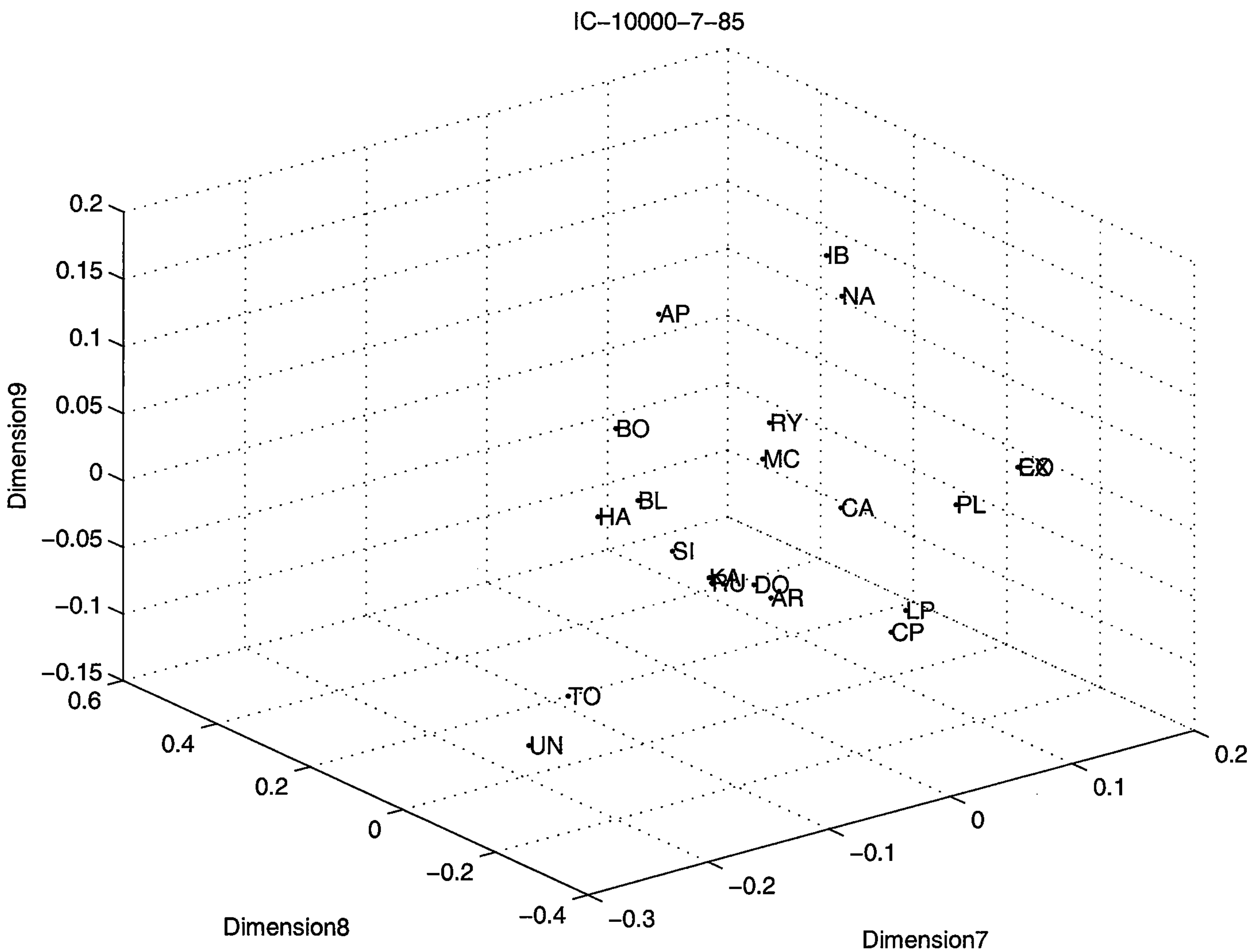

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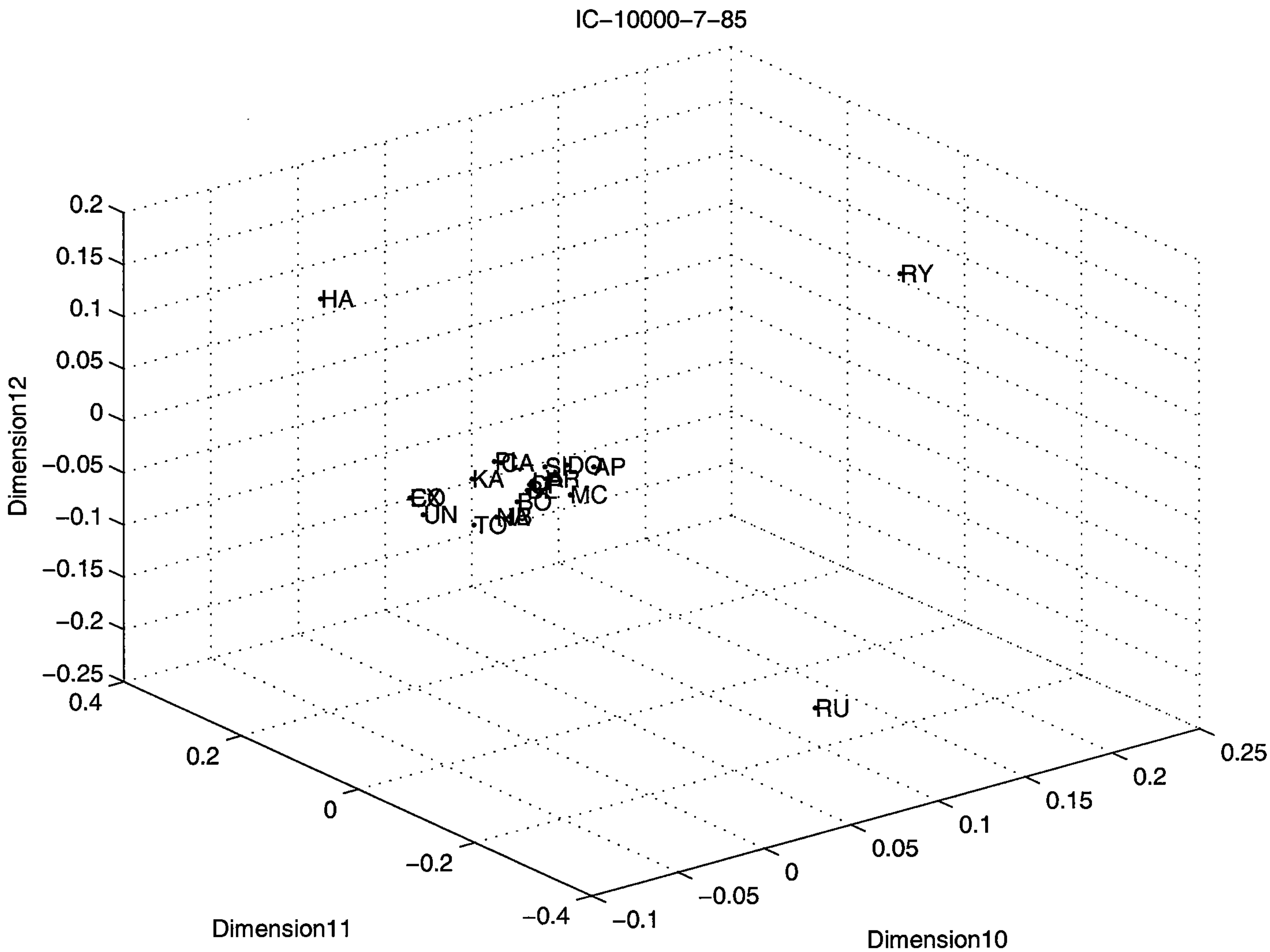

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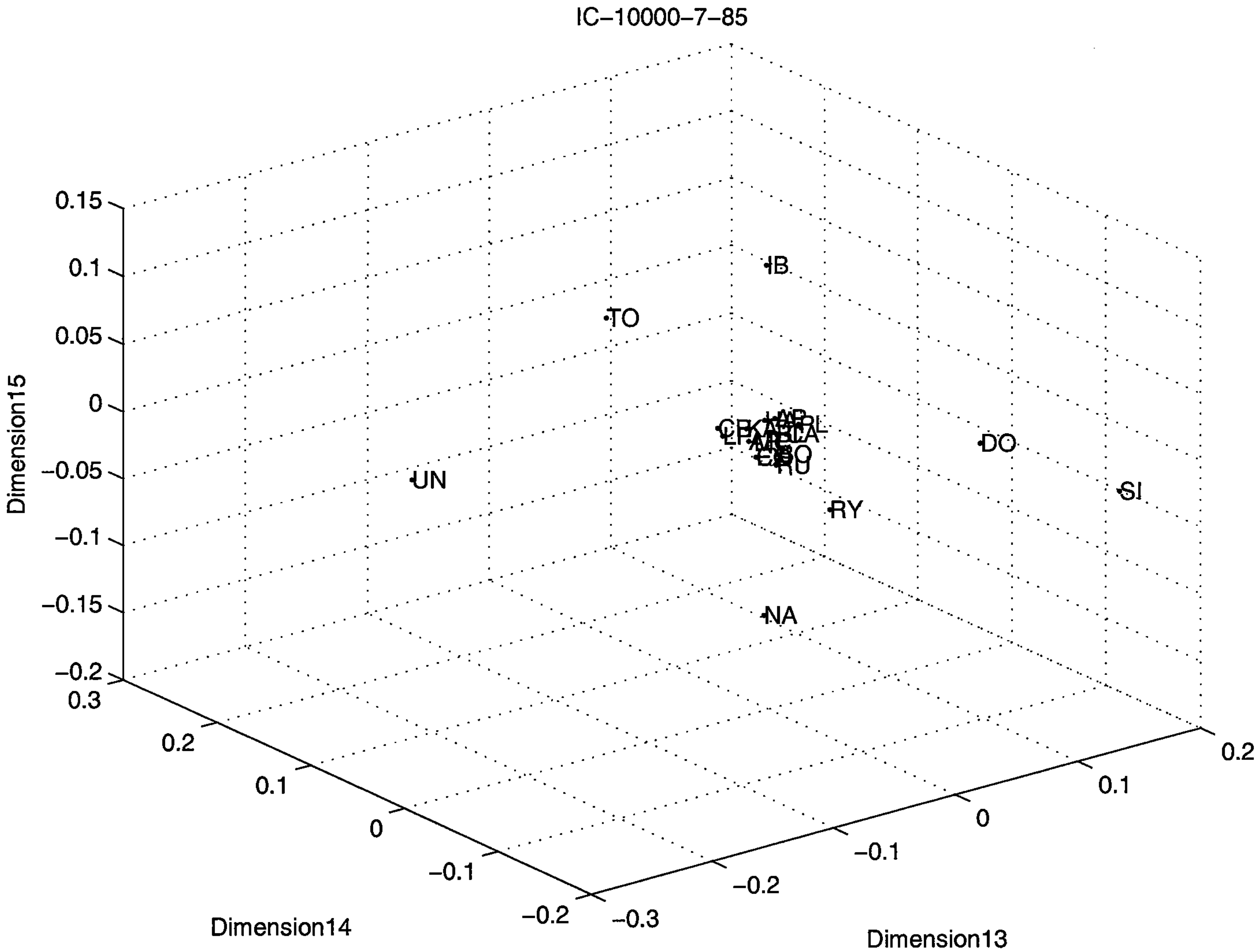
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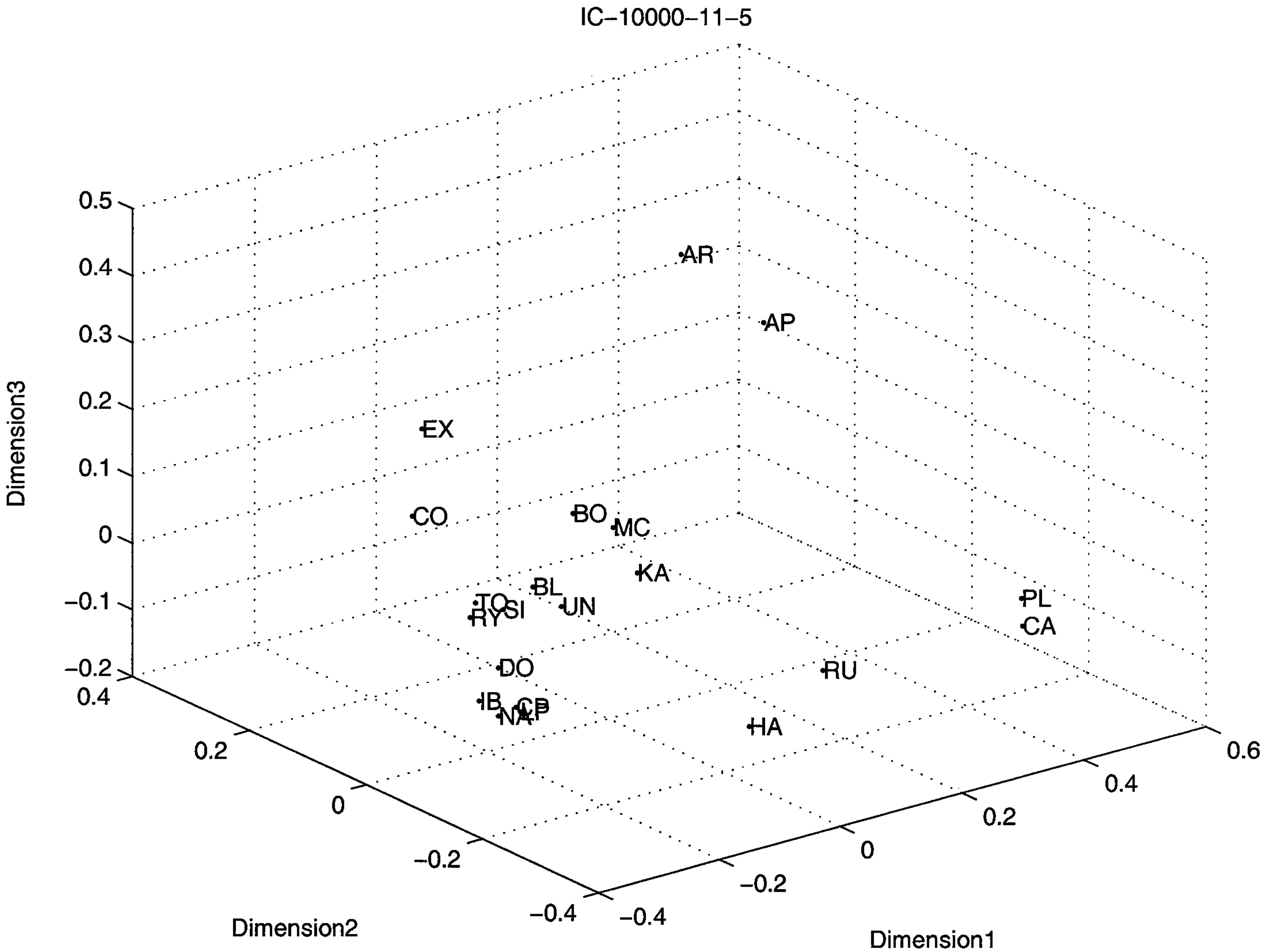

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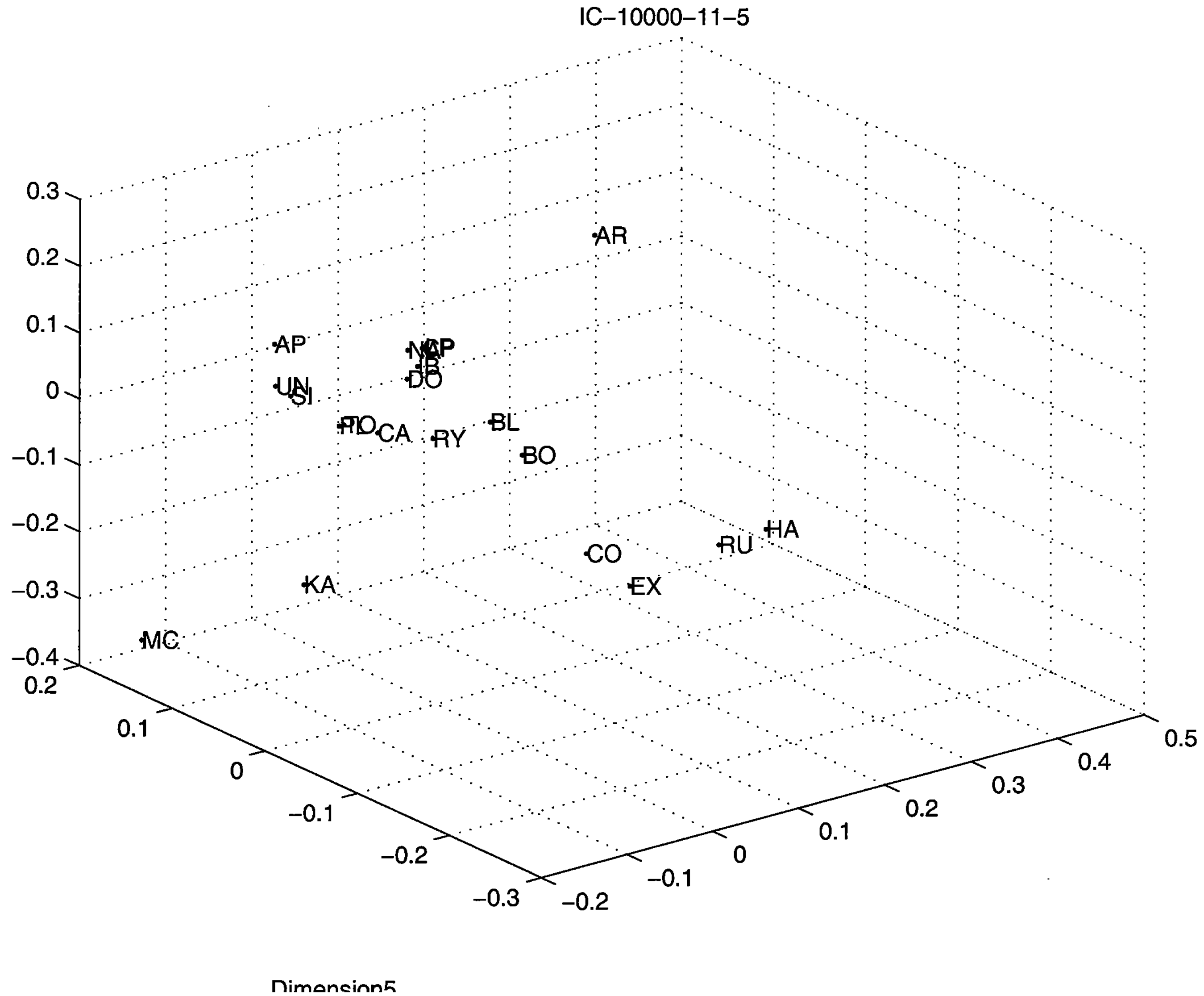
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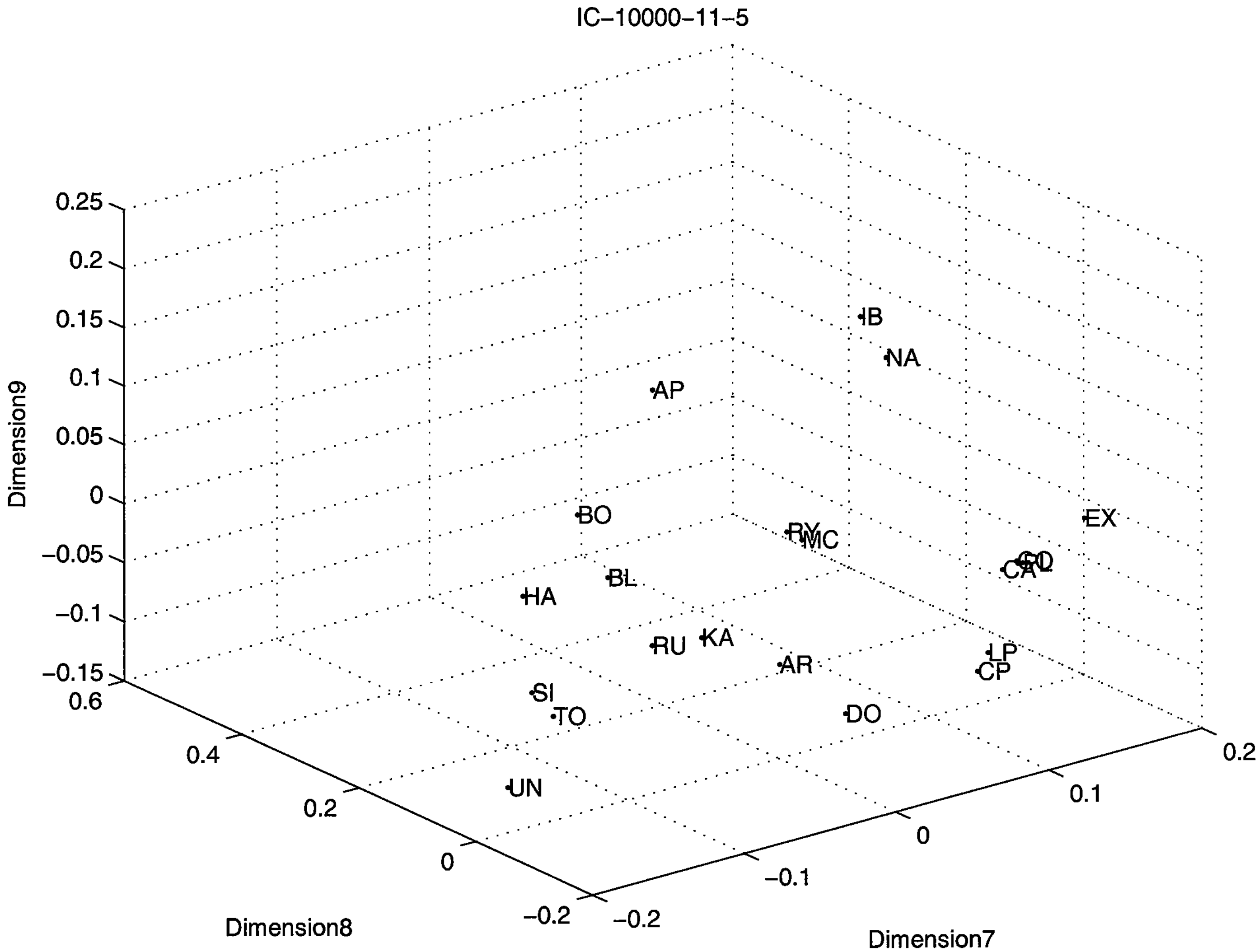
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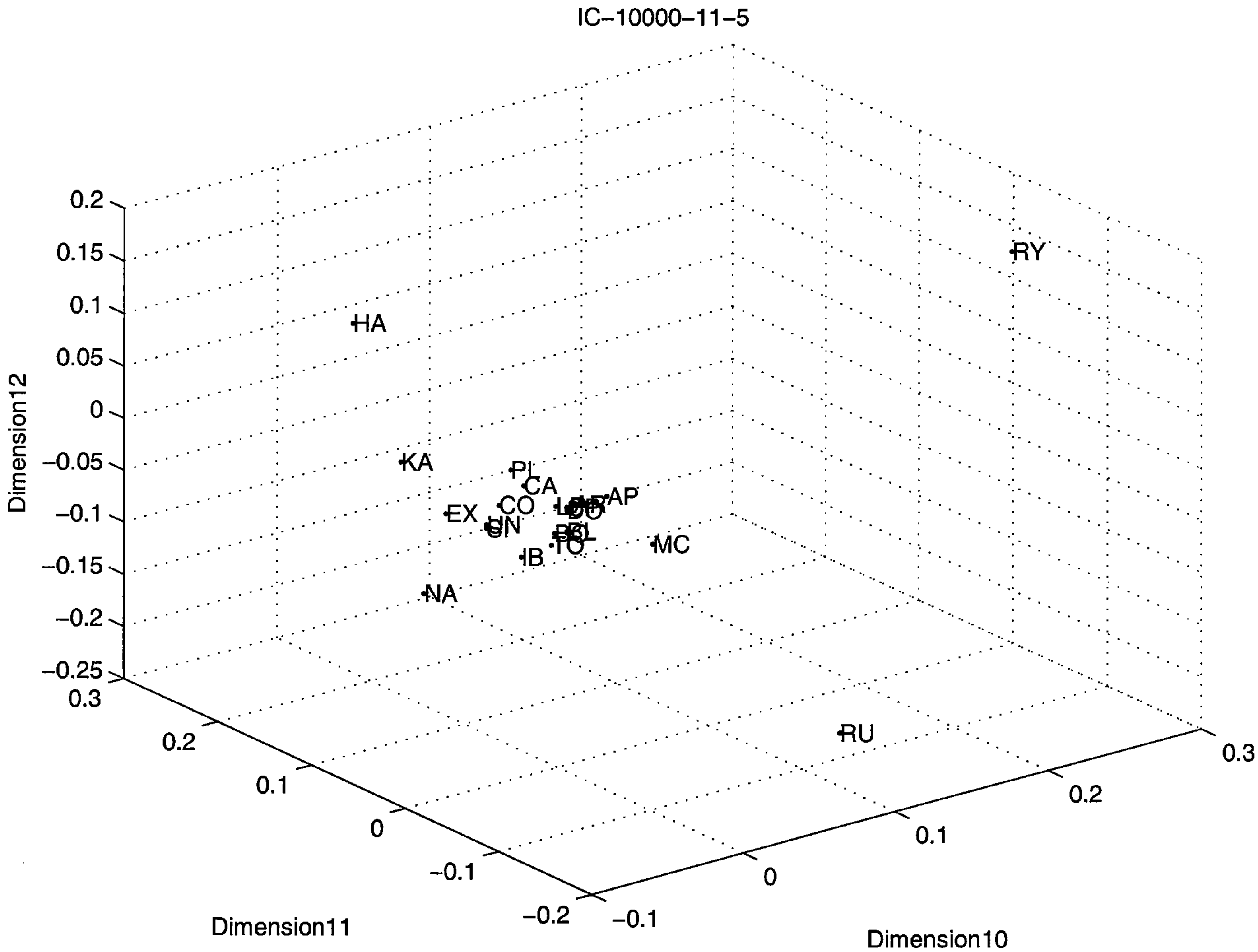
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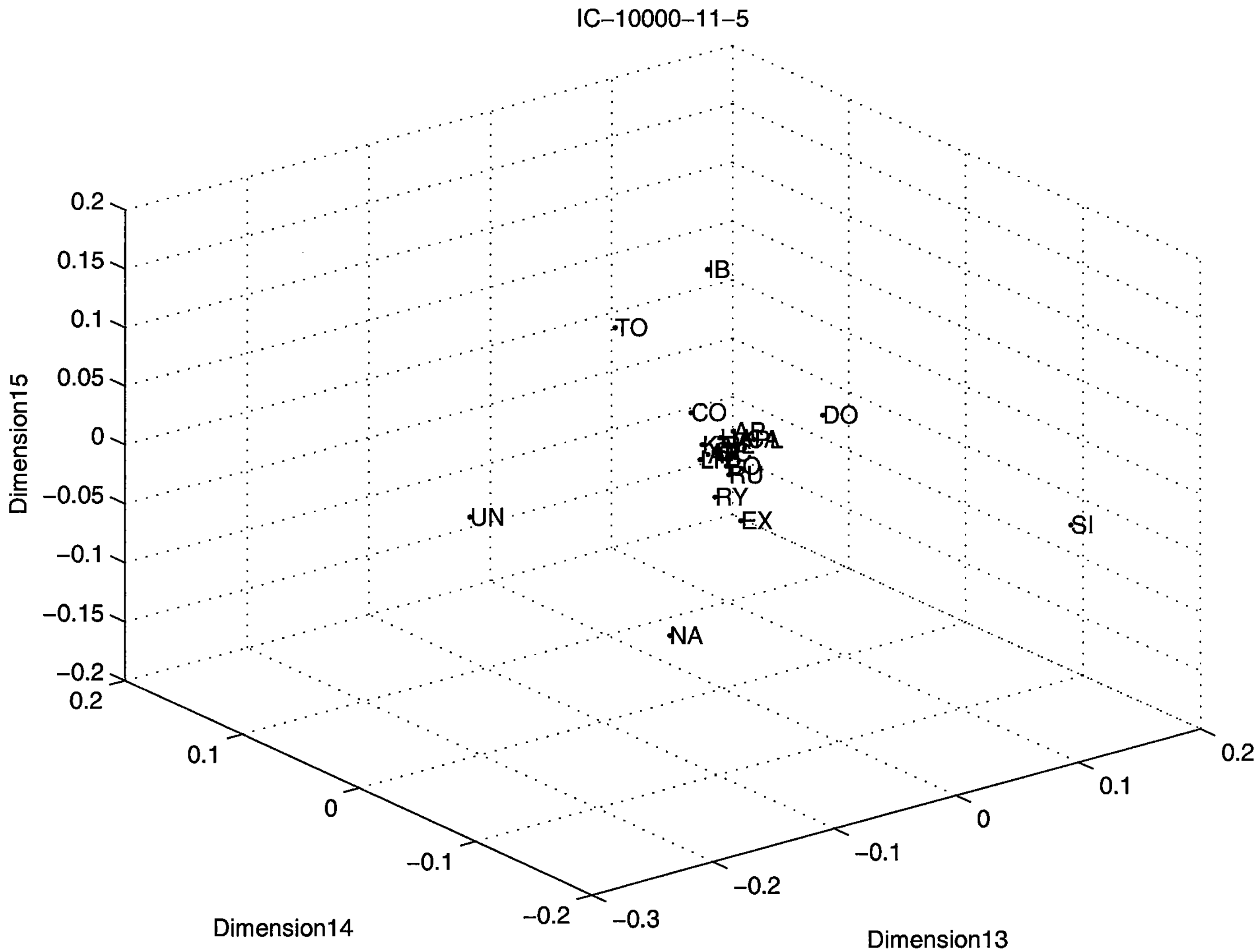
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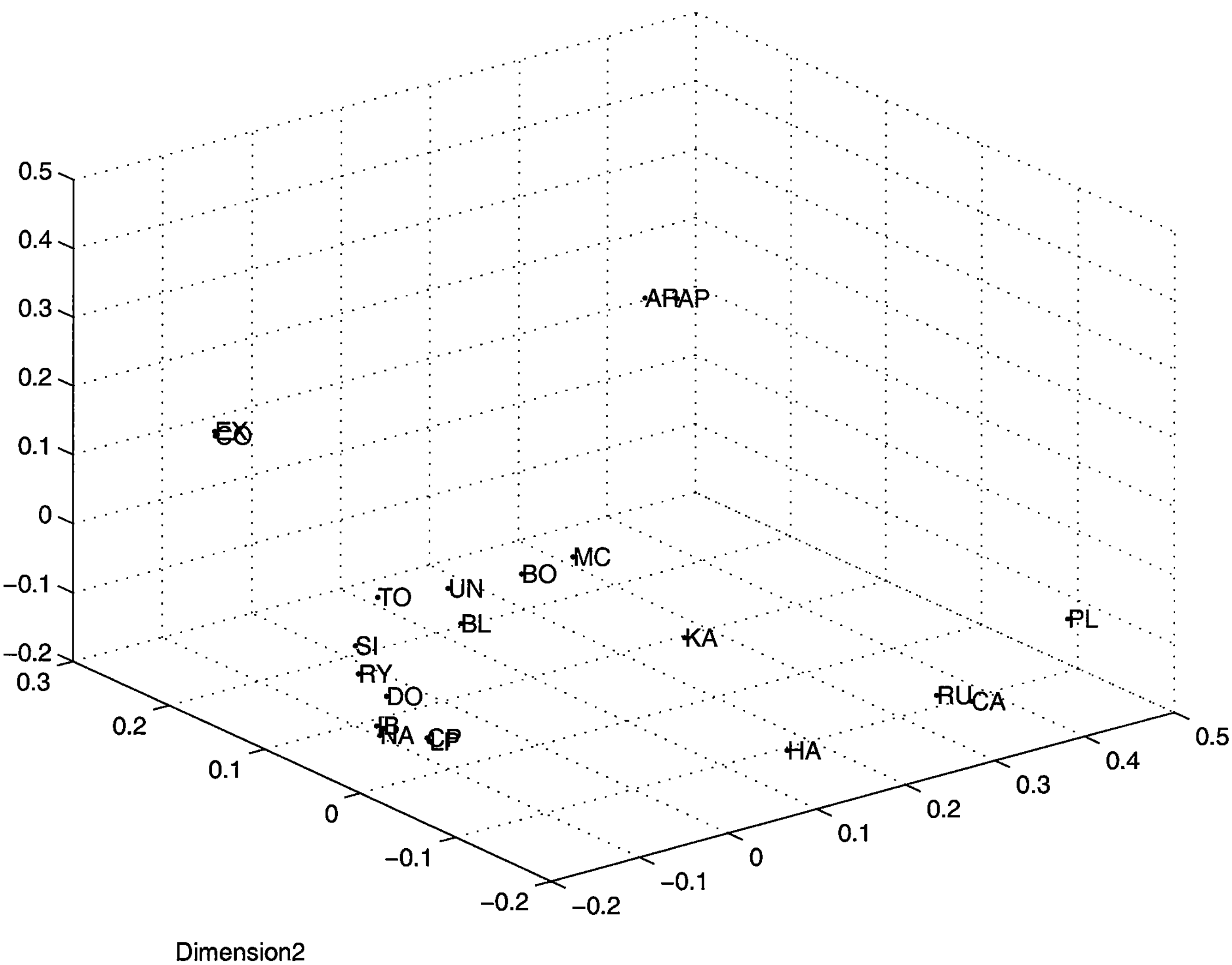
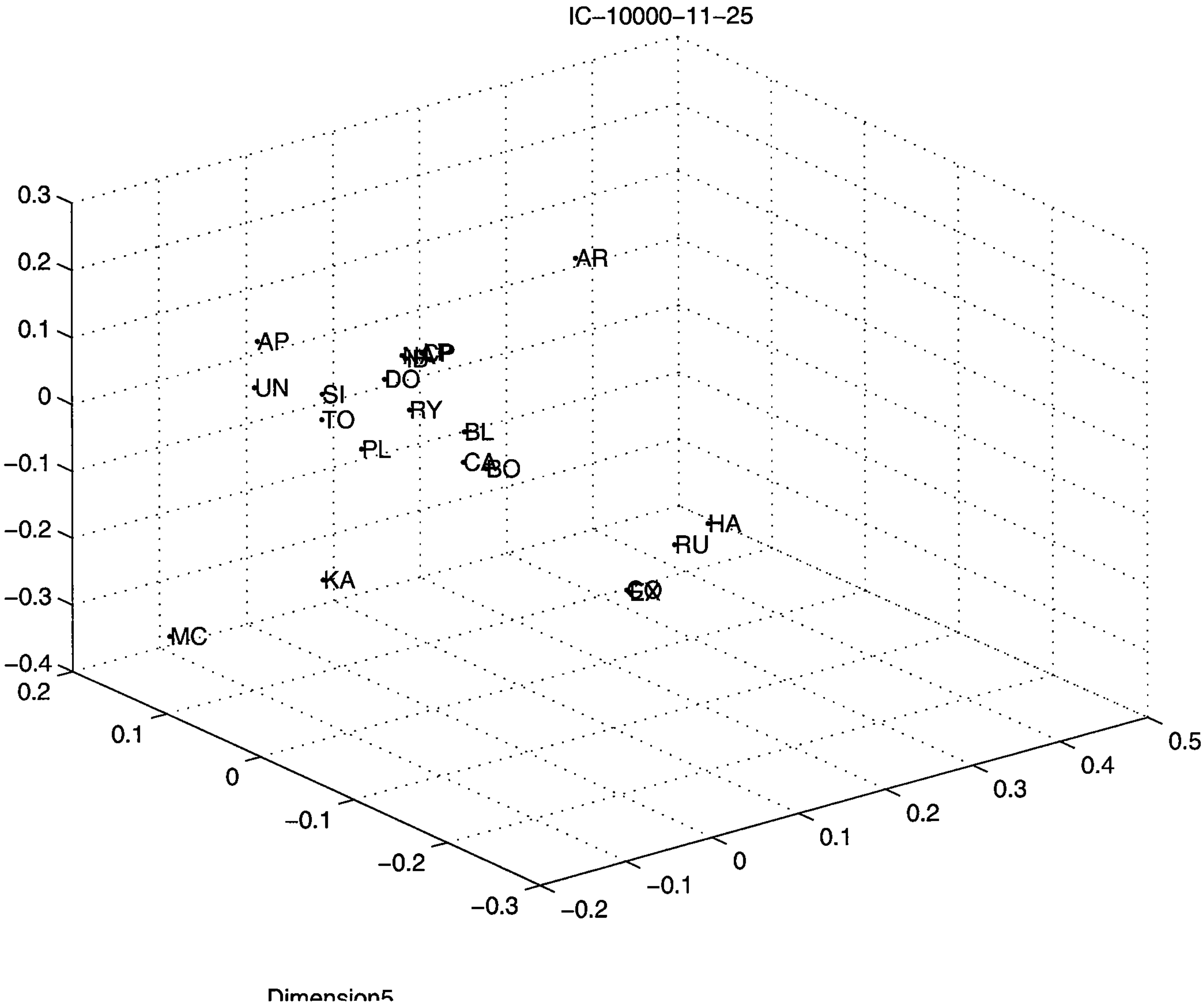
IC–10000–11–25

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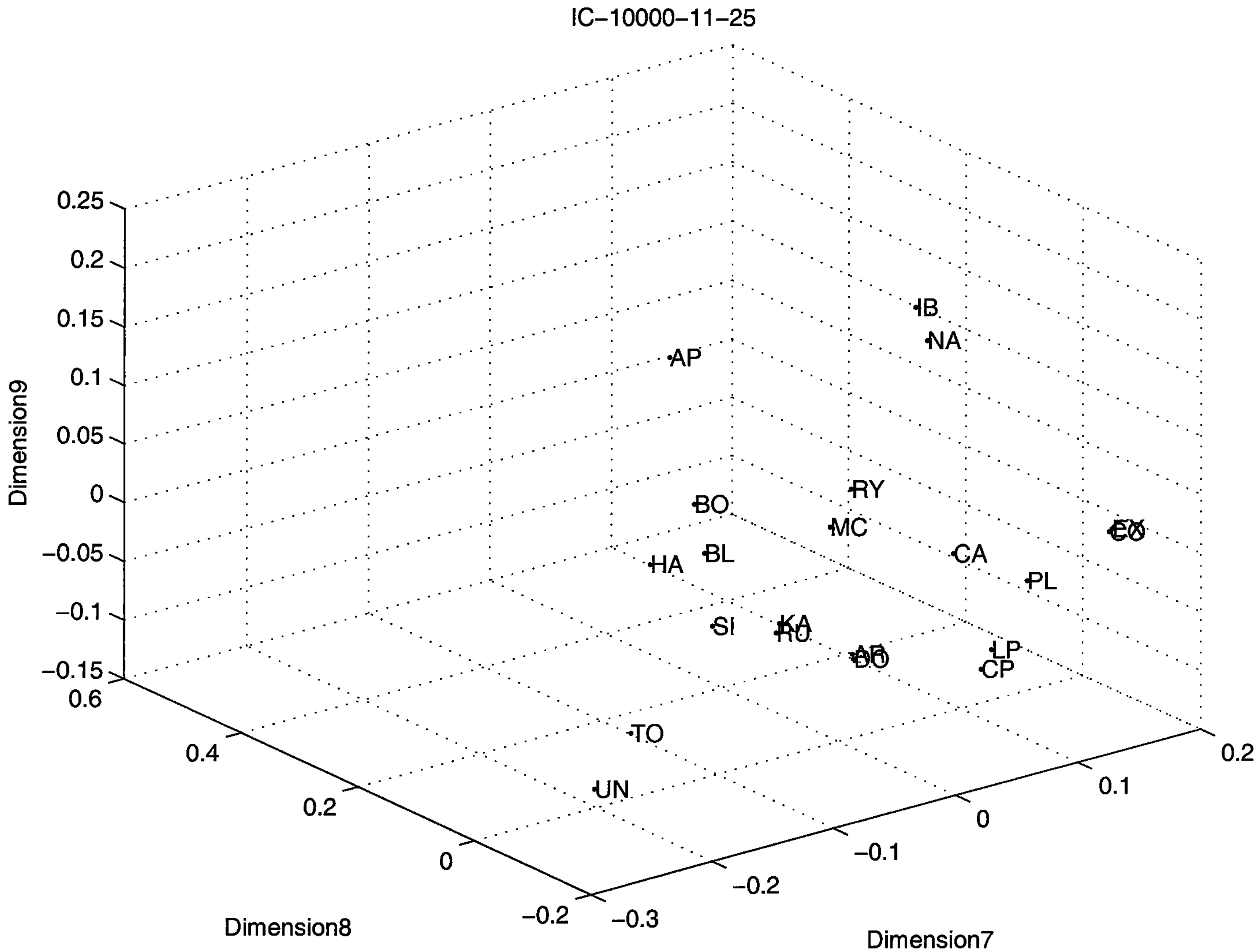
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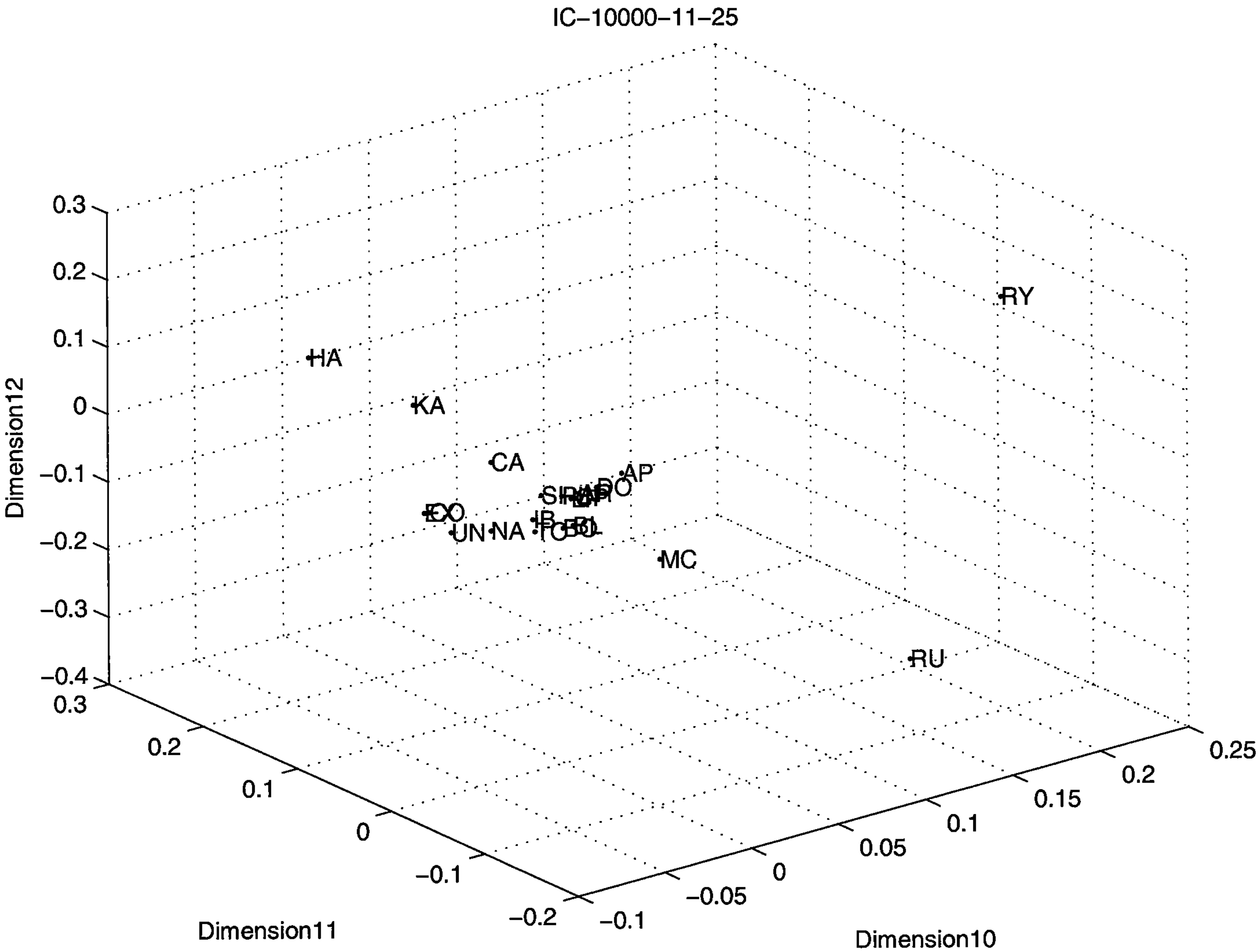

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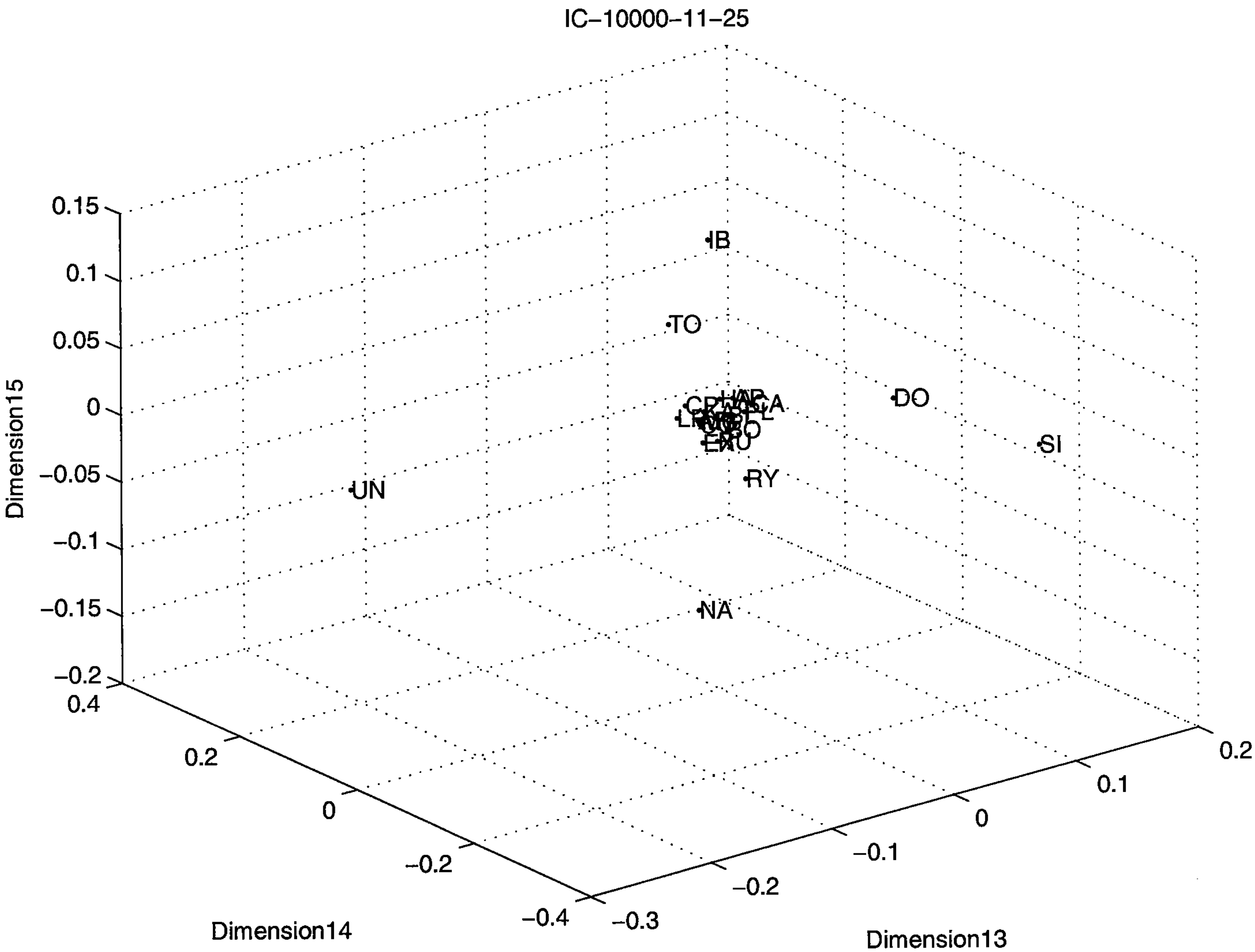

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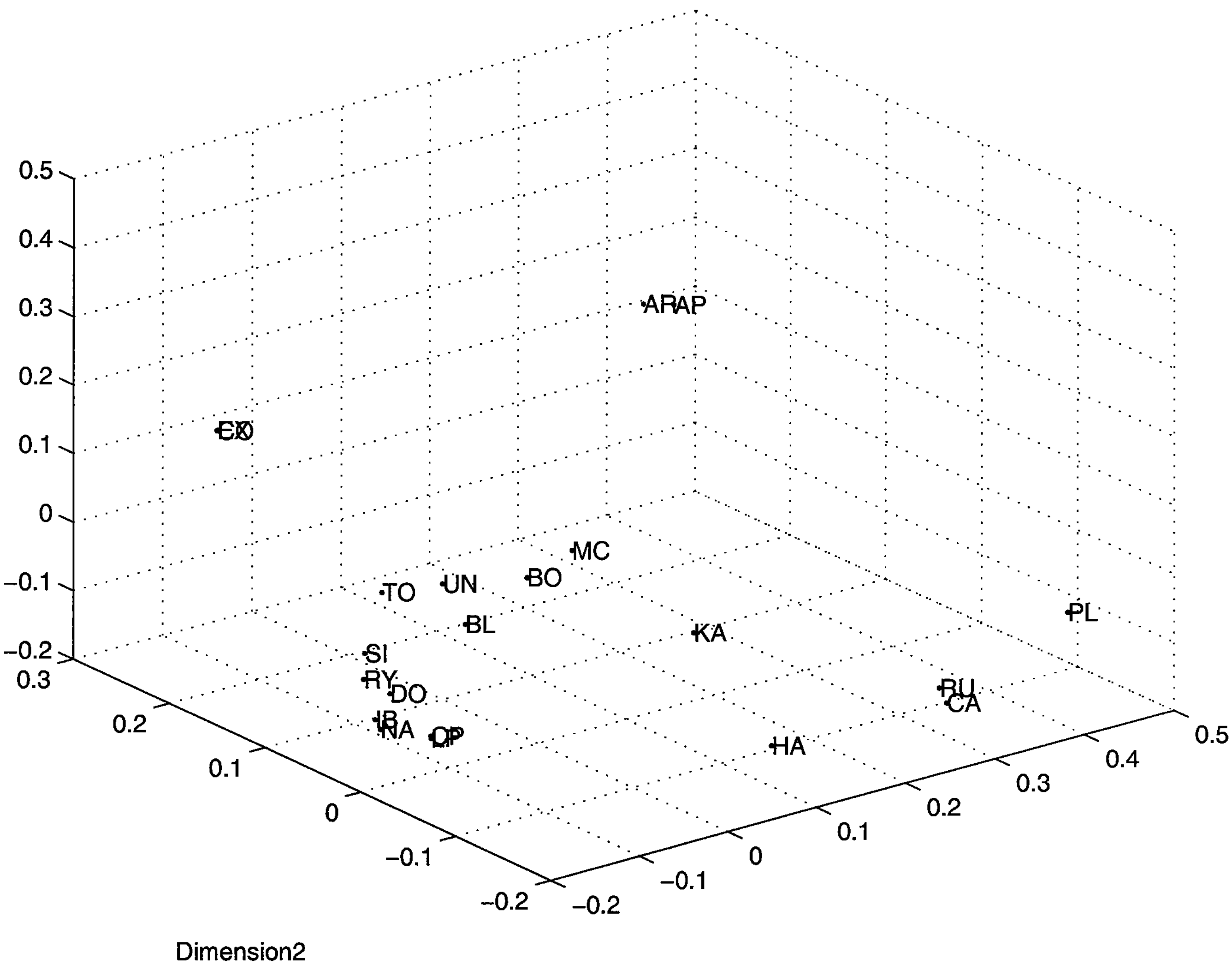

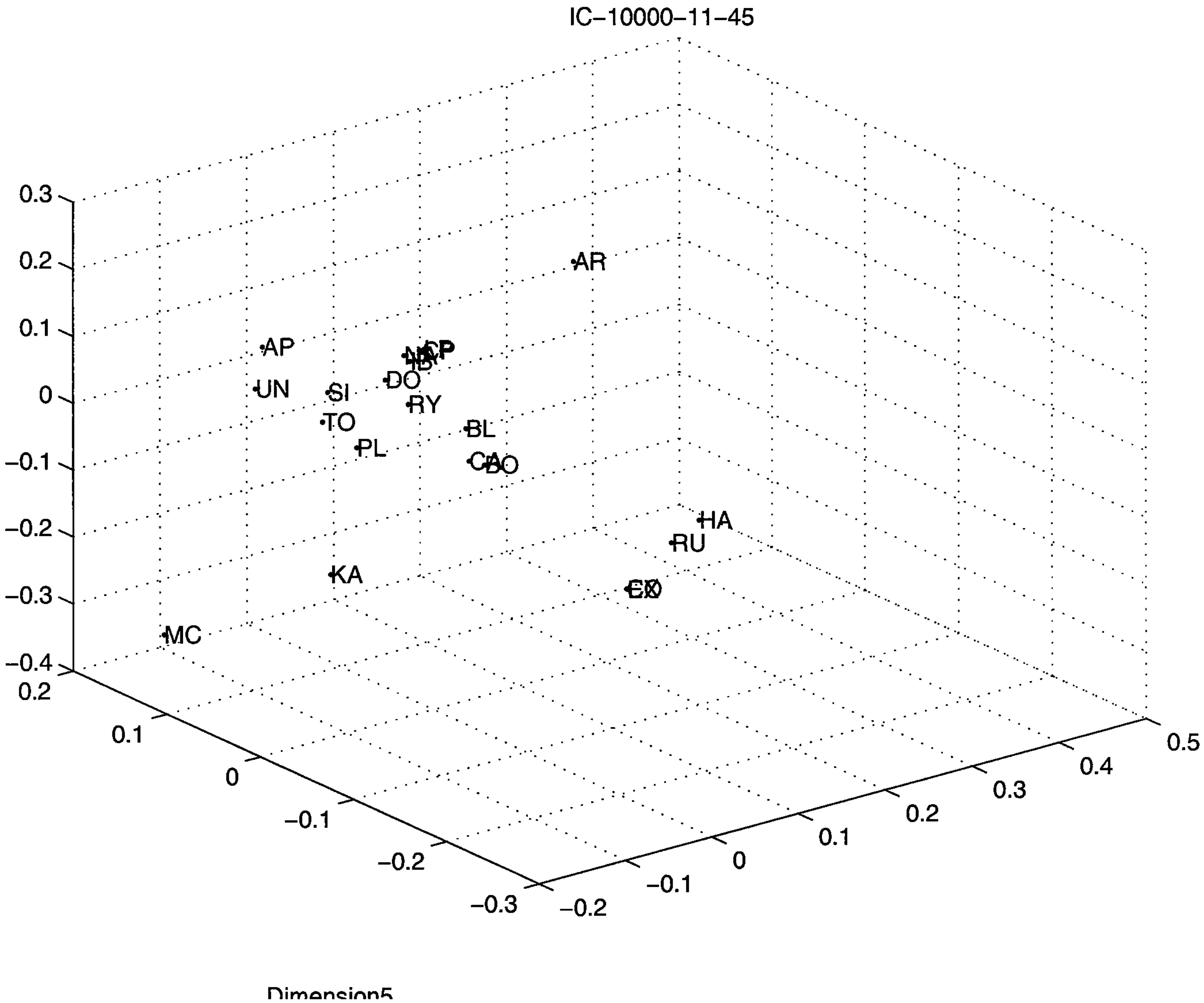
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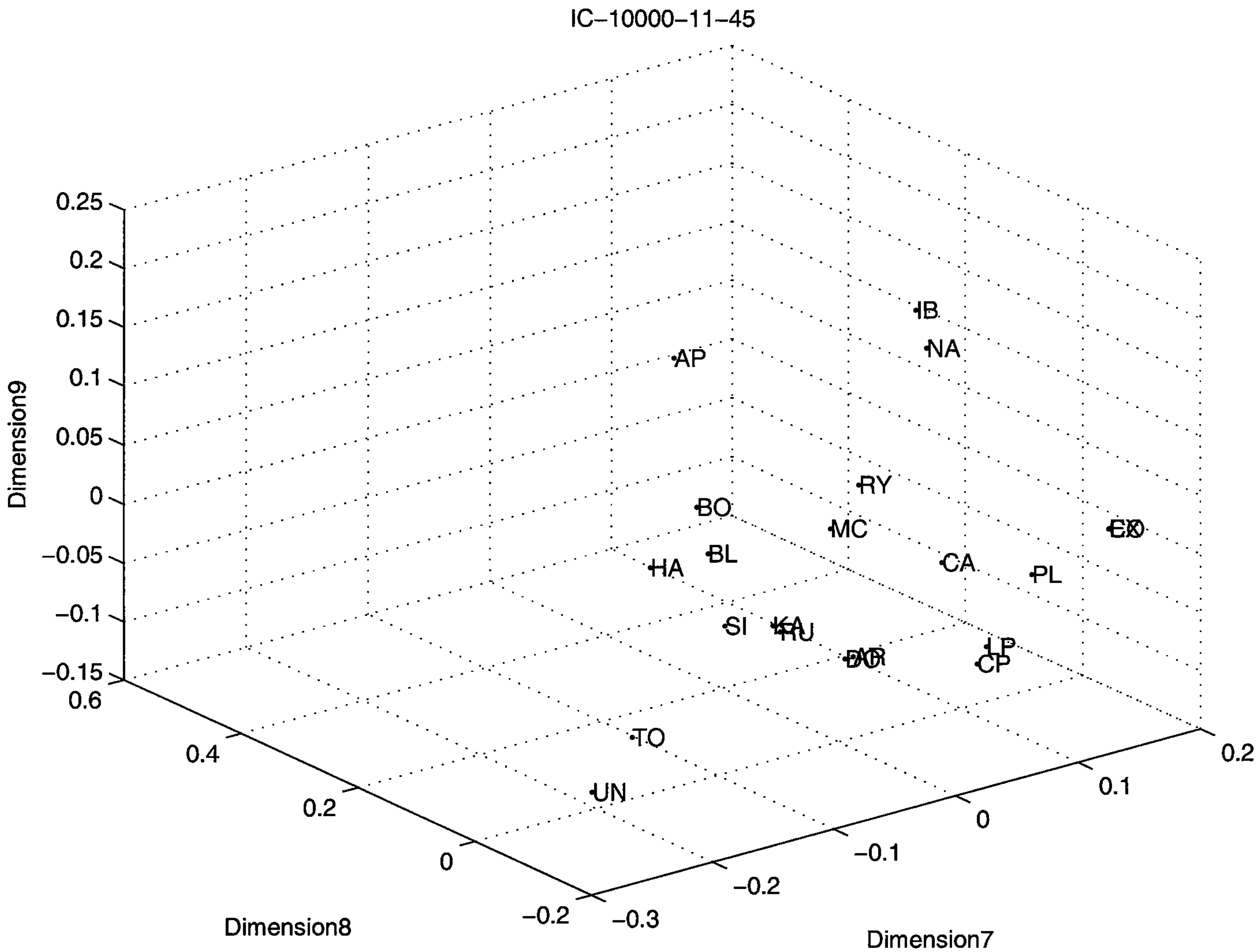

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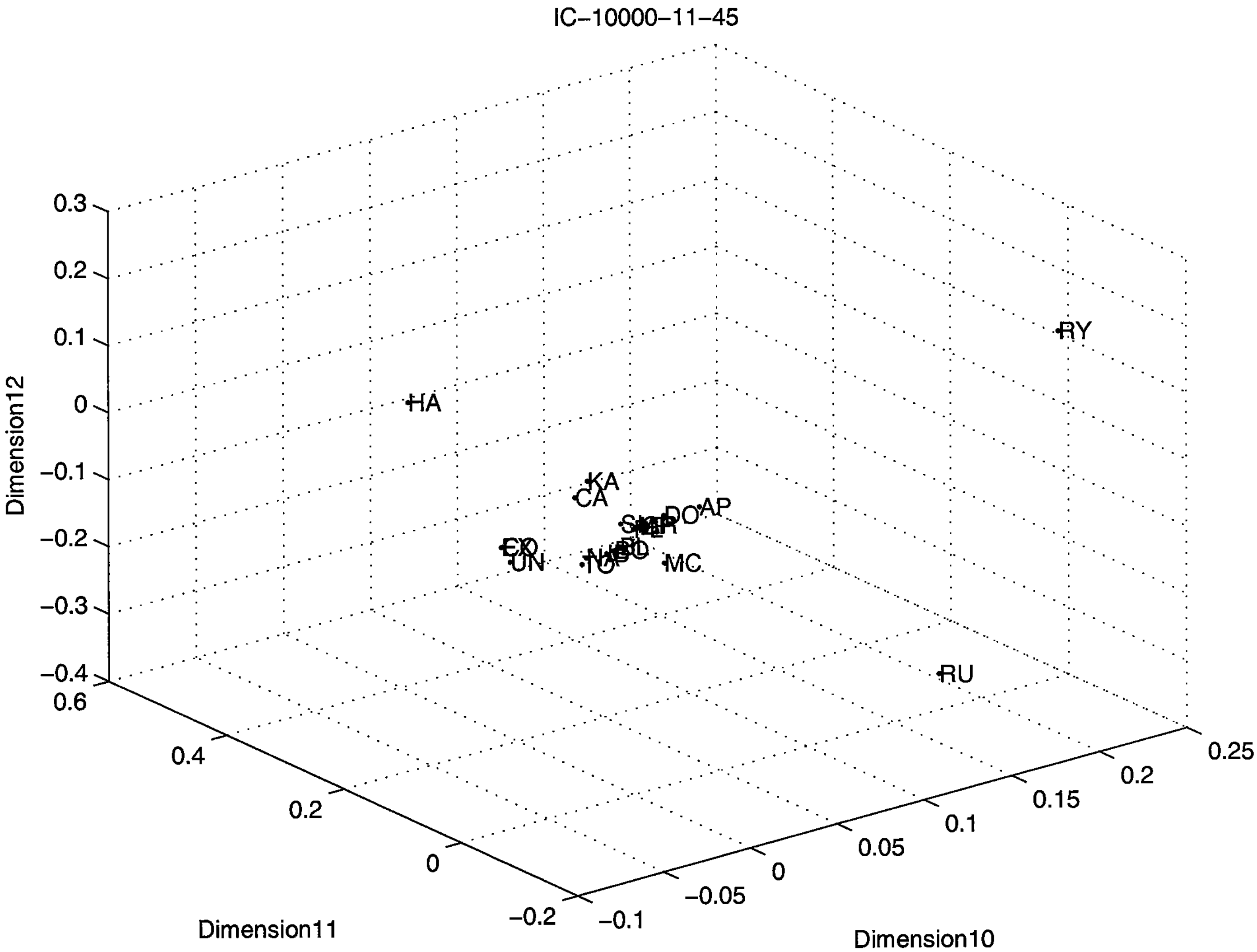
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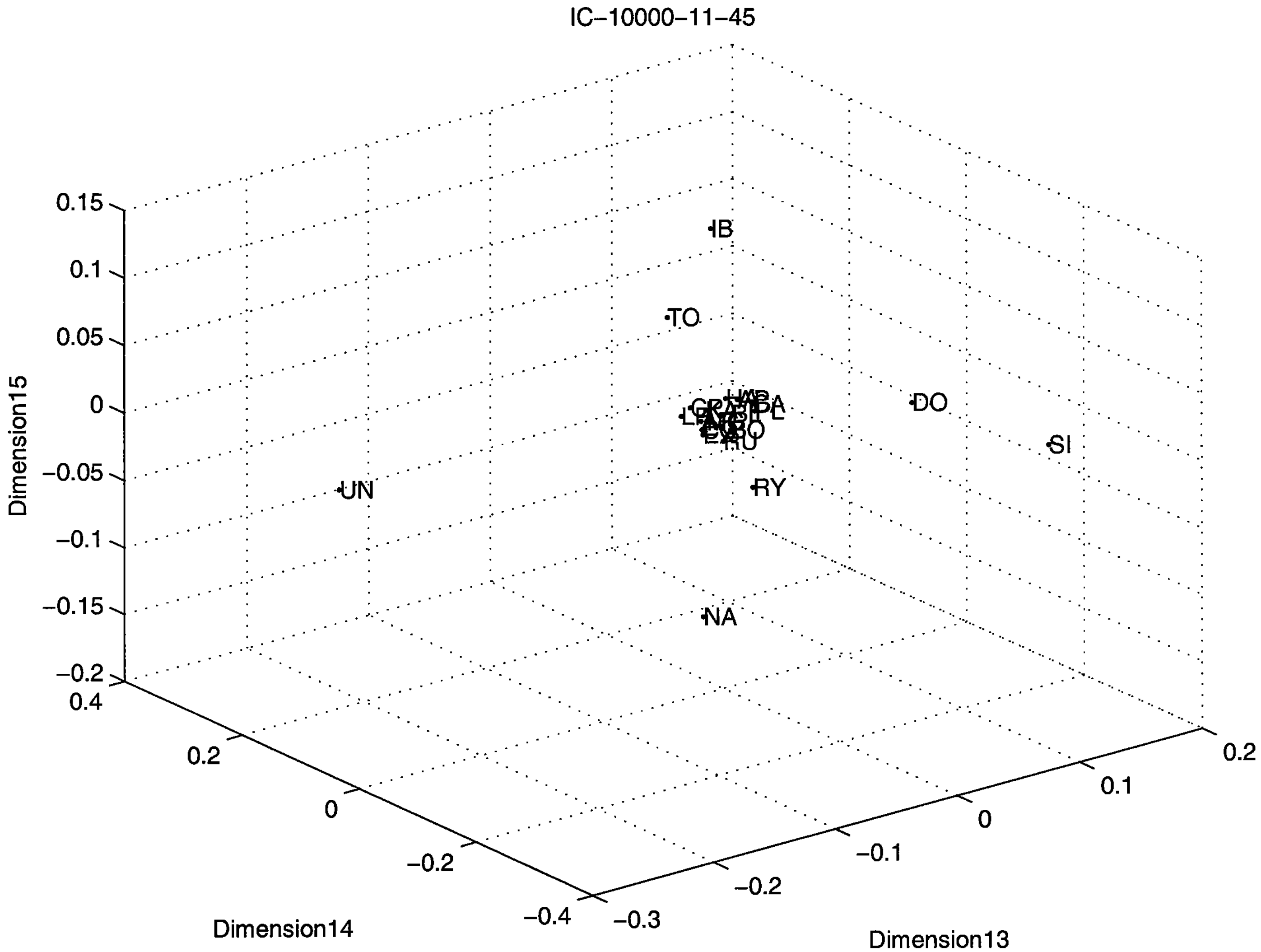
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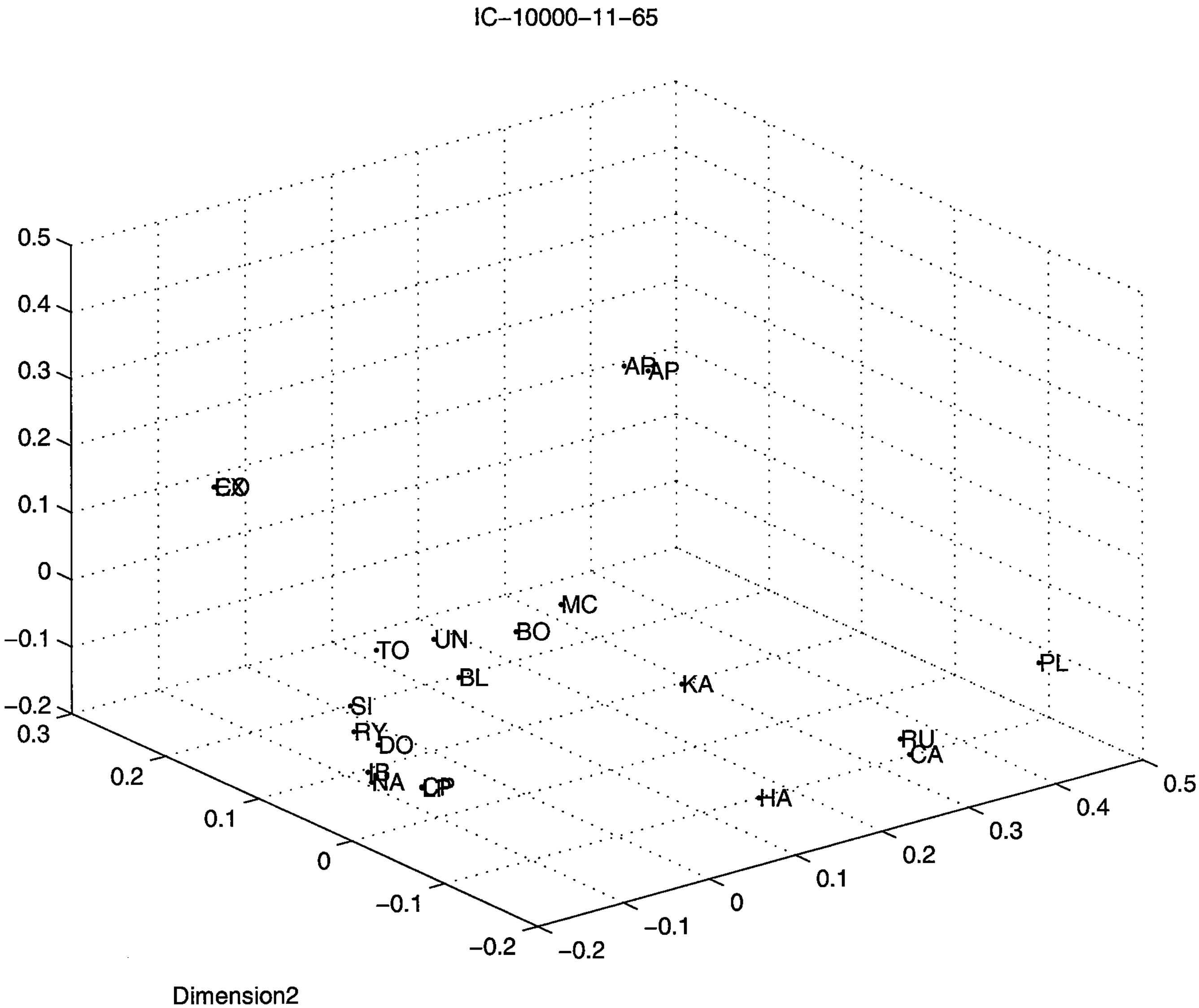
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HA
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0.2
0.1
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-0.2
0.3
0.2
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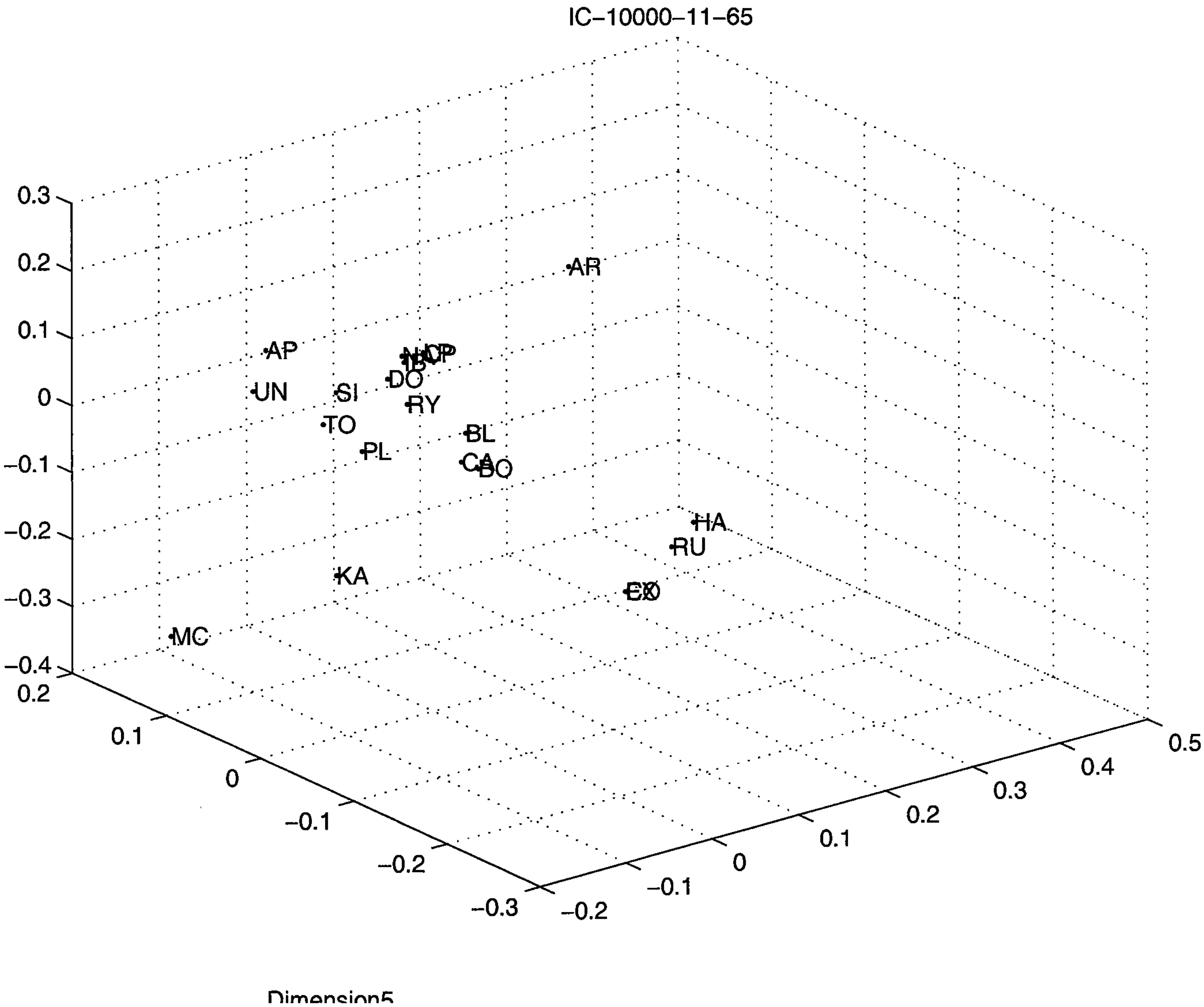

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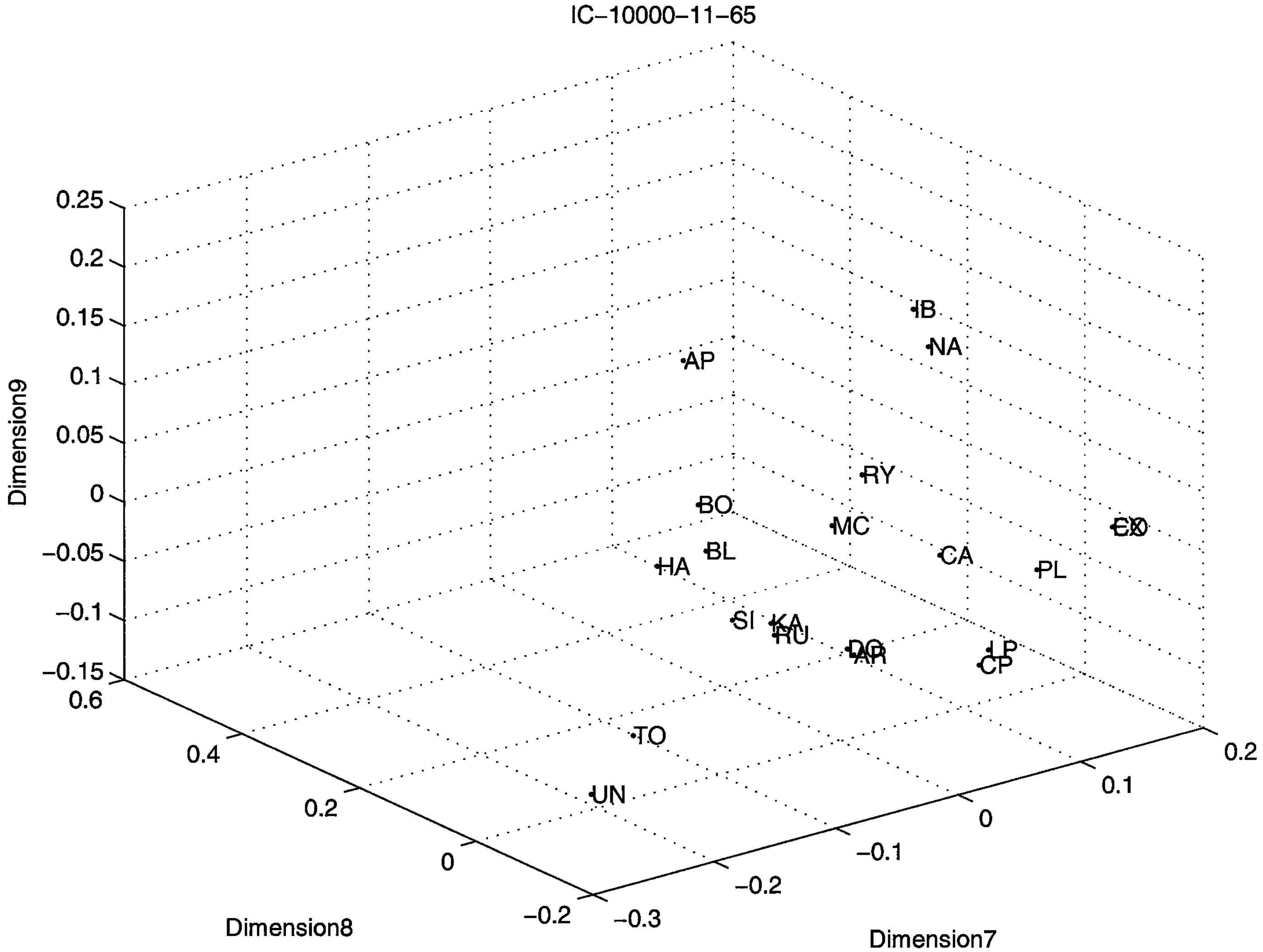

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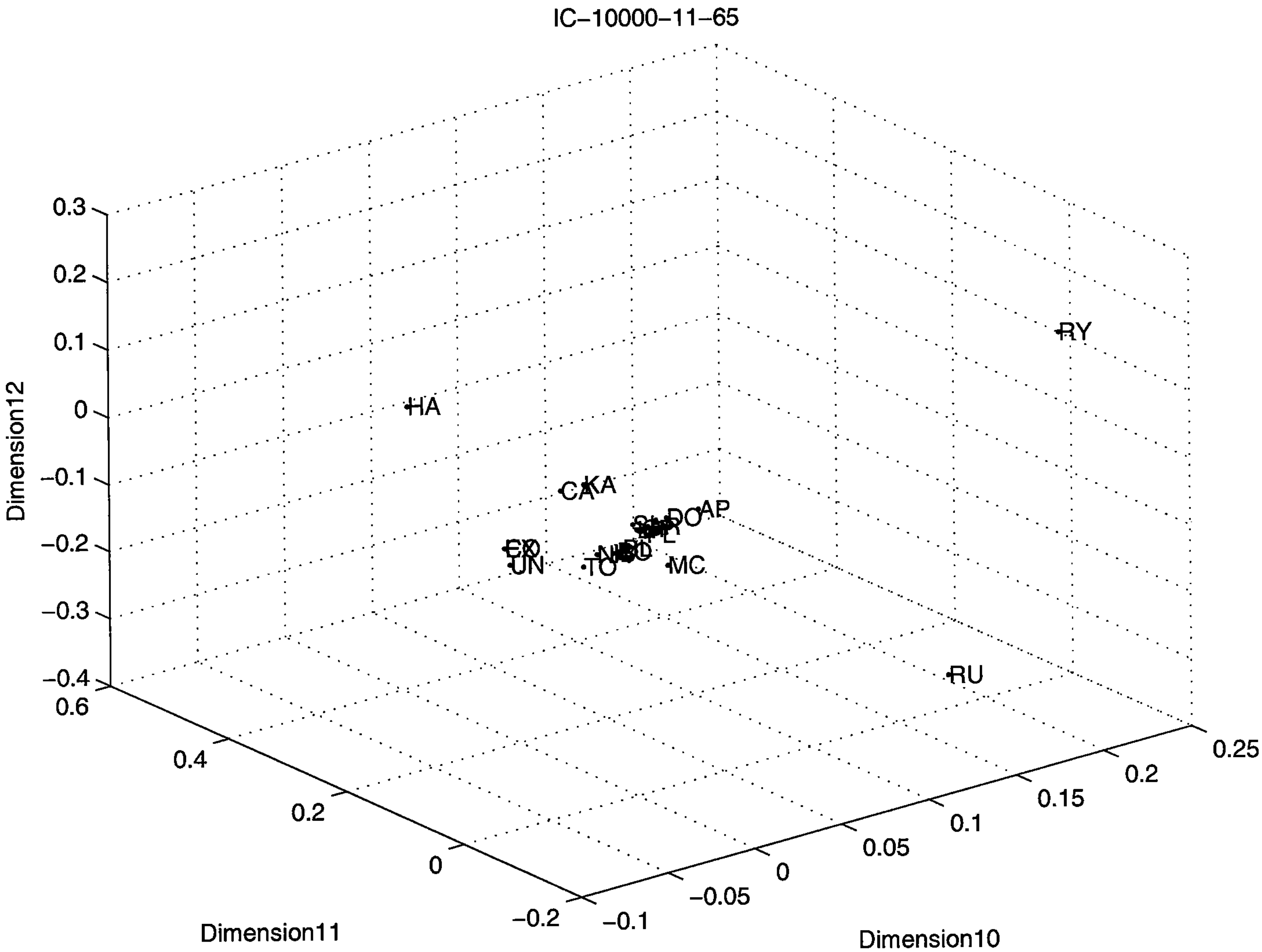
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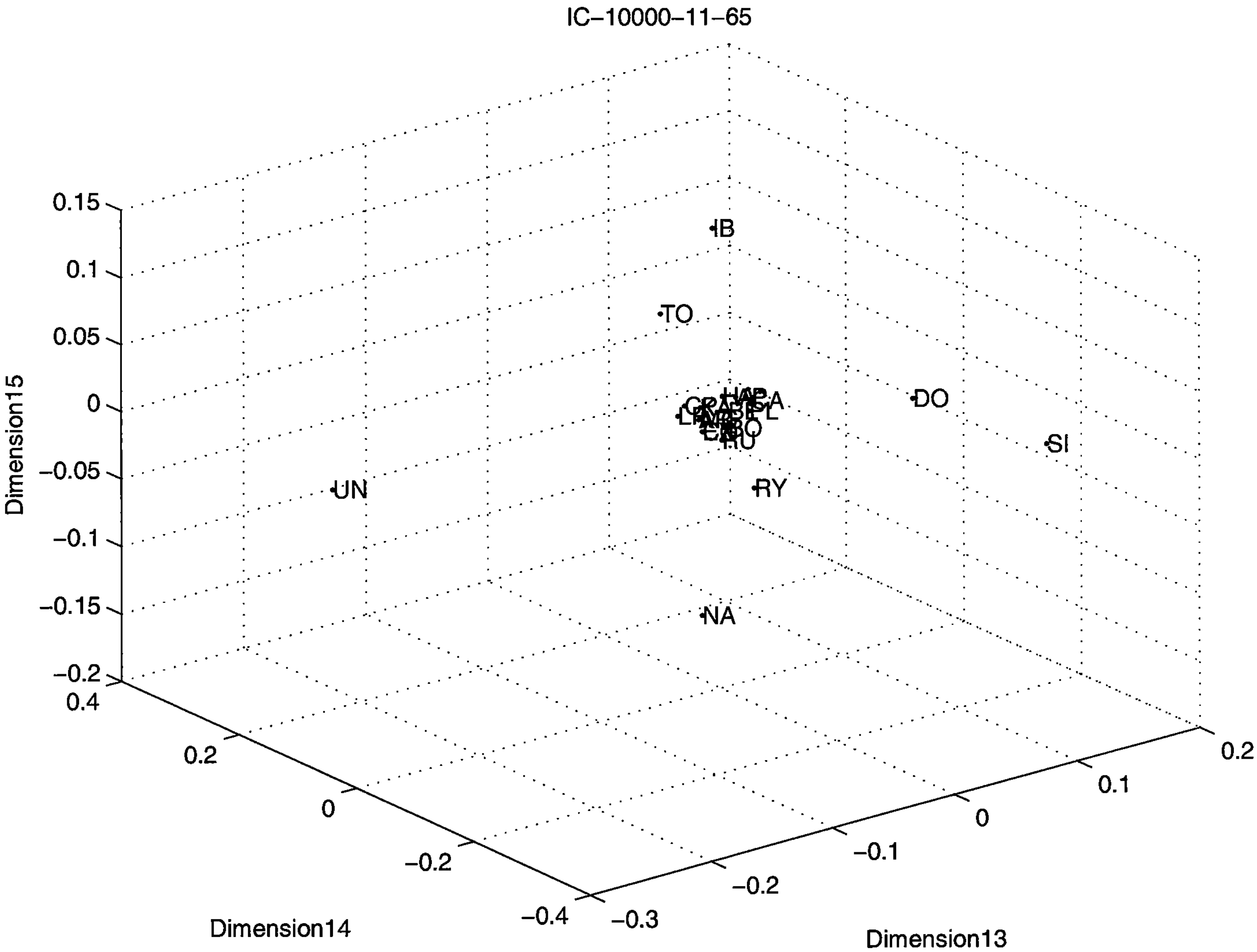
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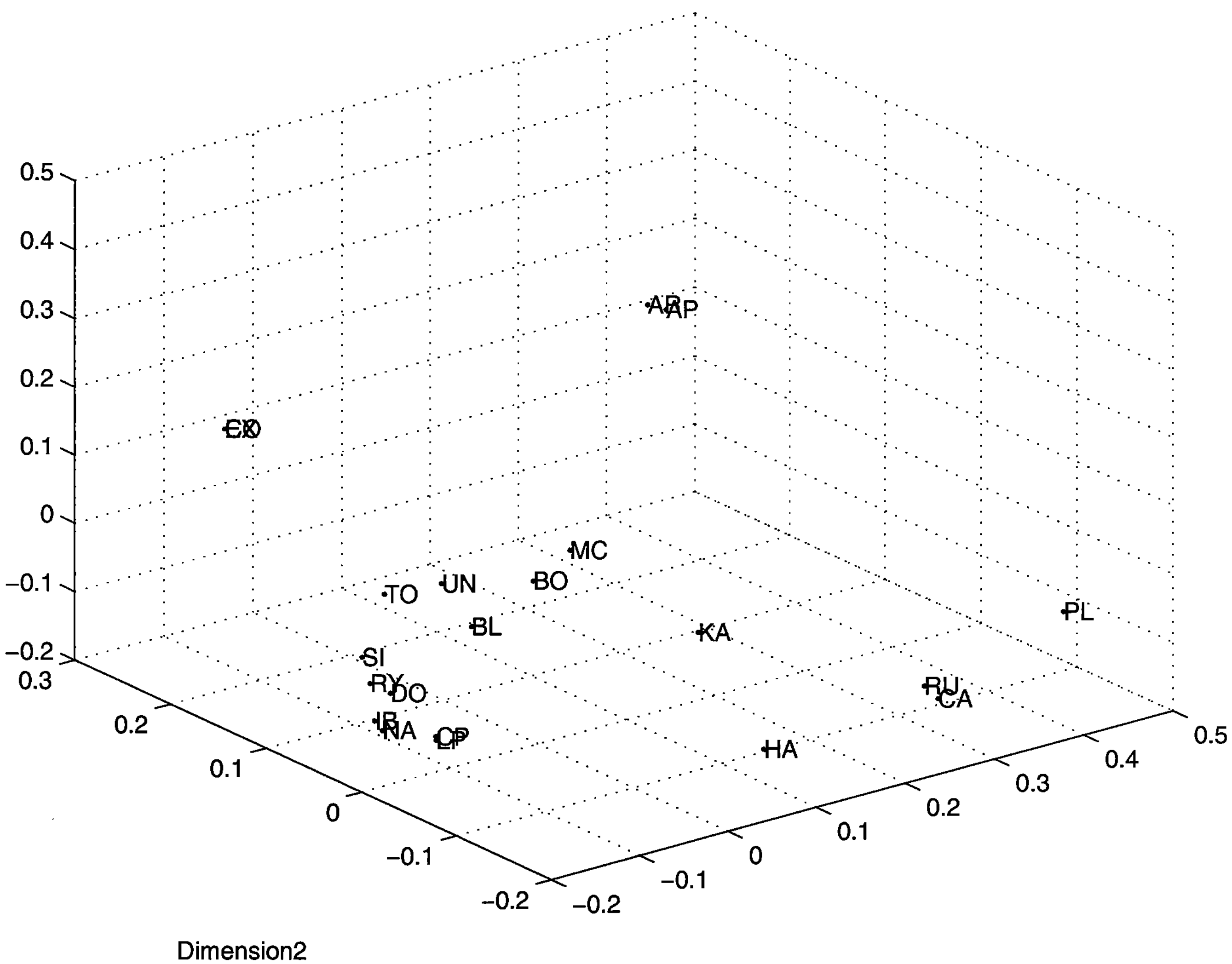

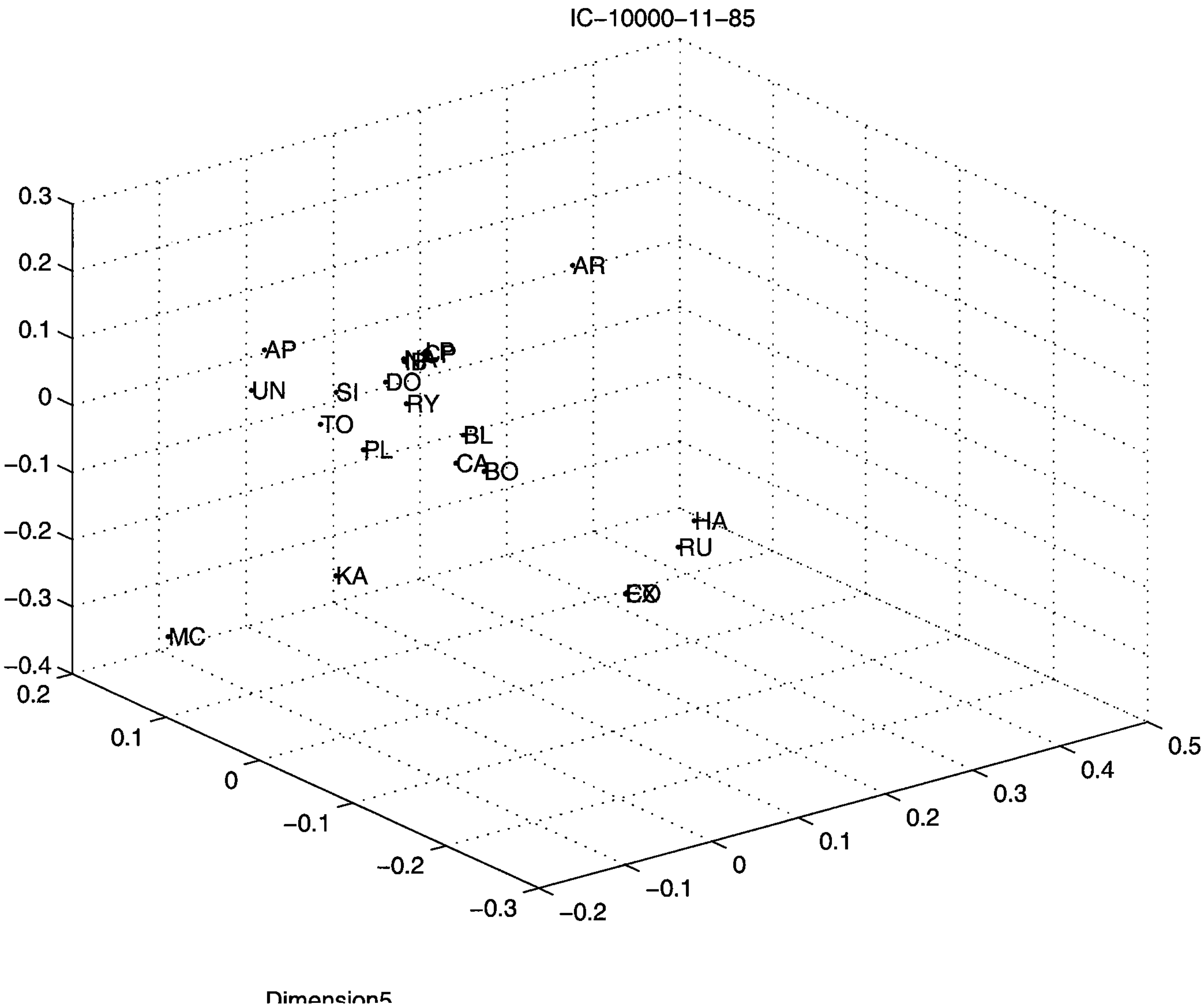

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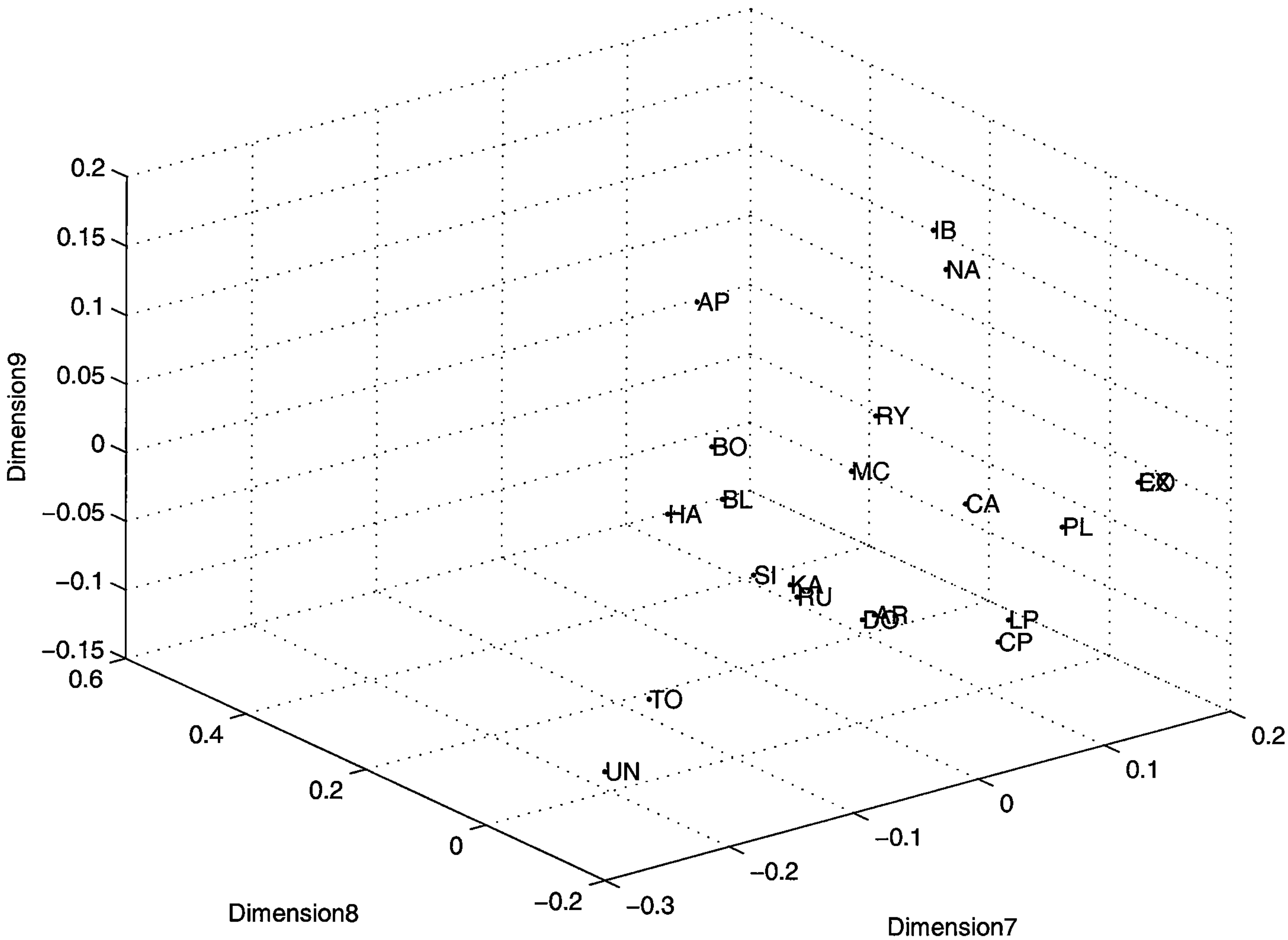

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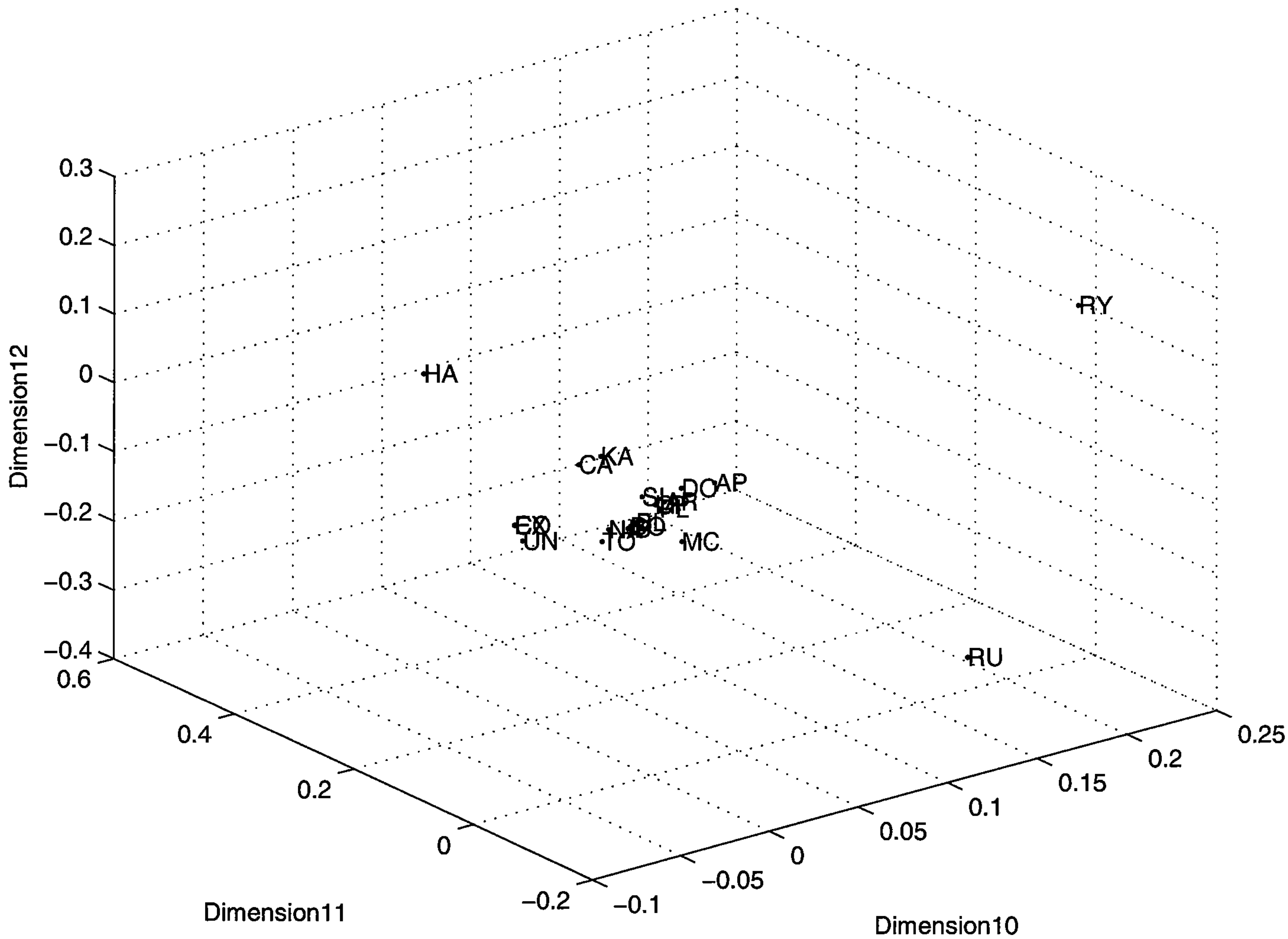

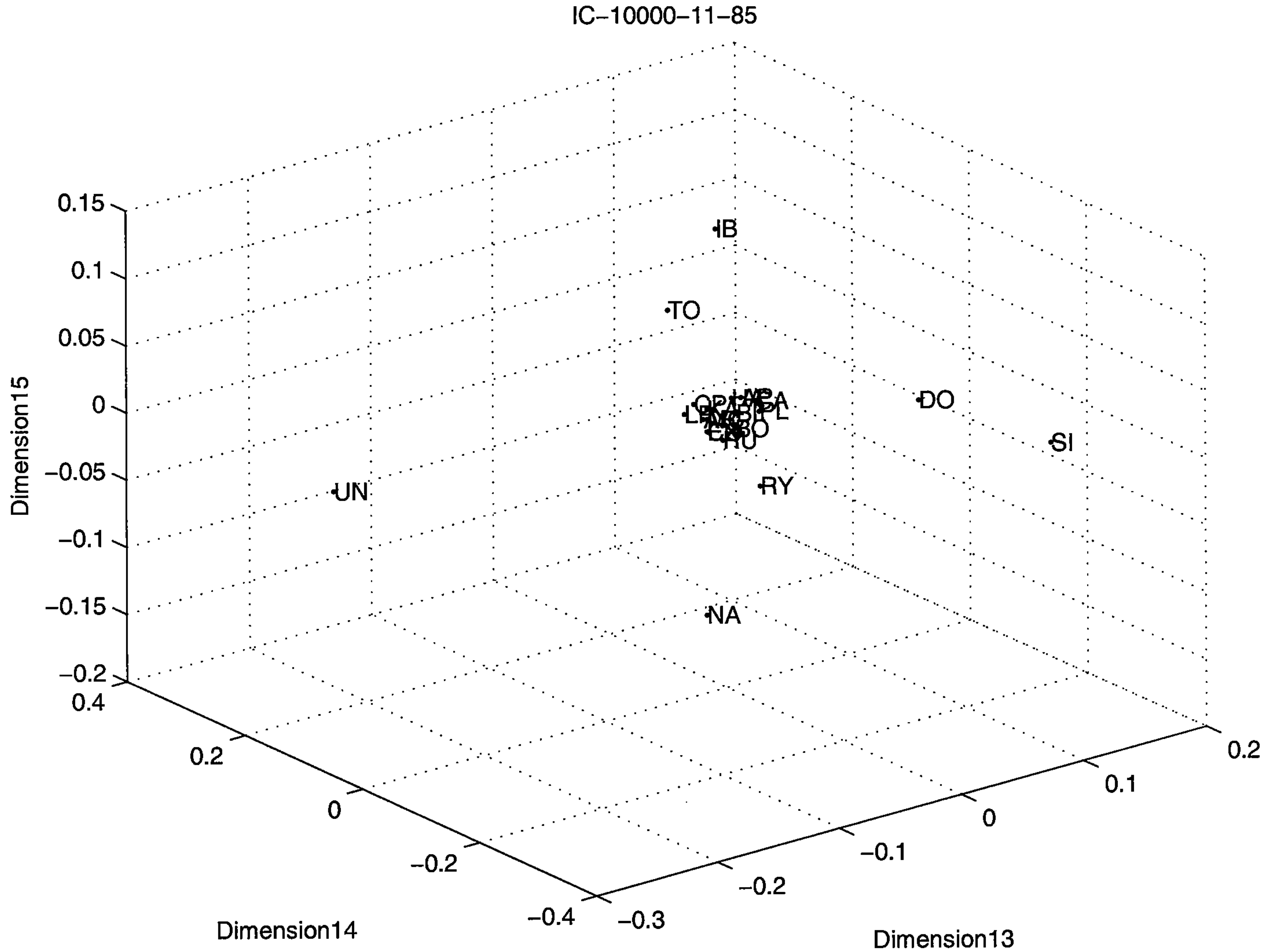
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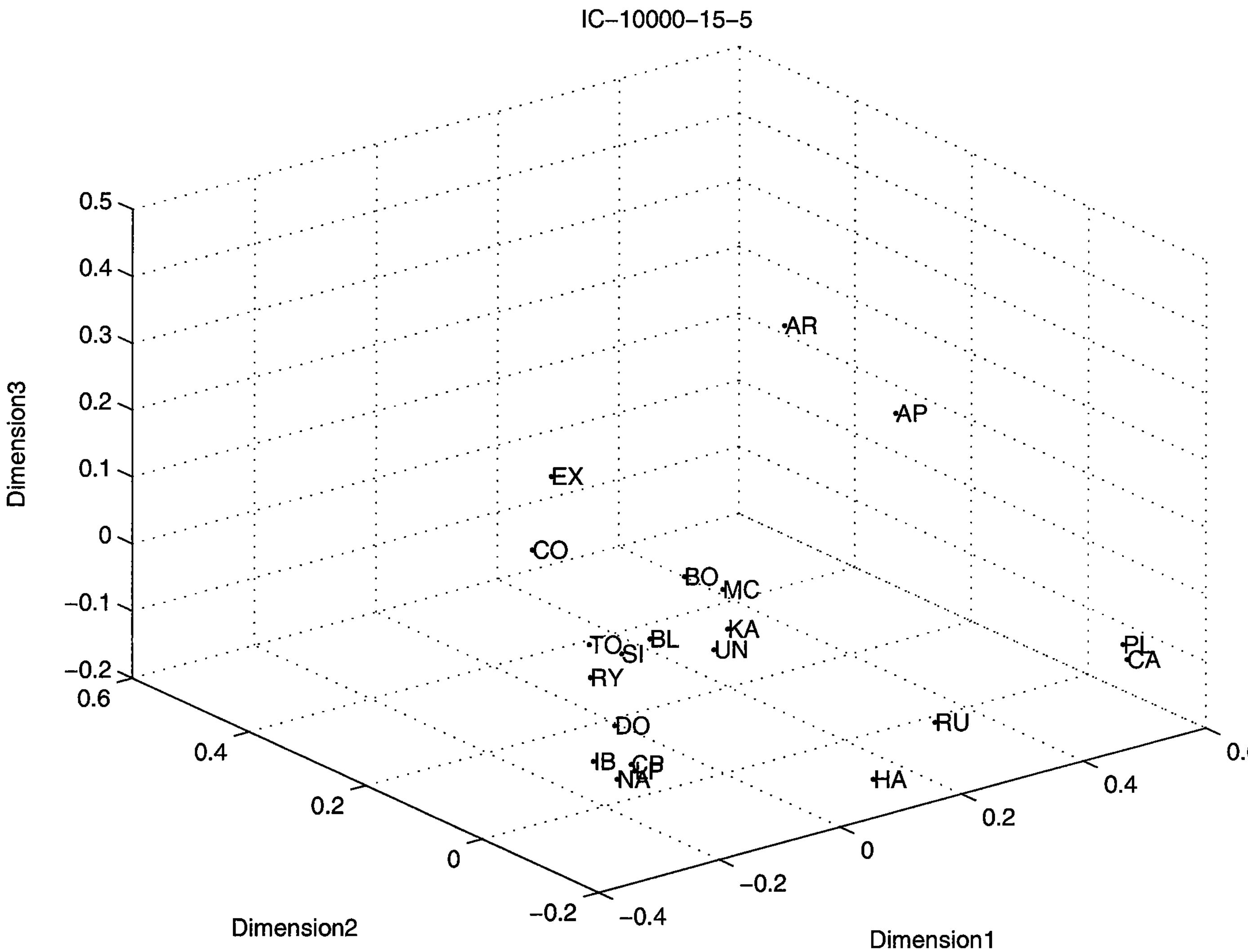
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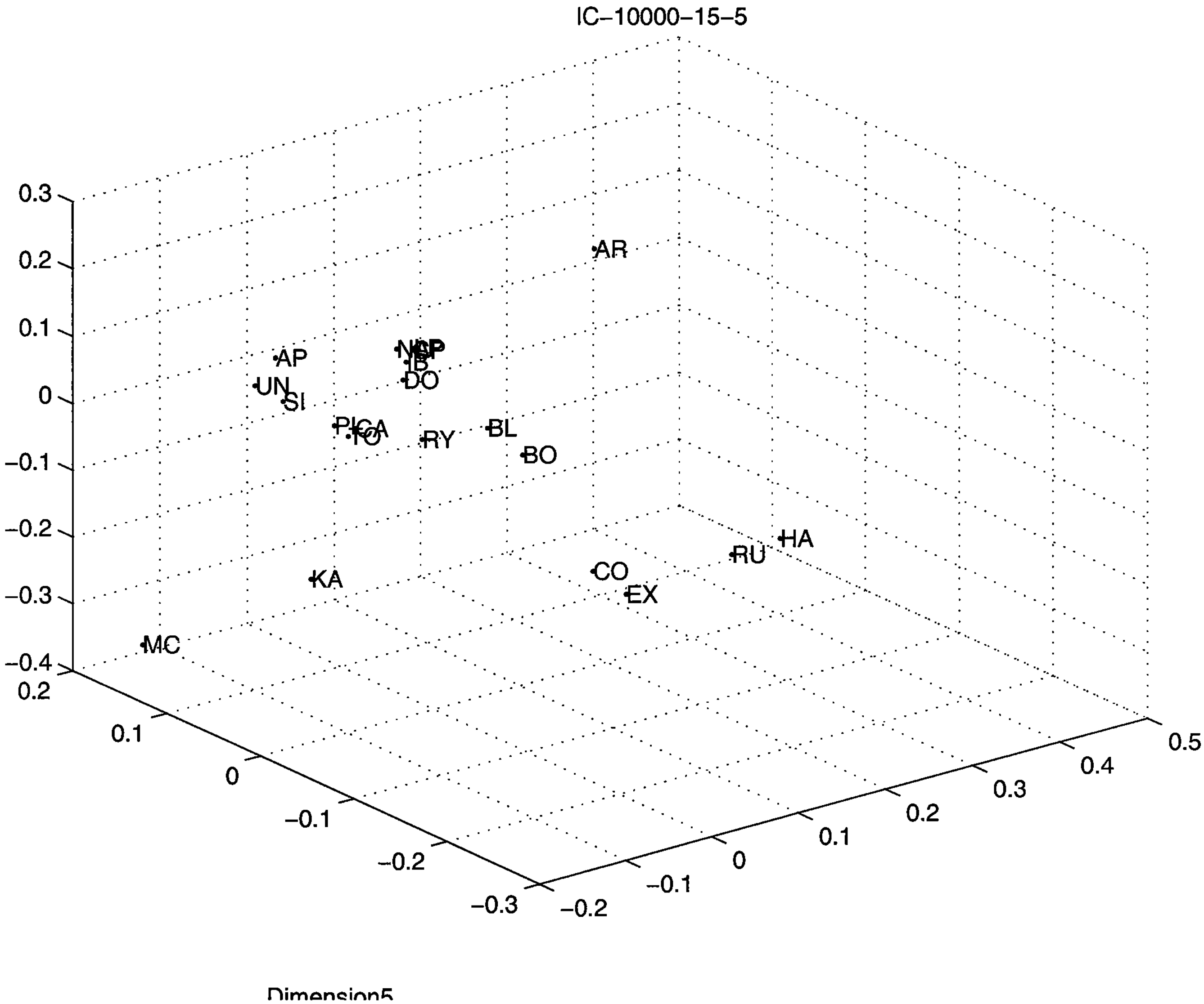

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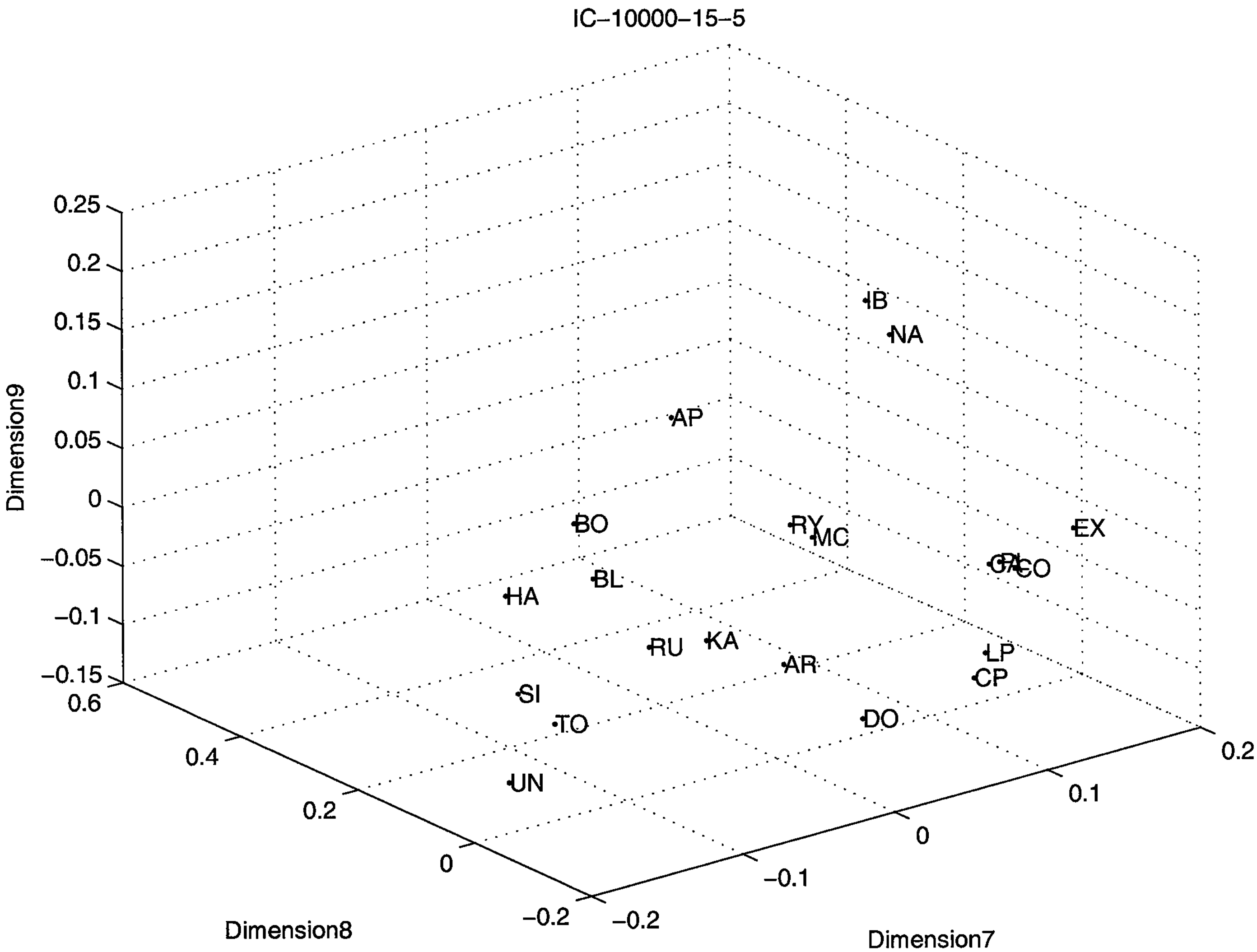

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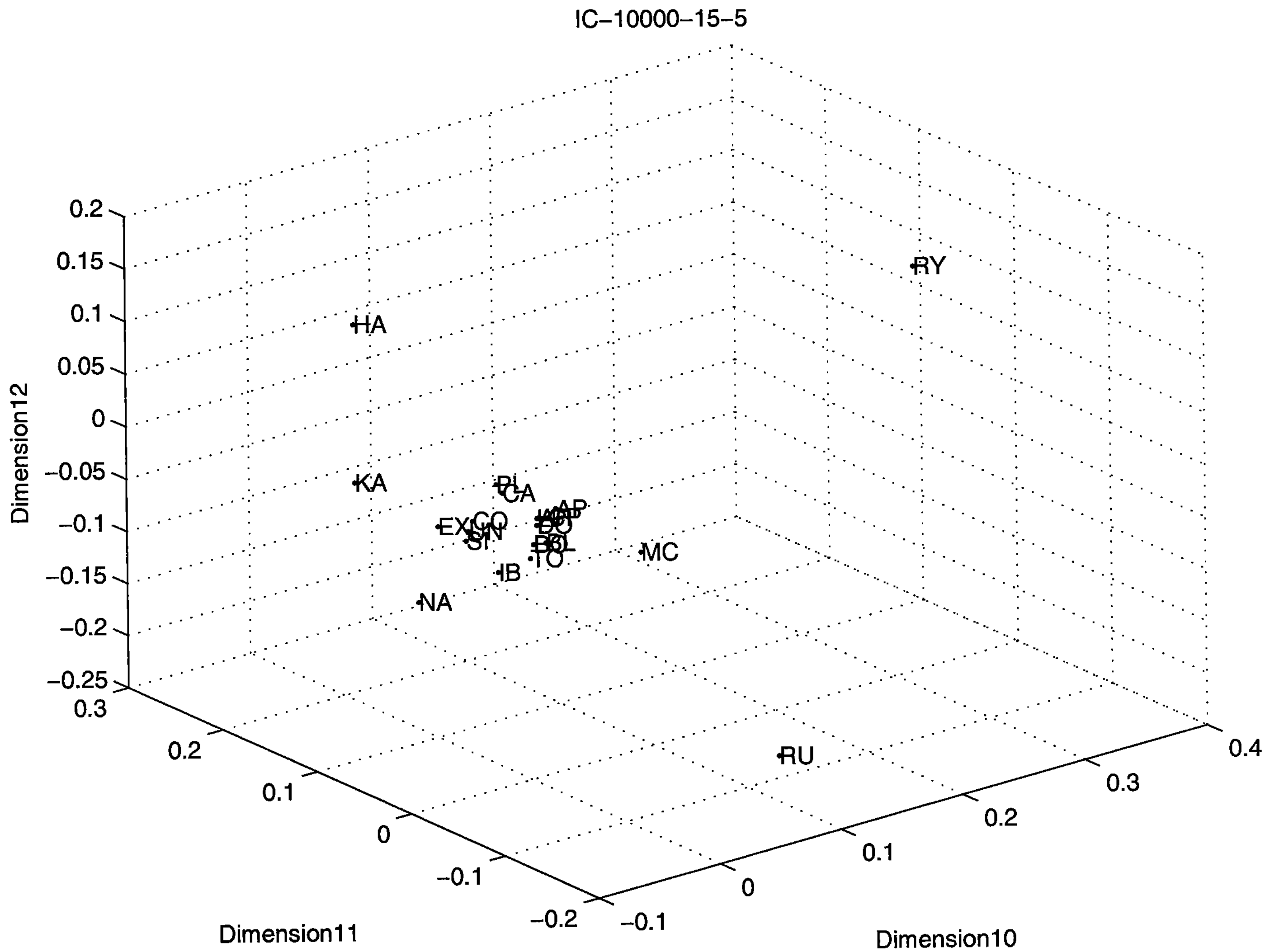

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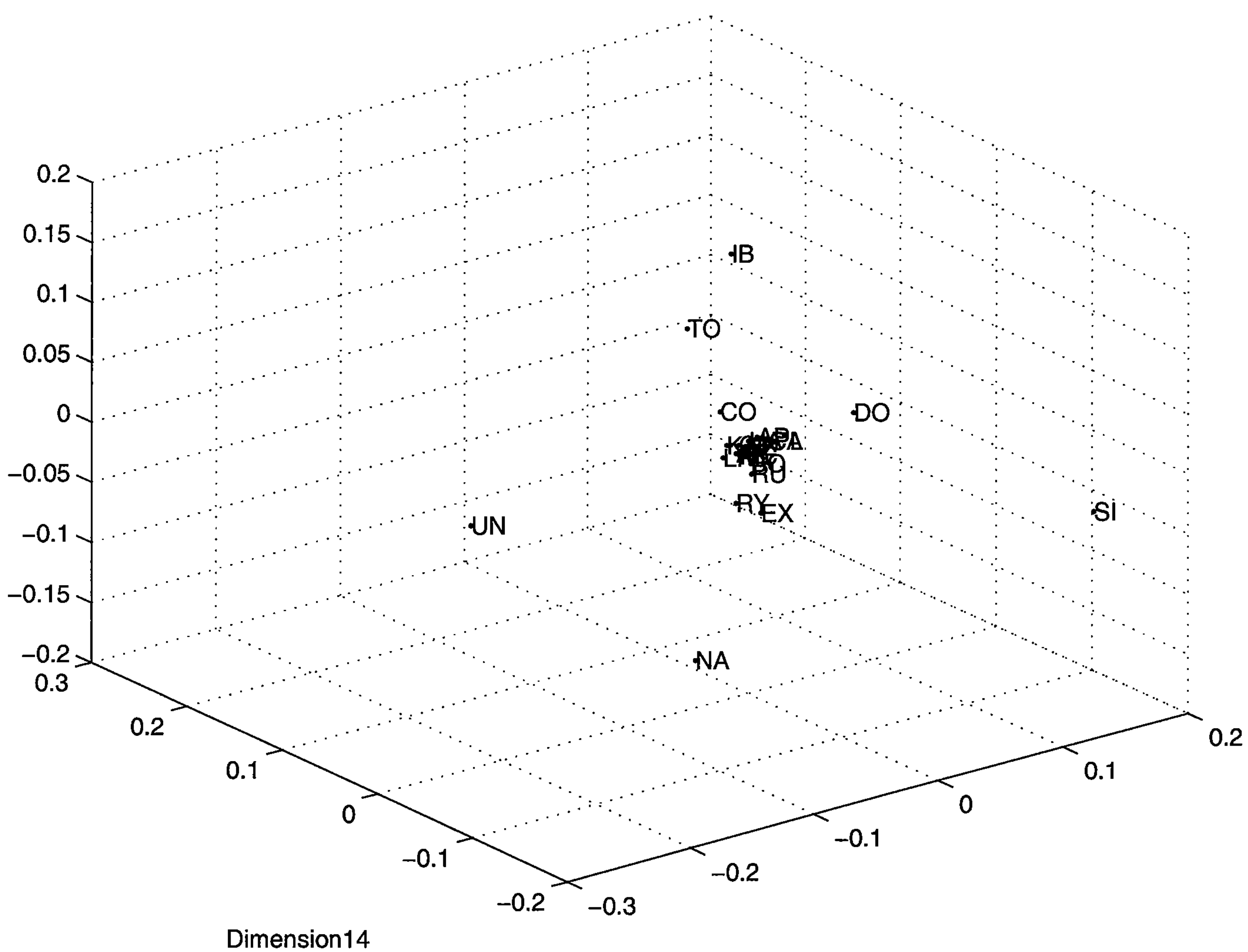

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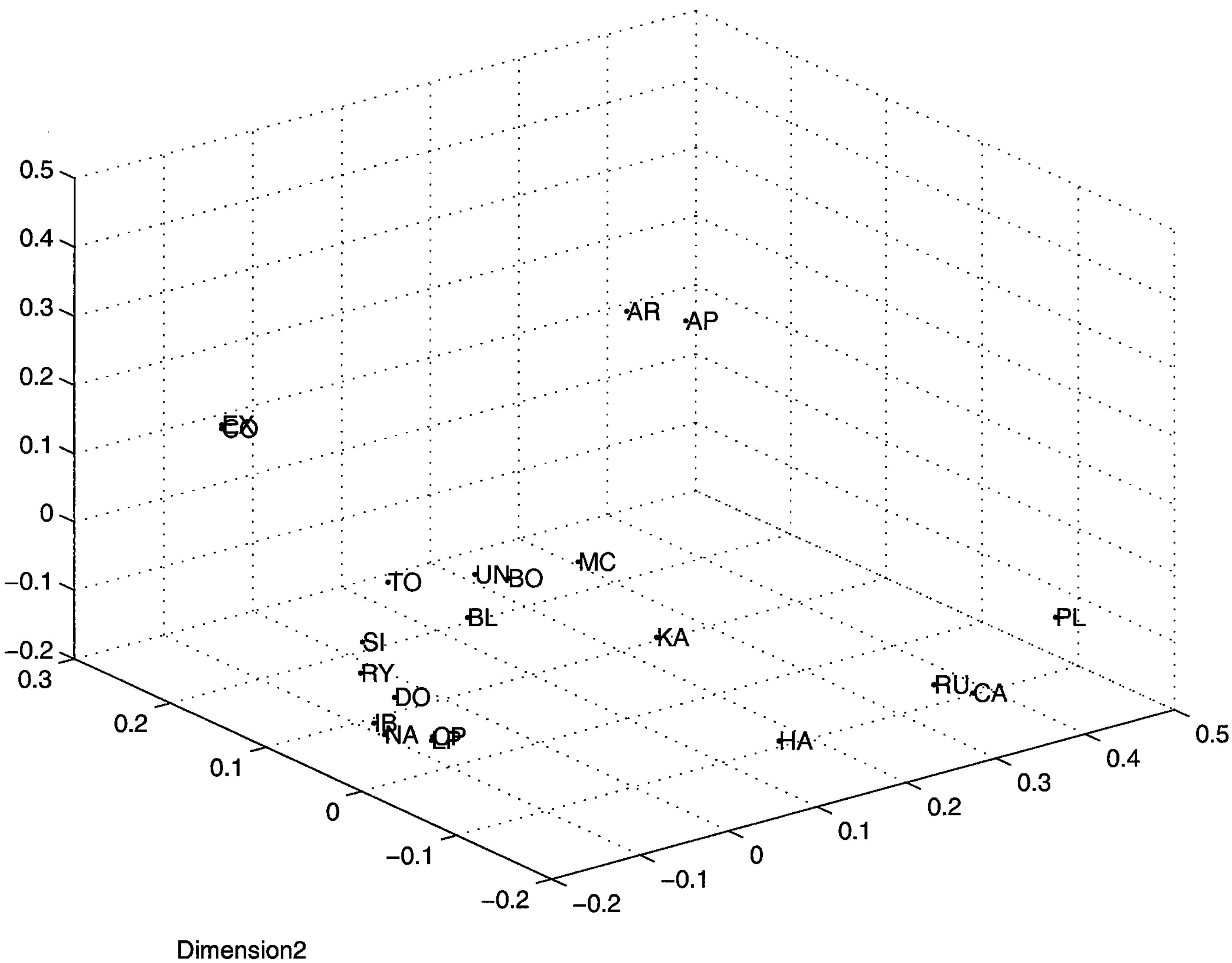

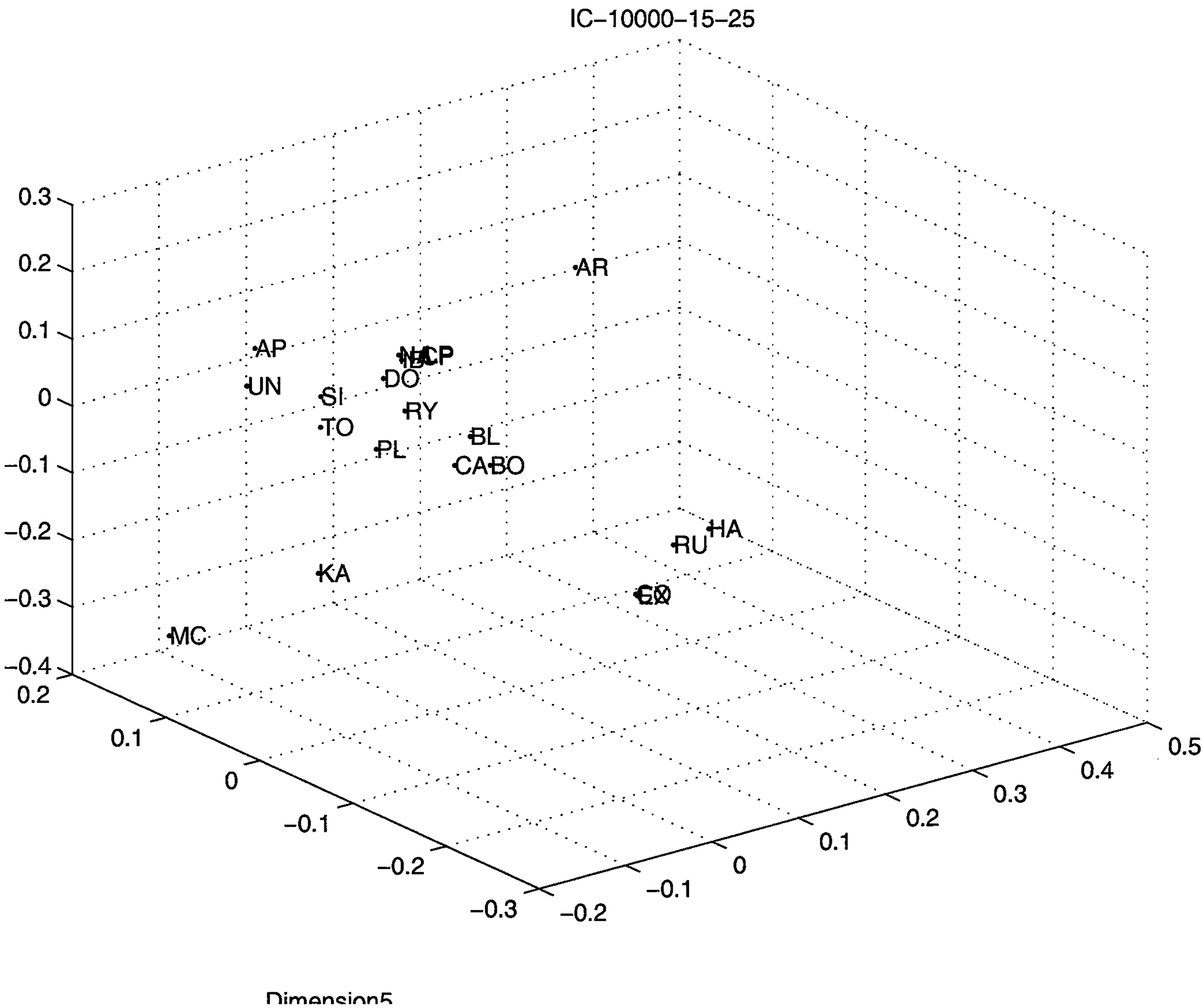
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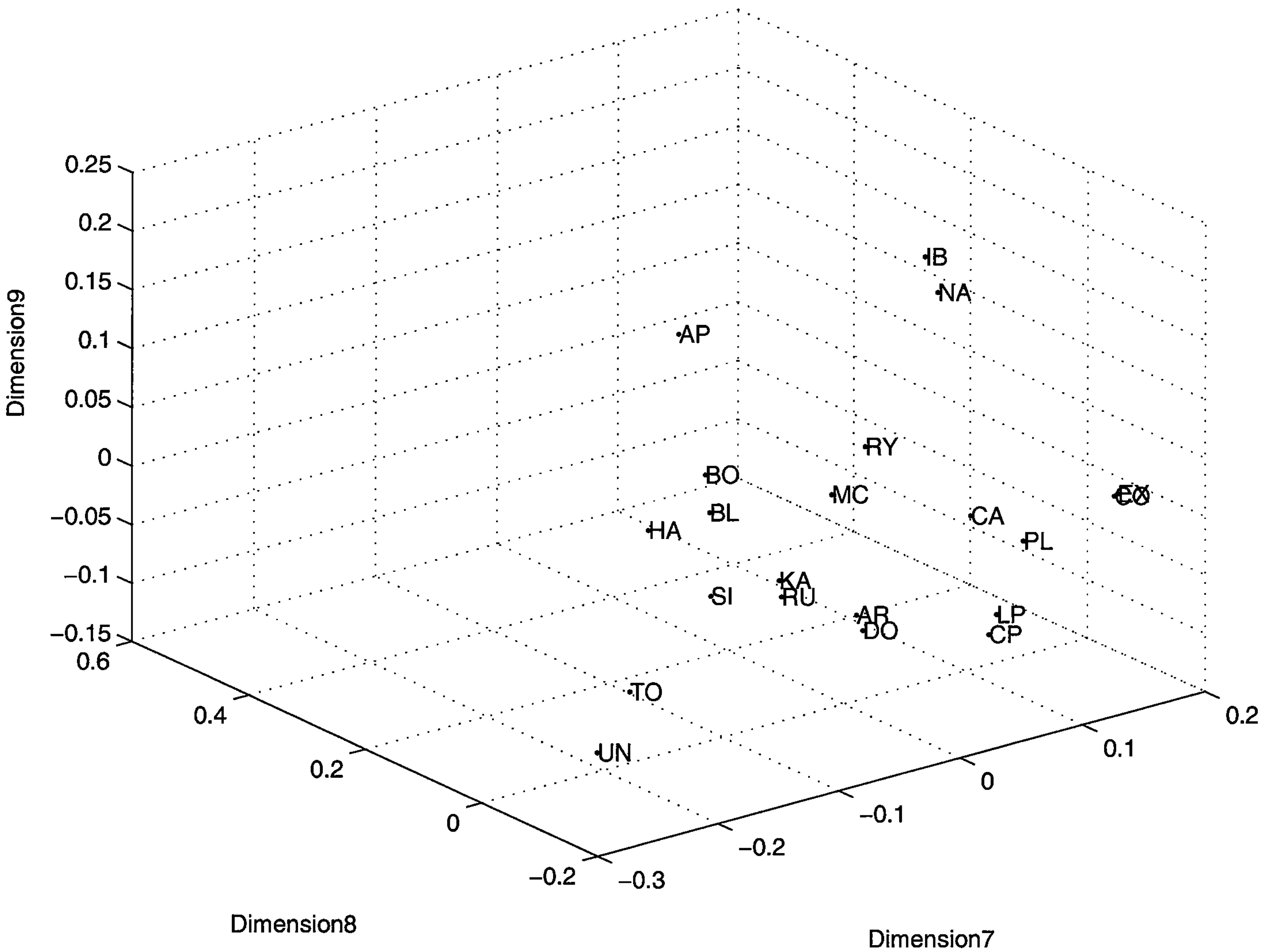

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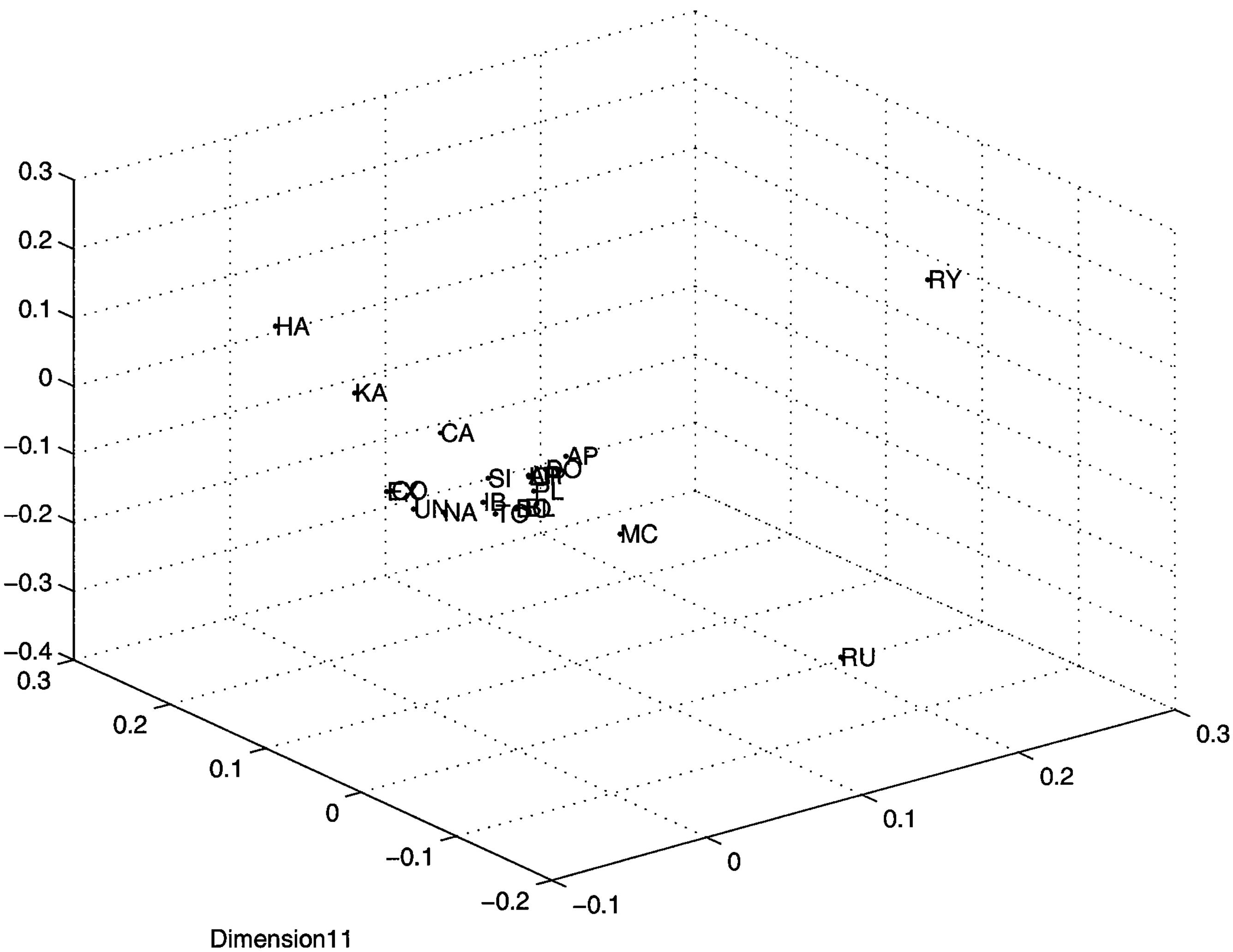

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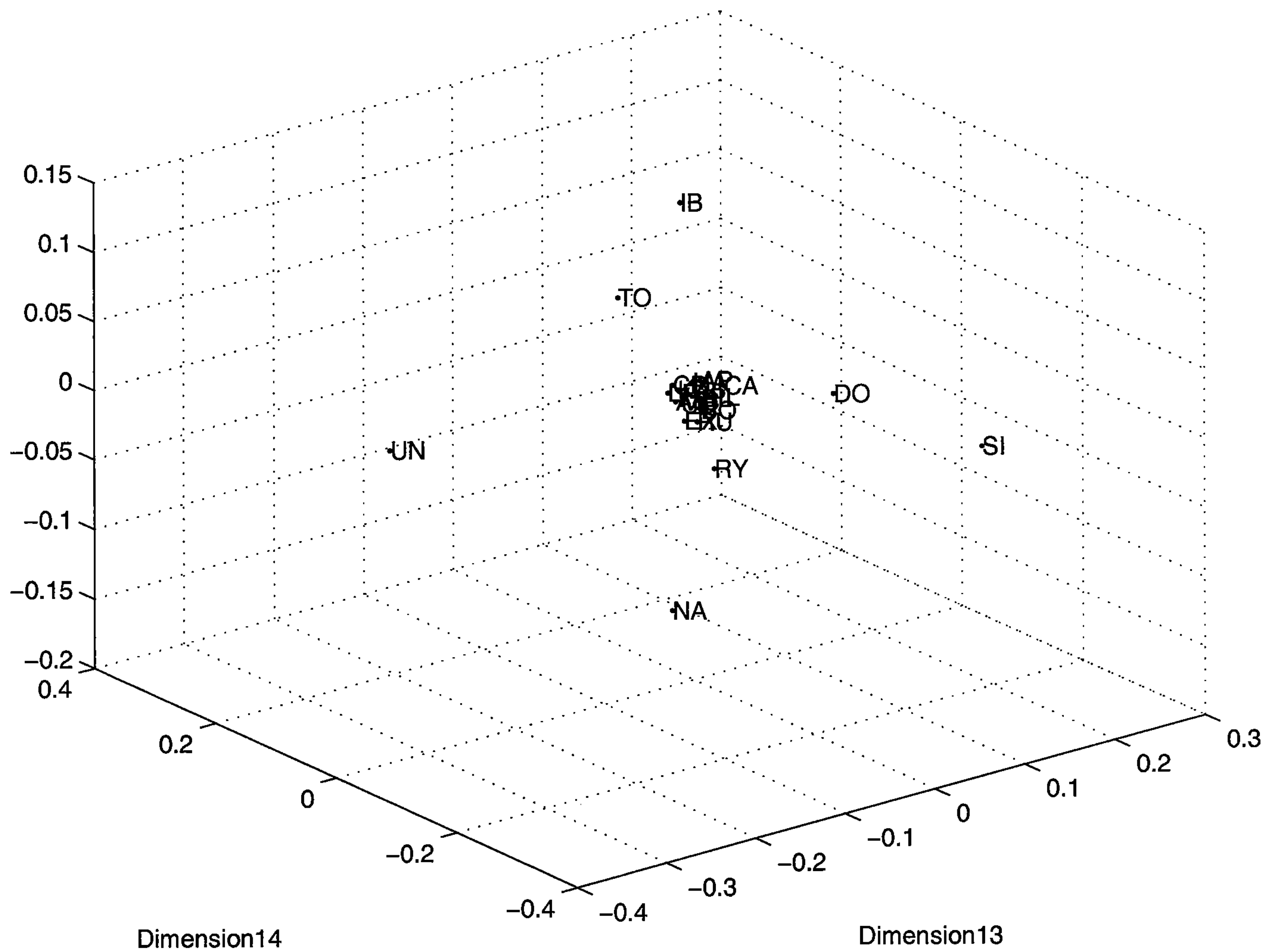

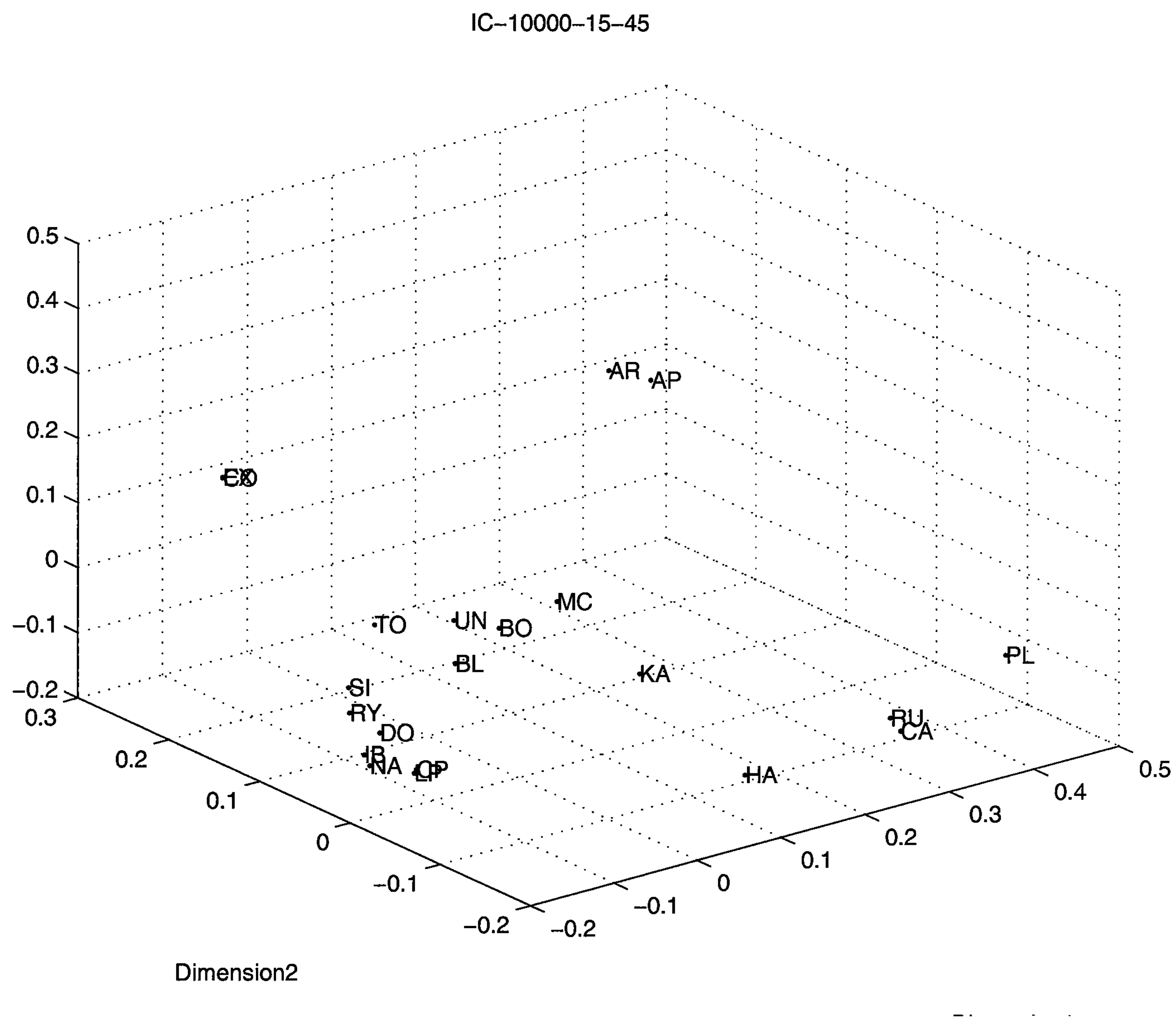

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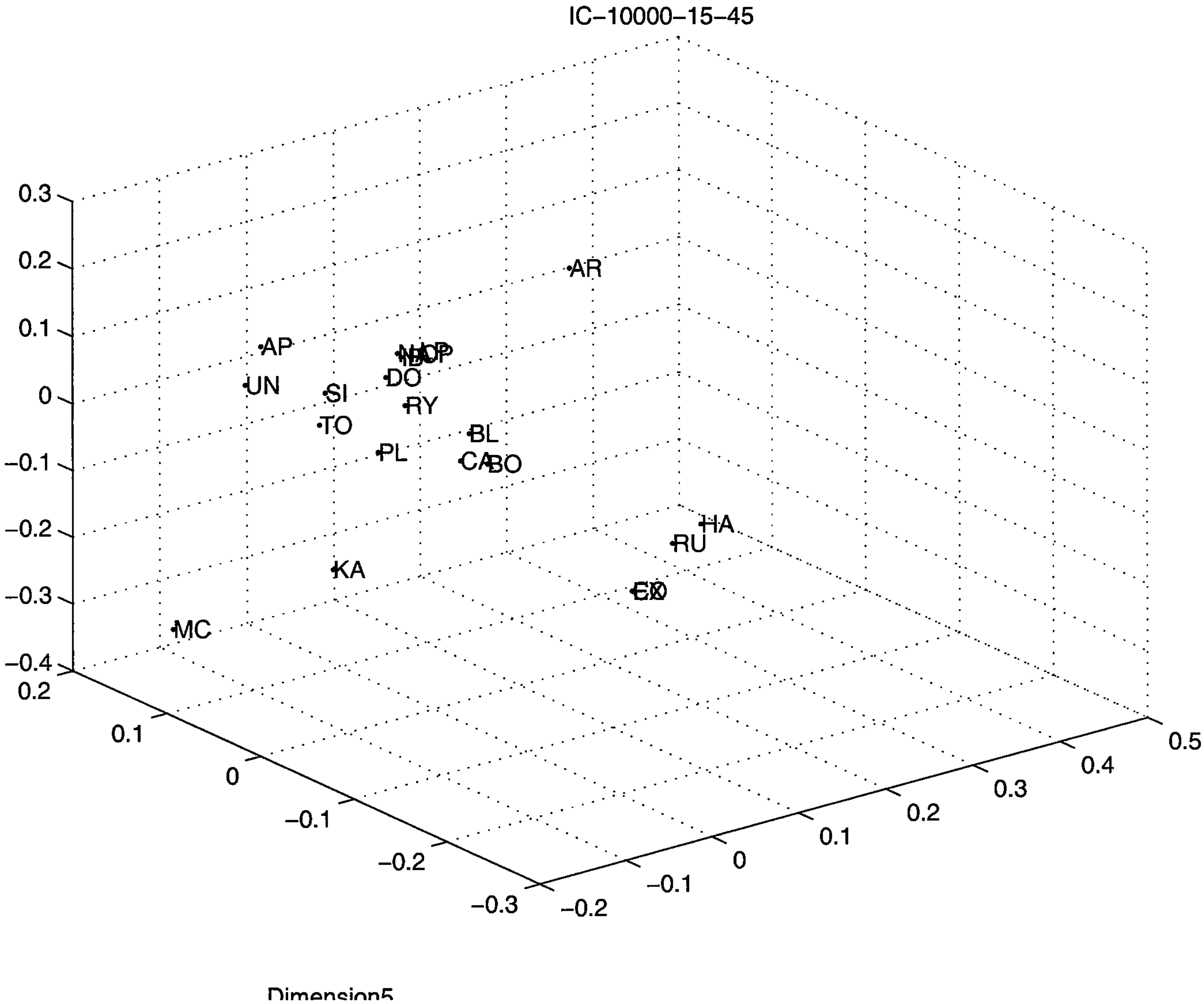
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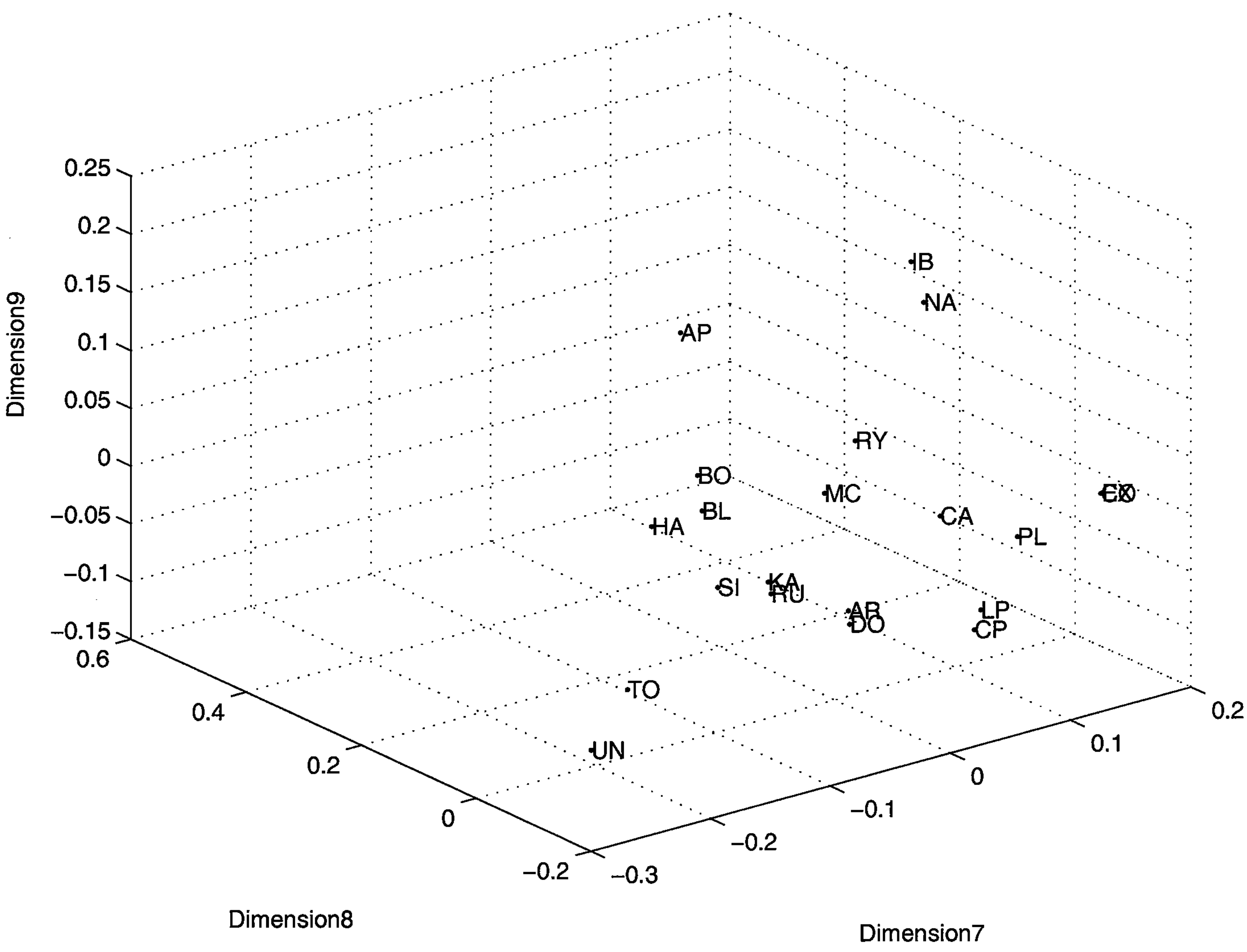

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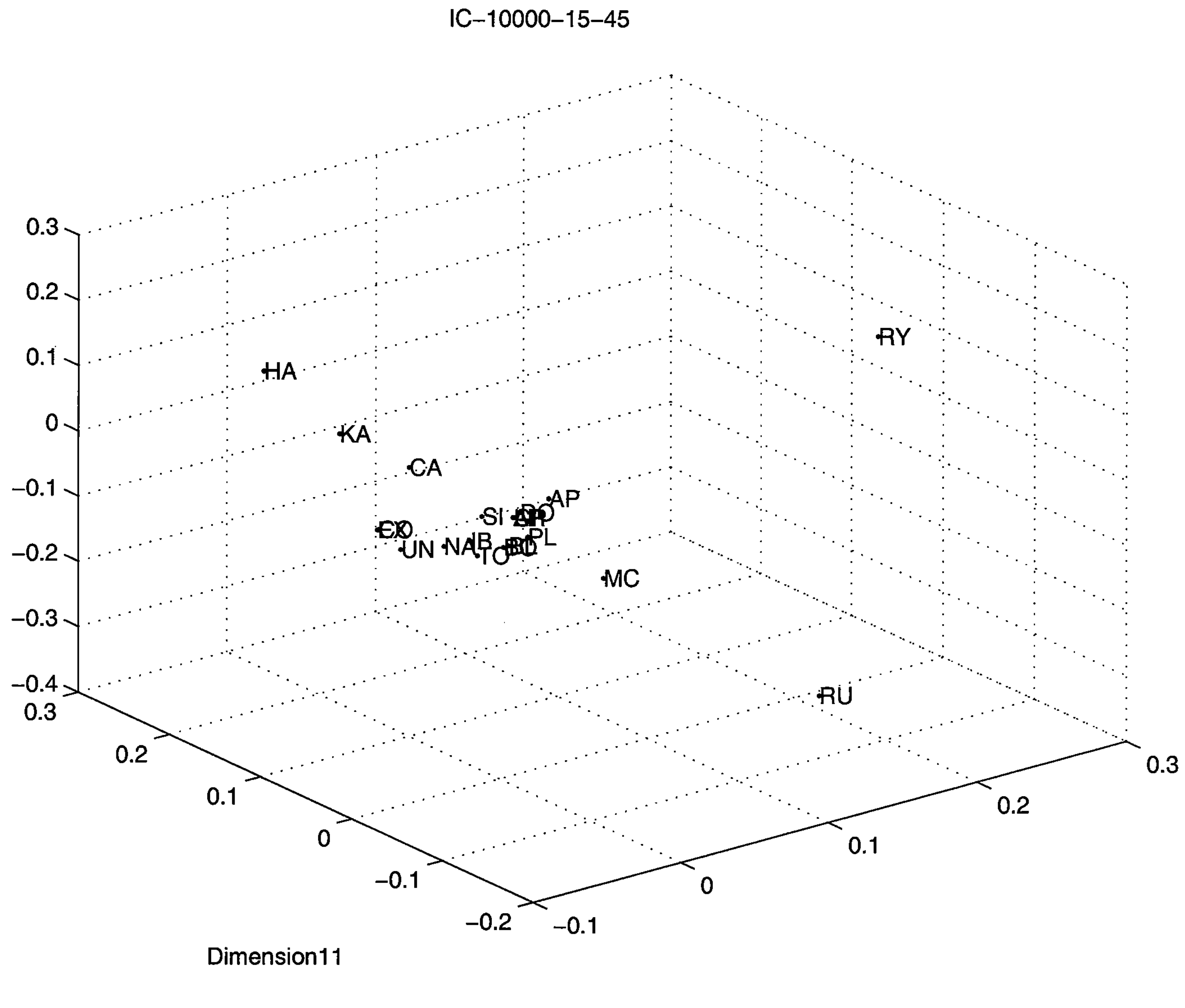
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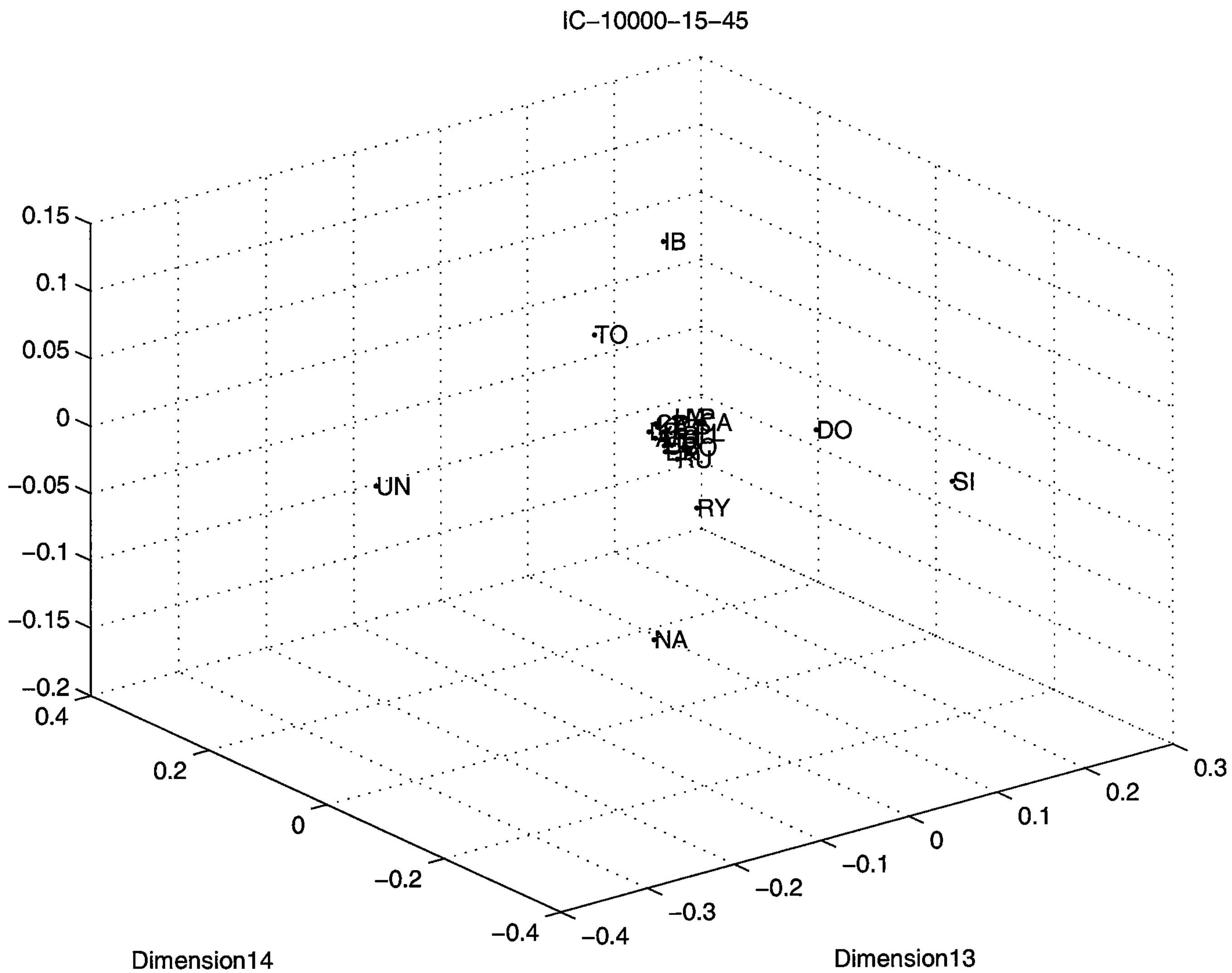
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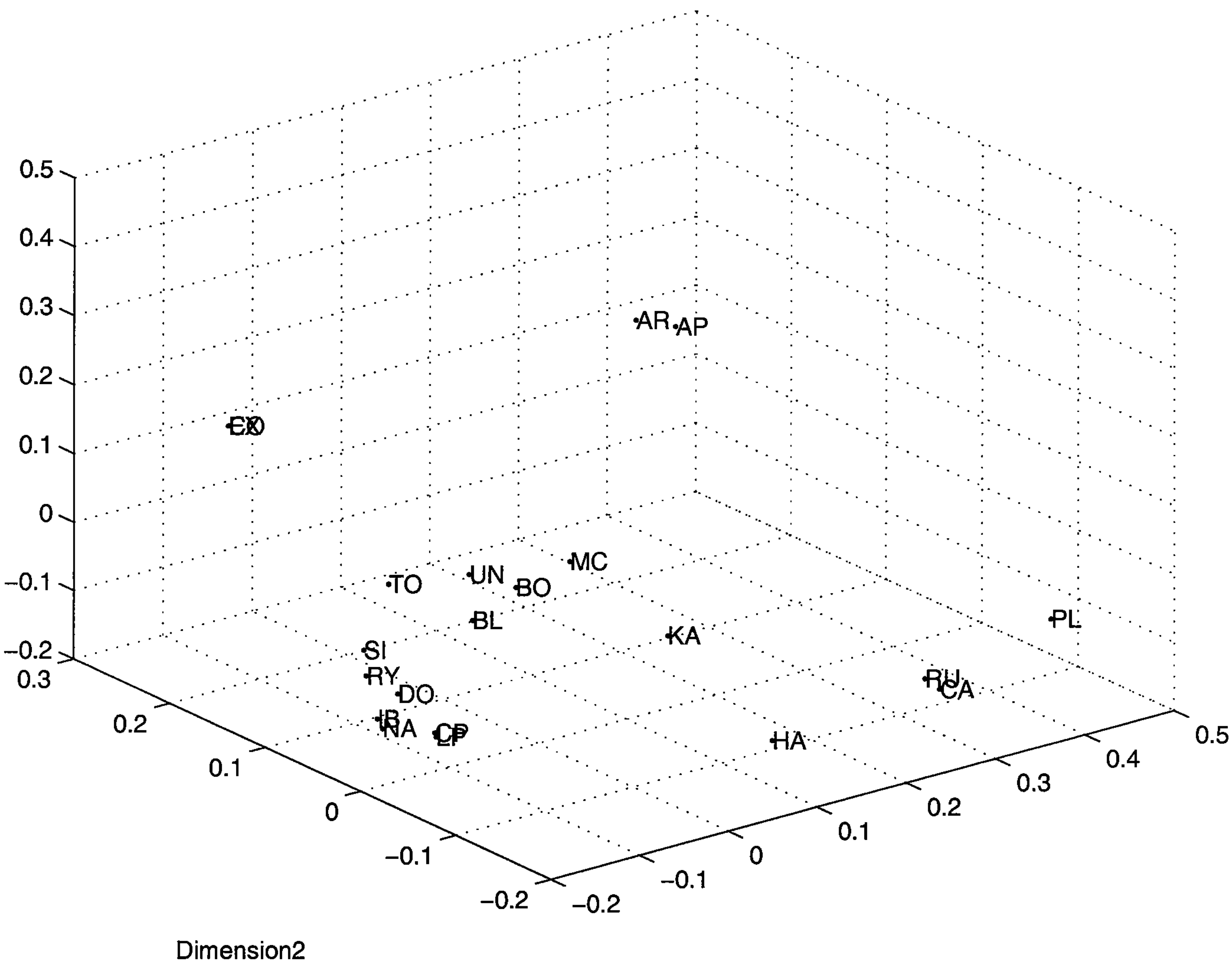

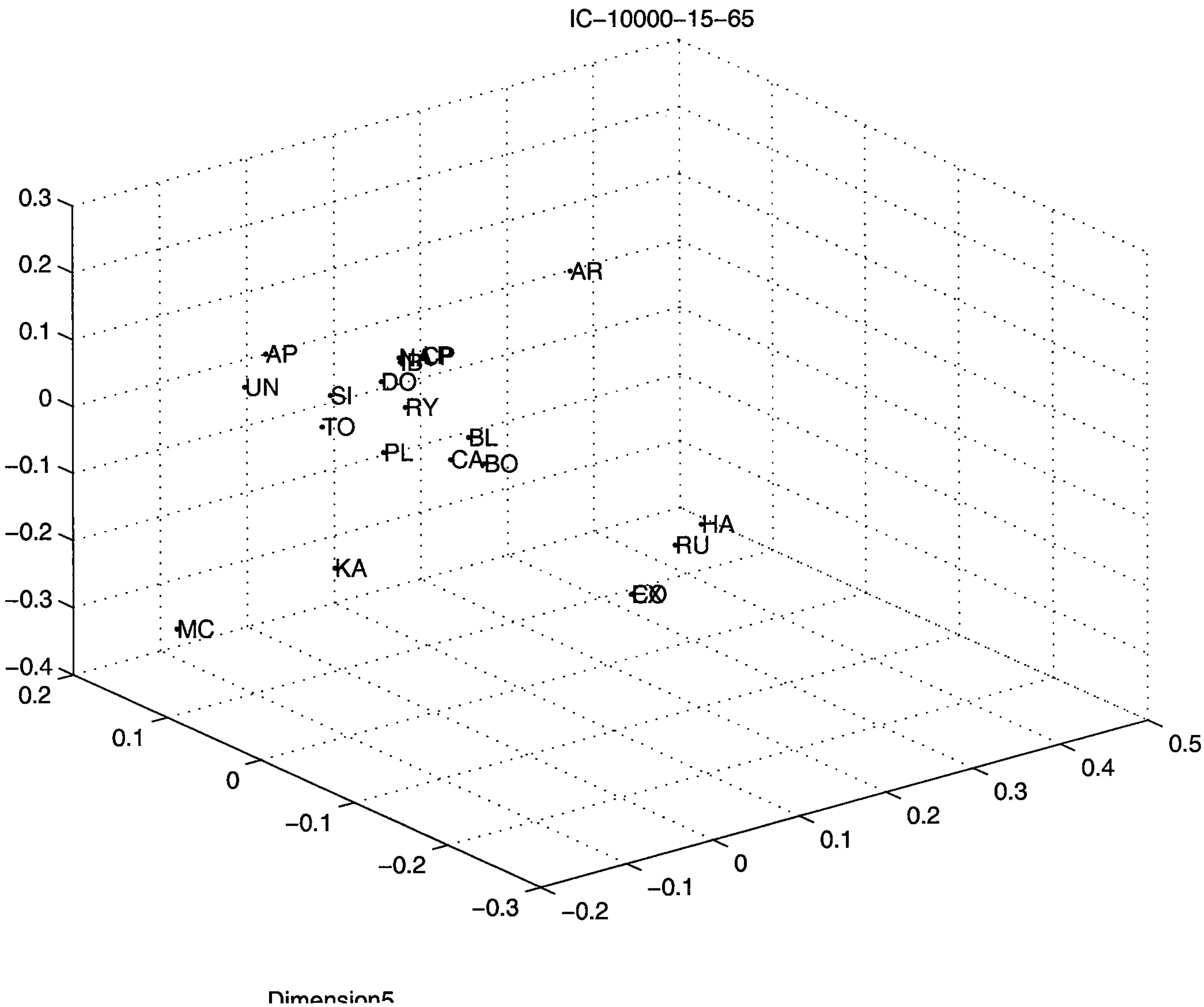
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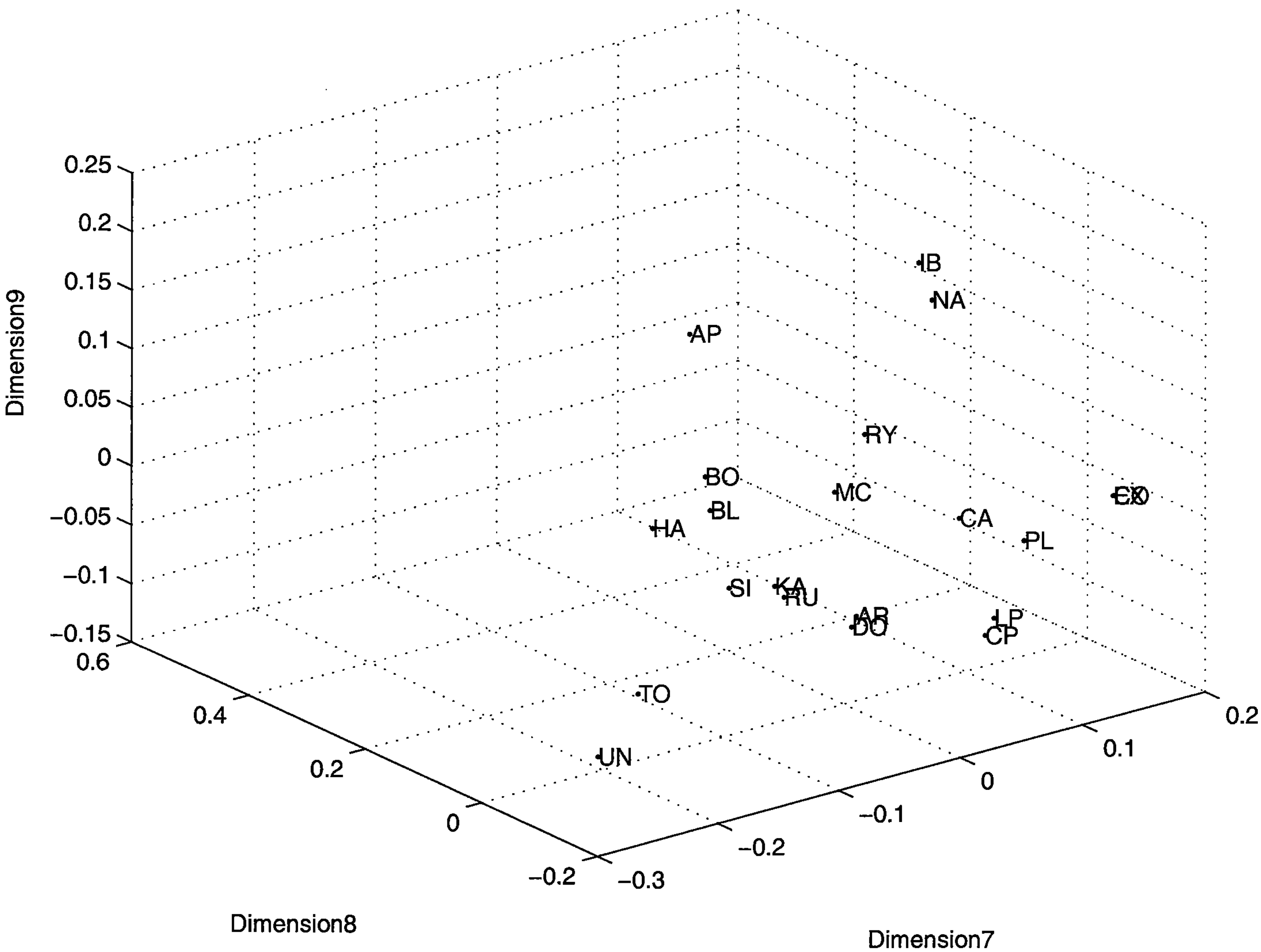

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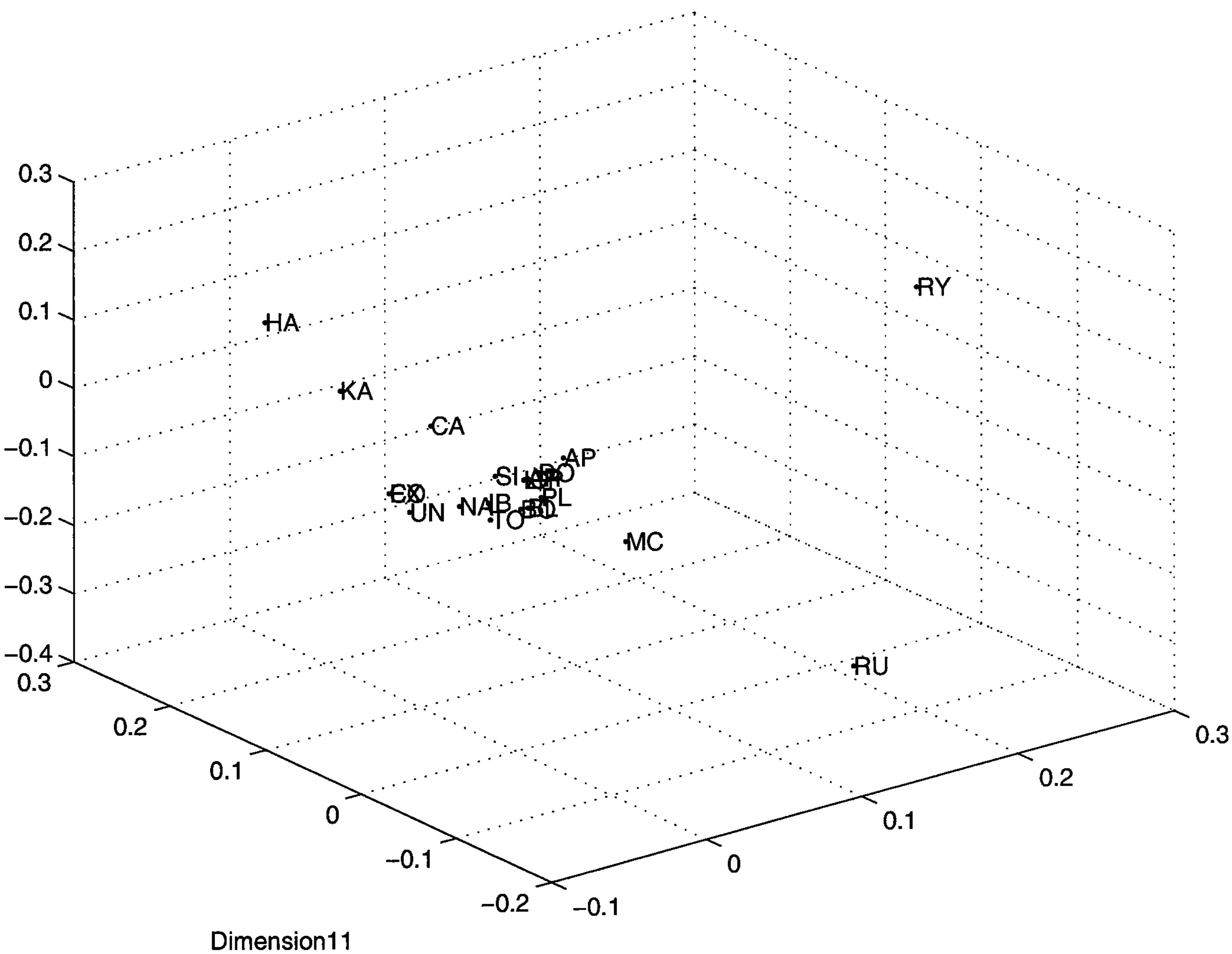
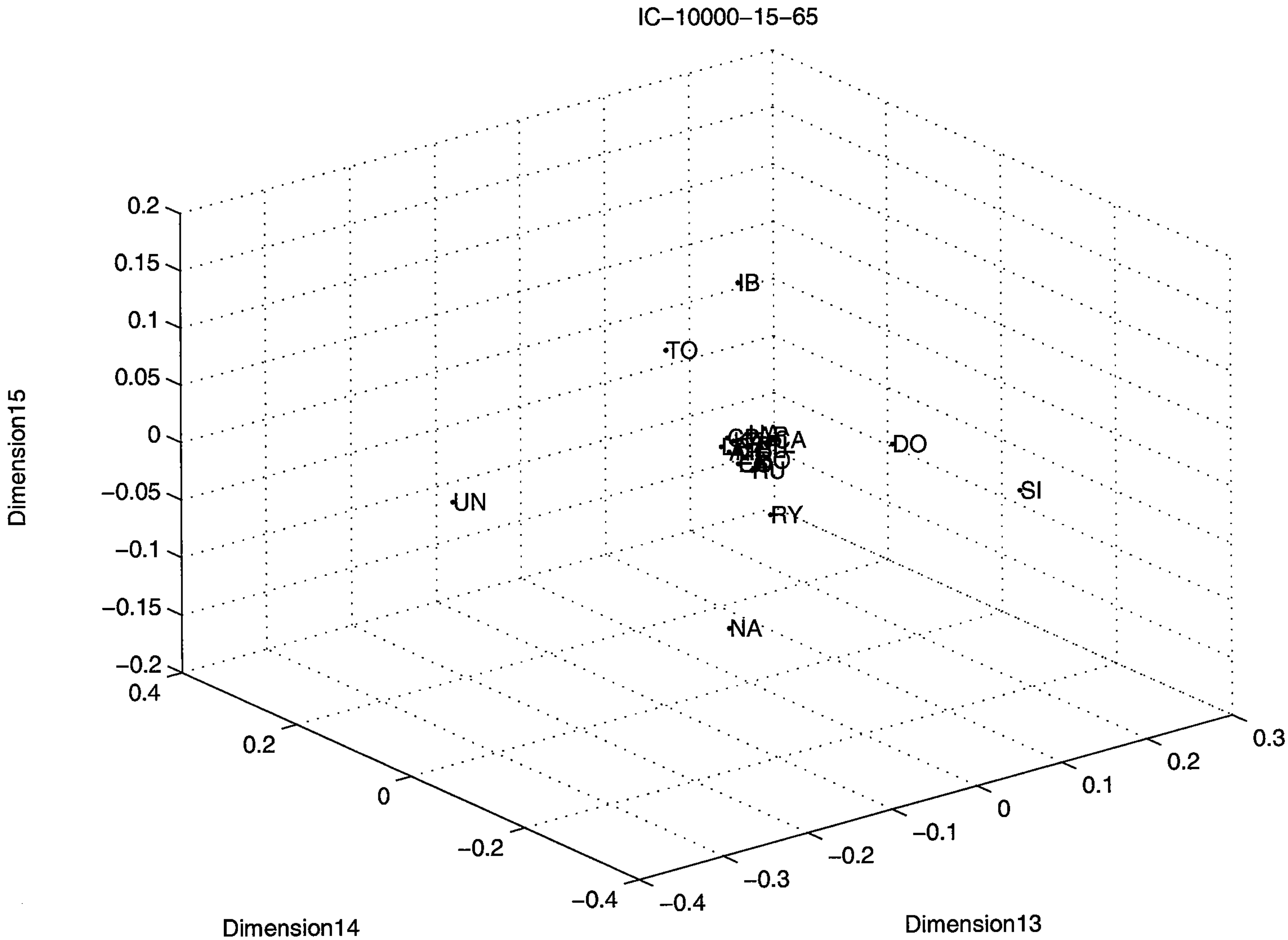
IC–10000–15–65

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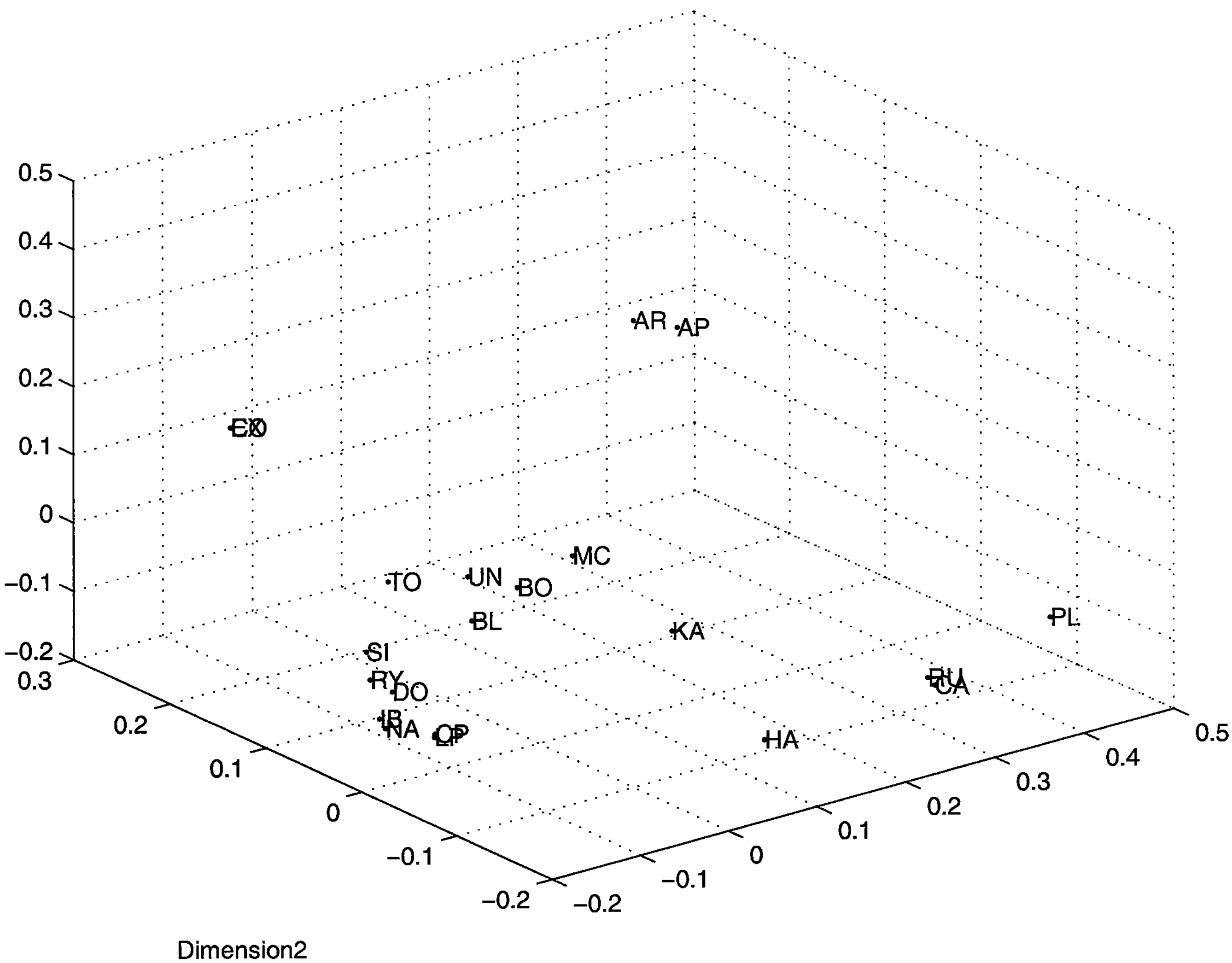
IC−10000−15−85



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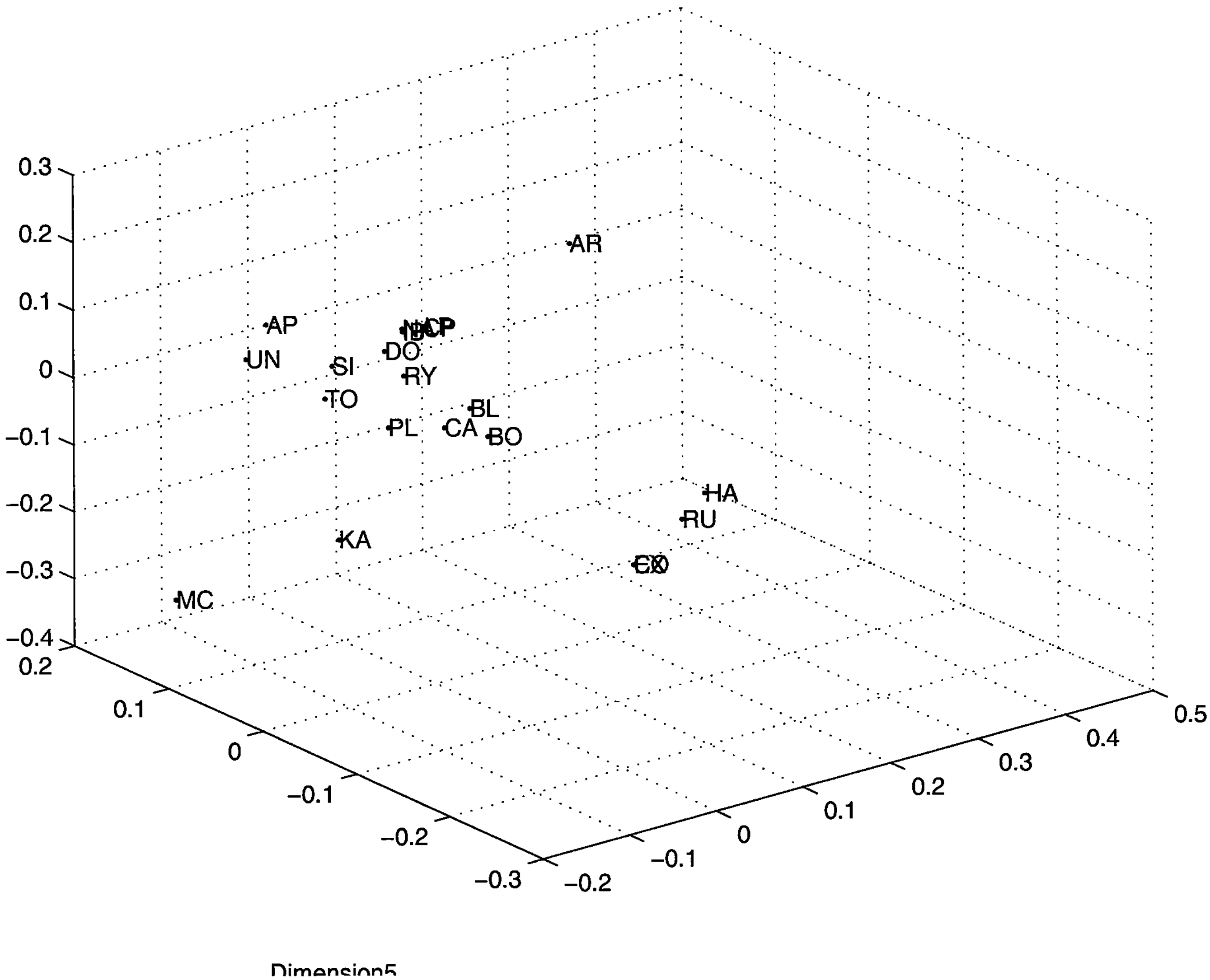

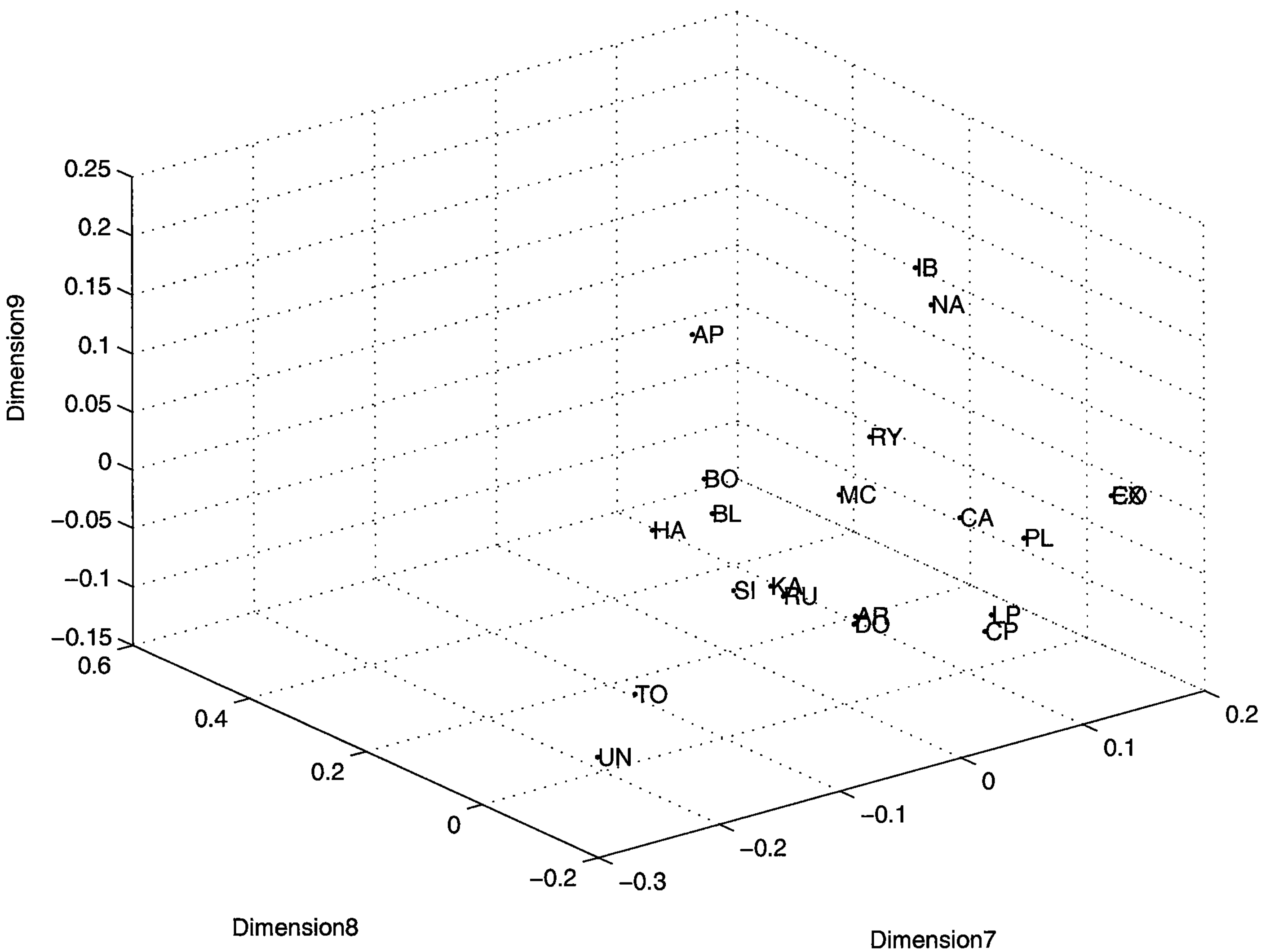

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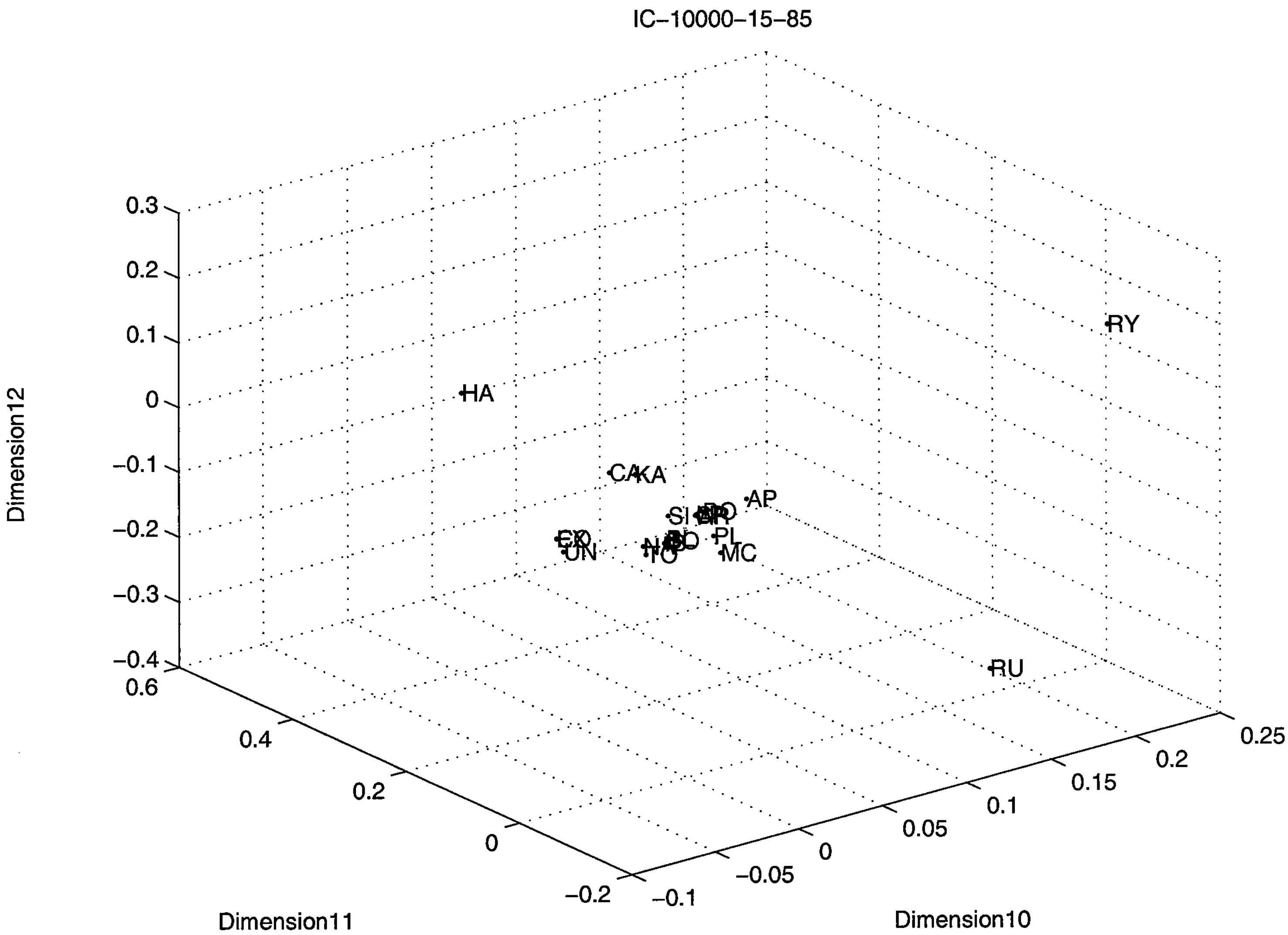

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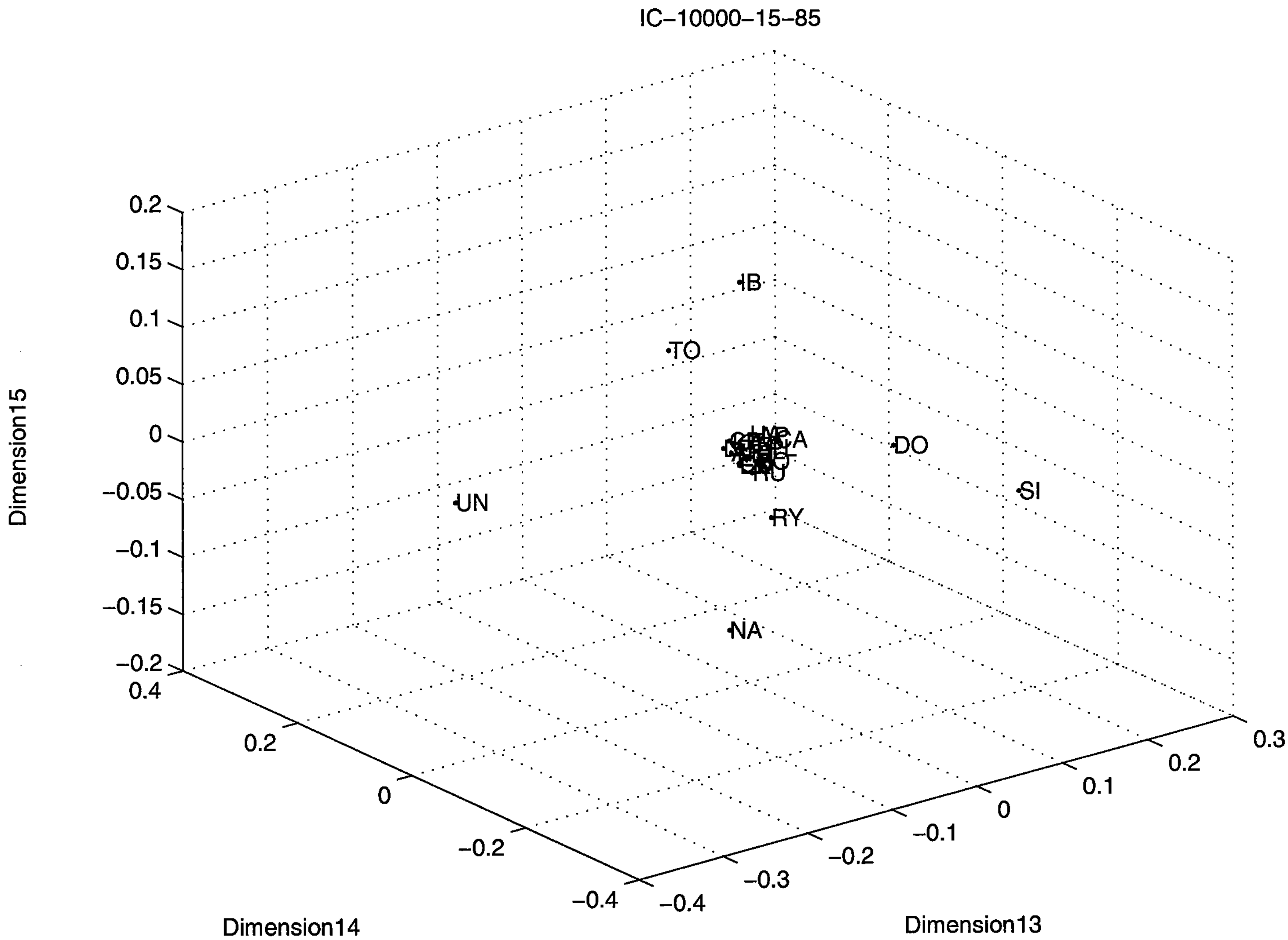
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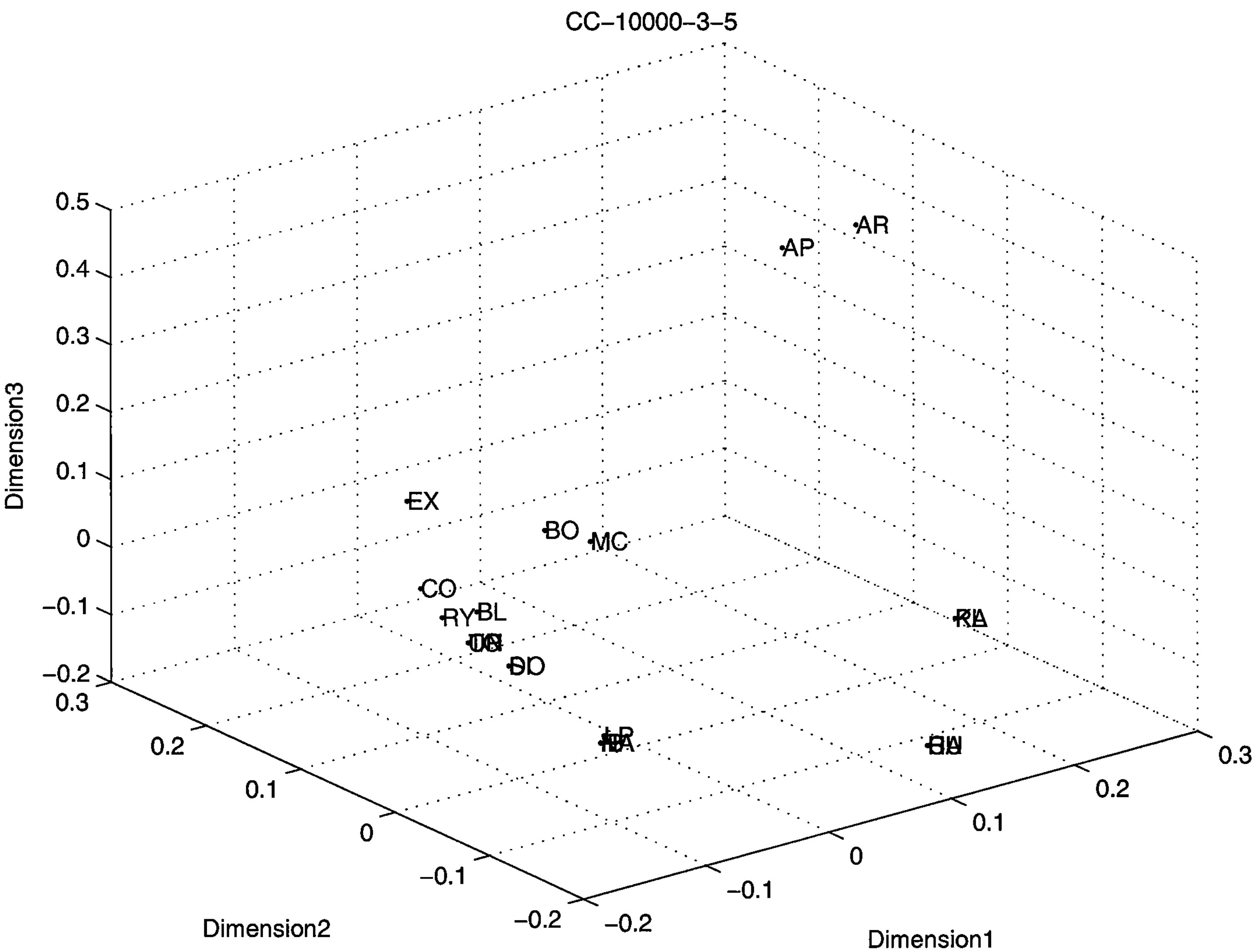

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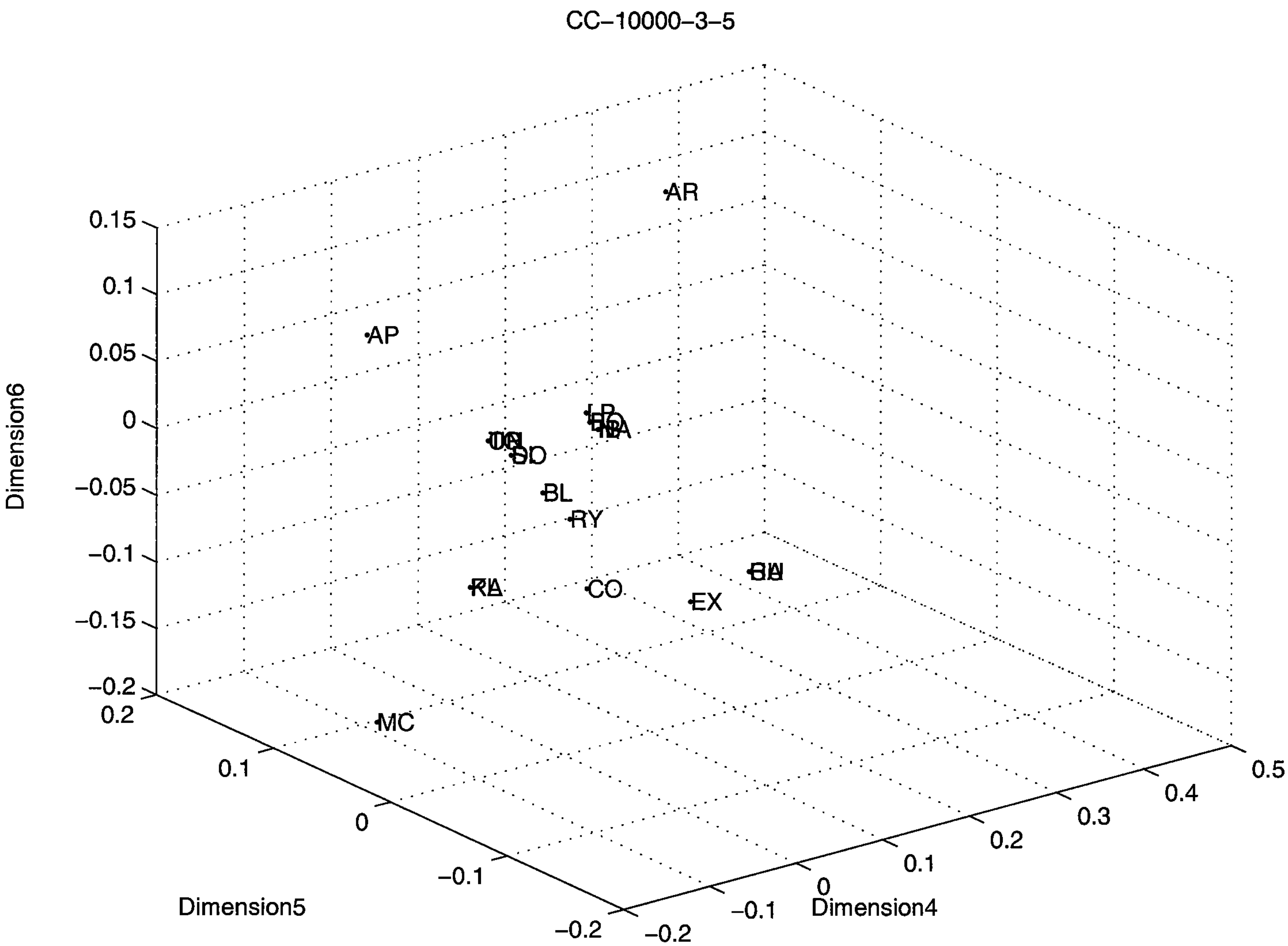

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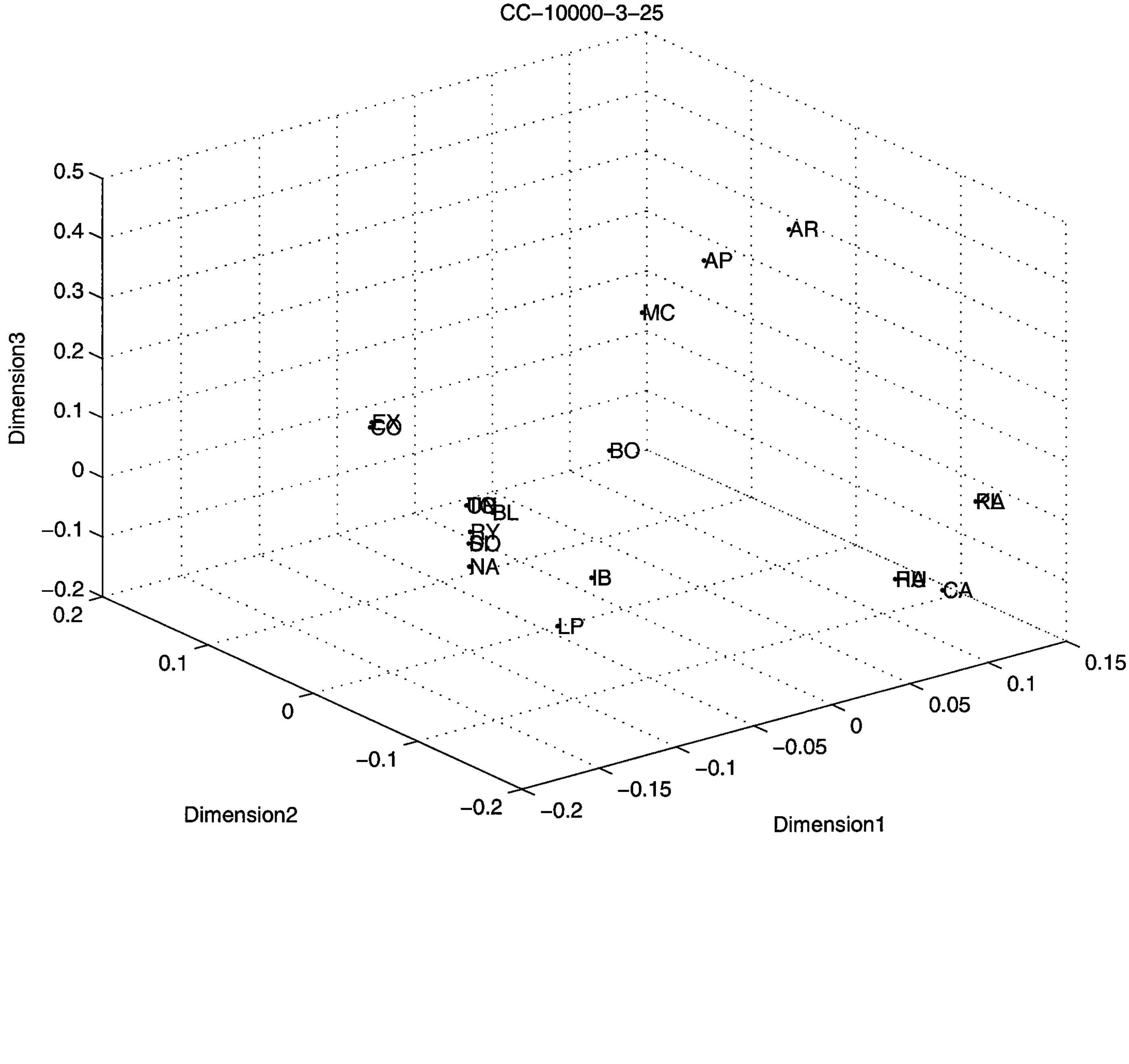

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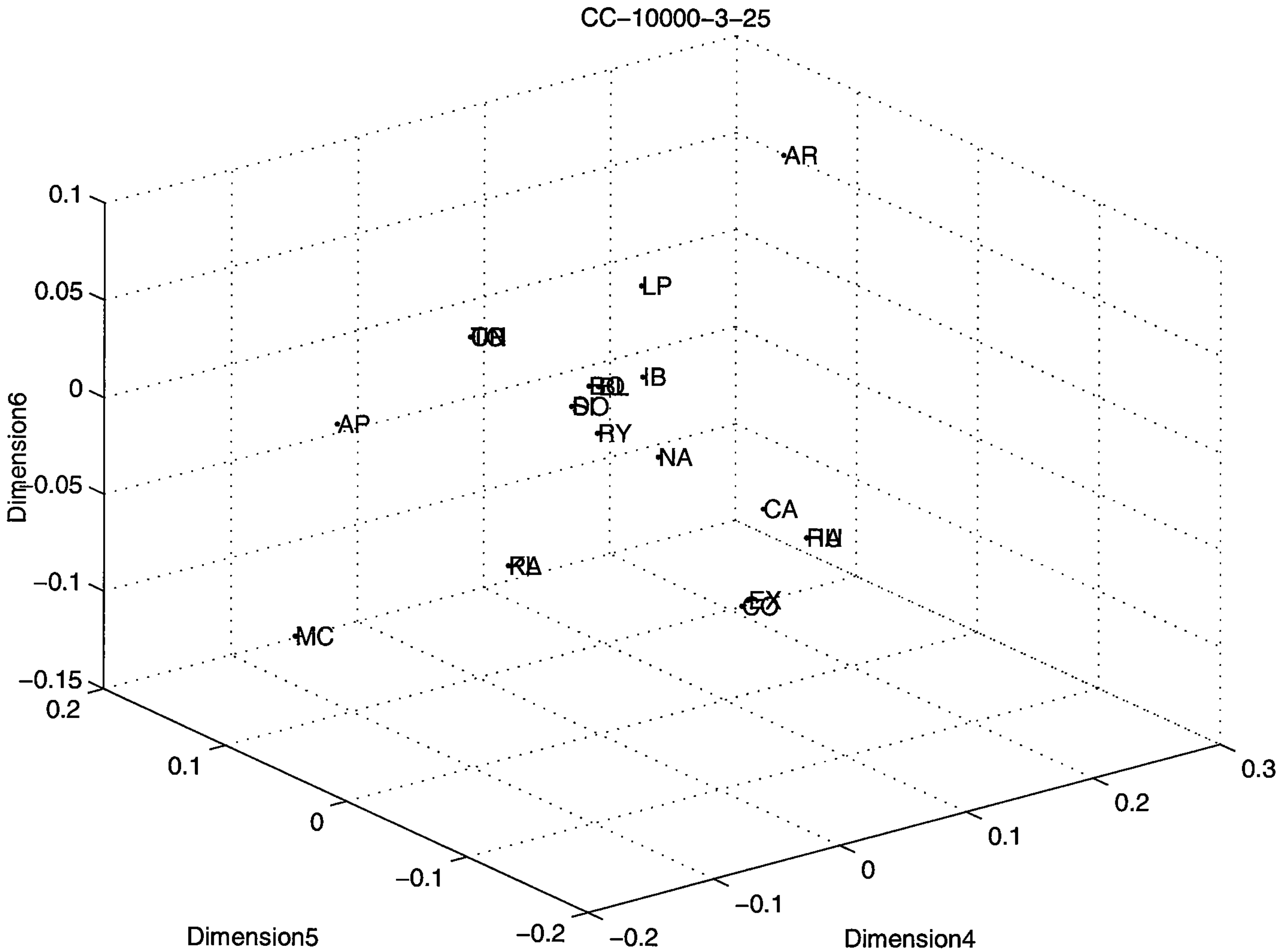

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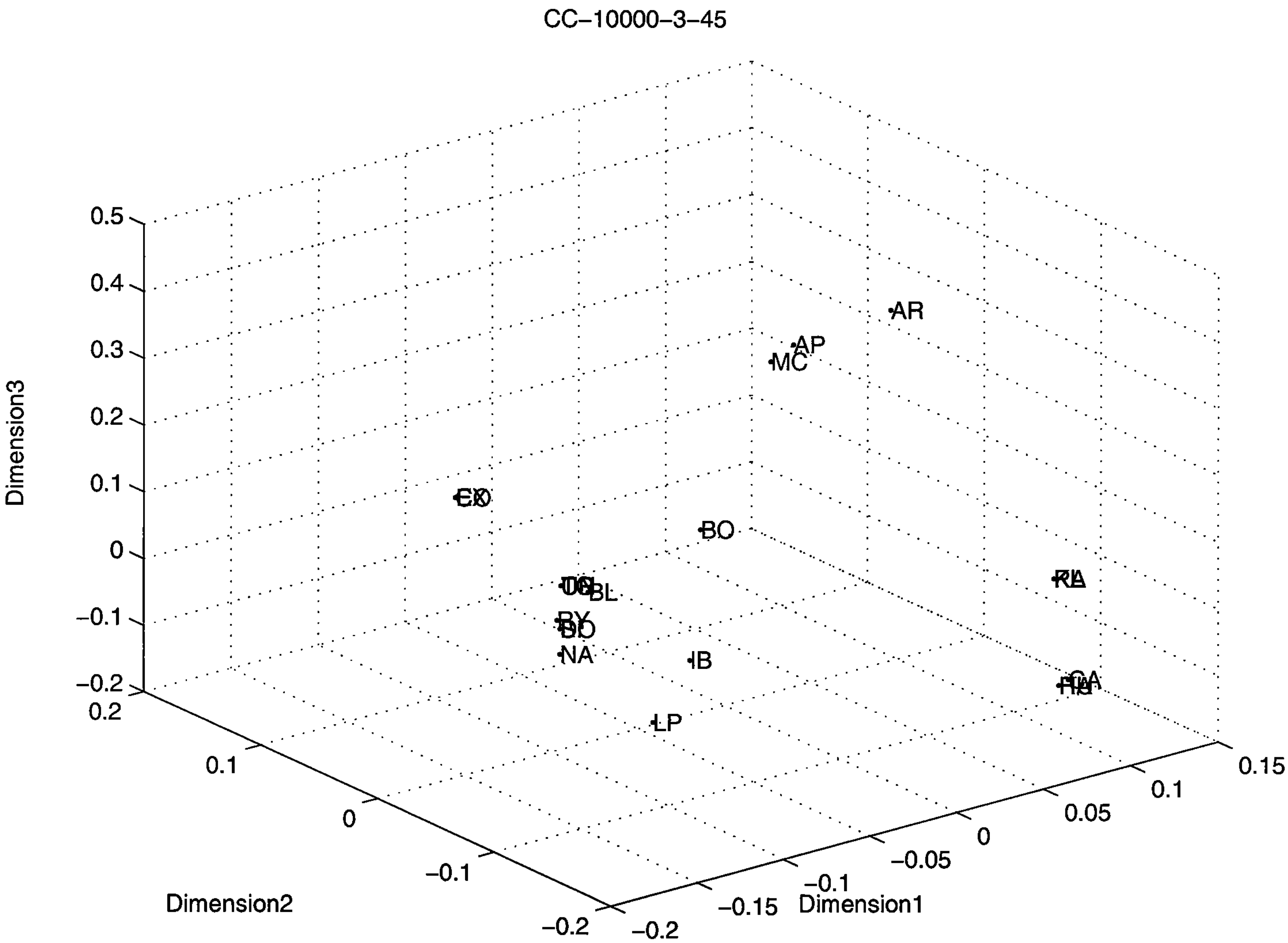

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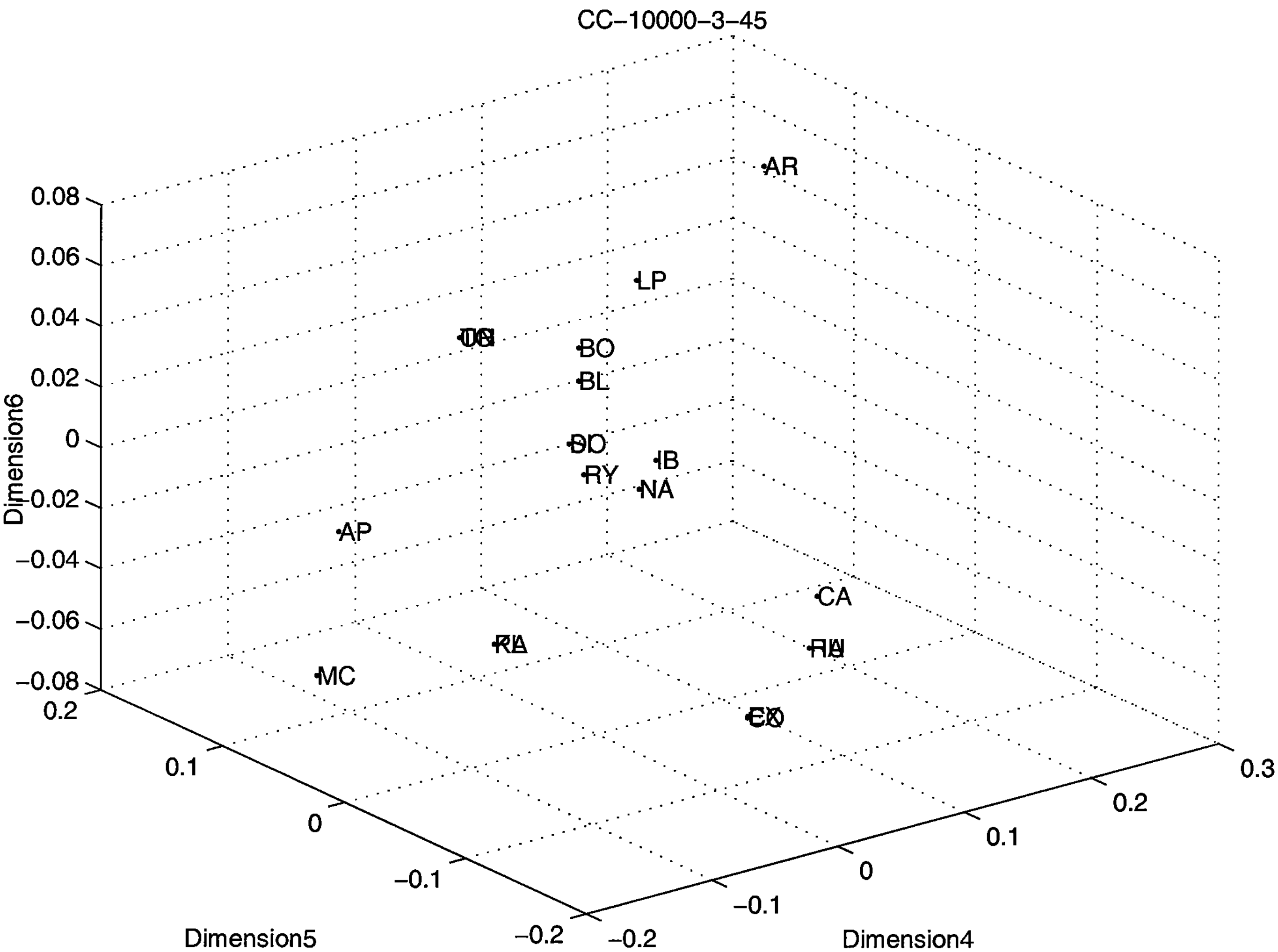

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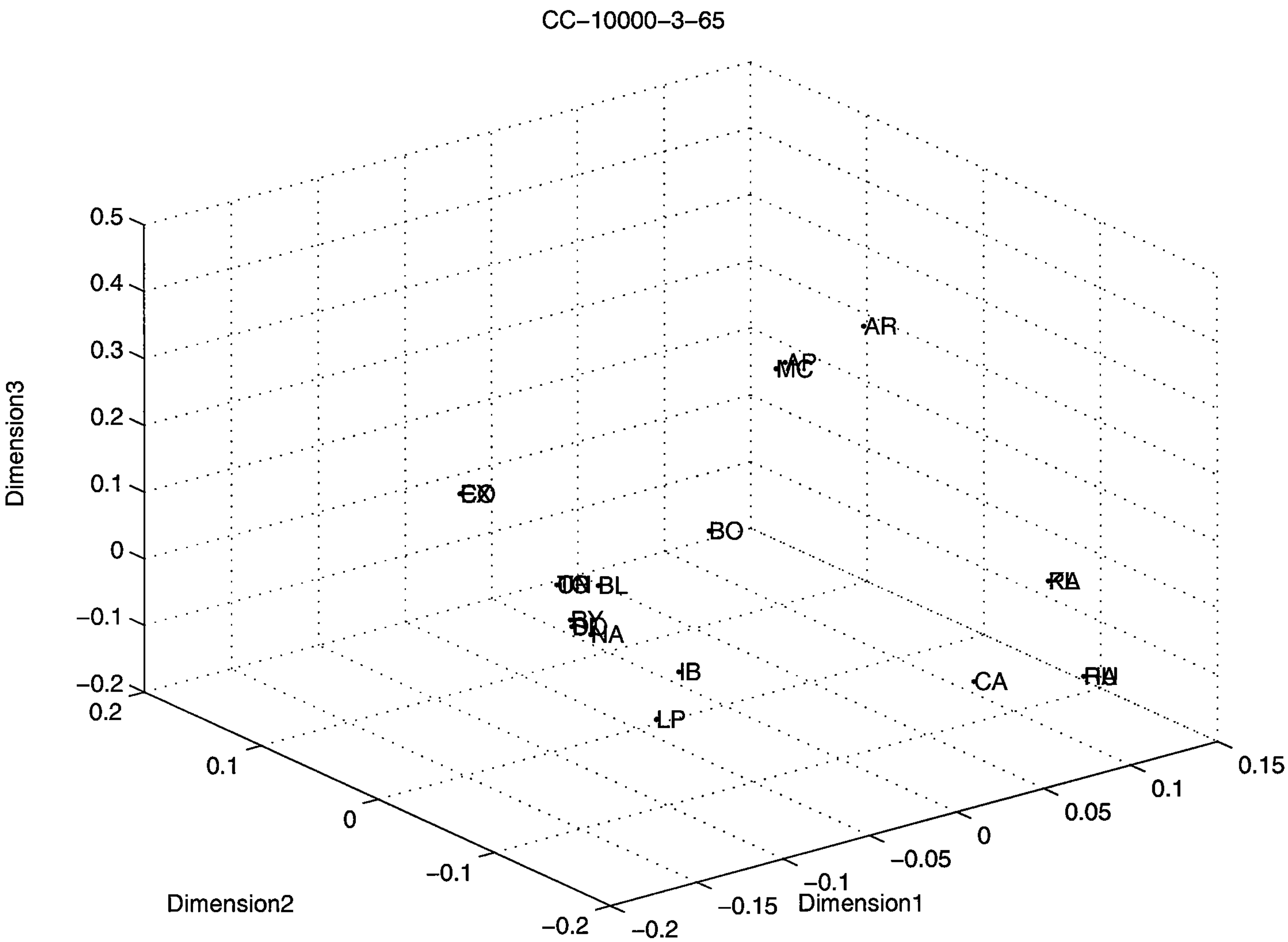
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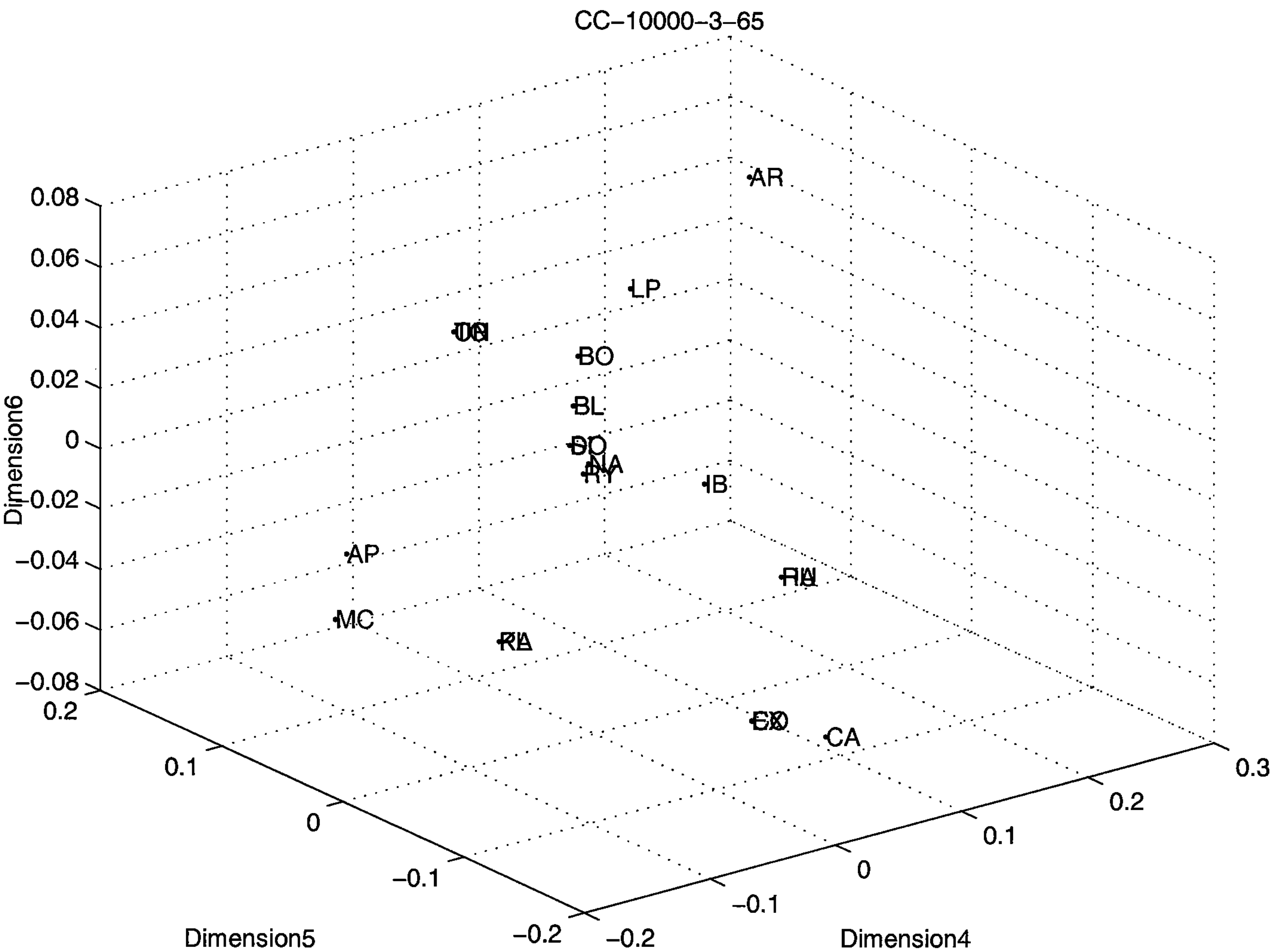
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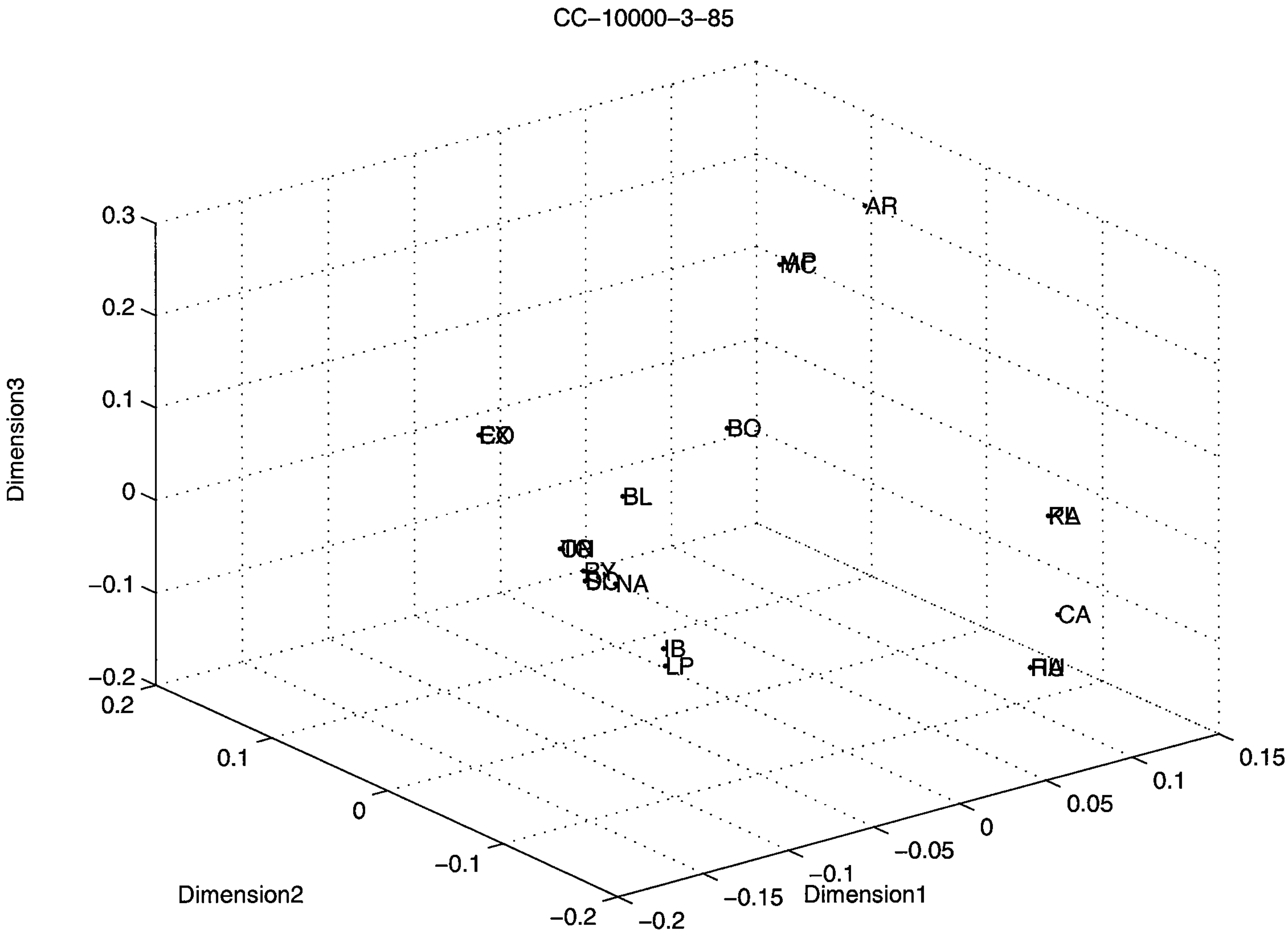
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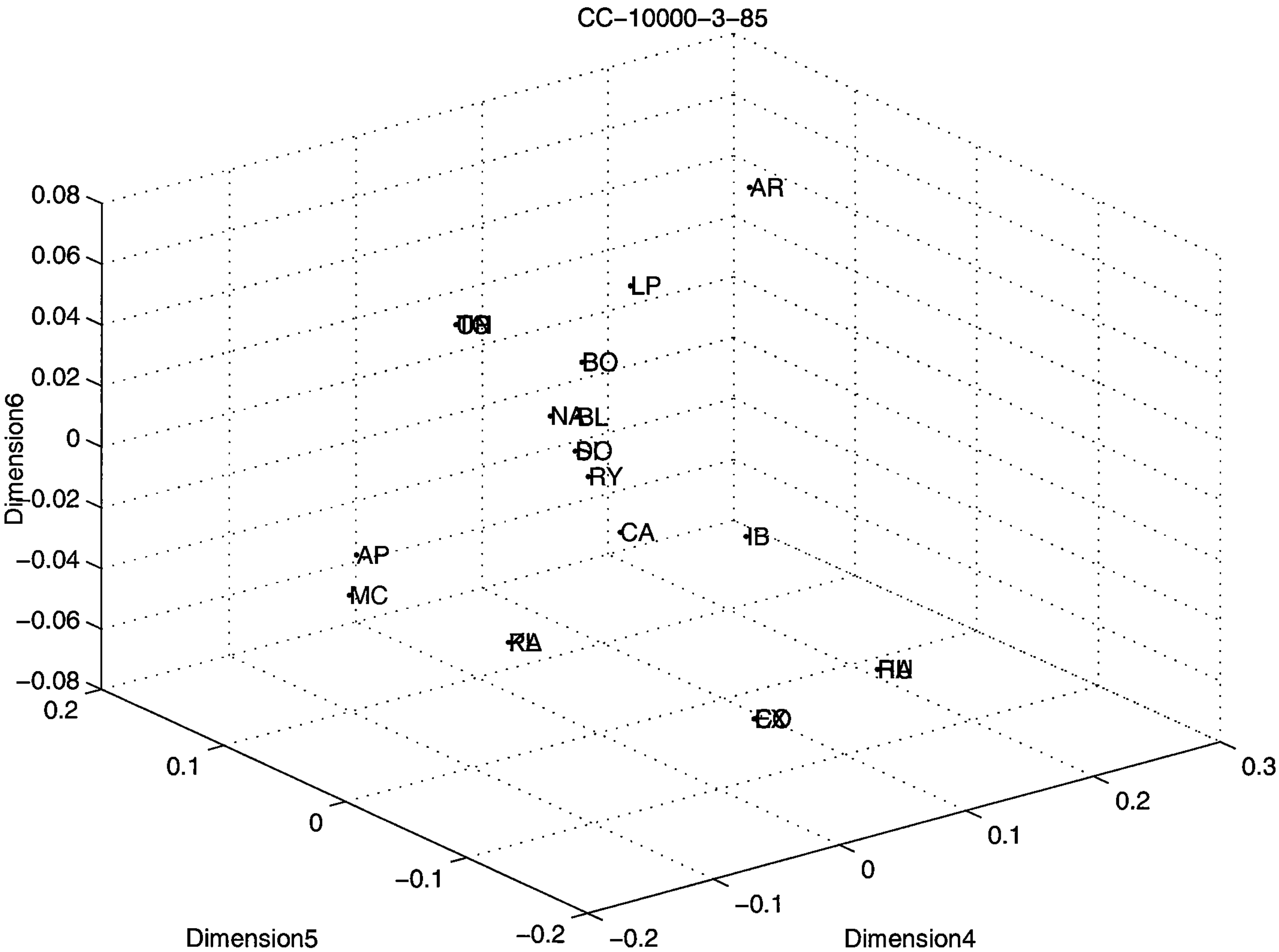
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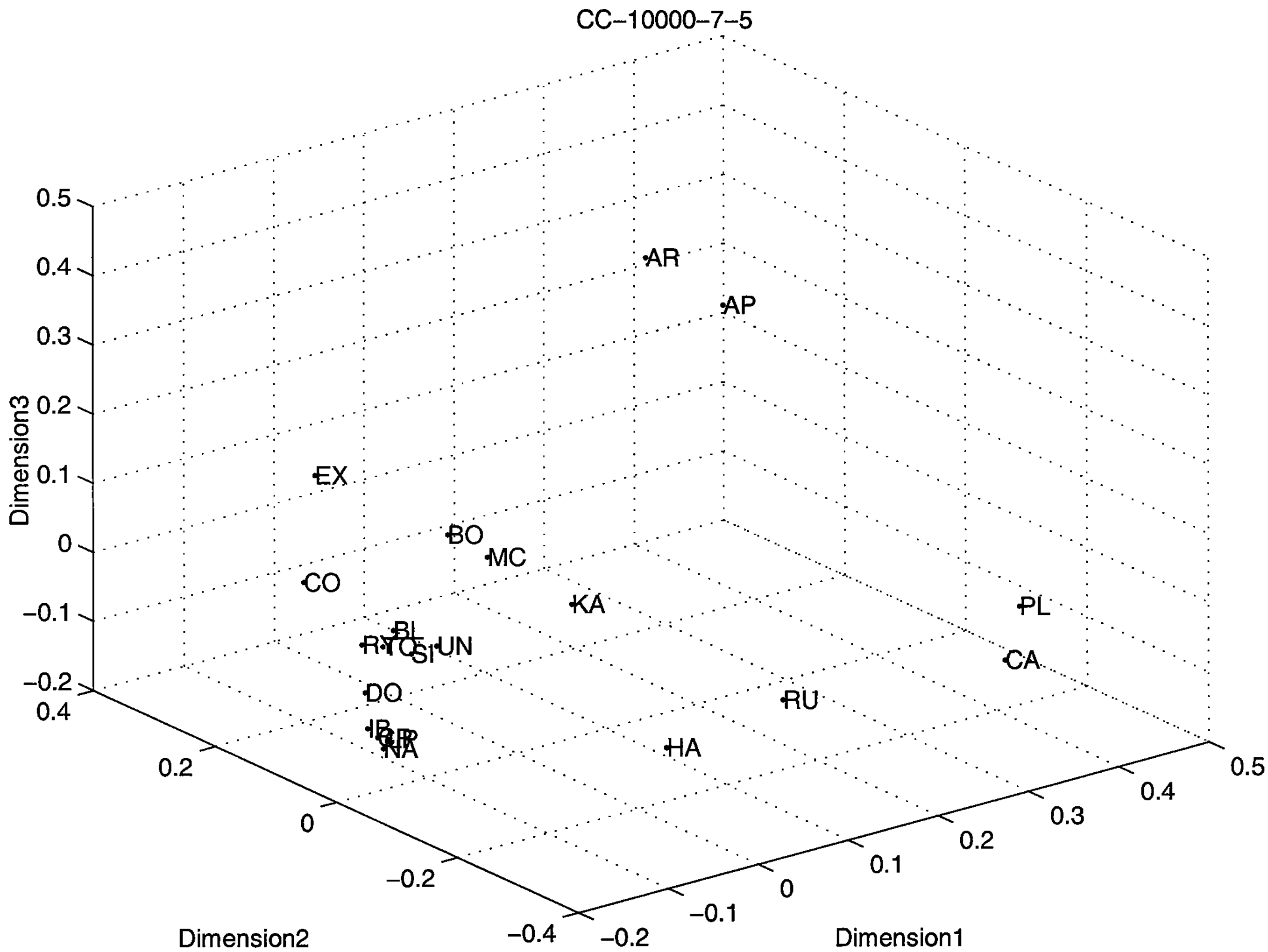
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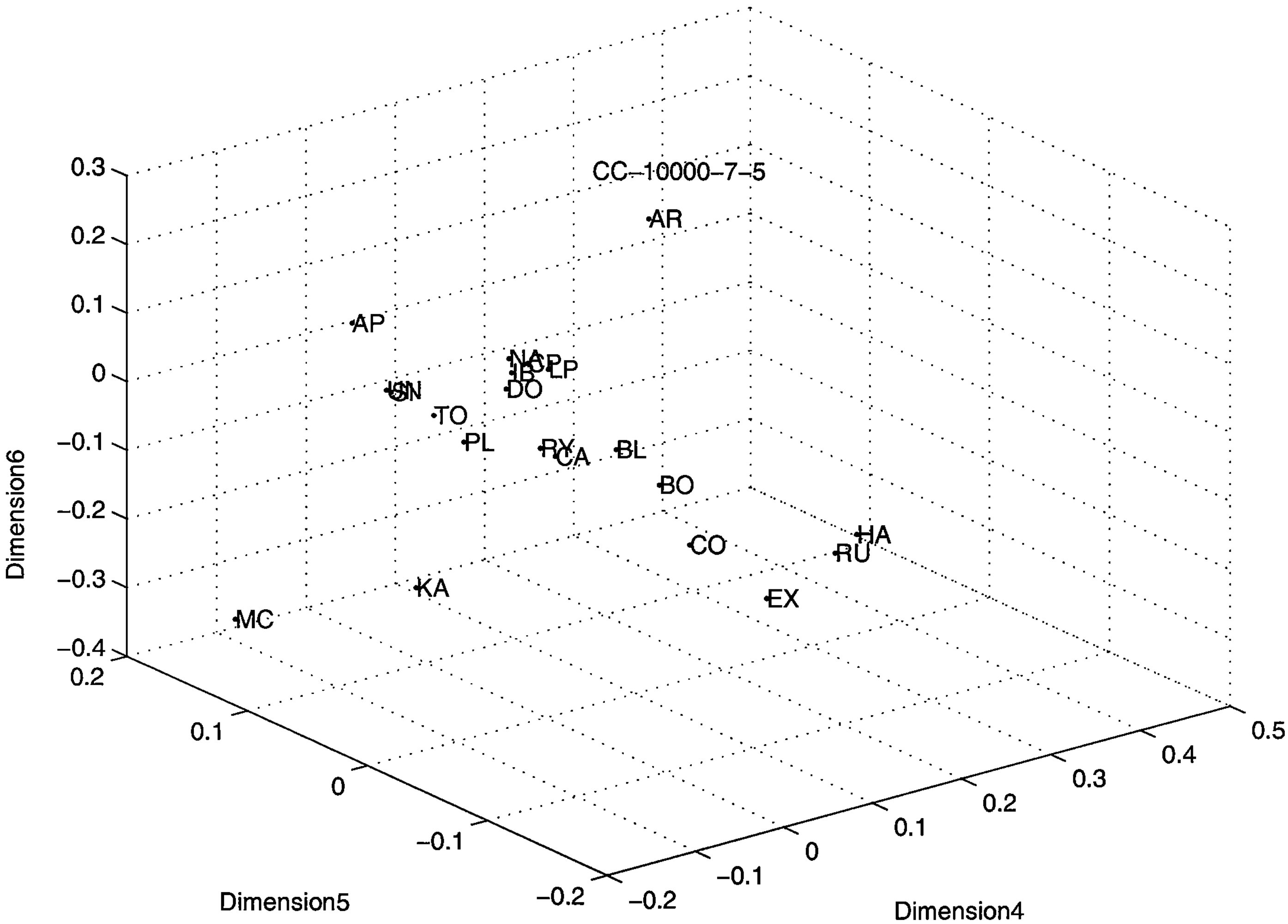

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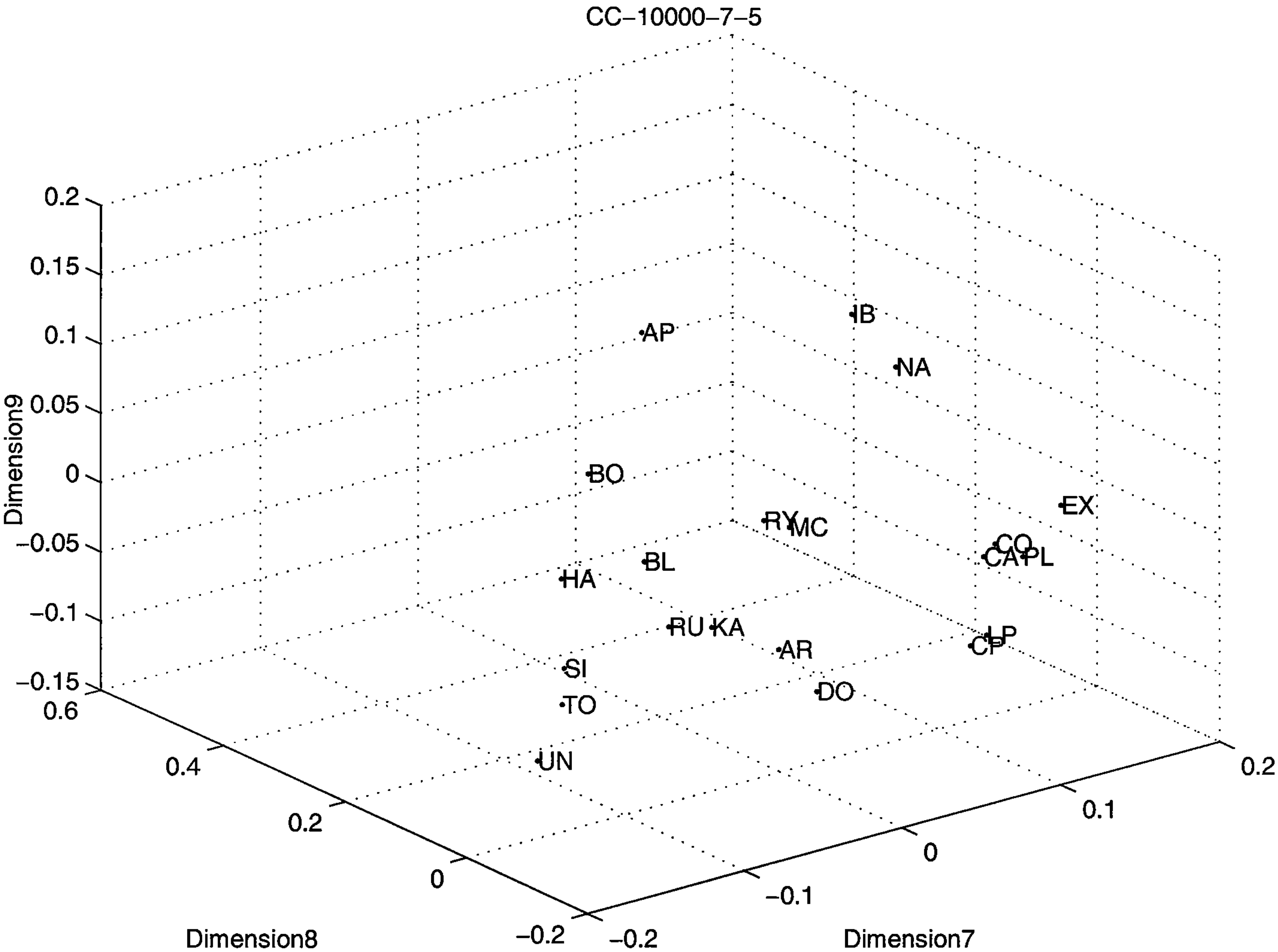
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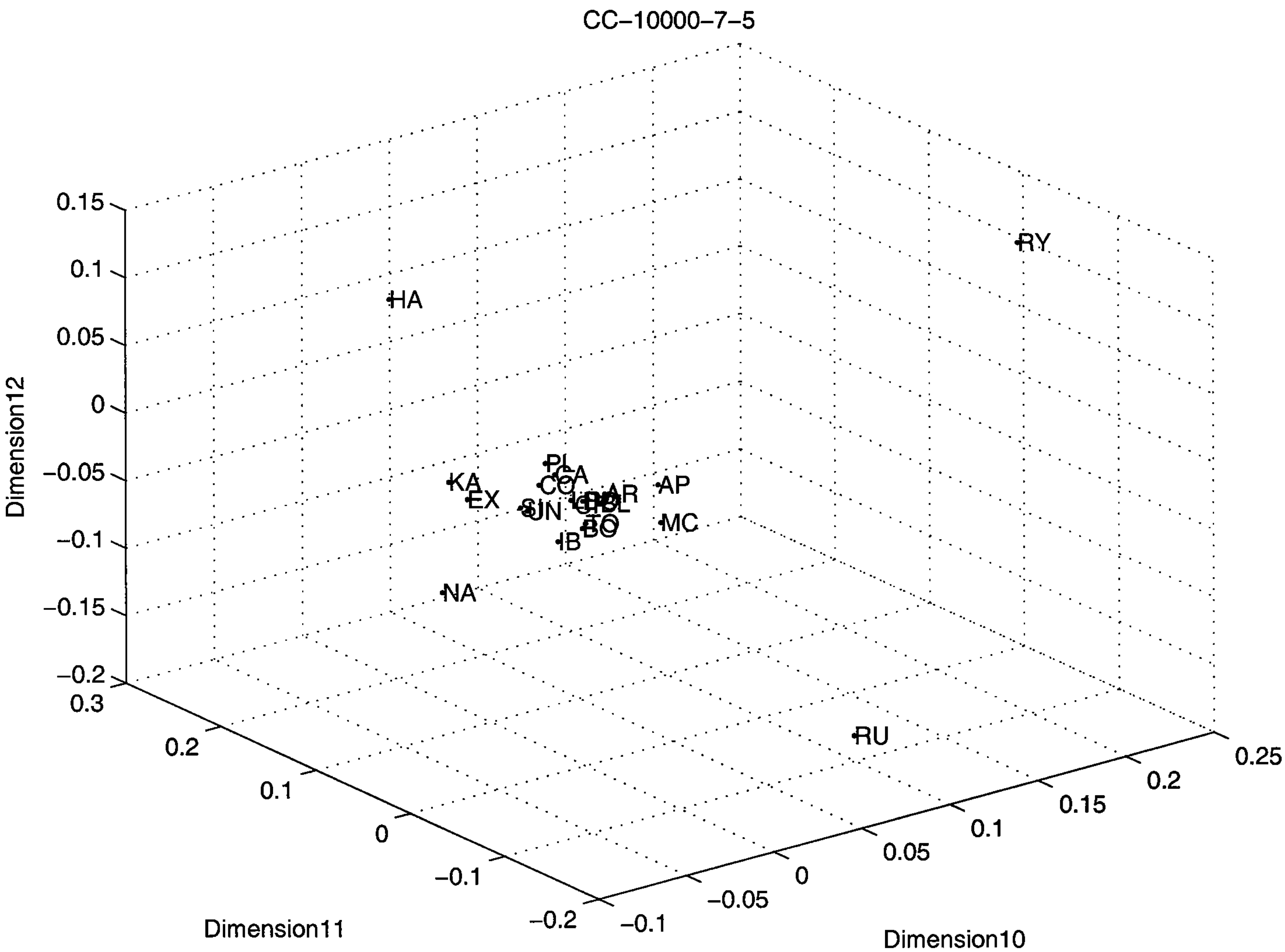
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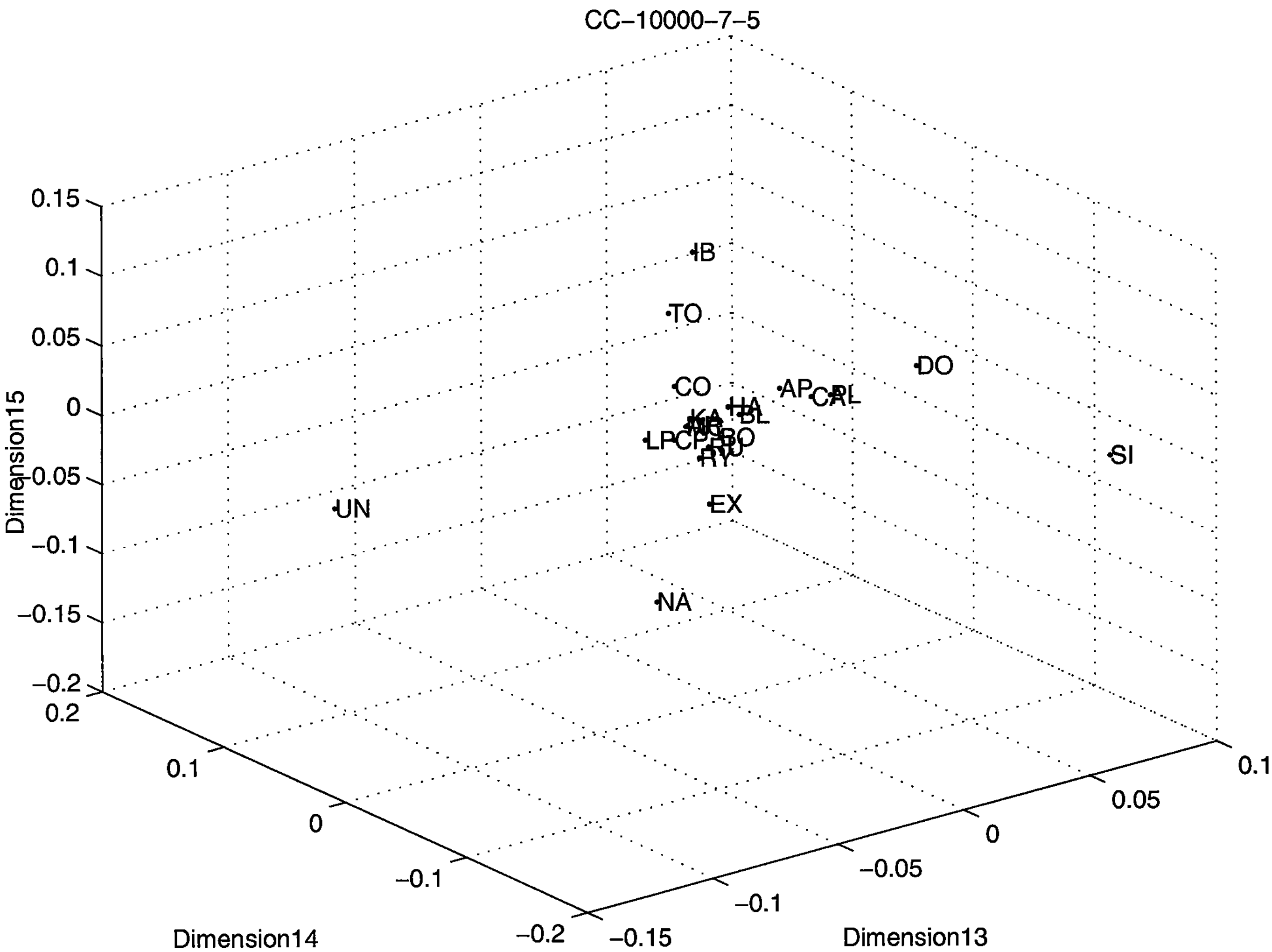

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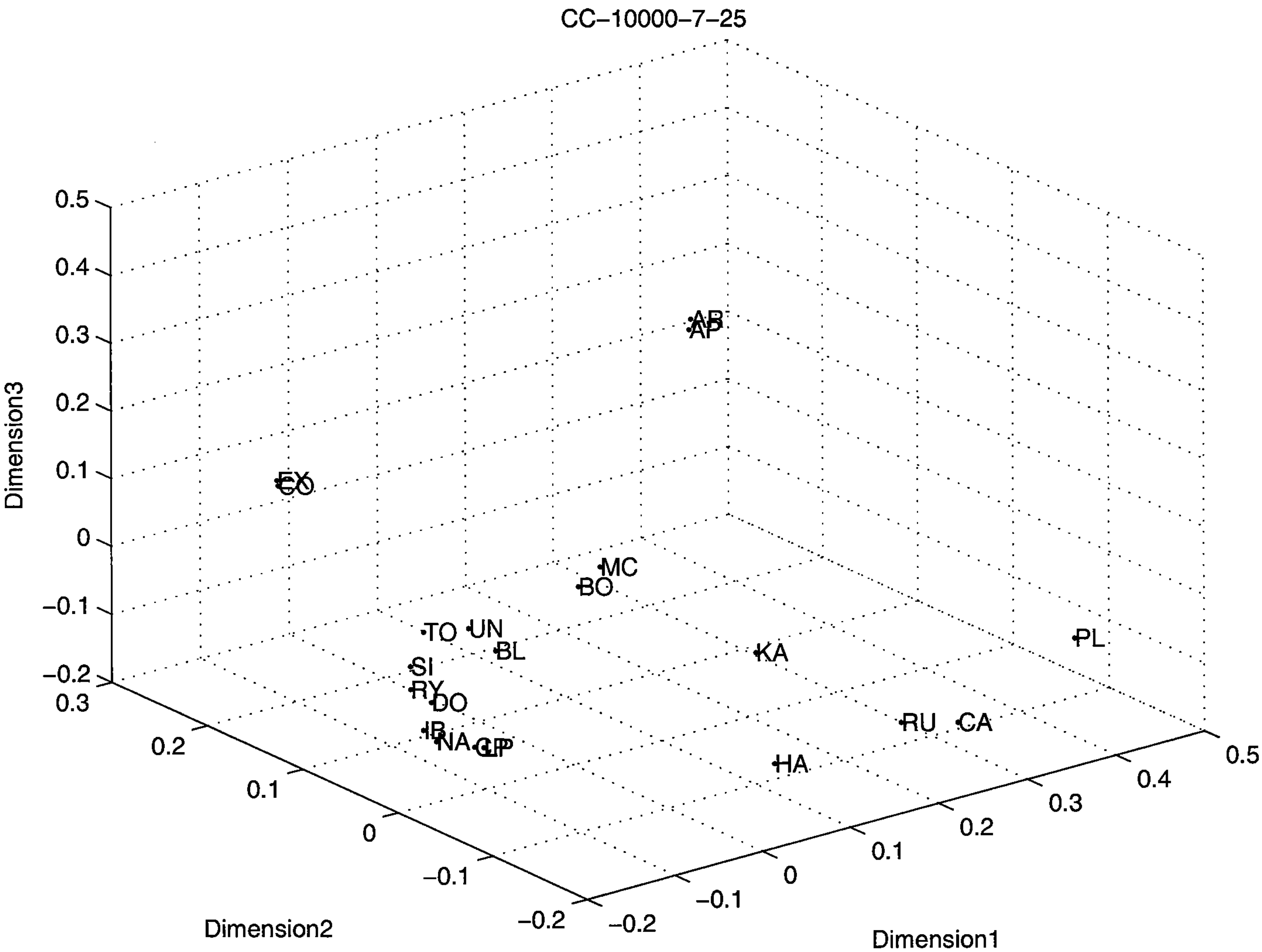

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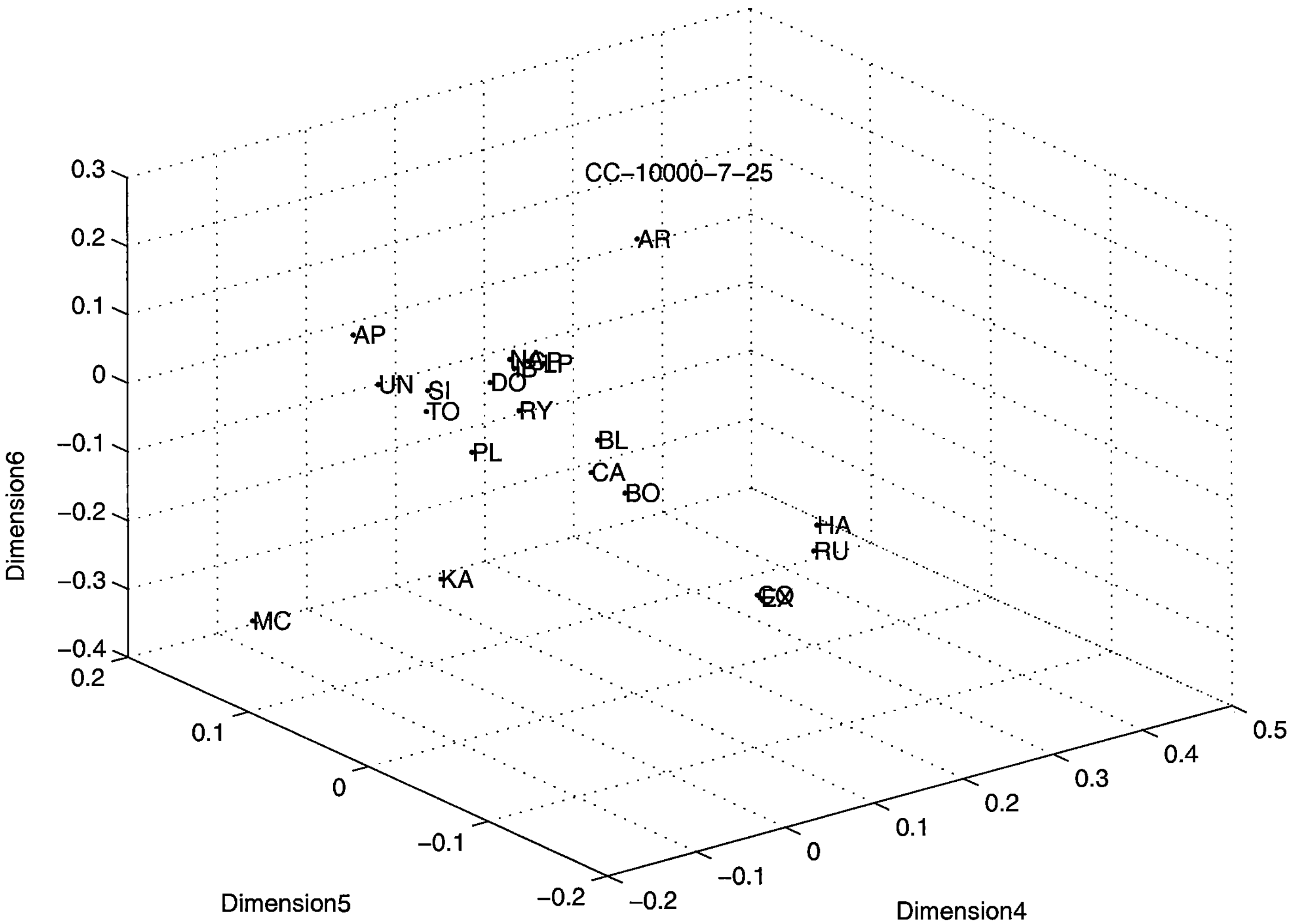

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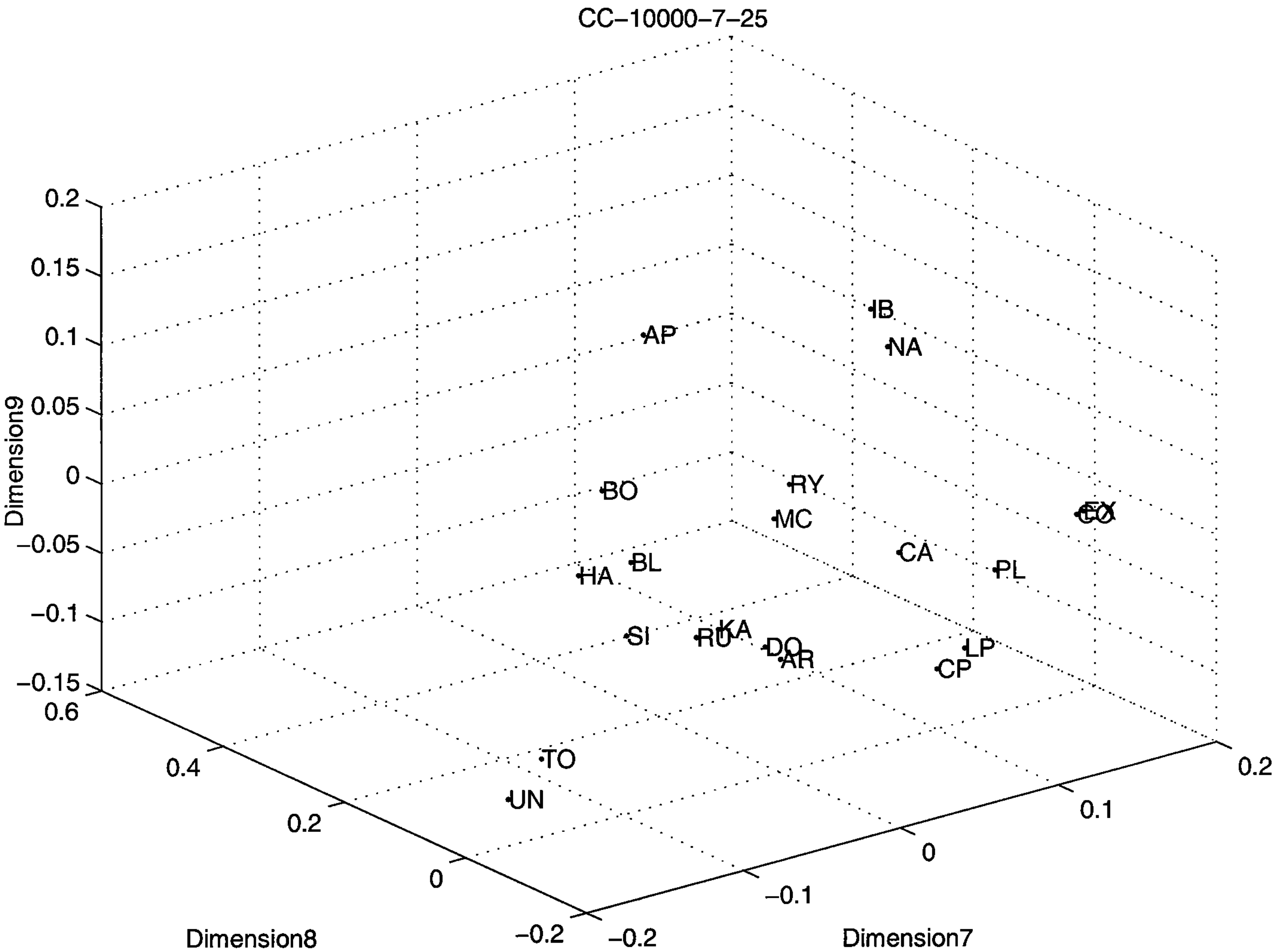

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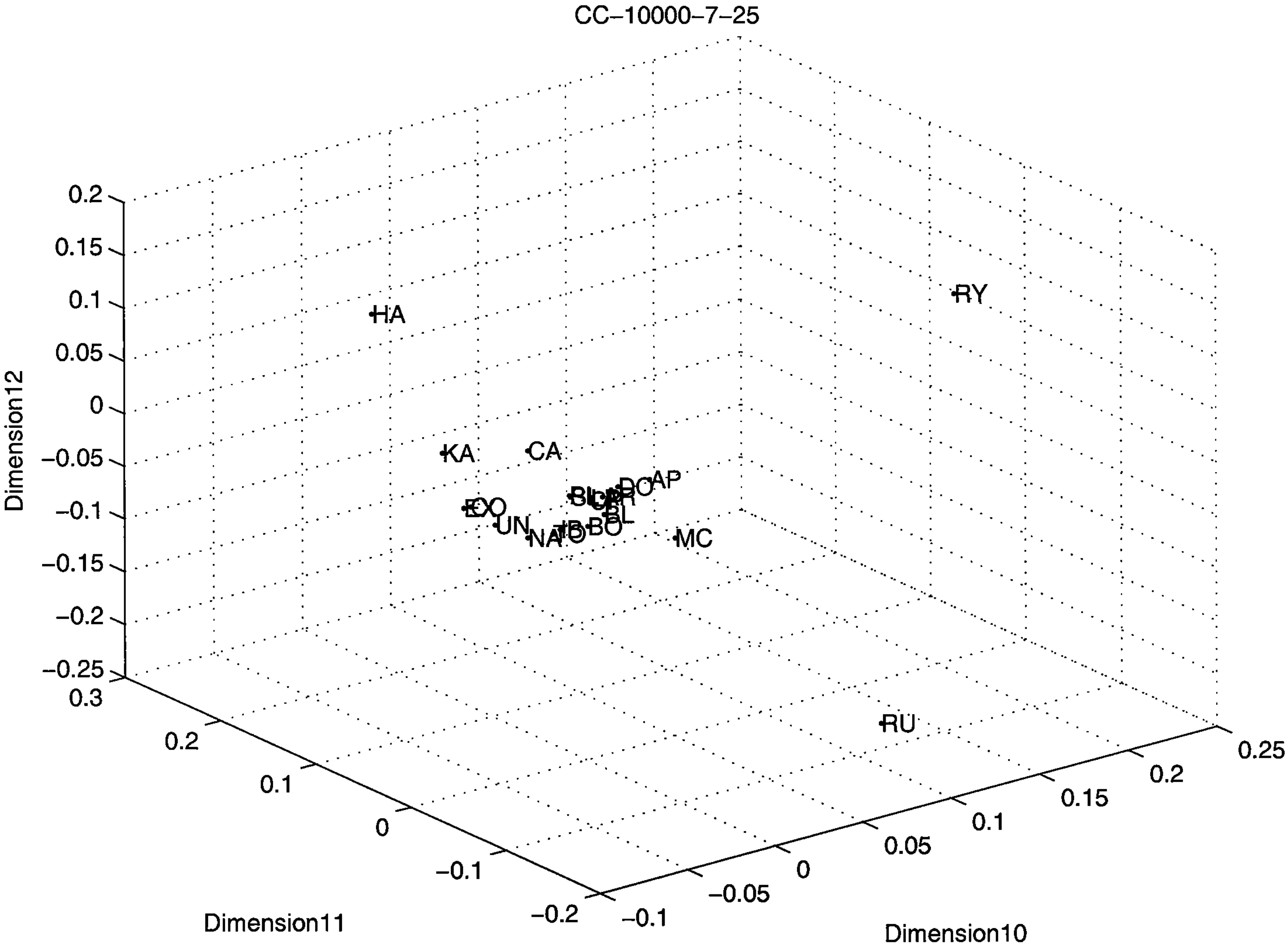

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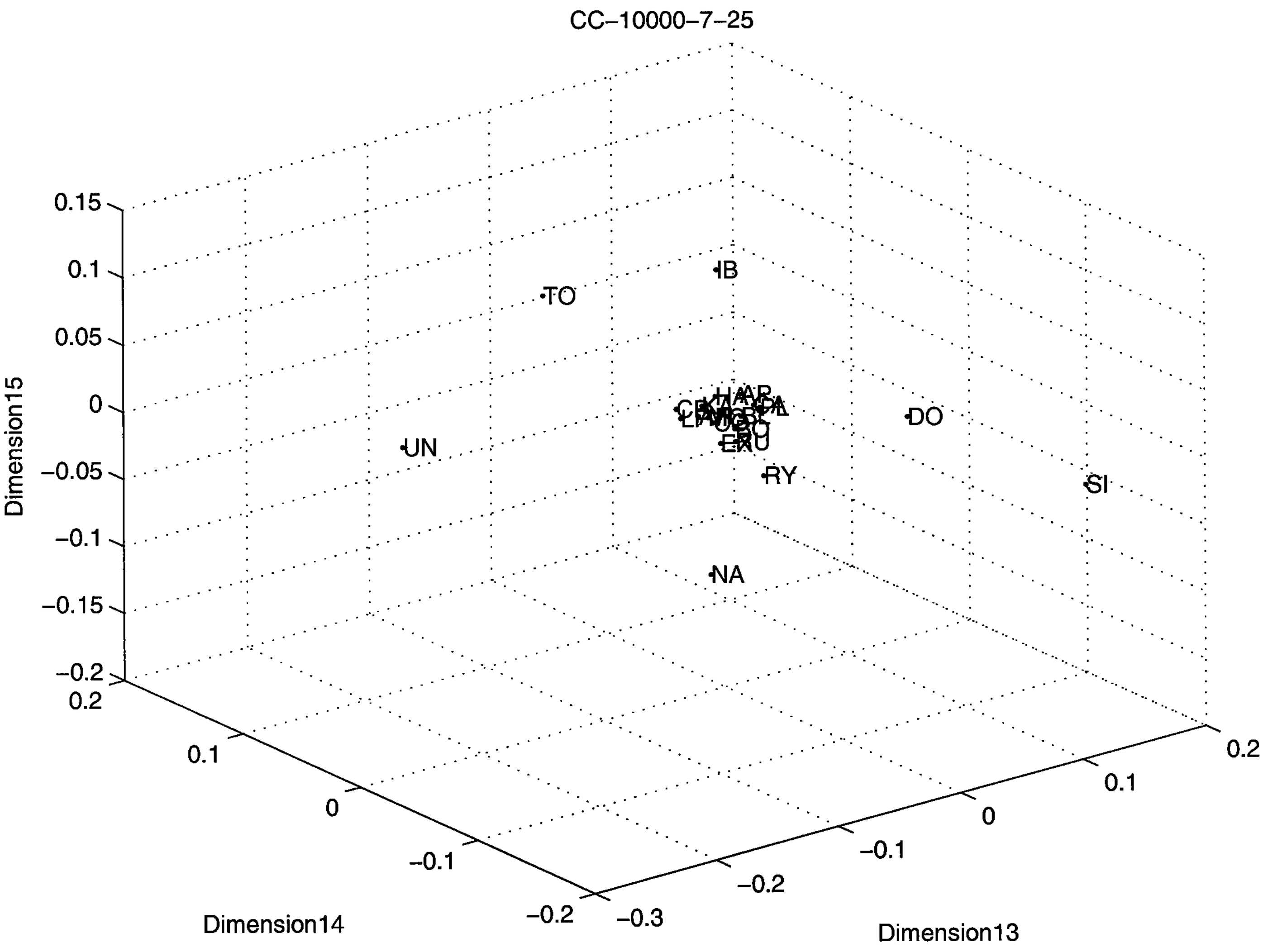

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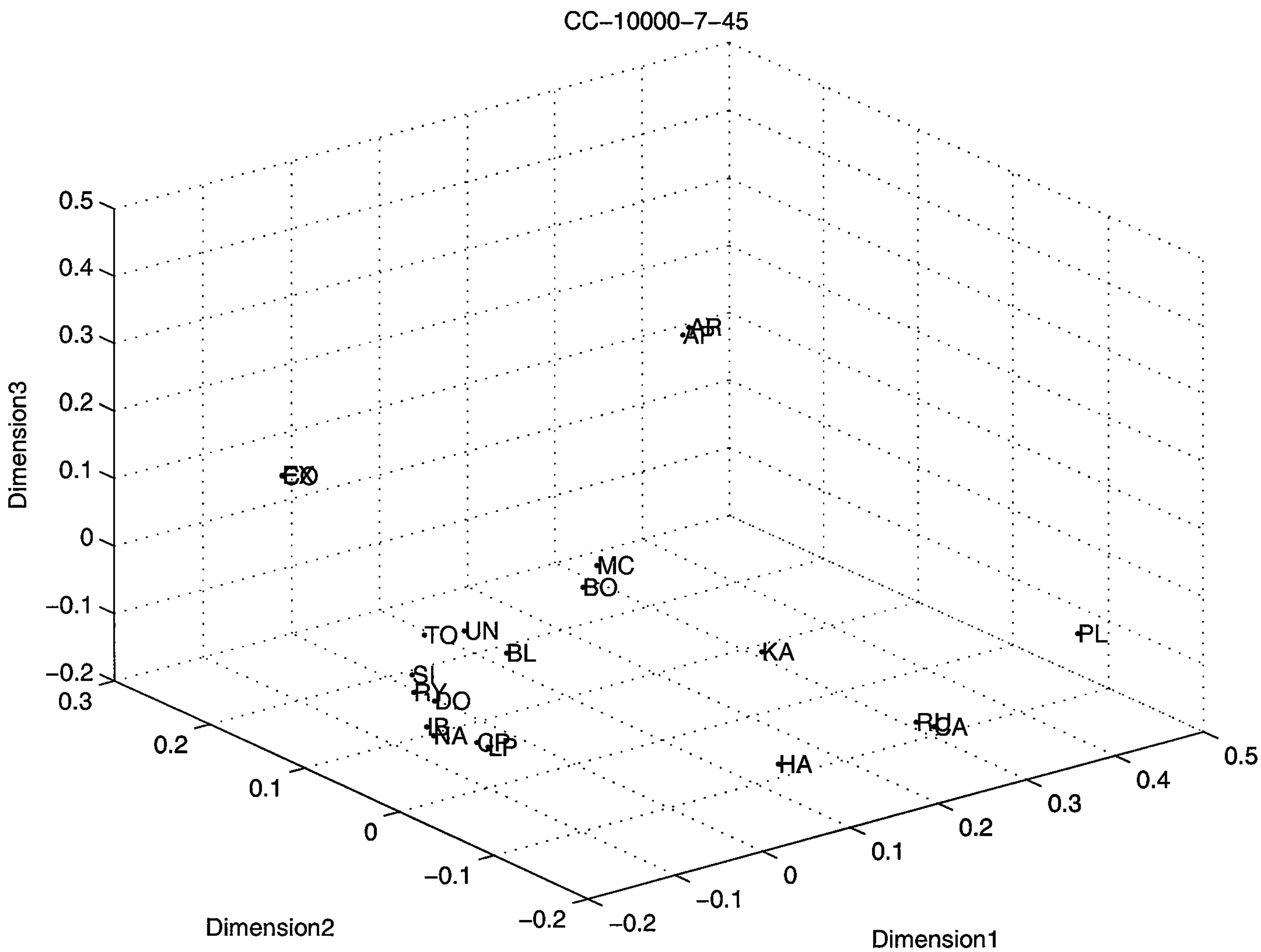

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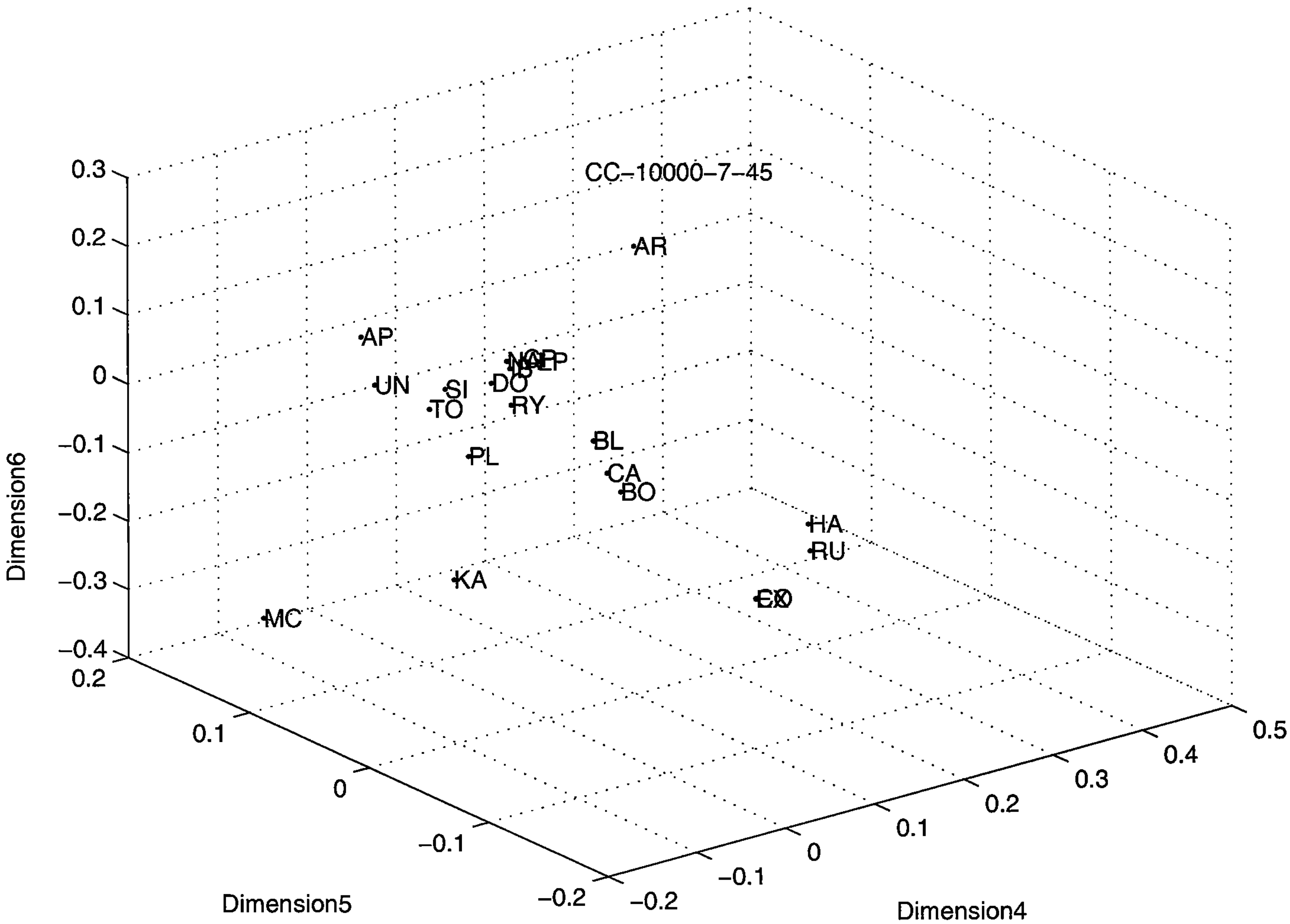

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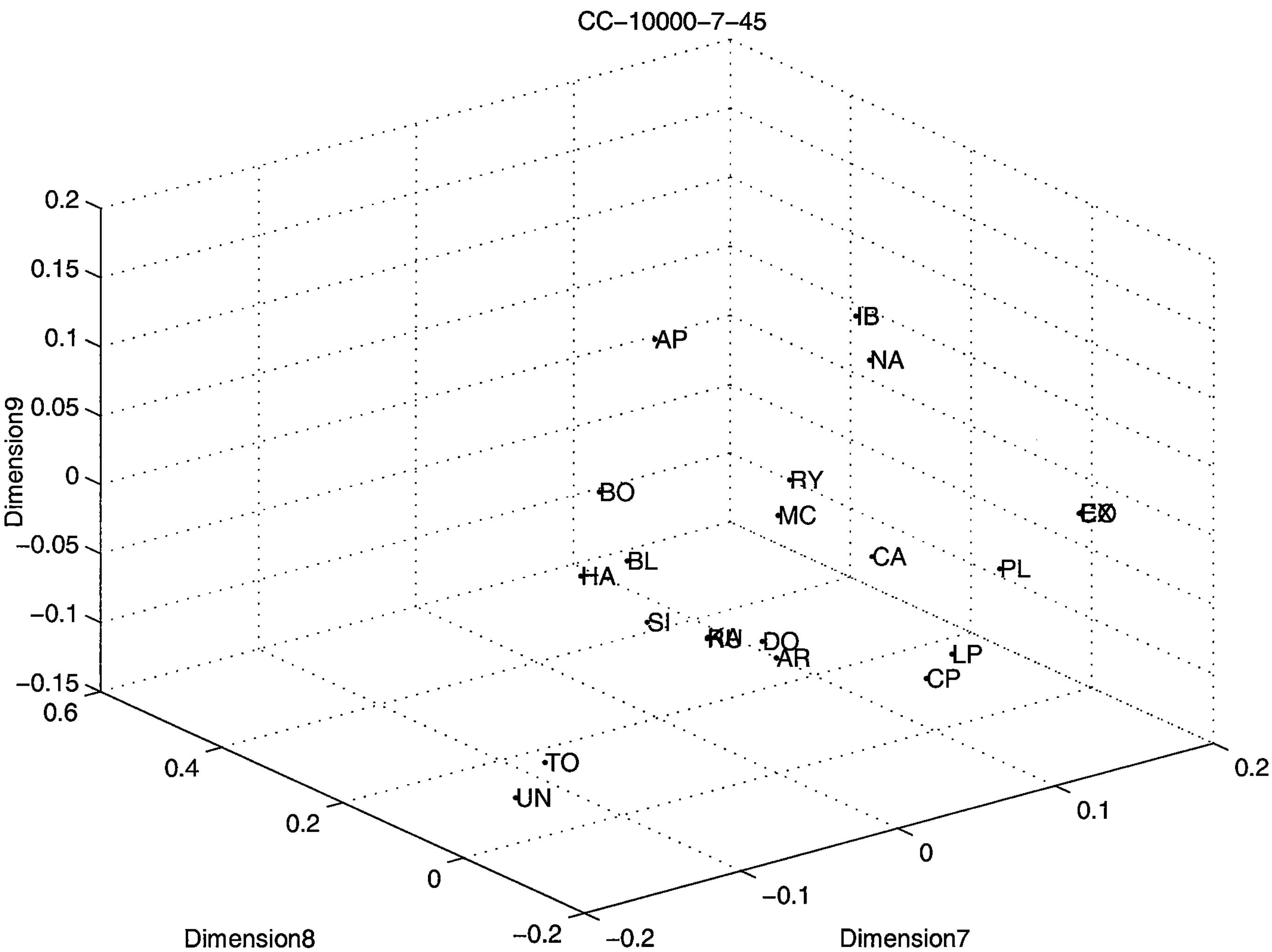
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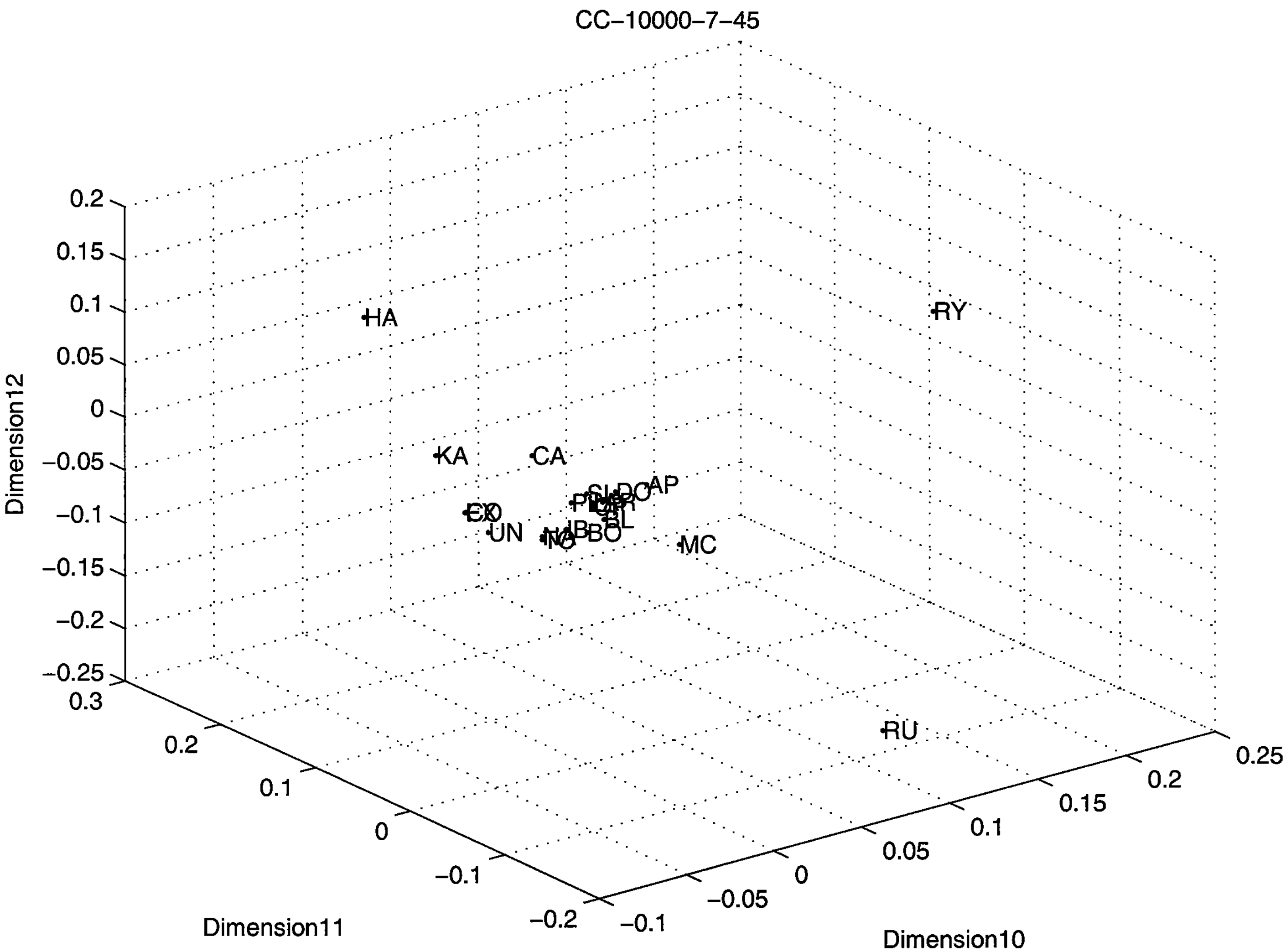

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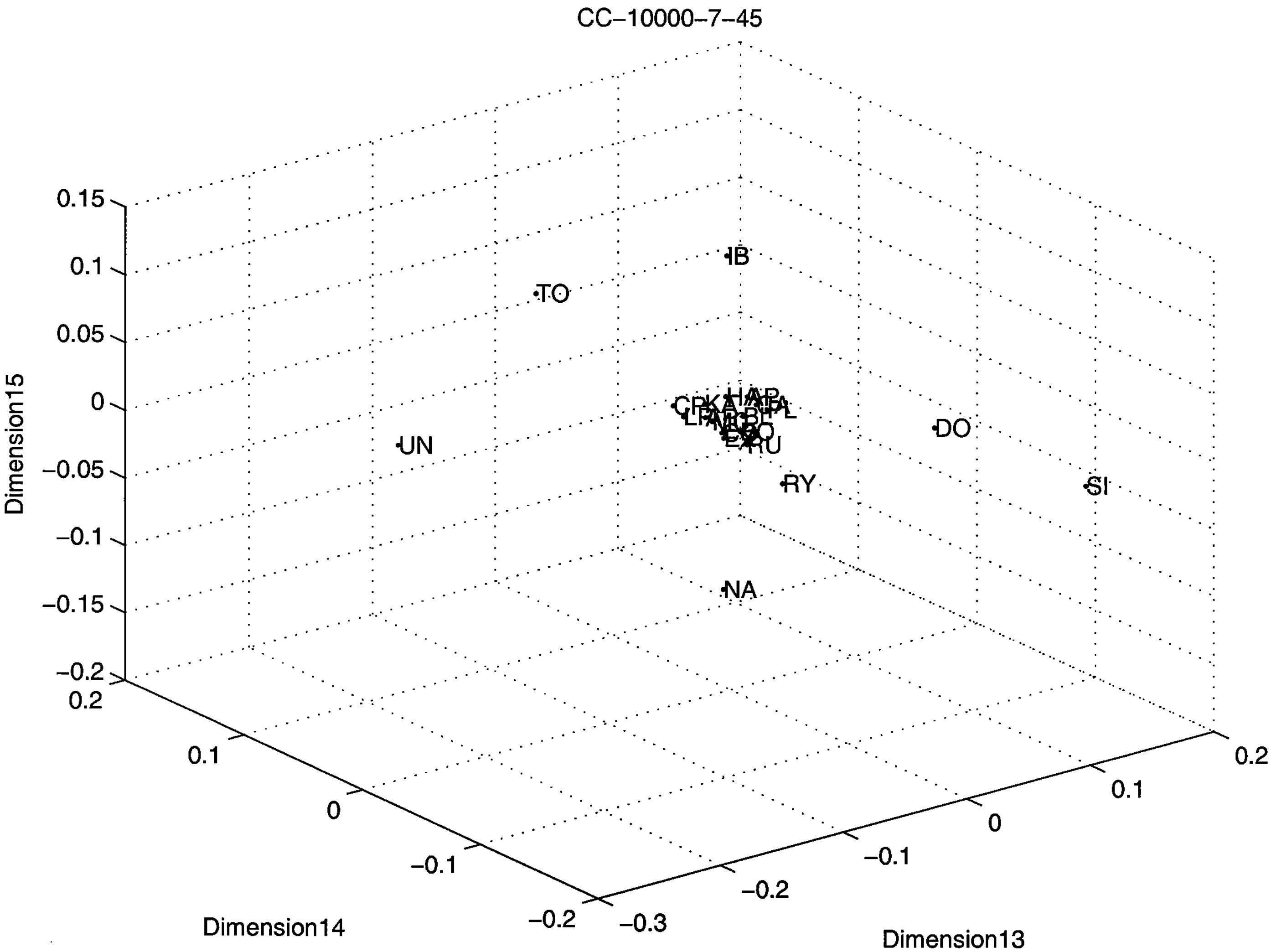

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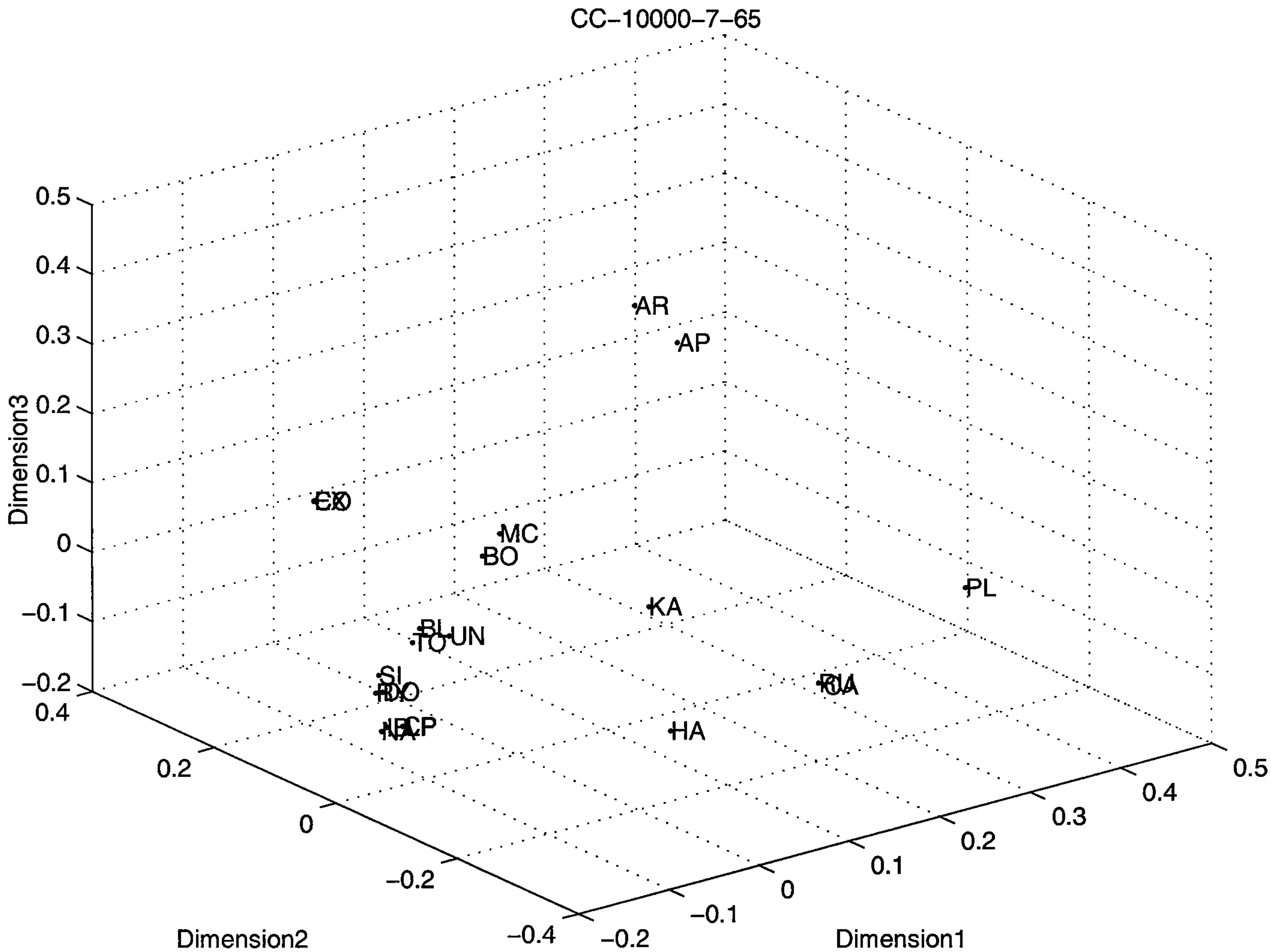

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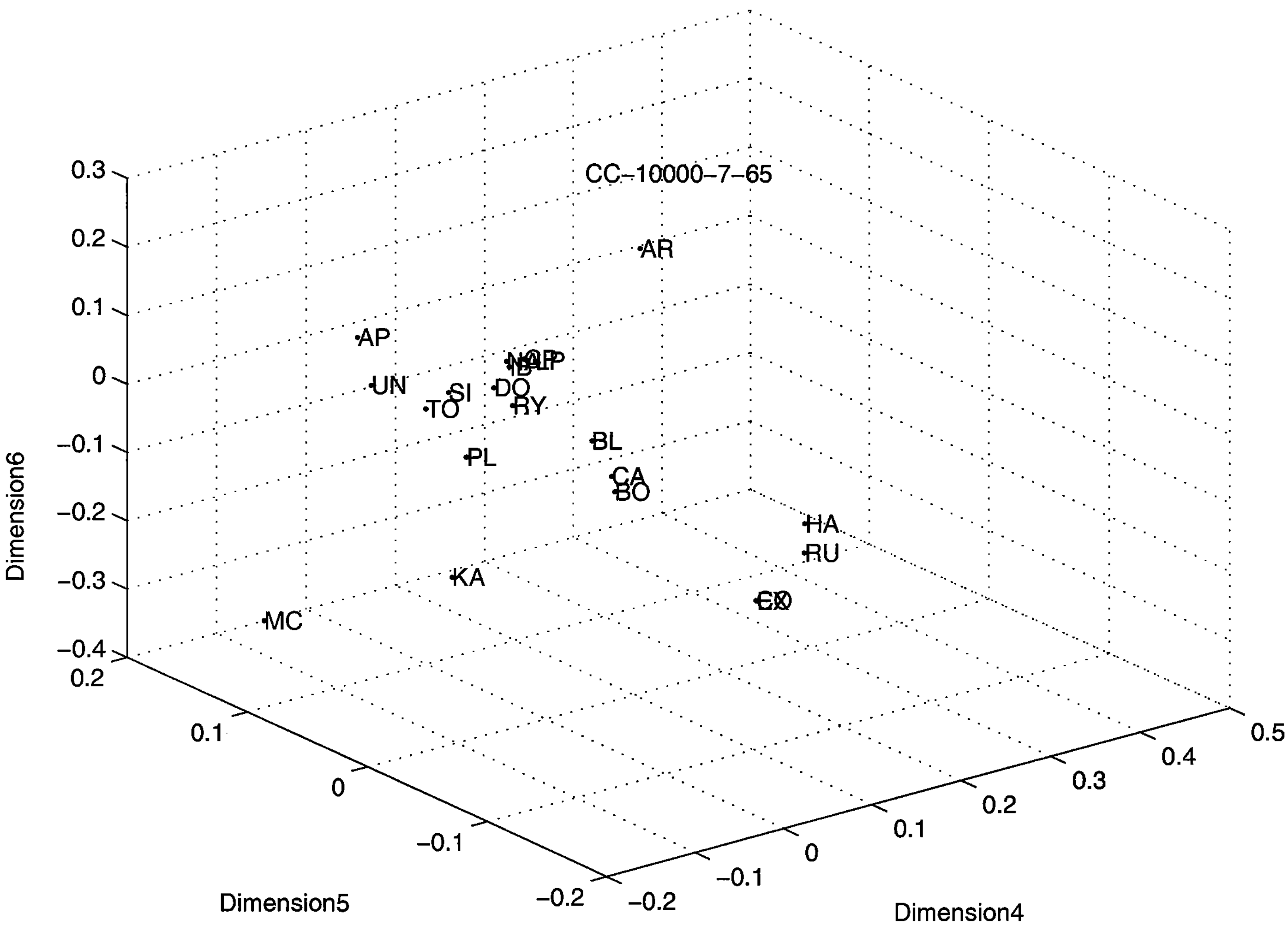

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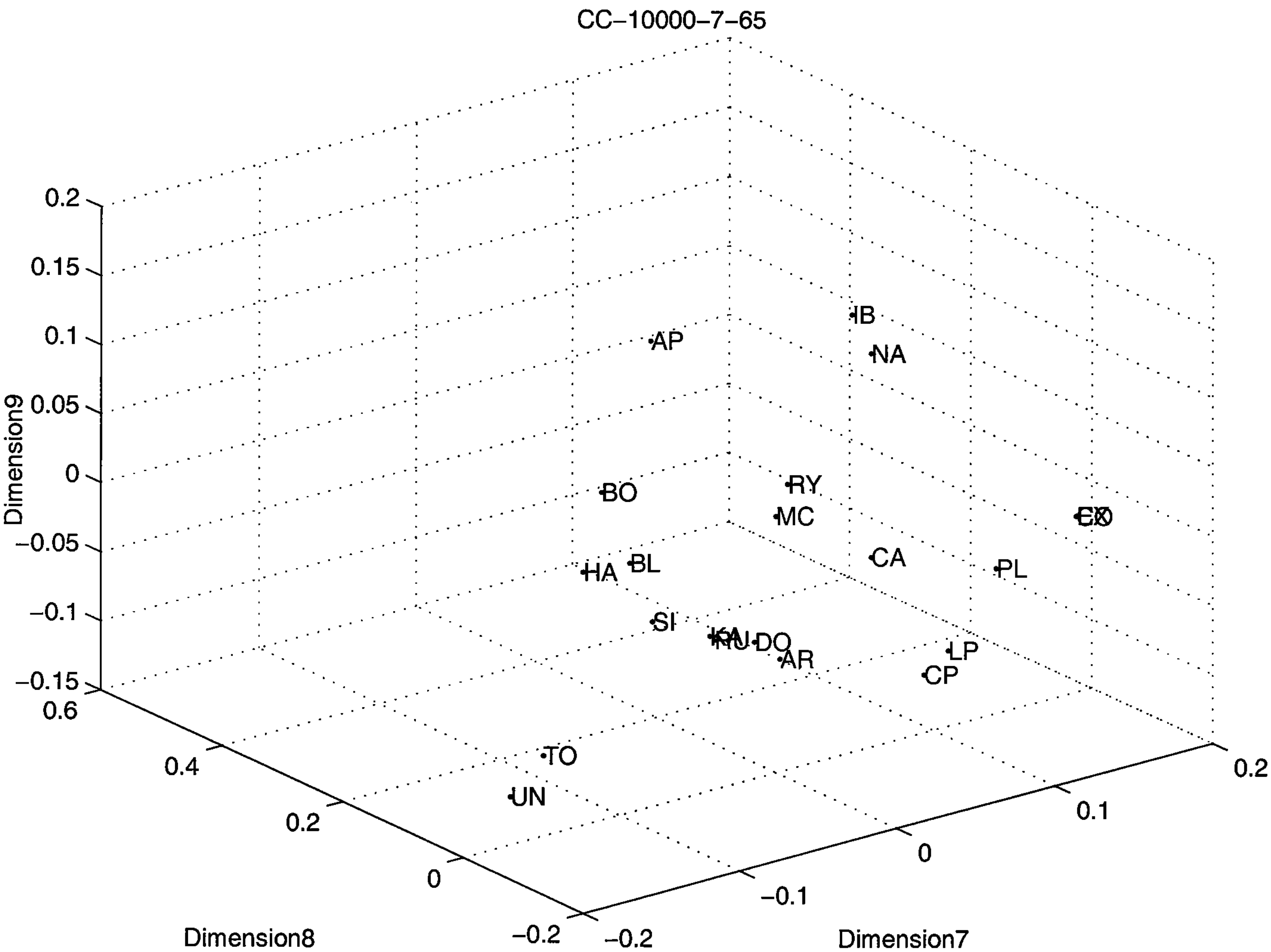
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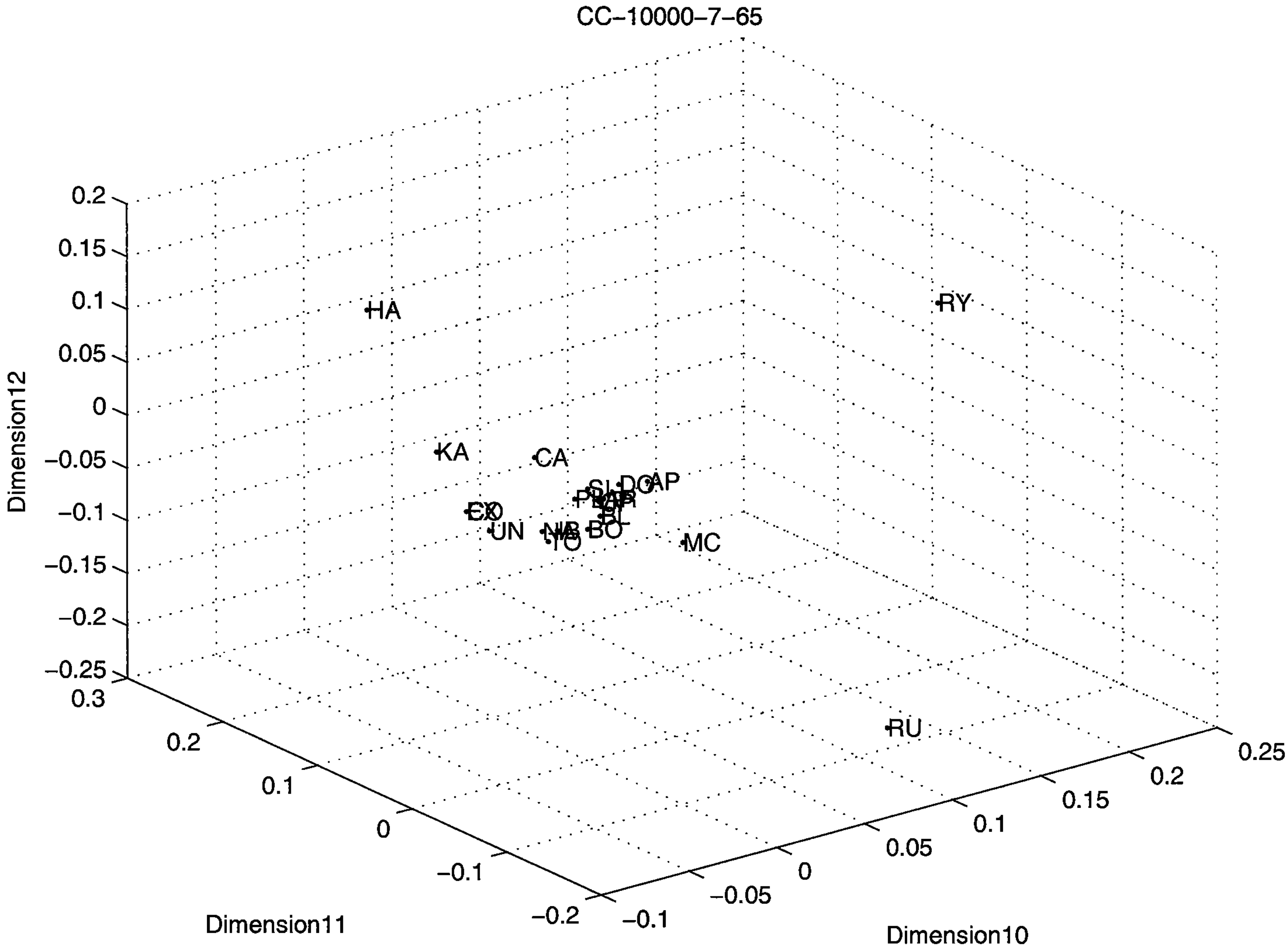

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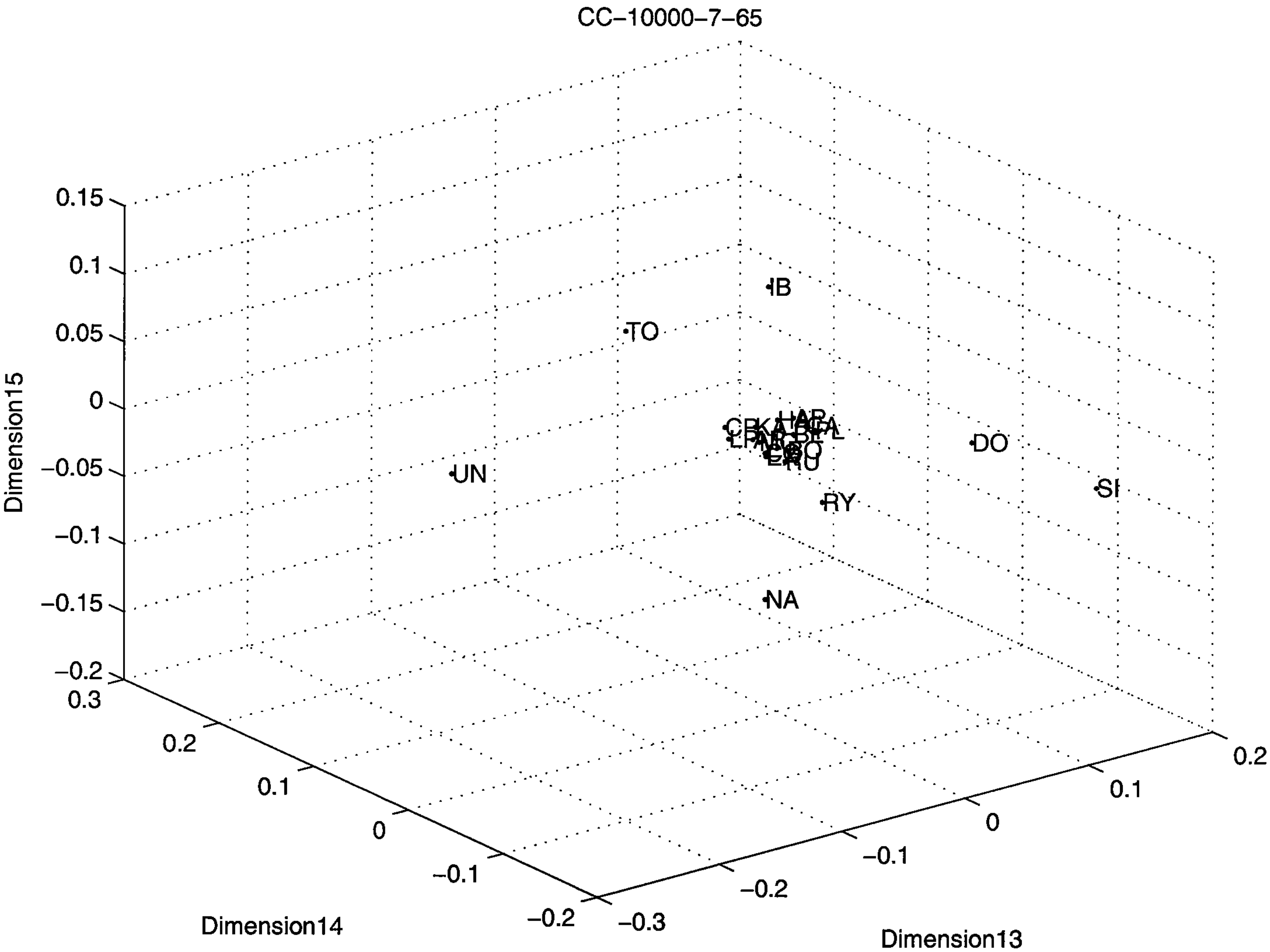
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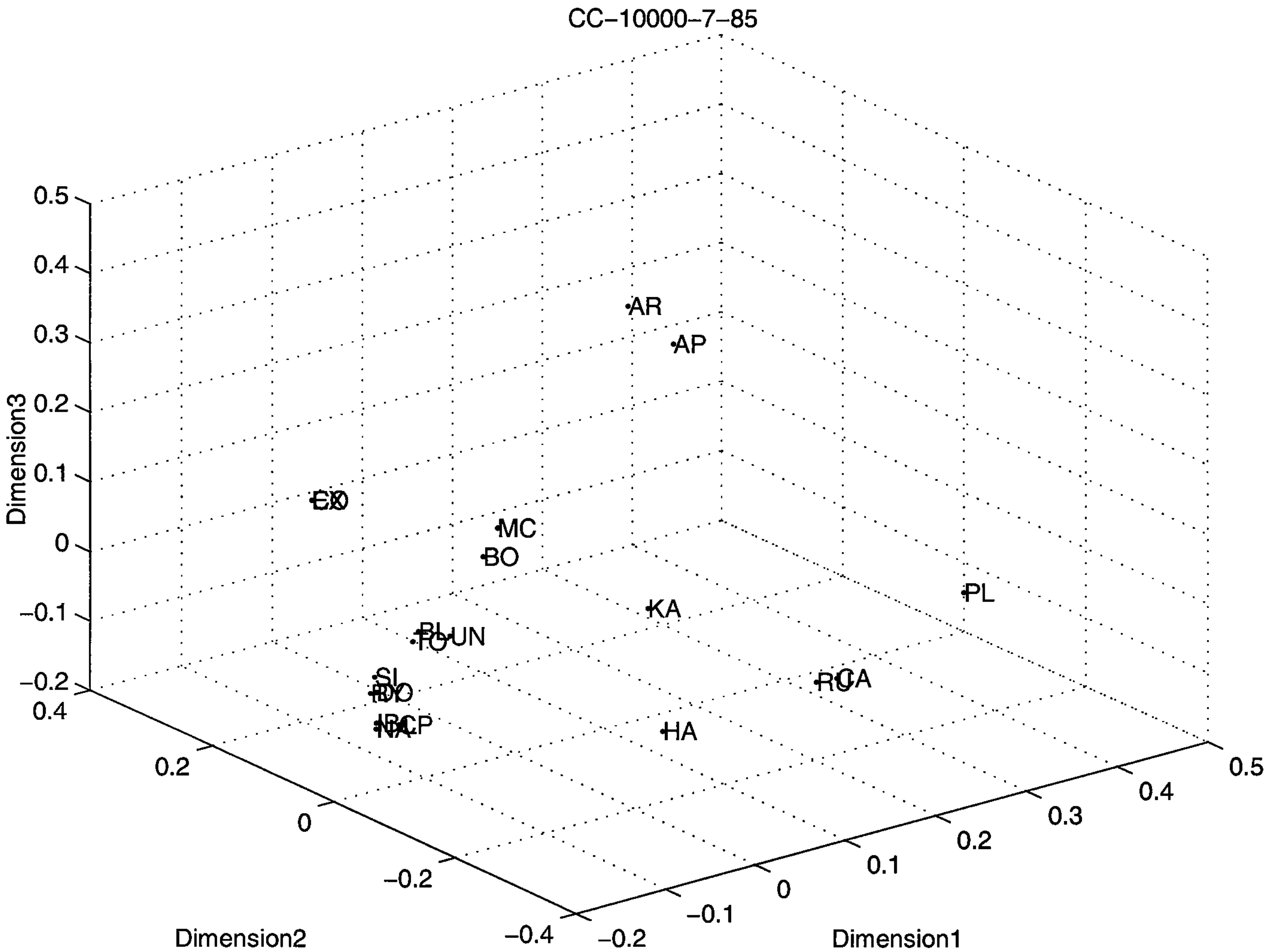
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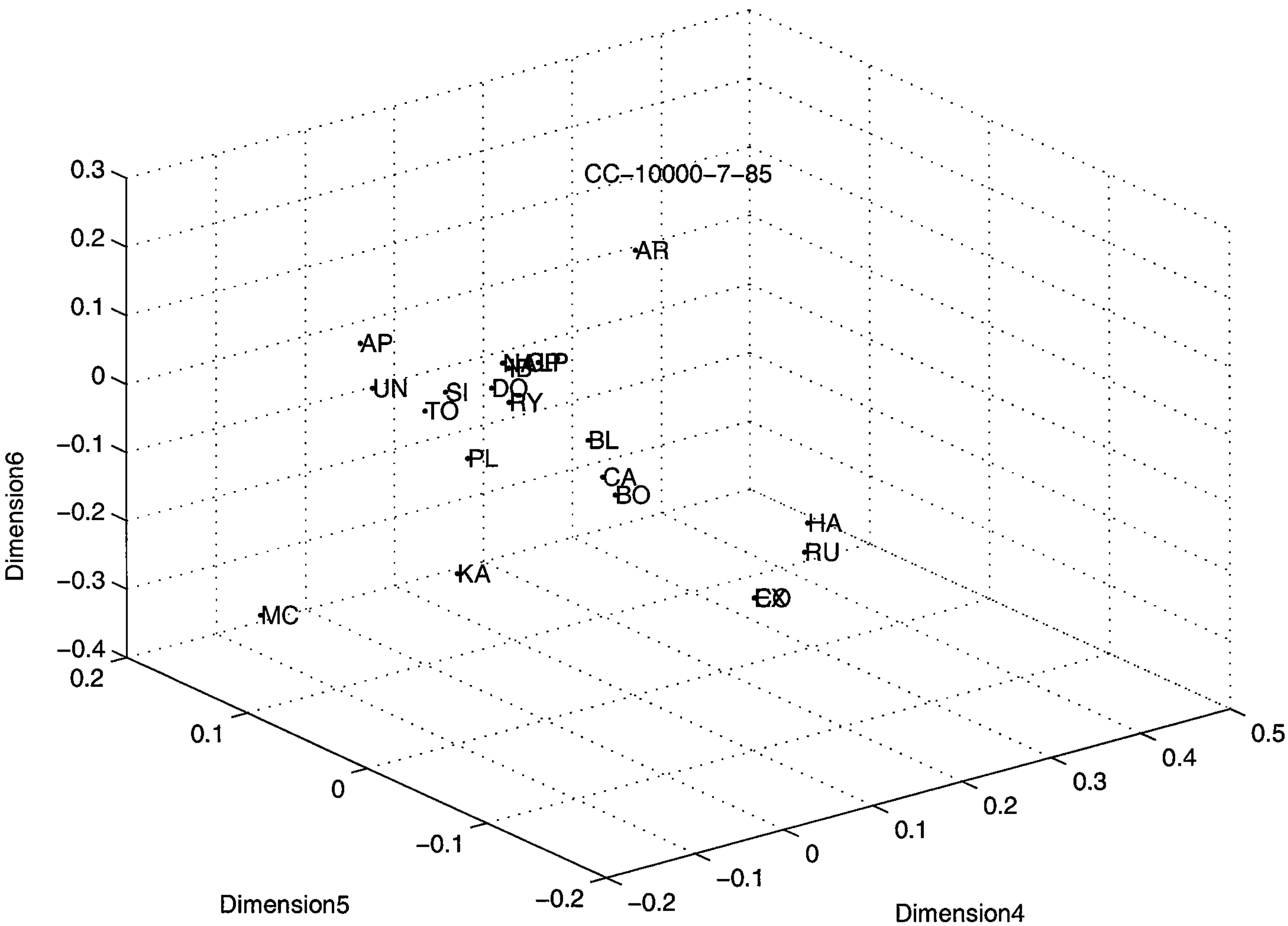
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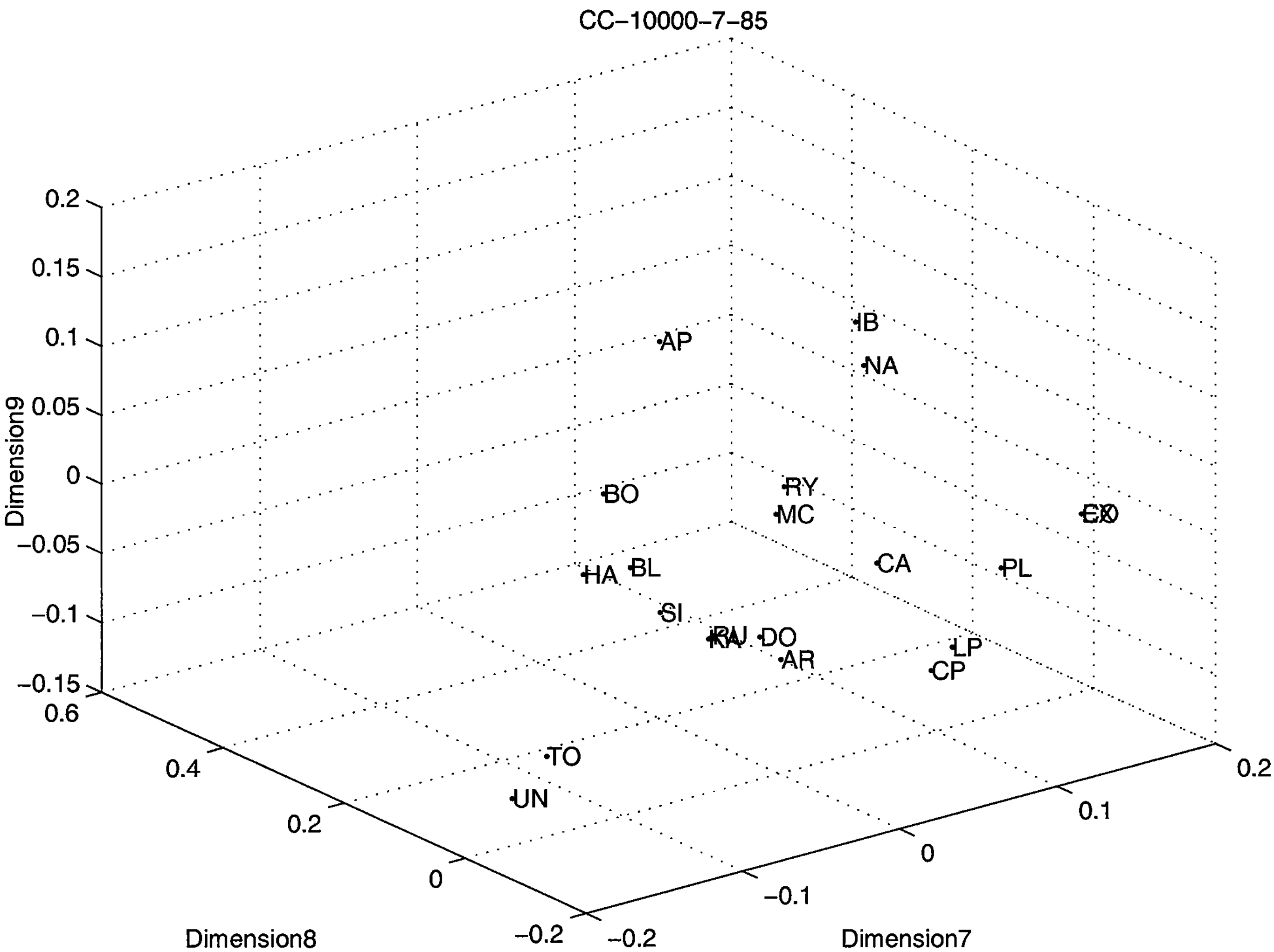
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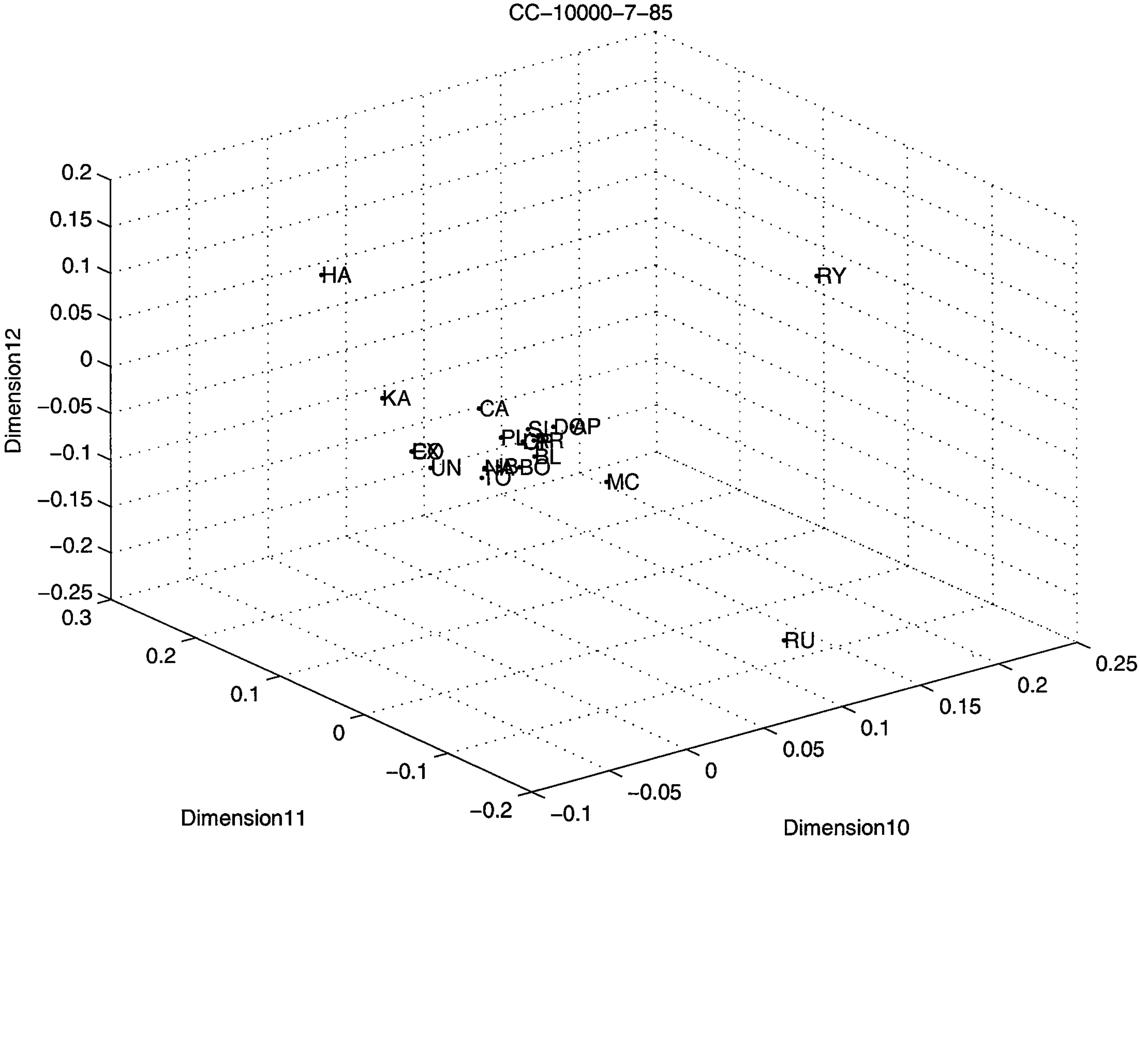
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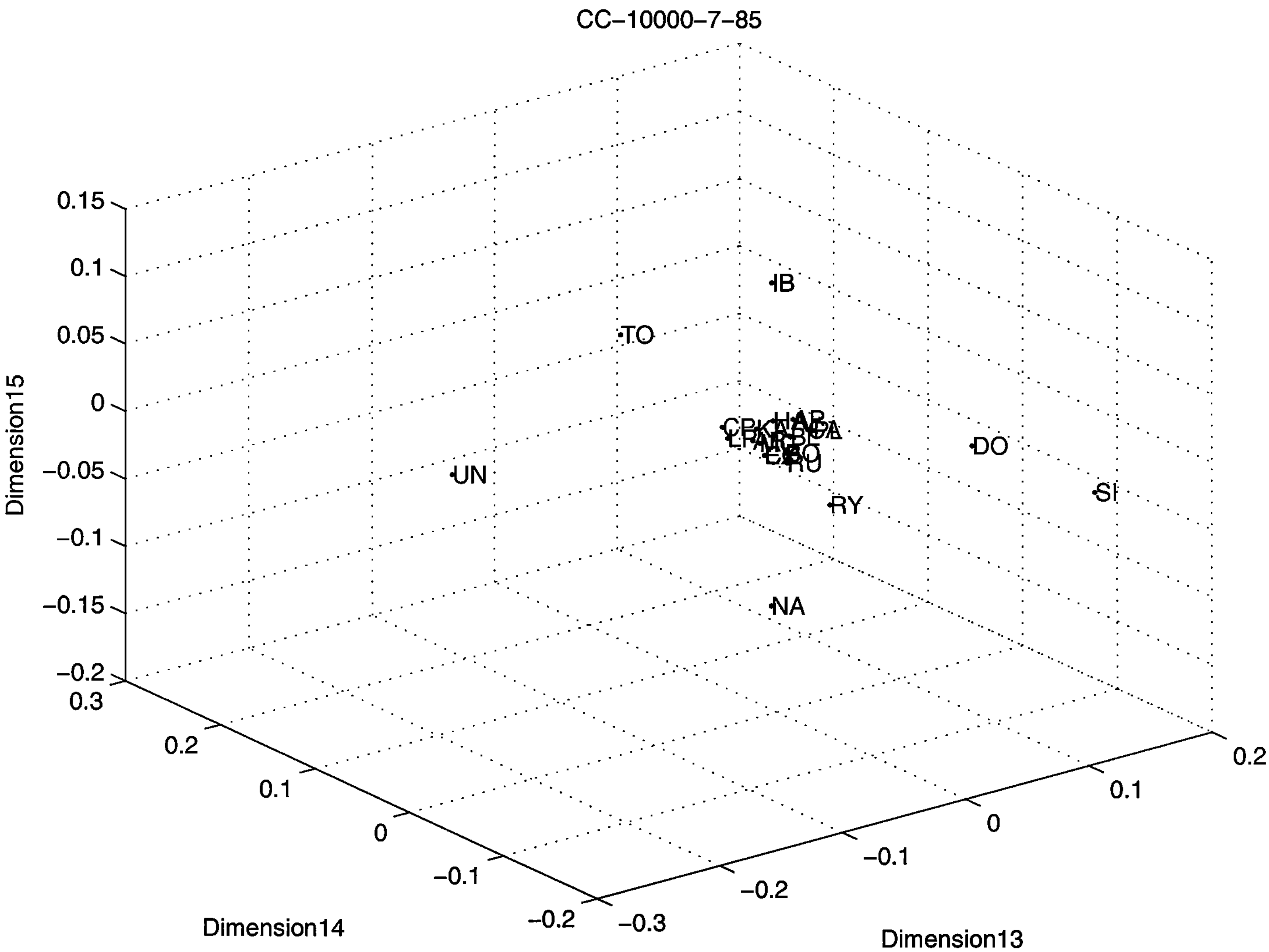
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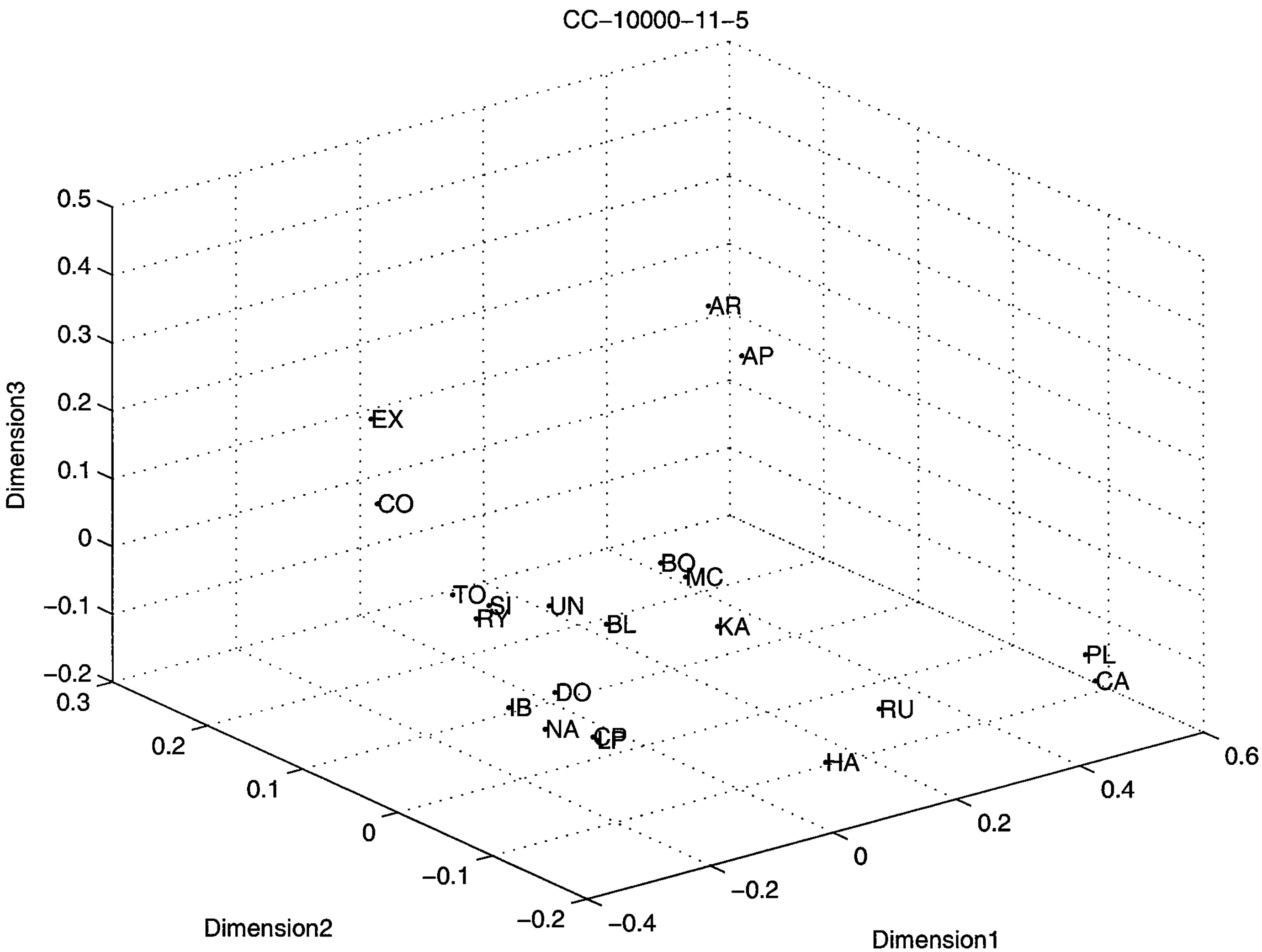
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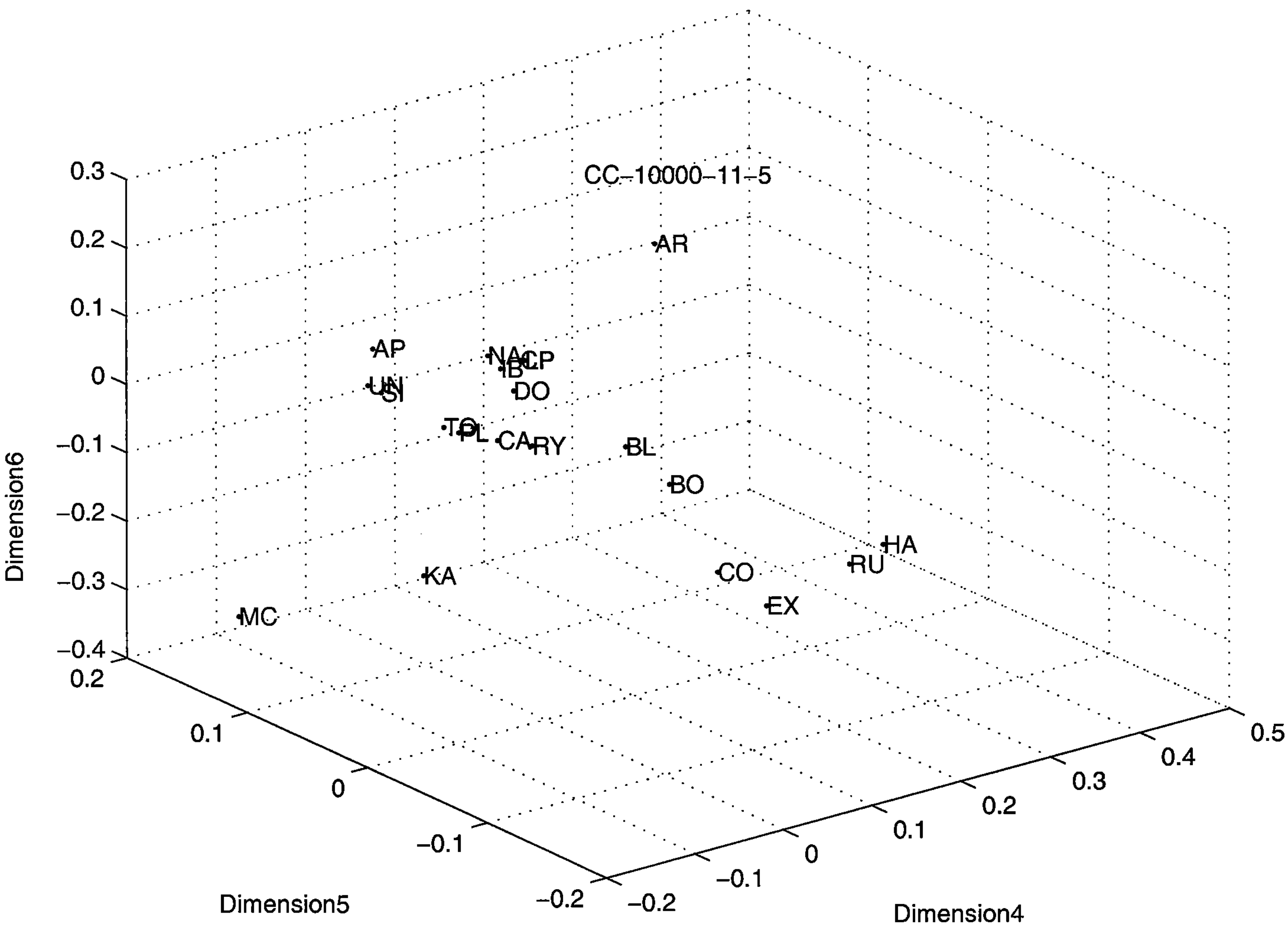

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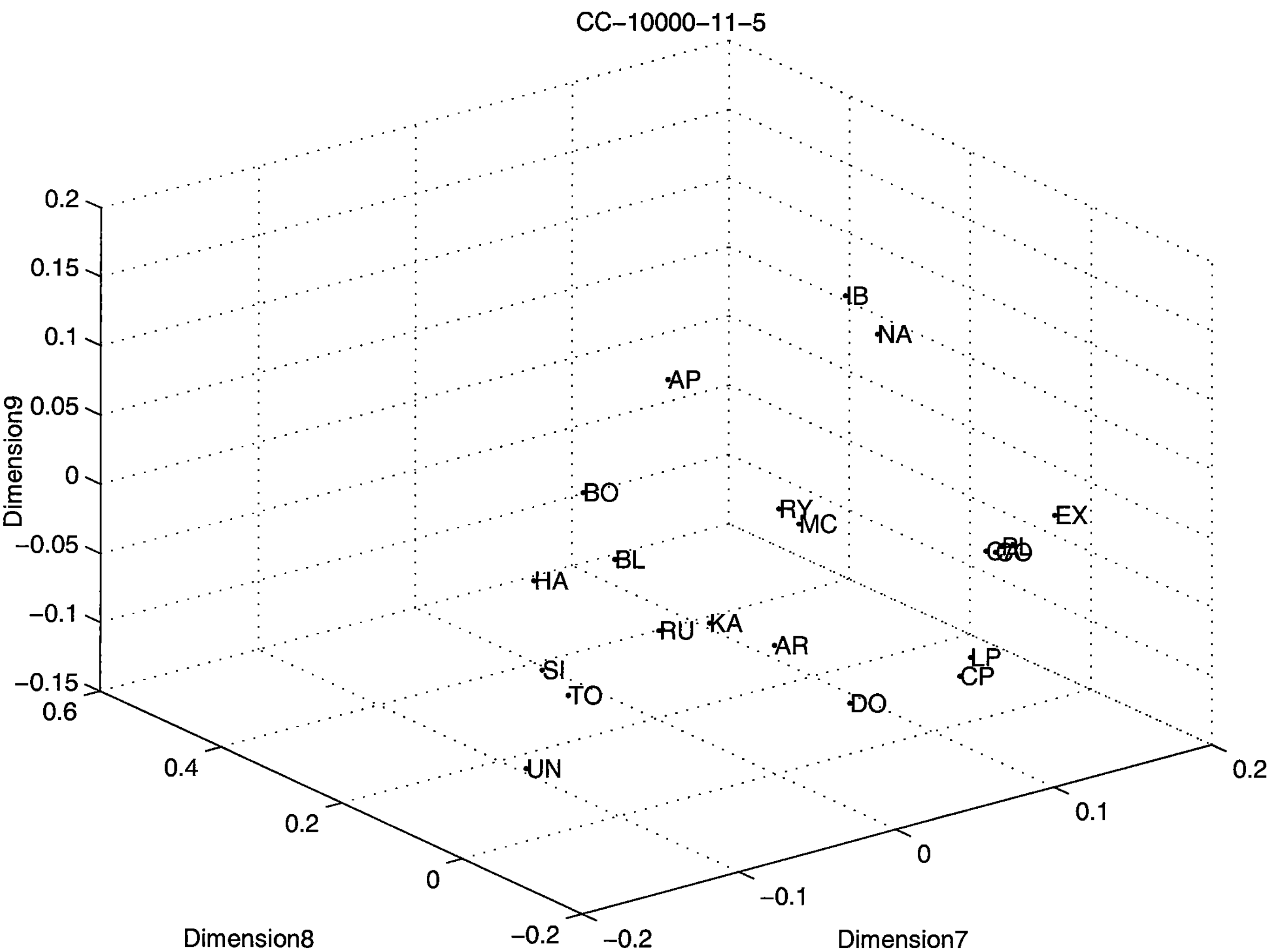

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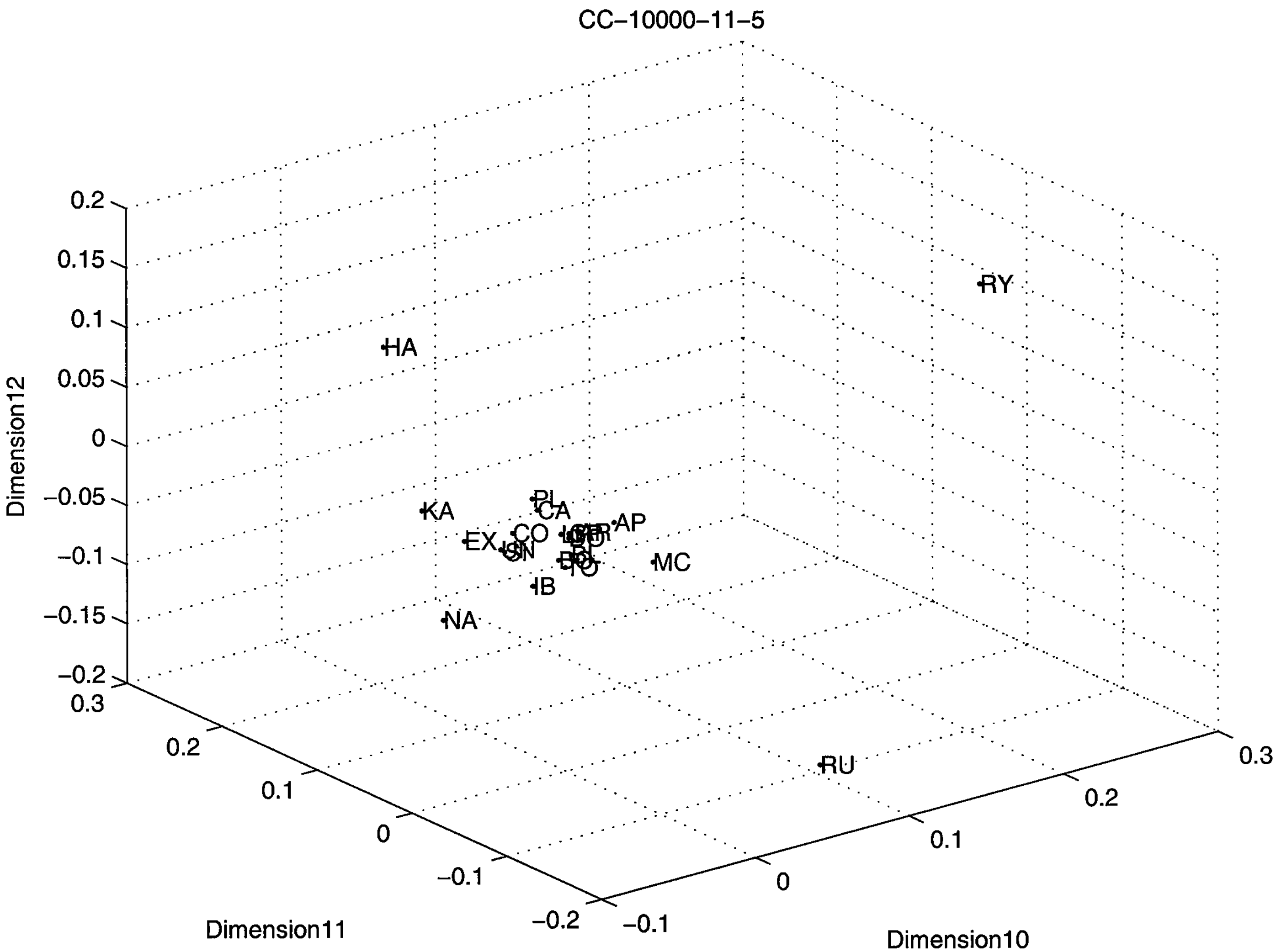

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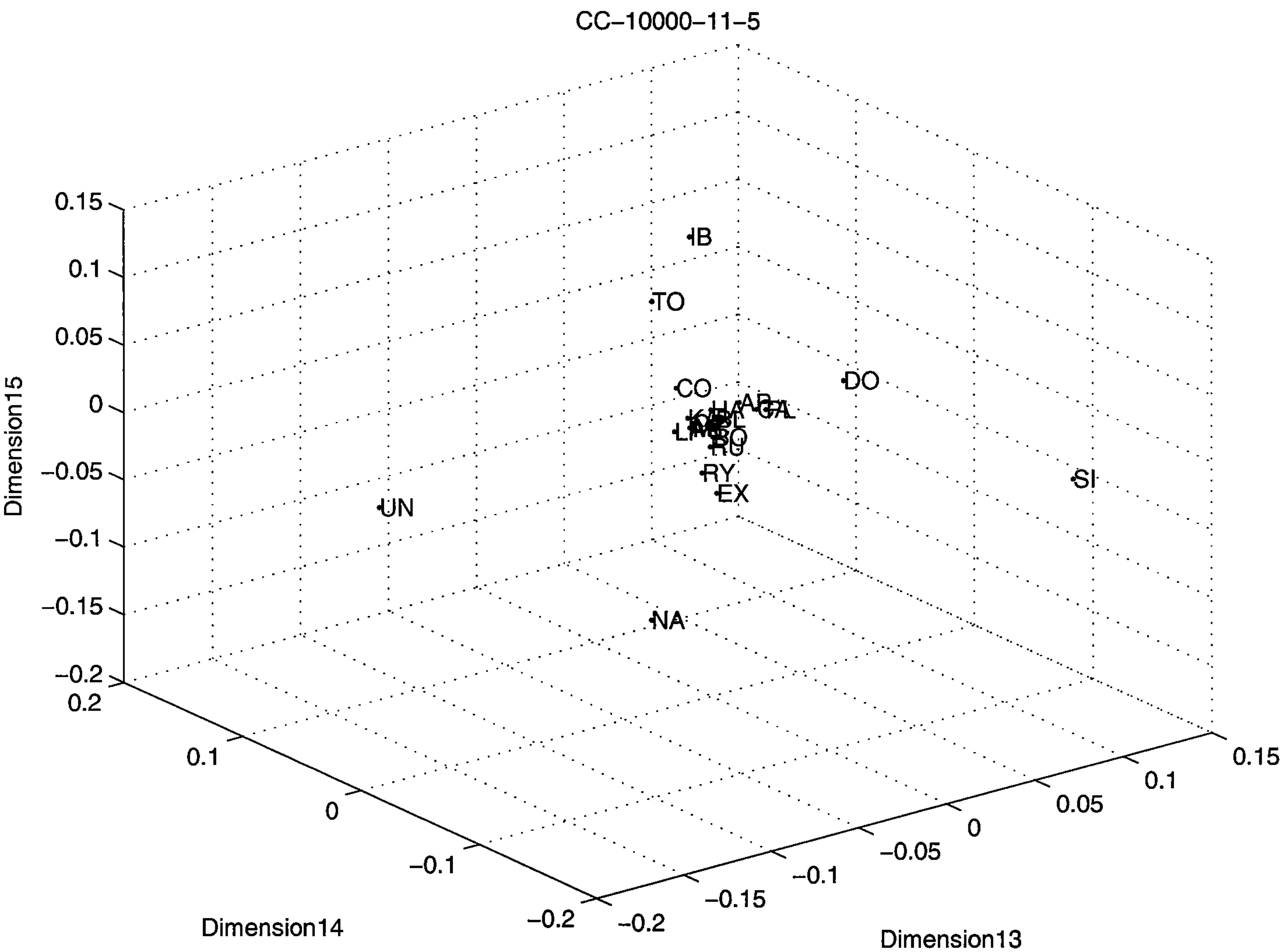
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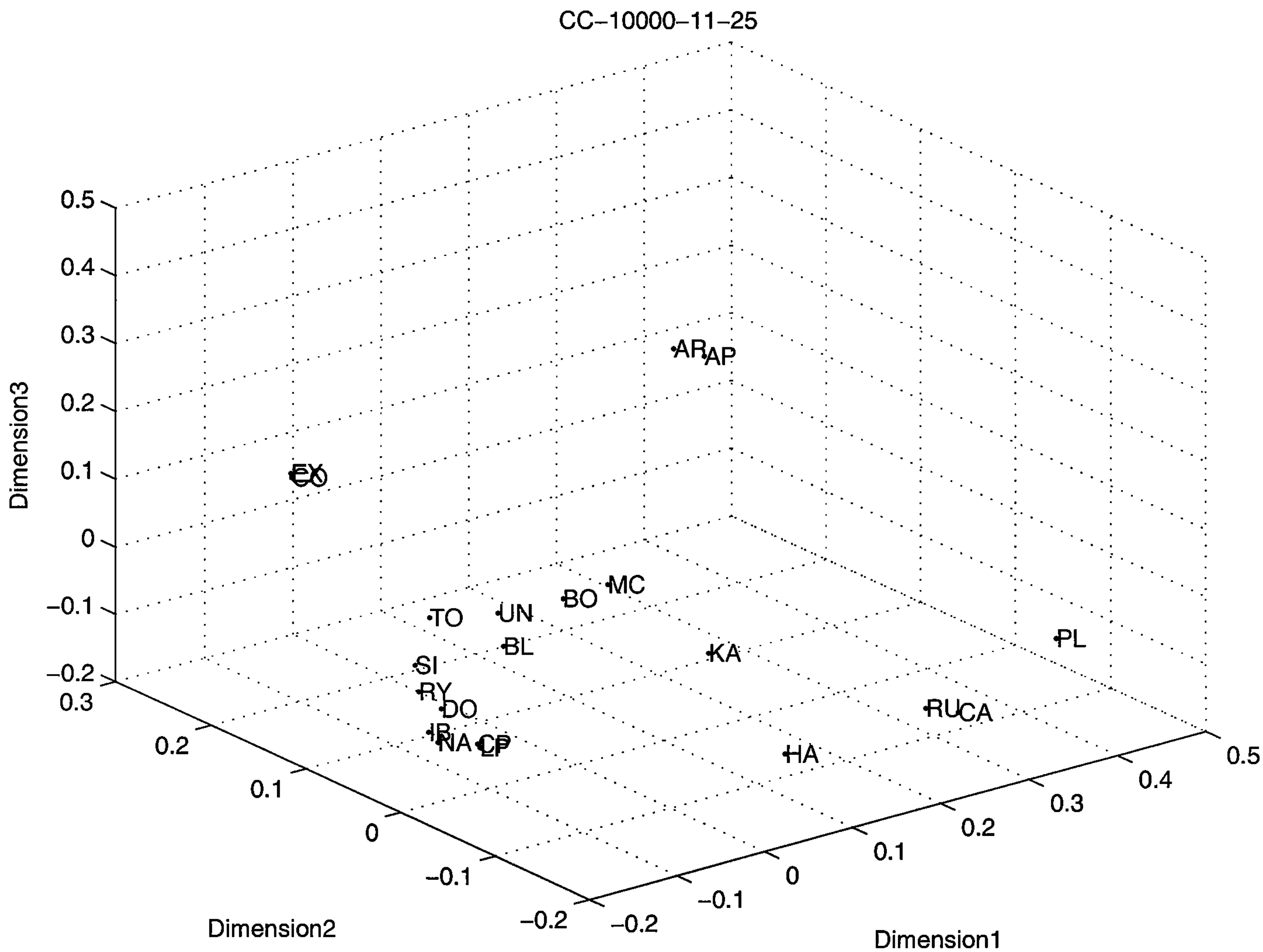

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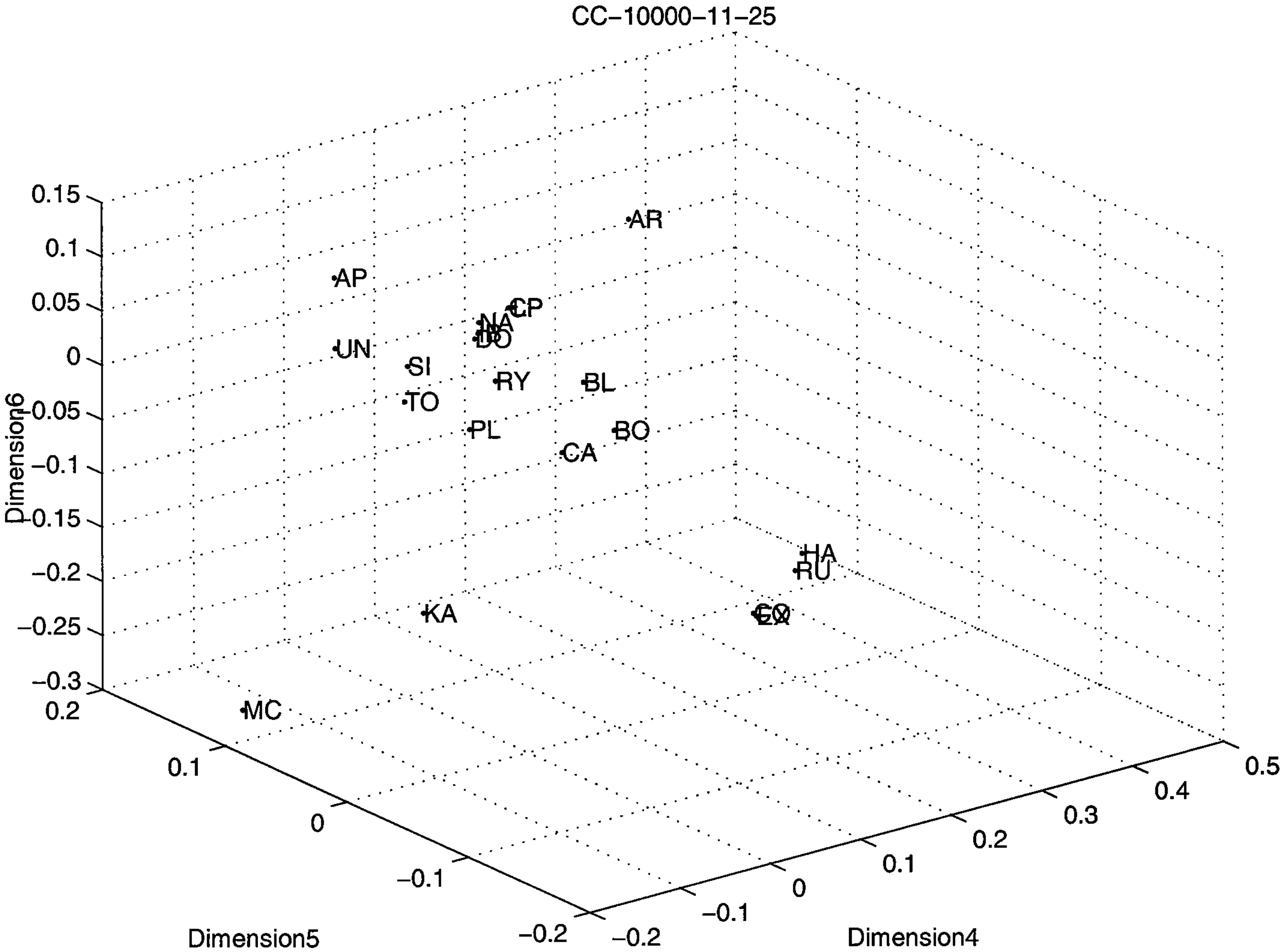

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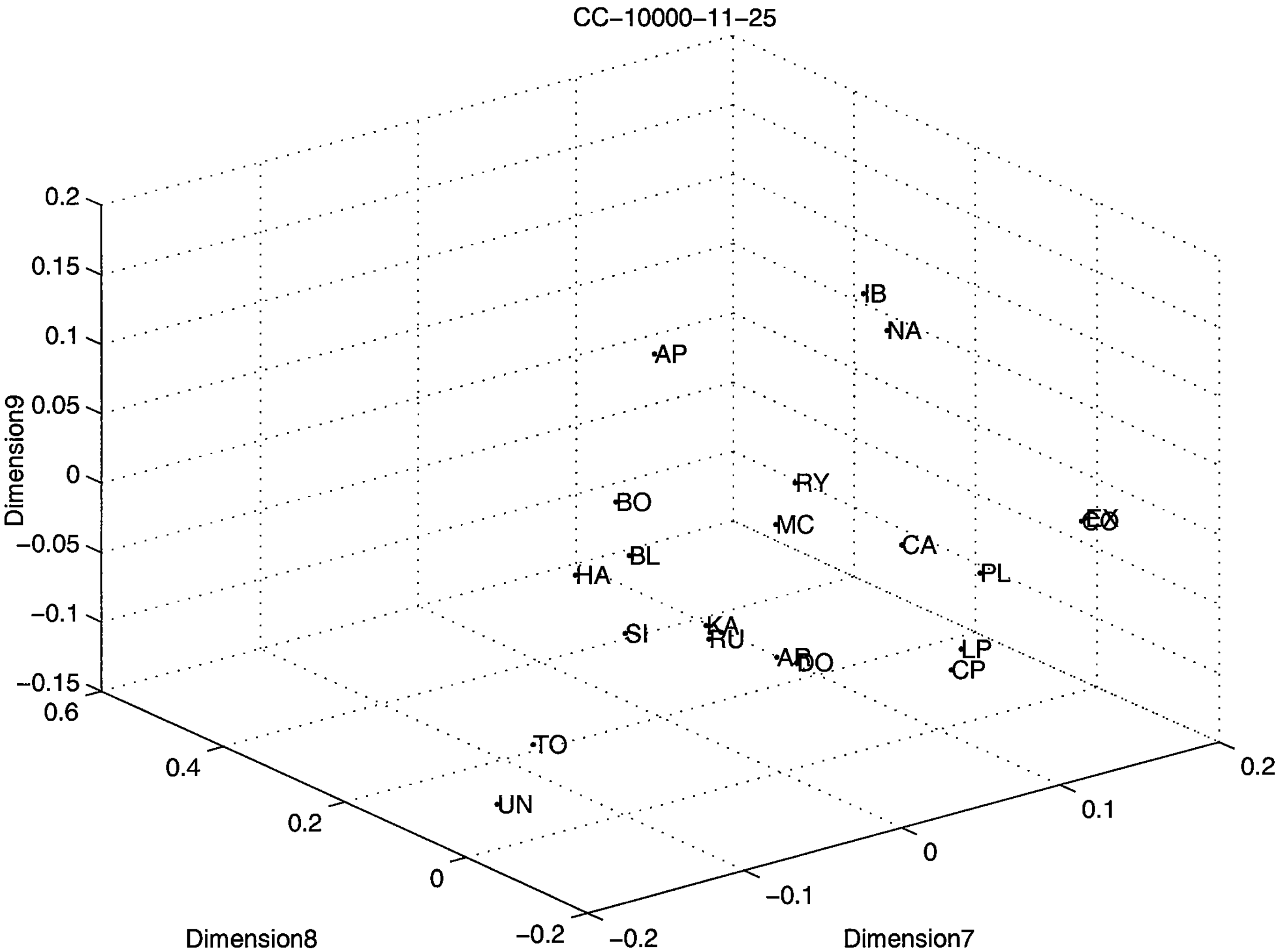

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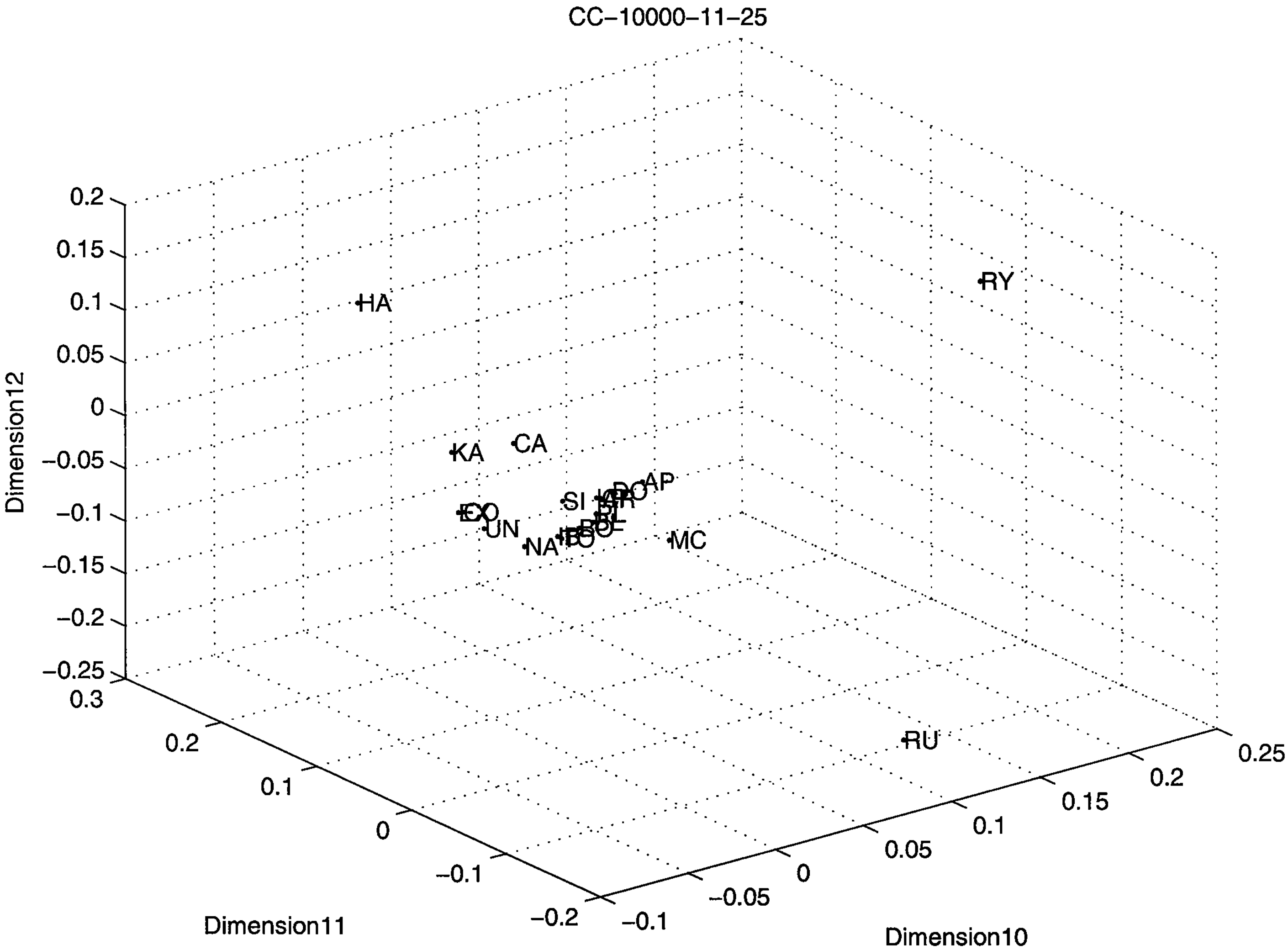

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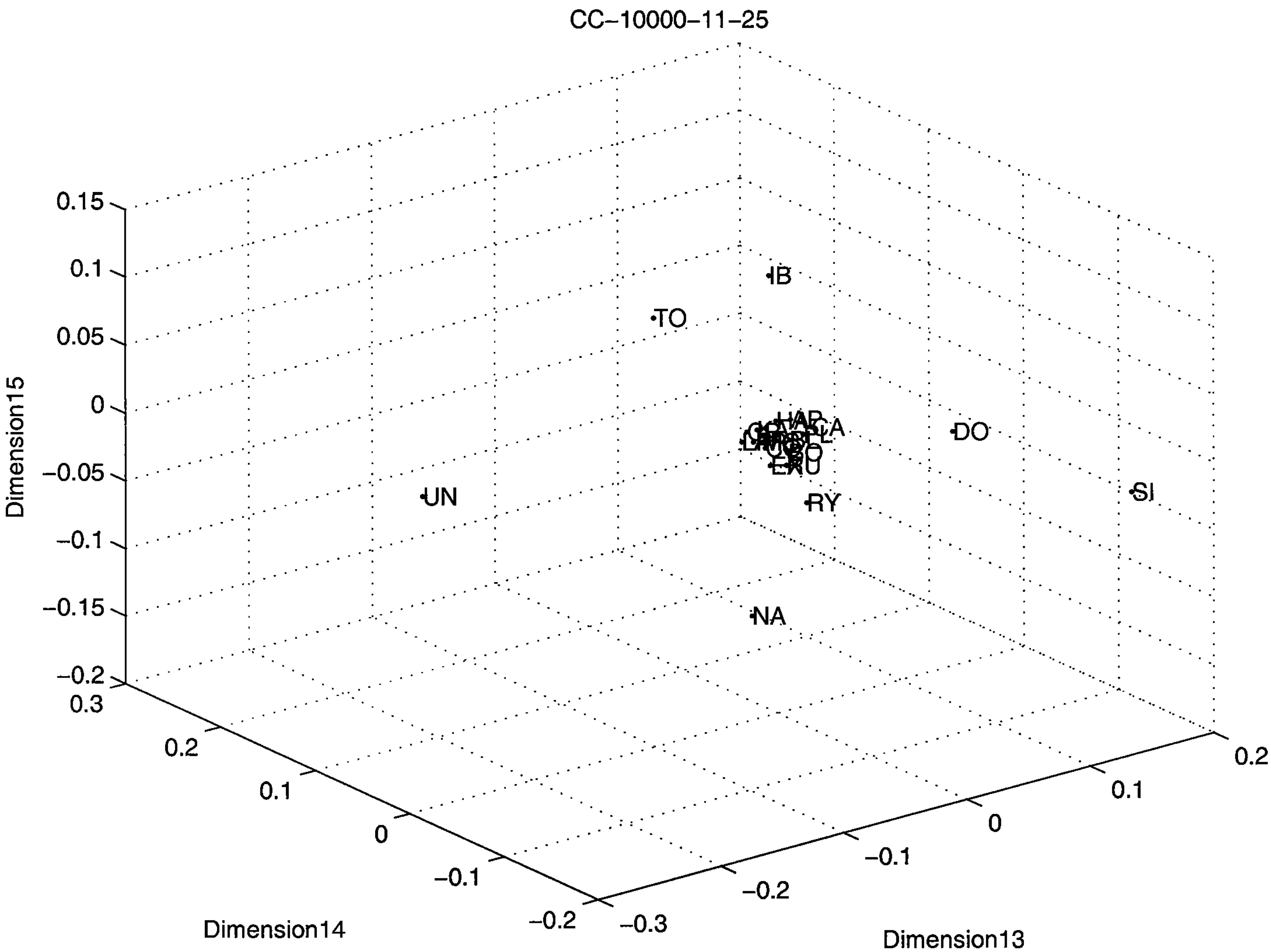

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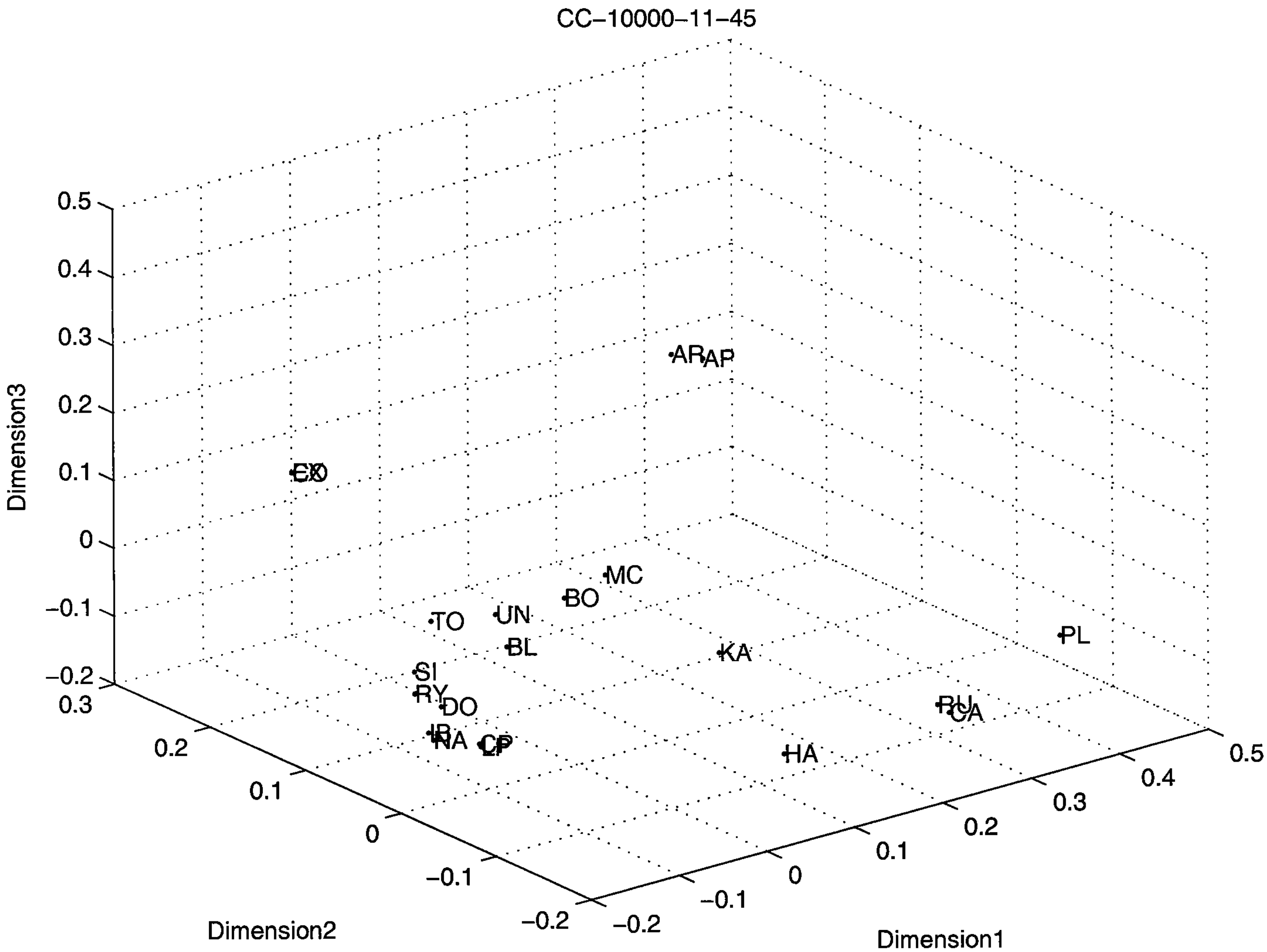
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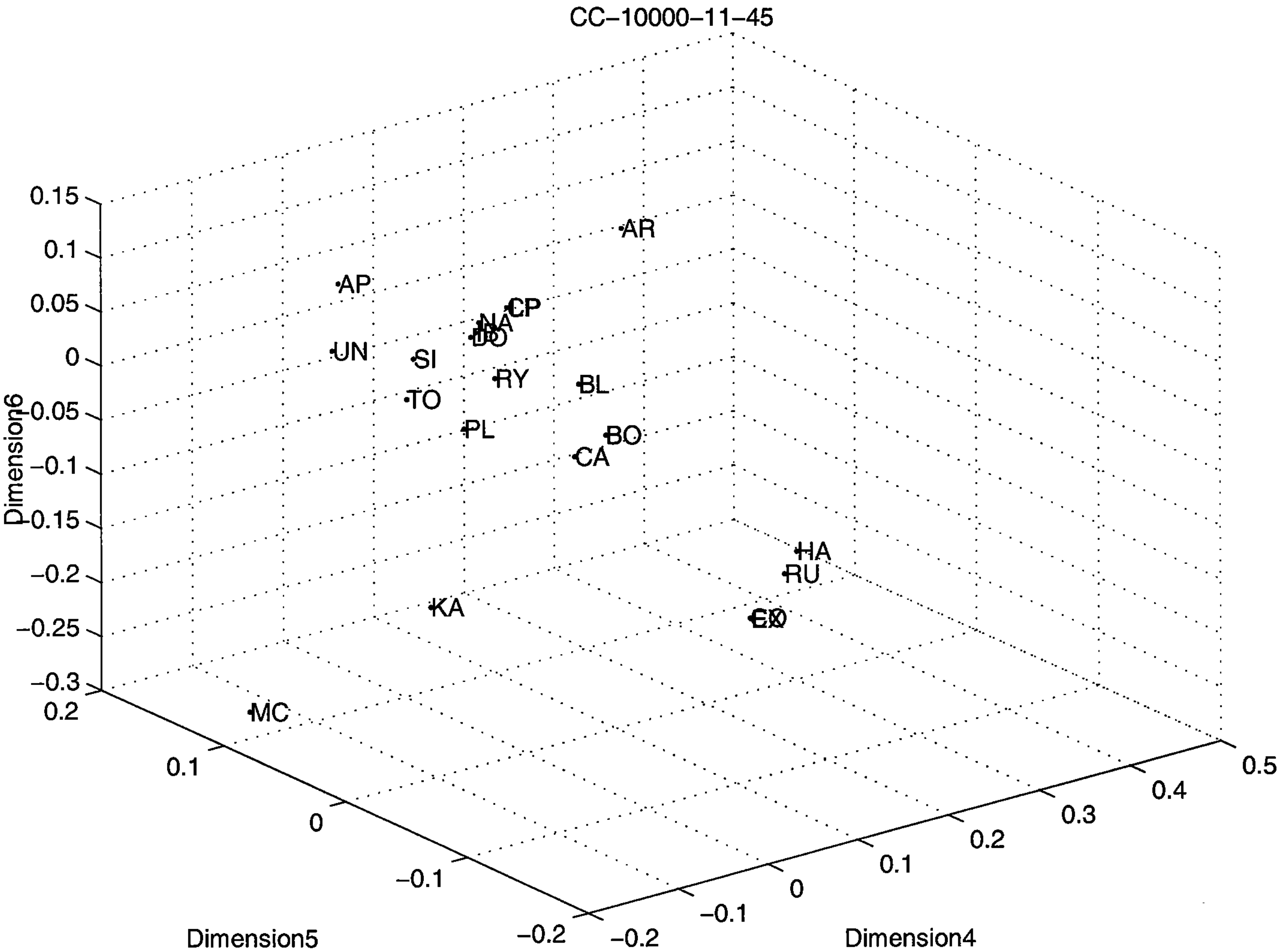

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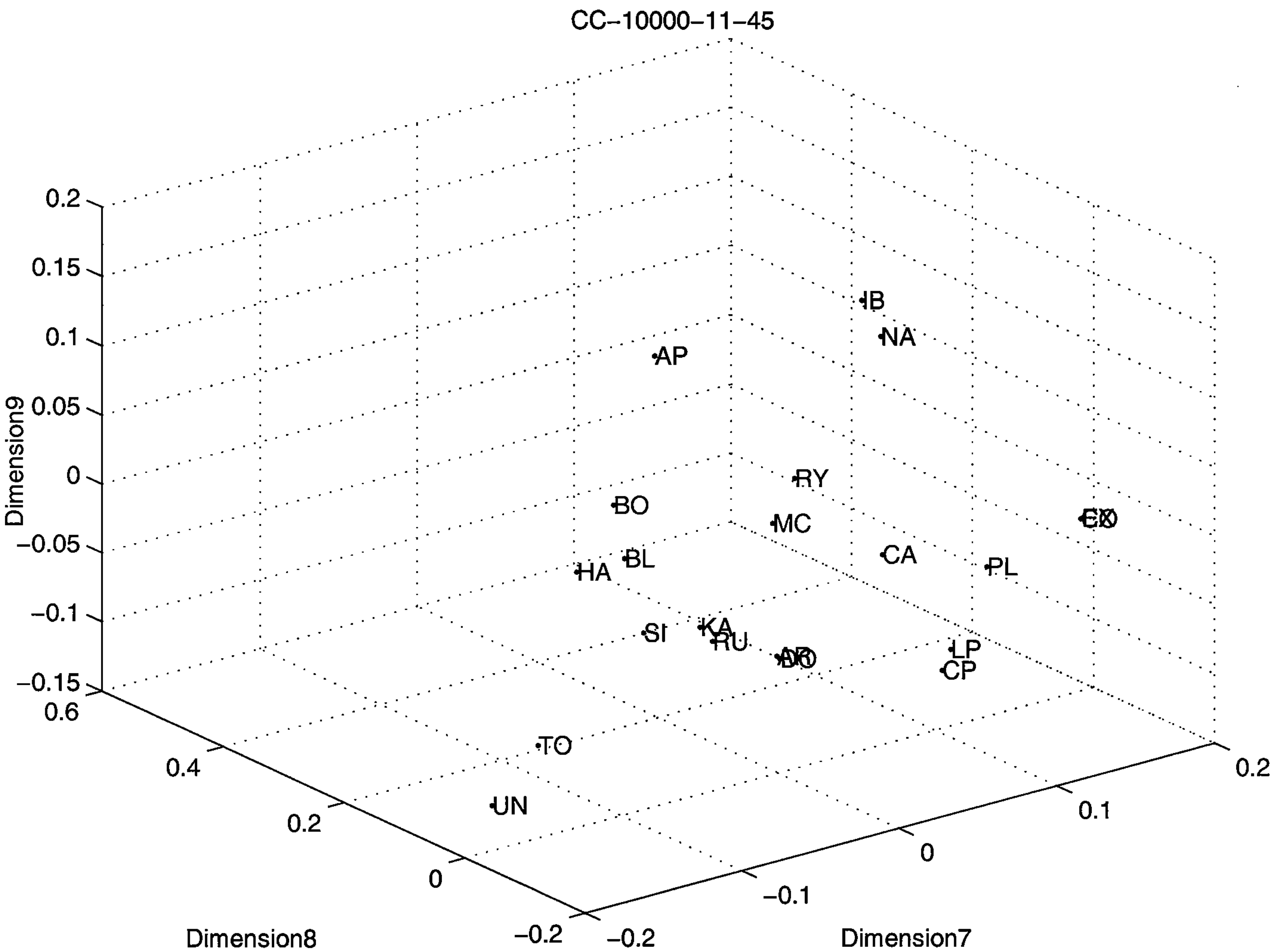

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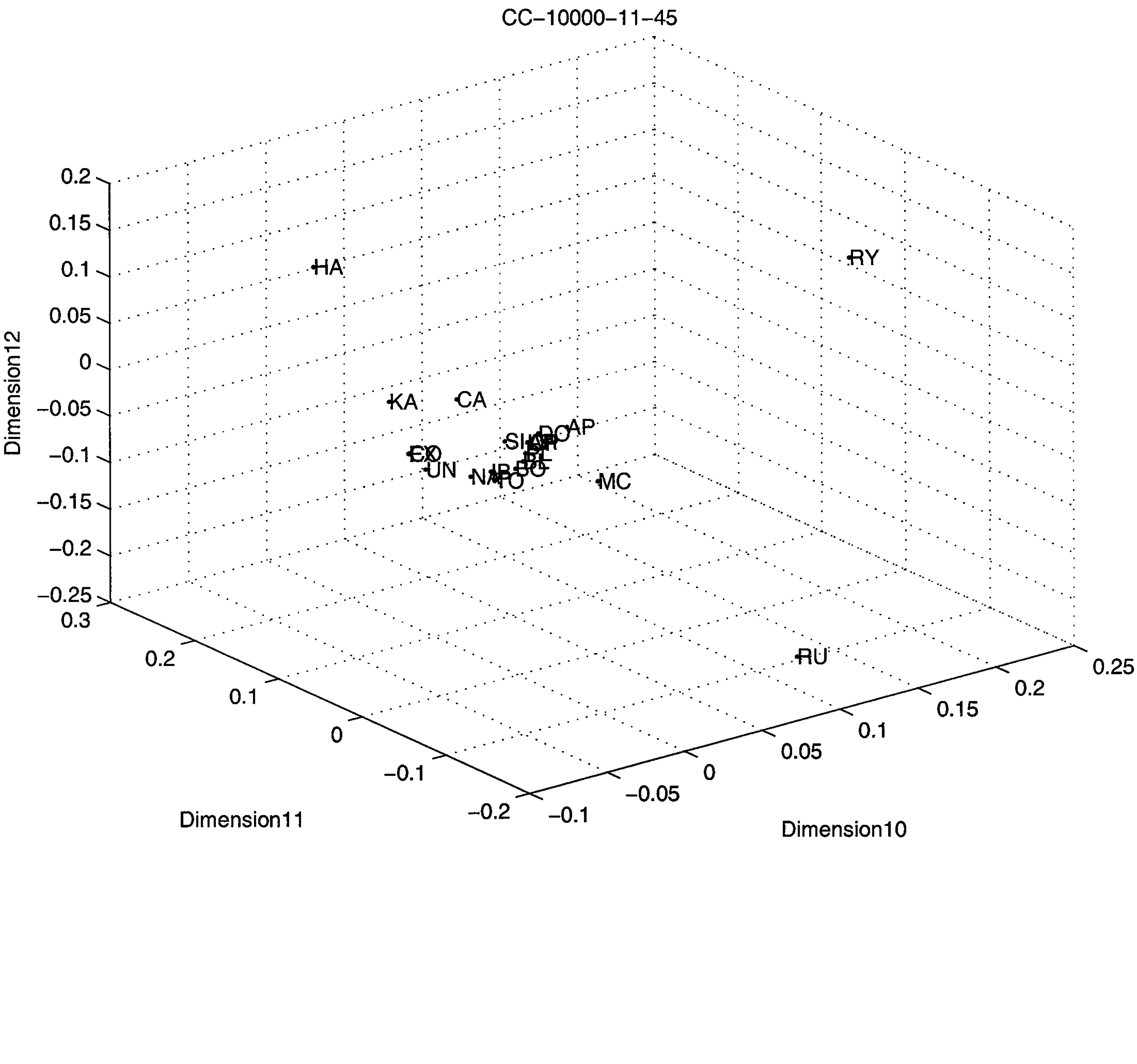

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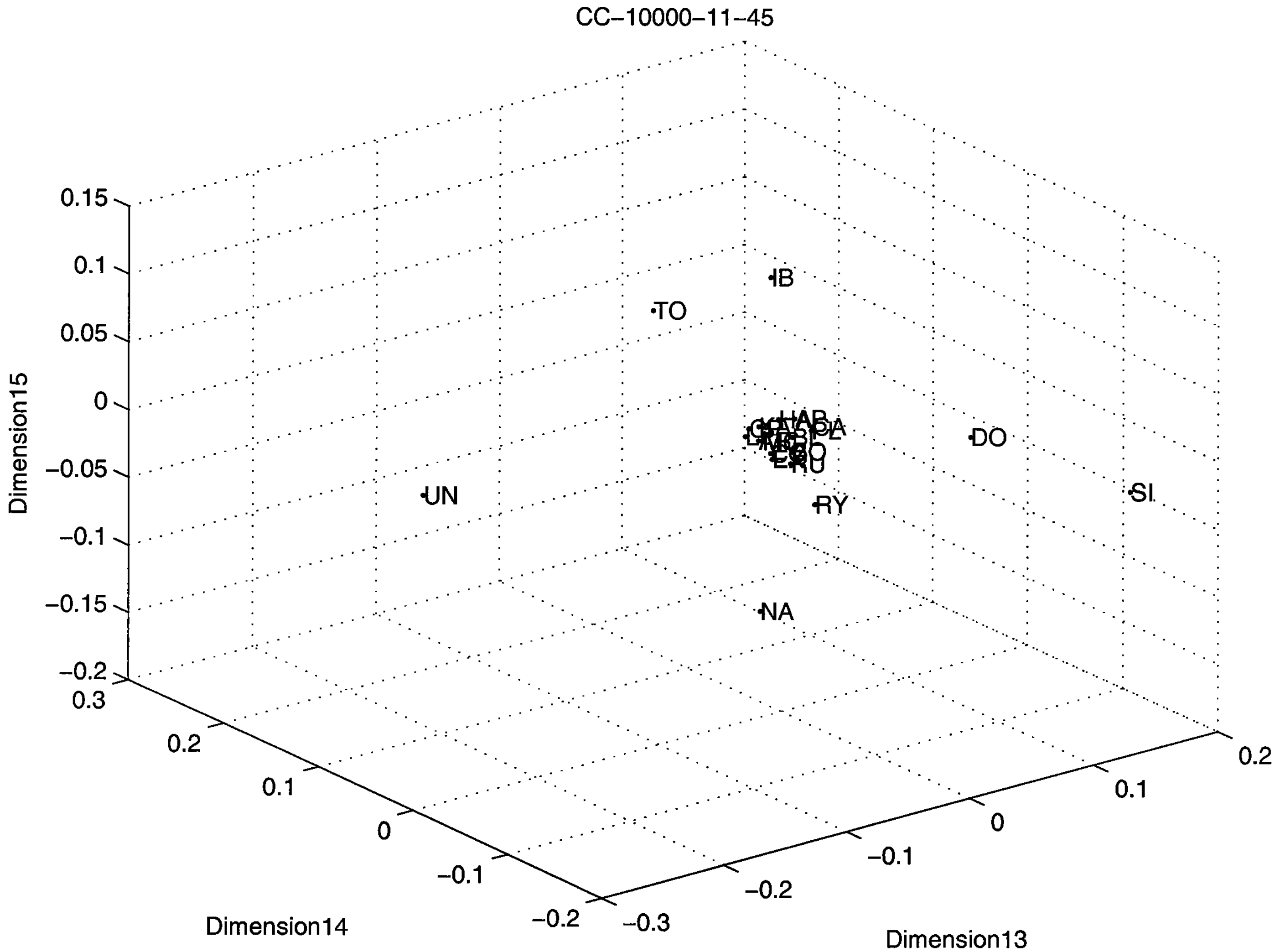
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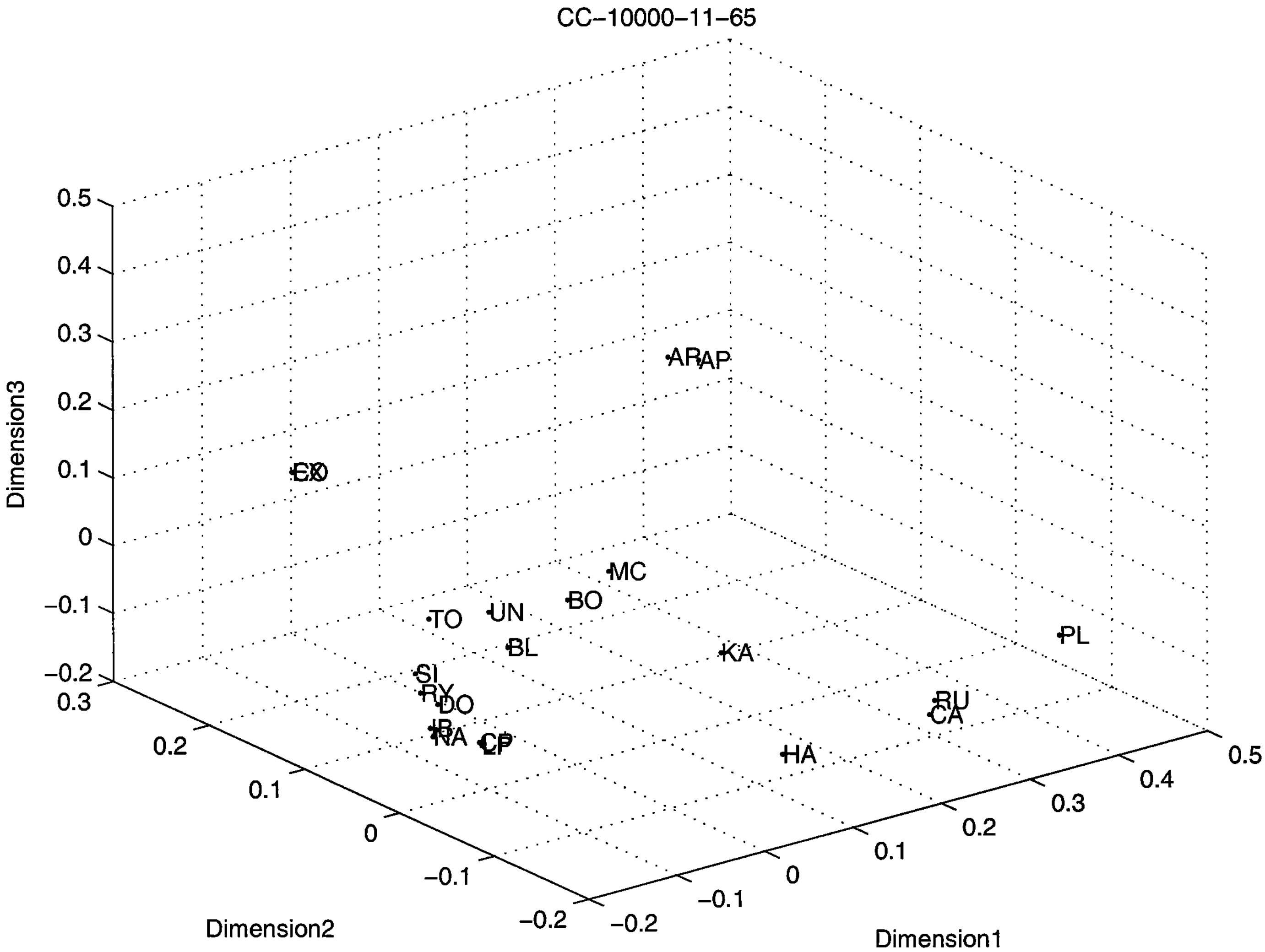

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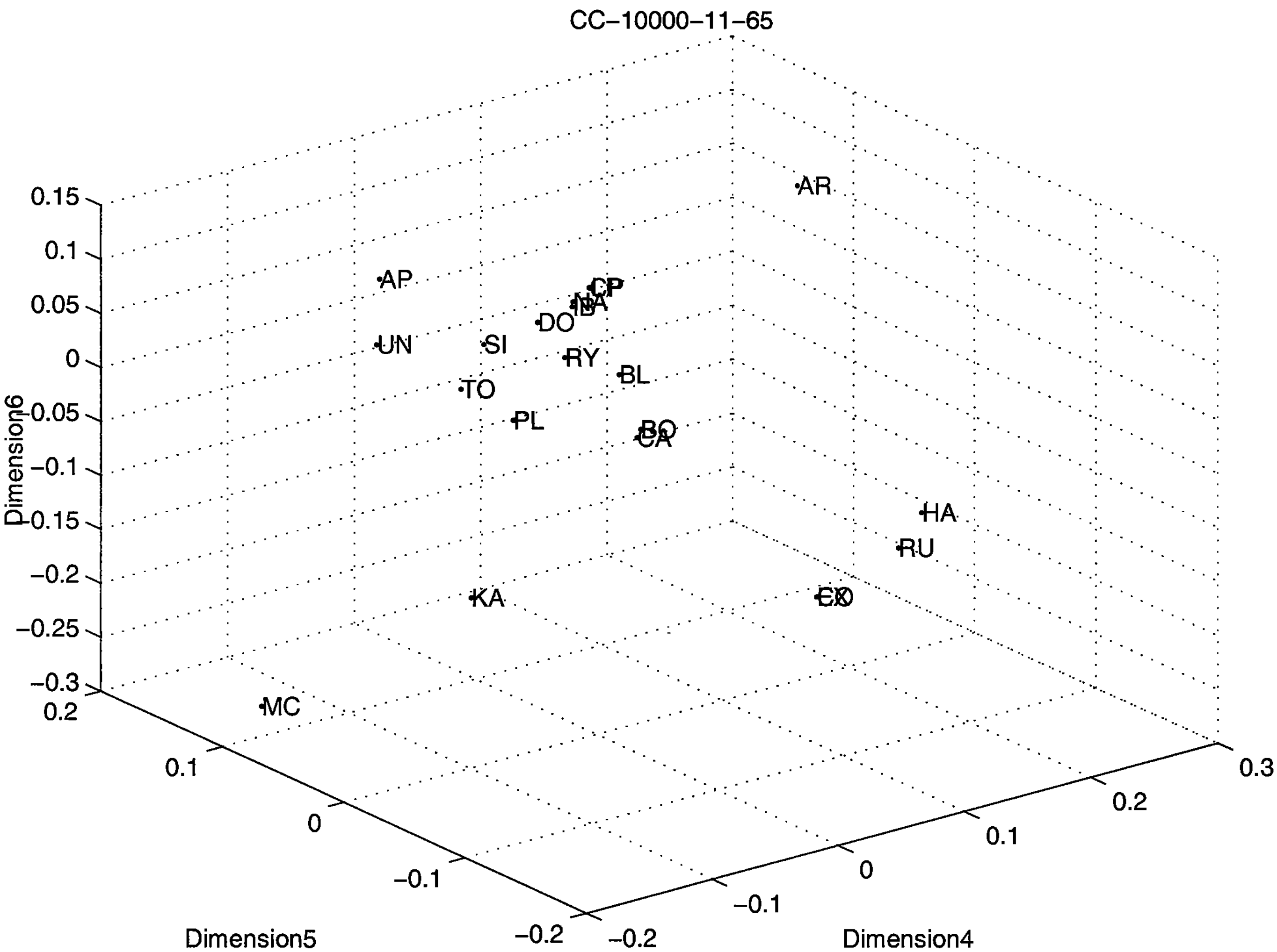

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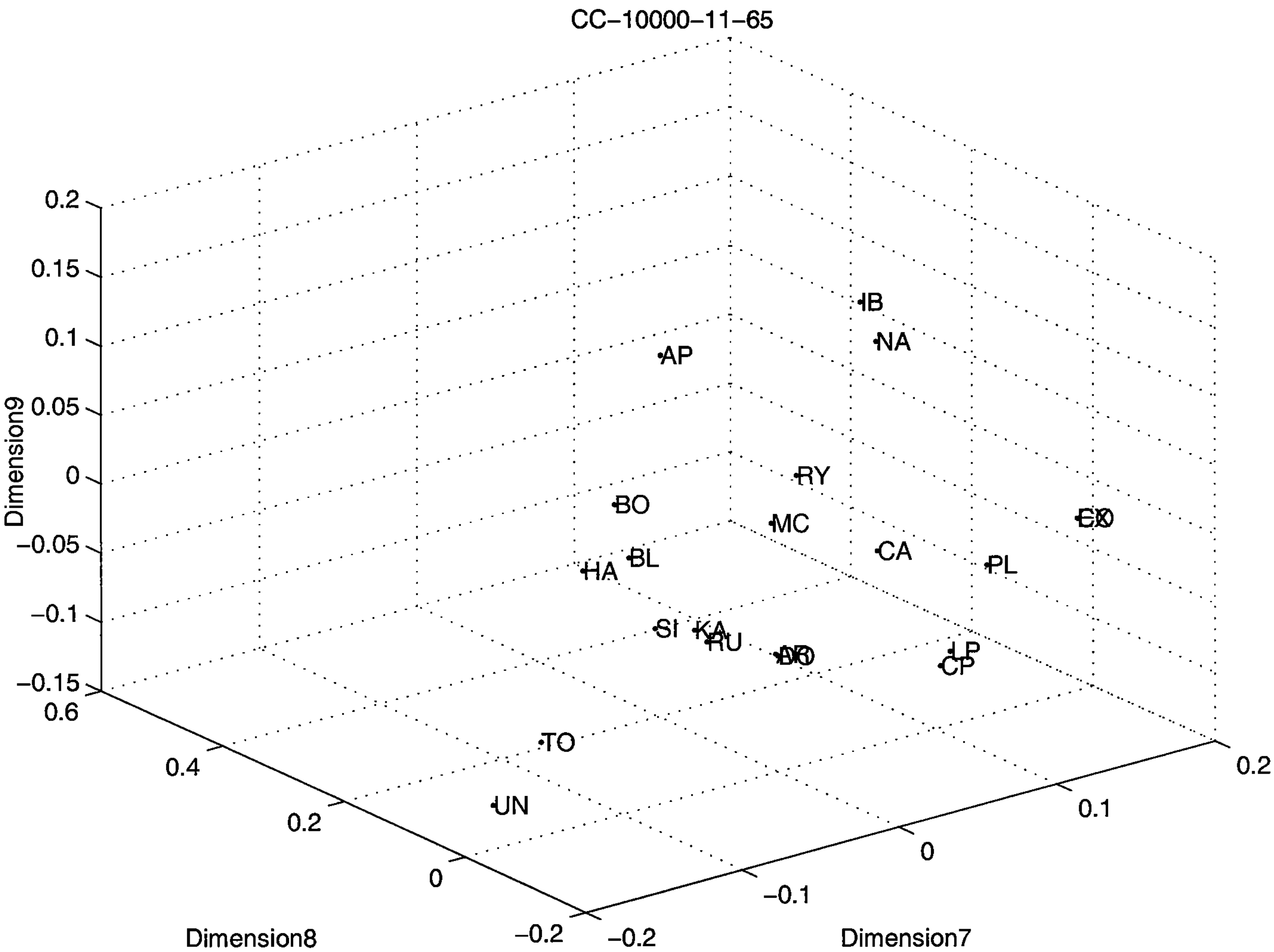
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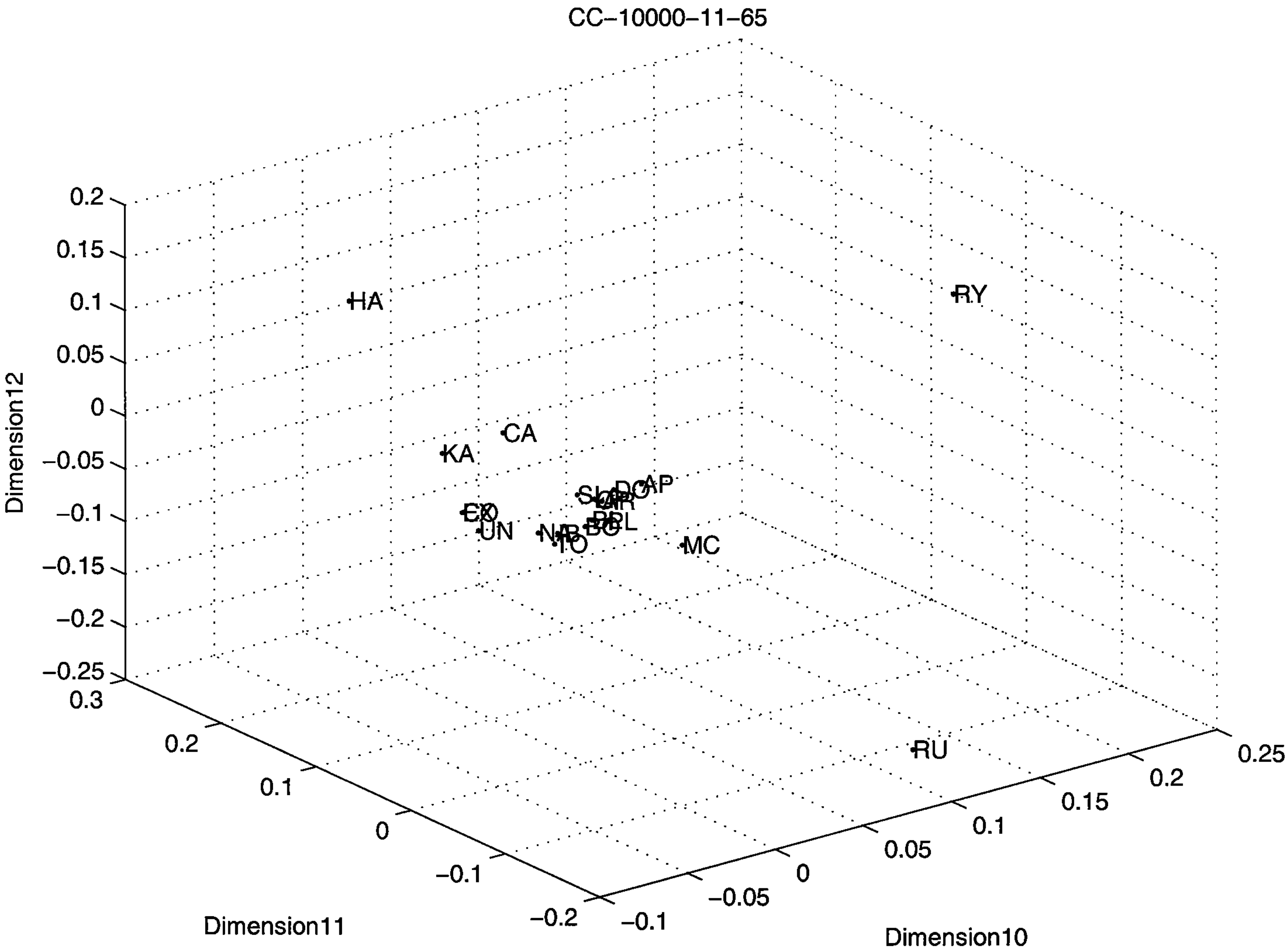

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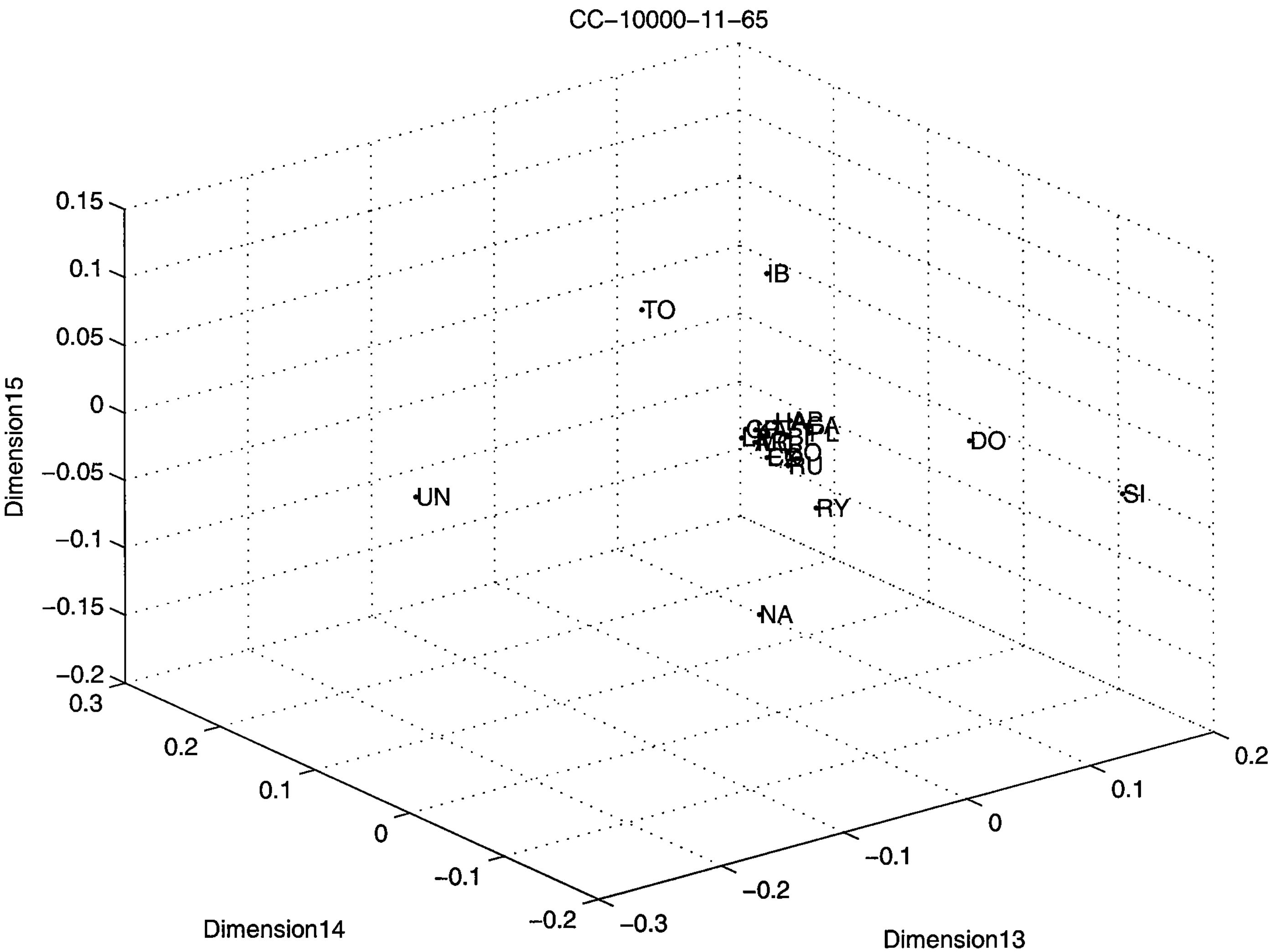
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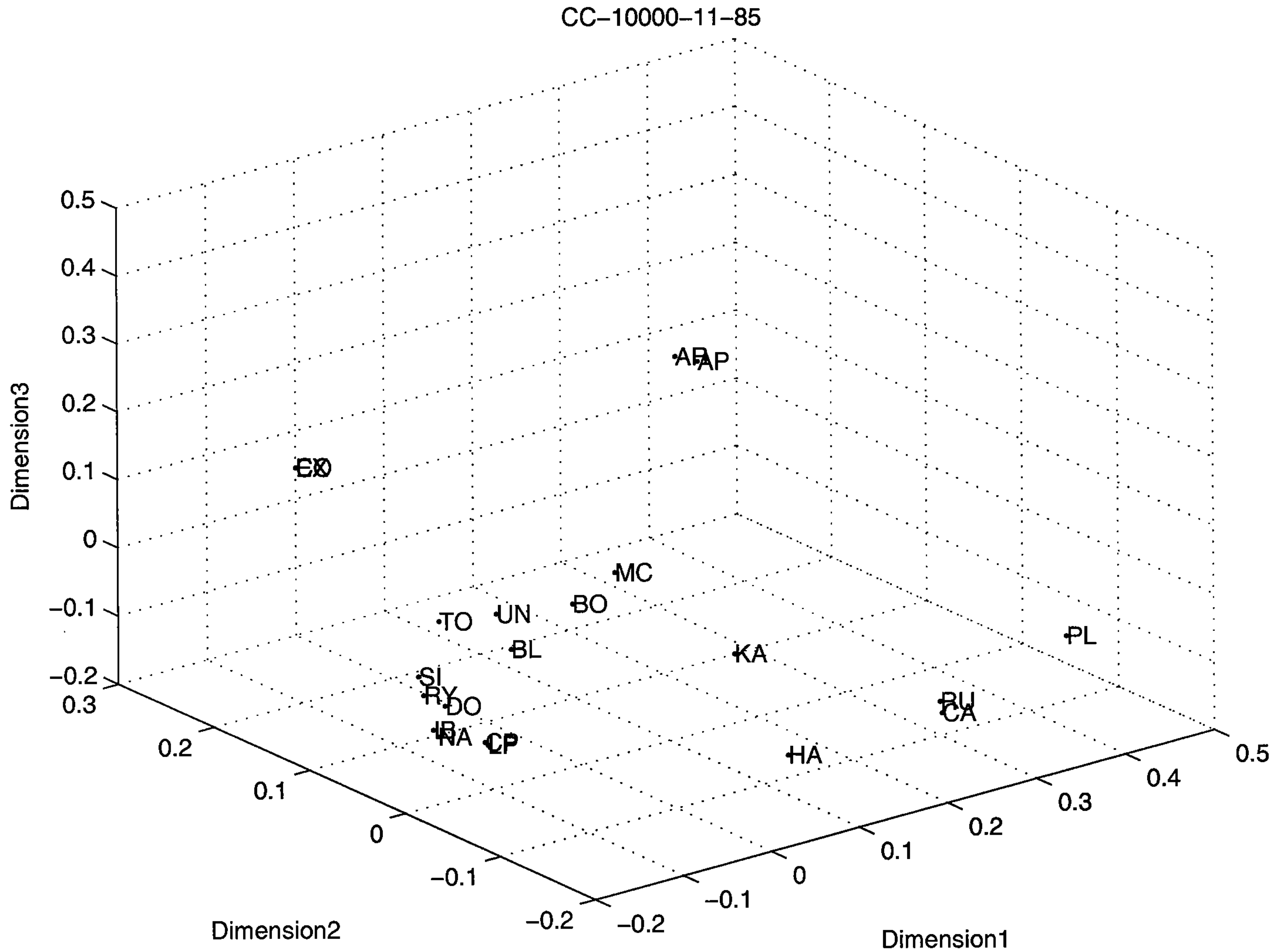
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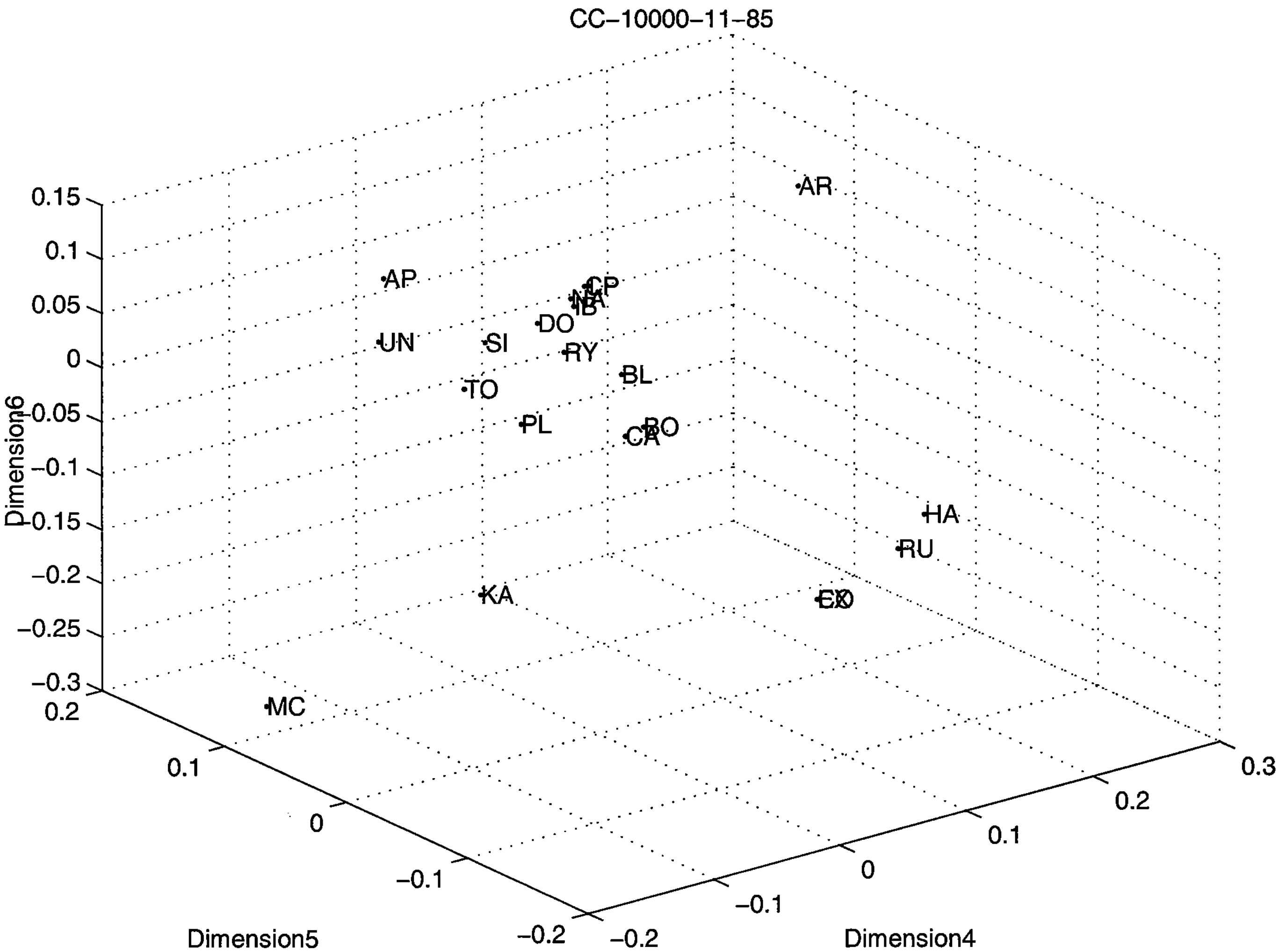

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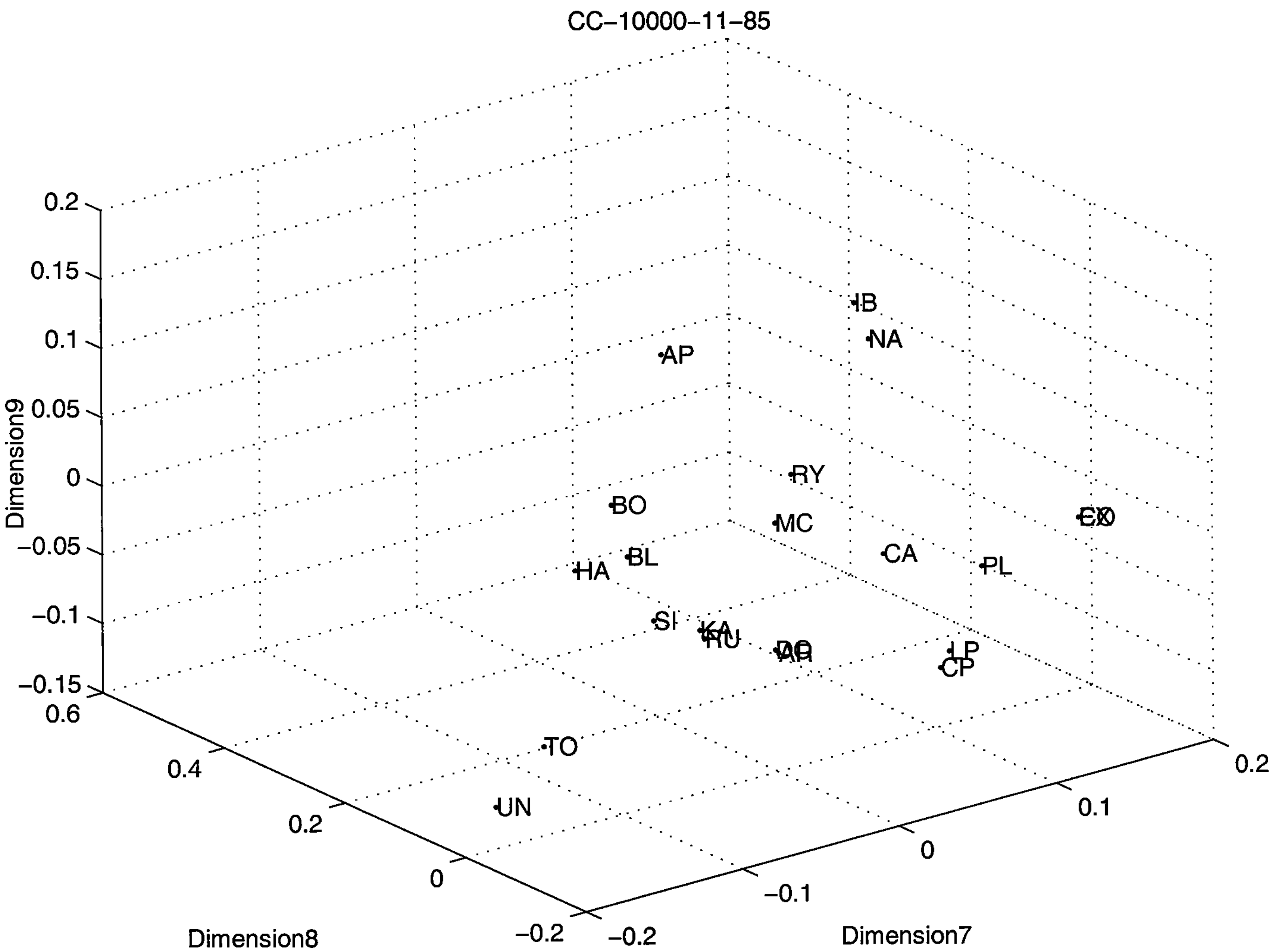
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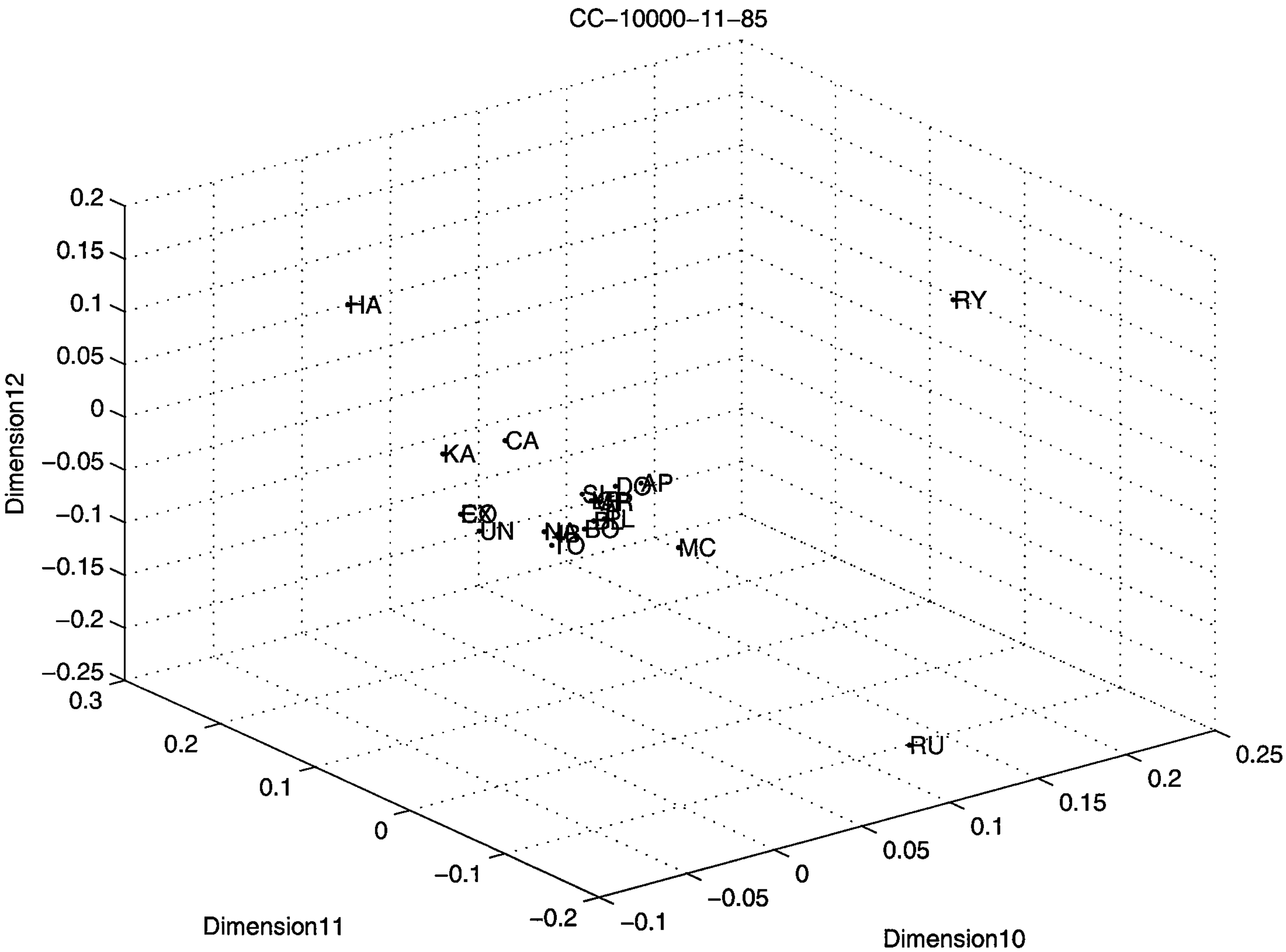

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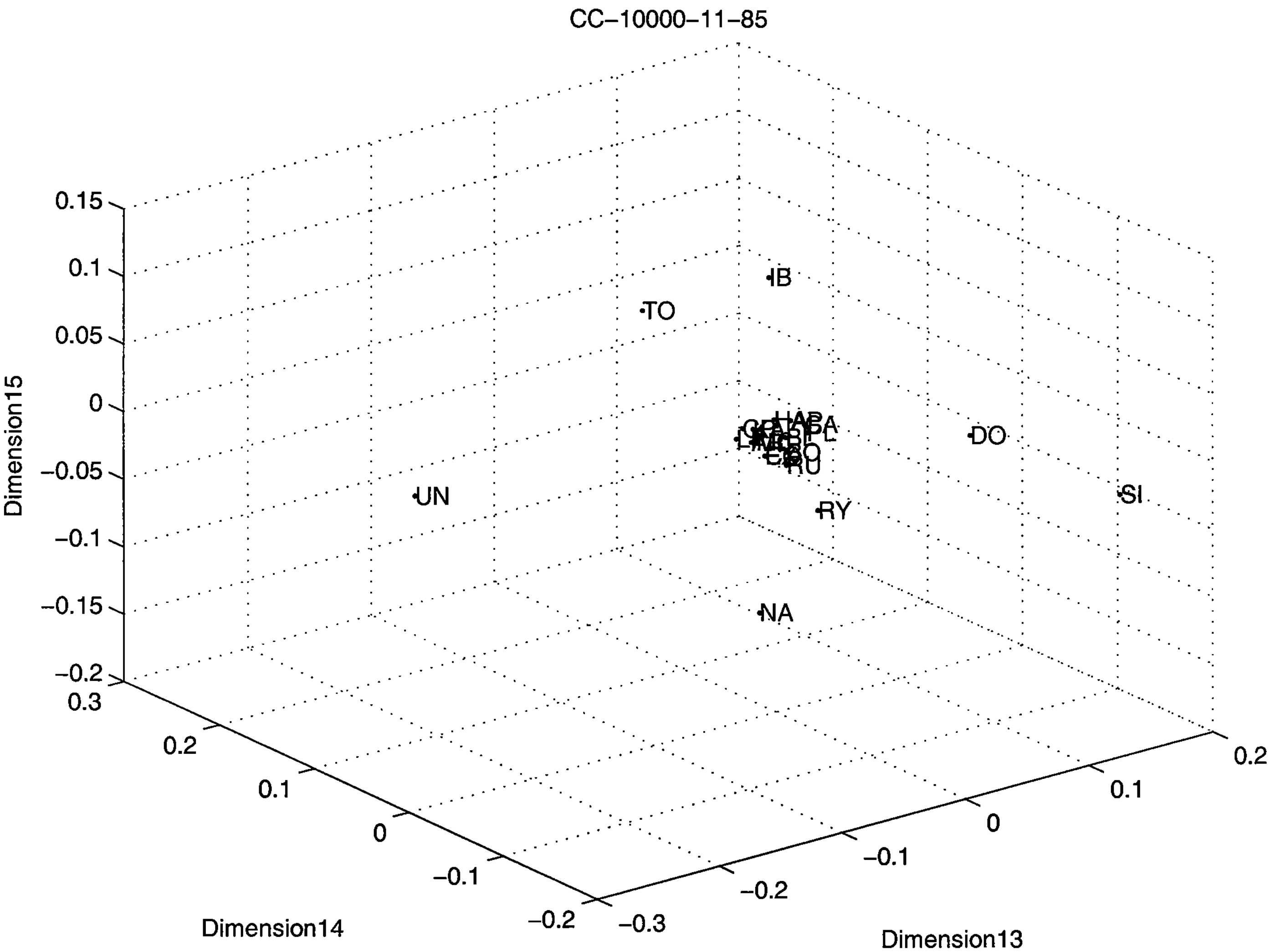
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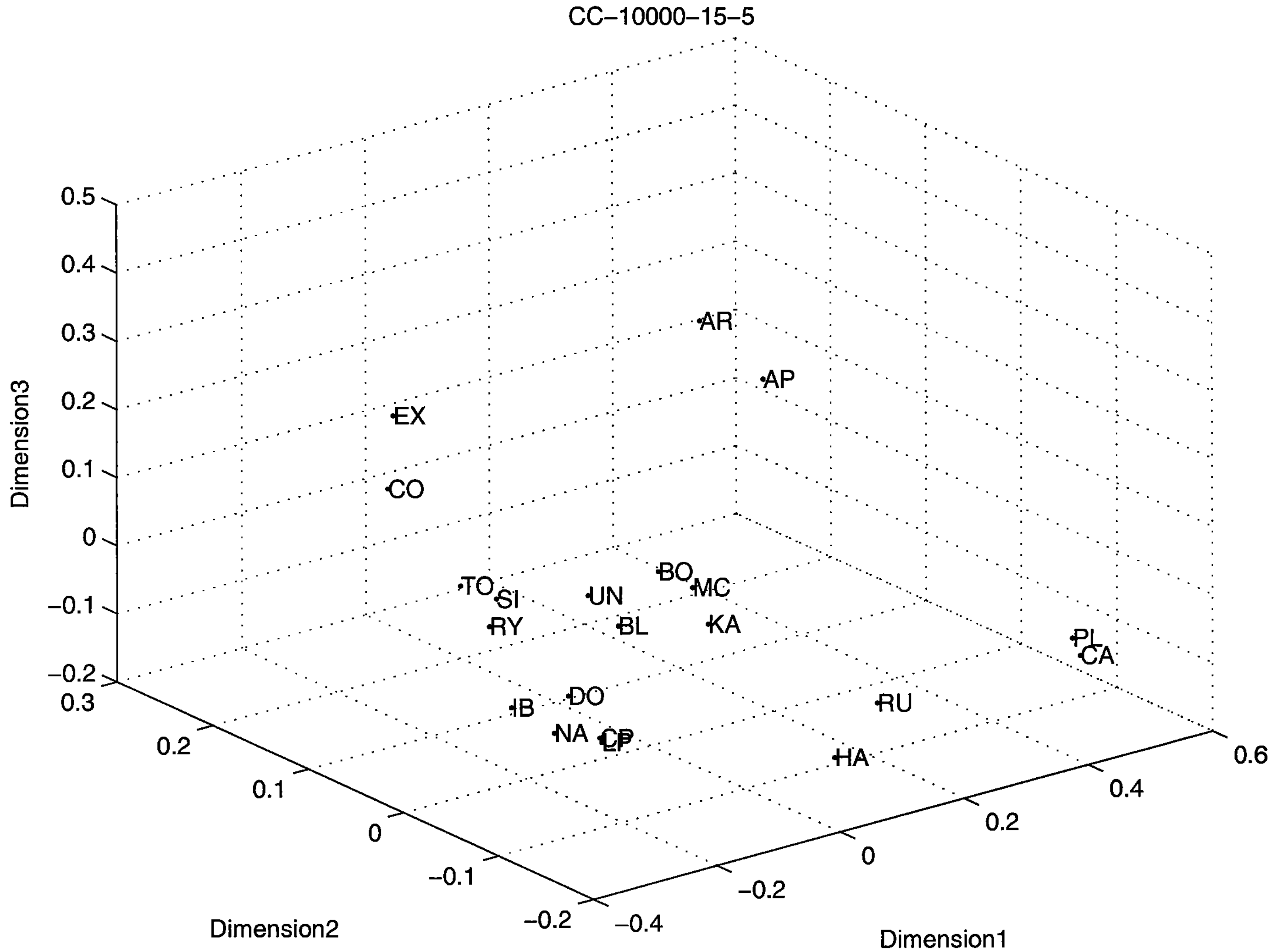

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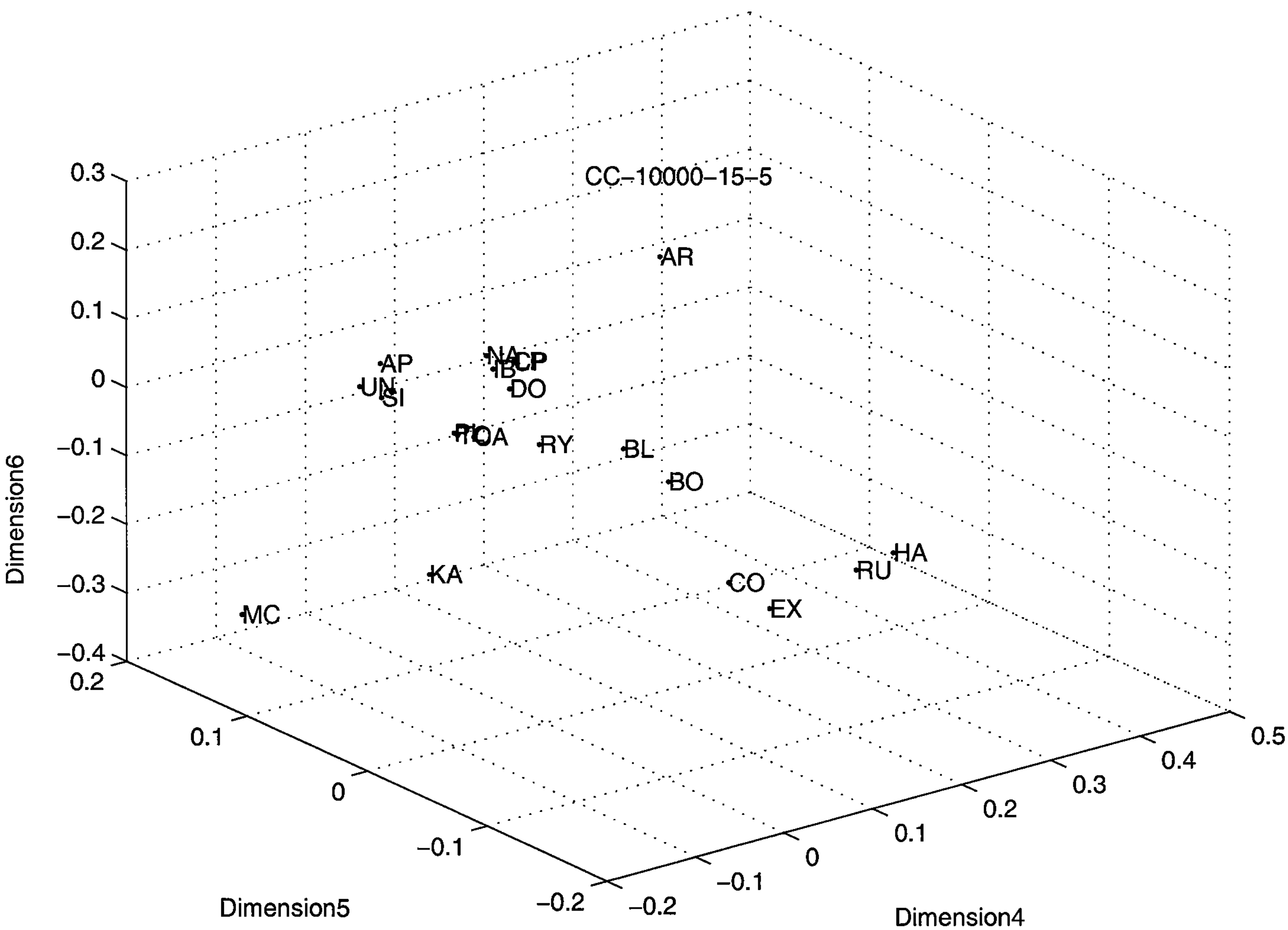

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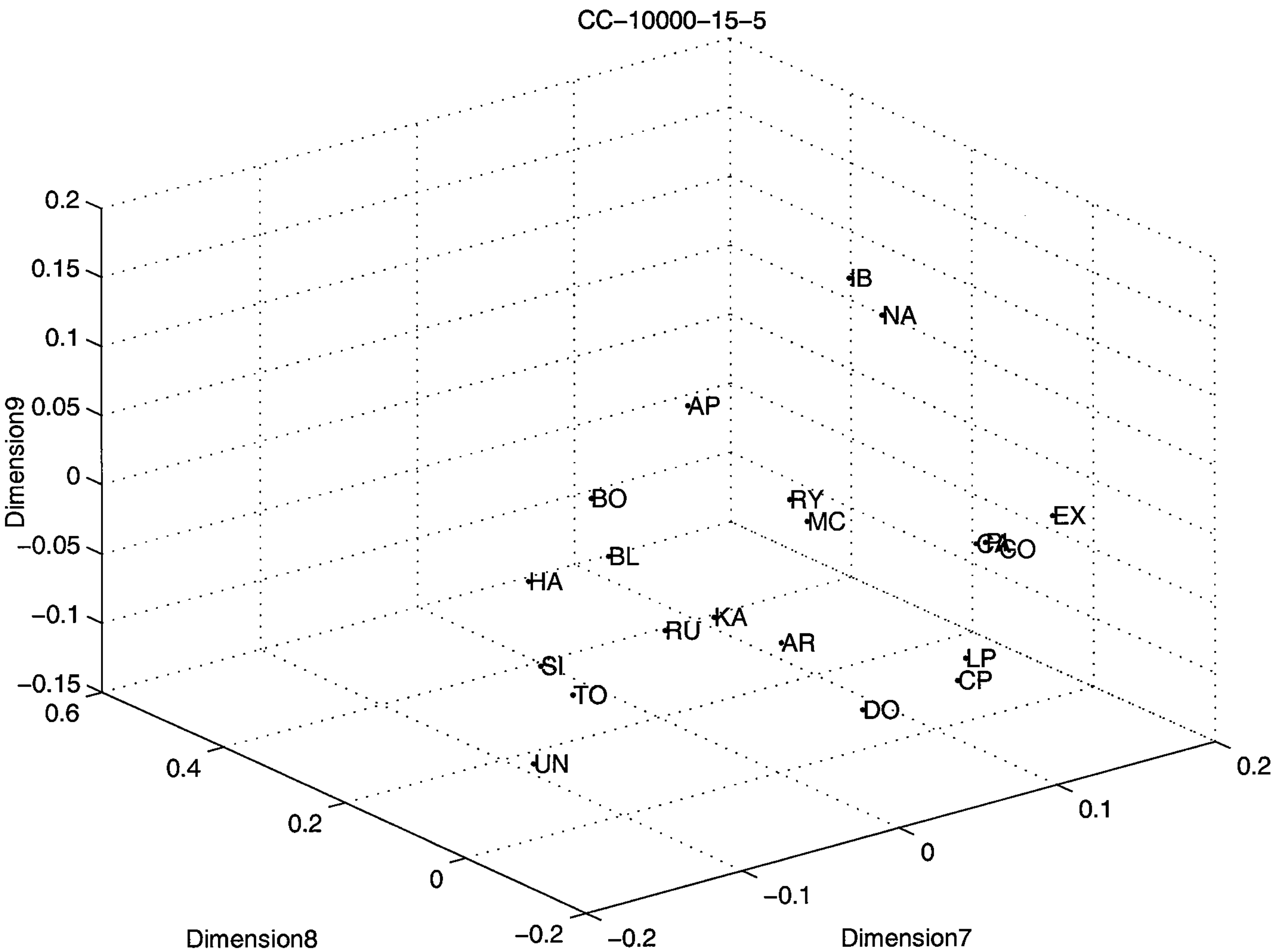

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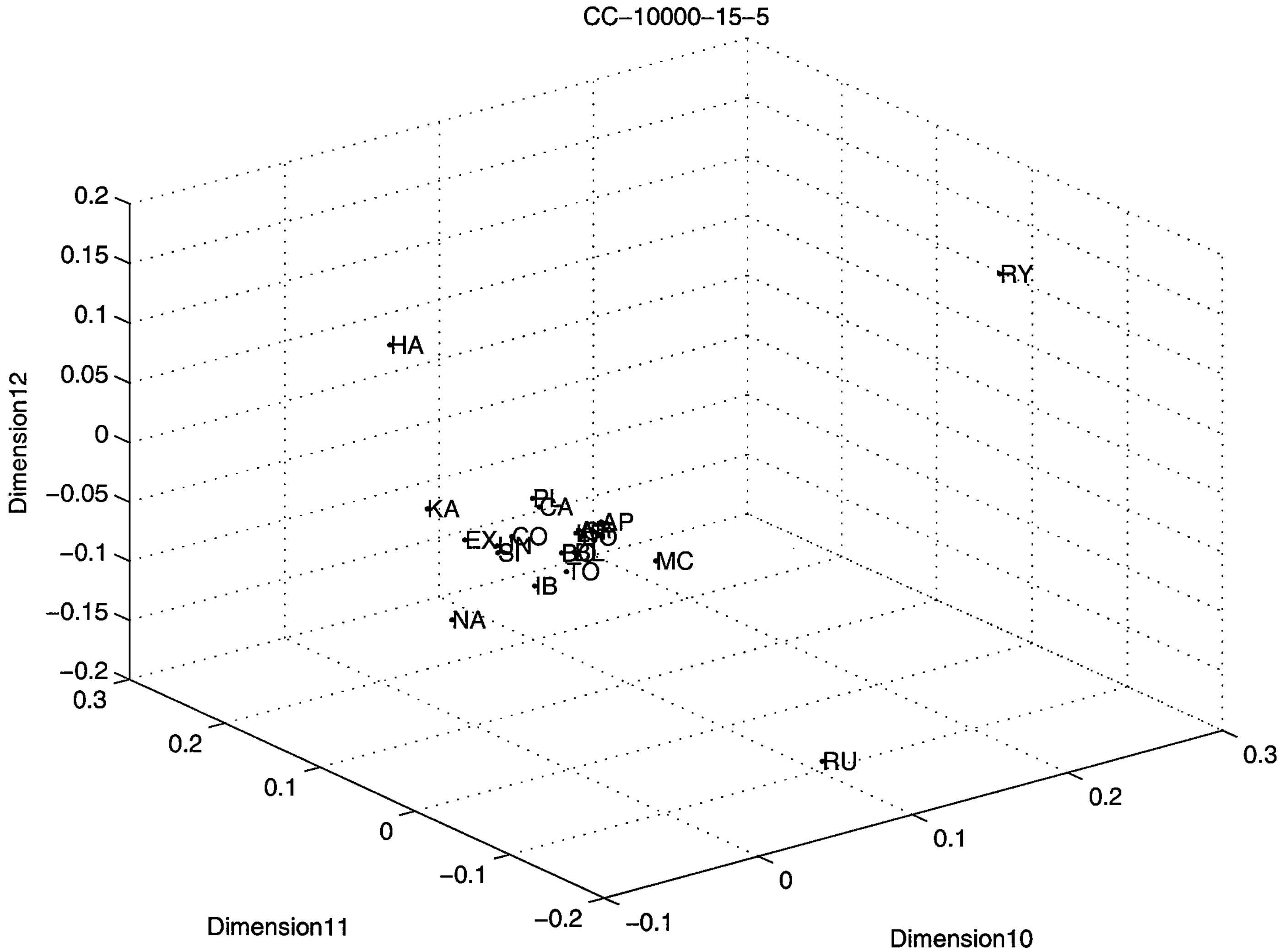

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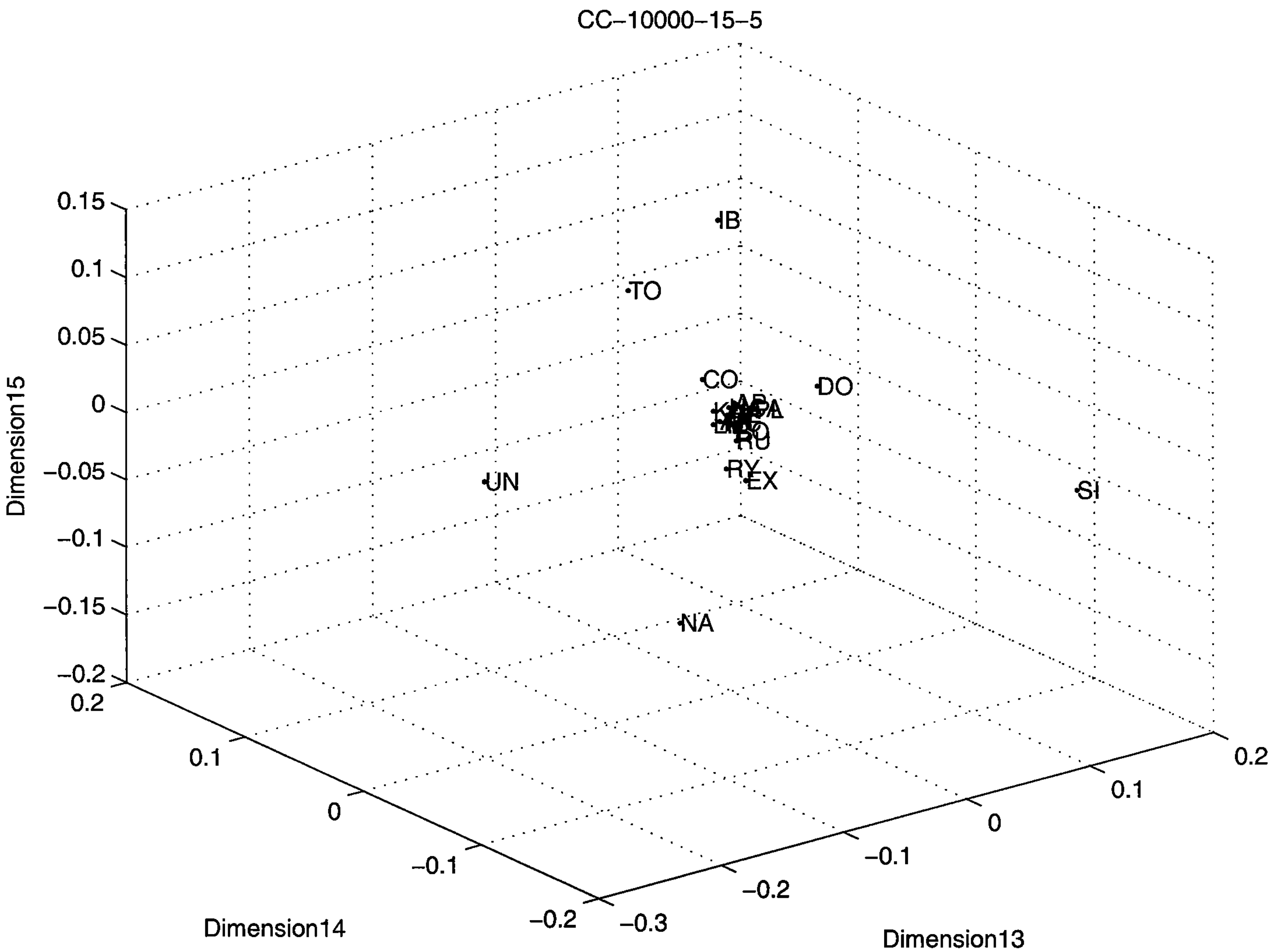

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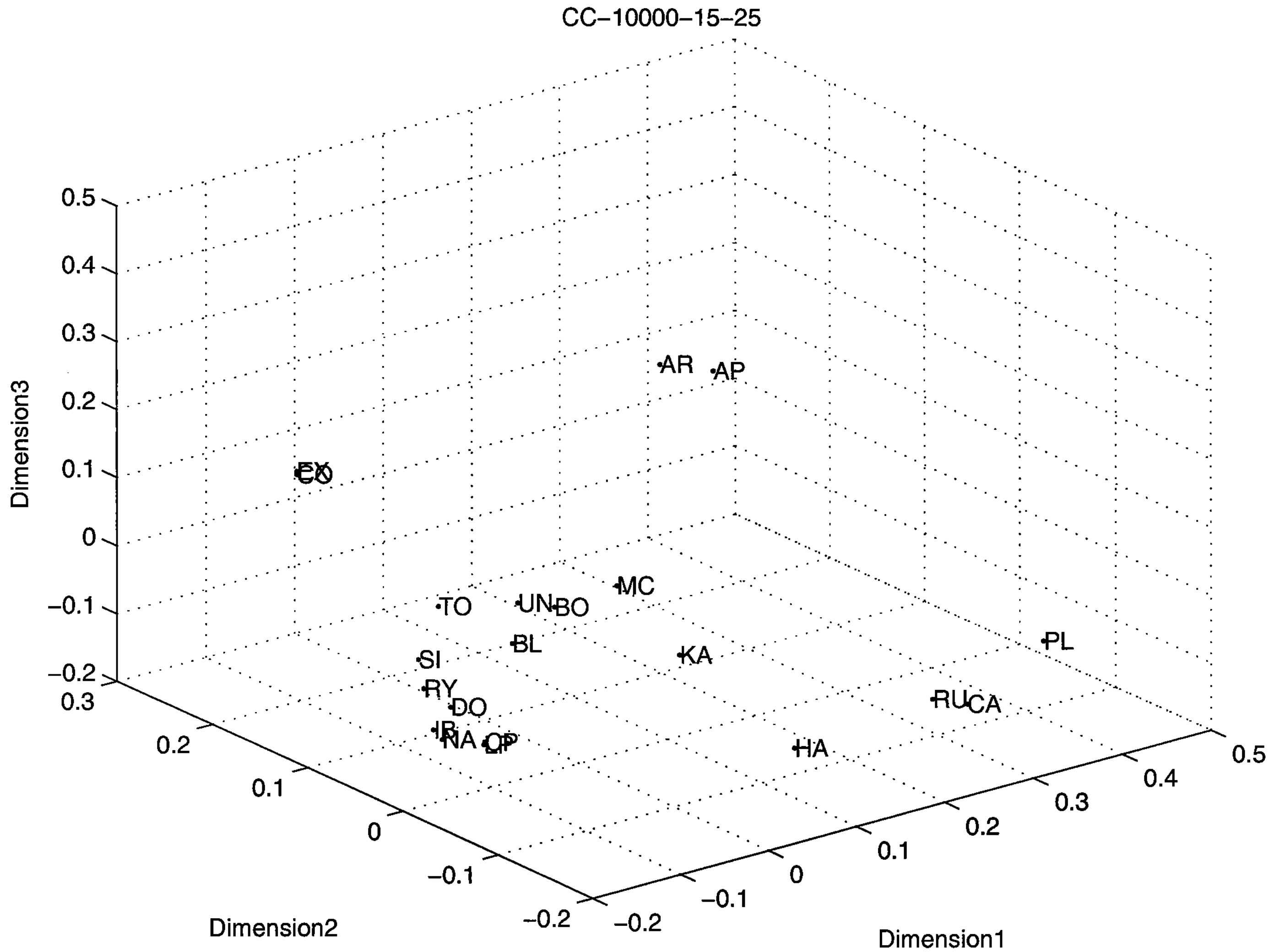
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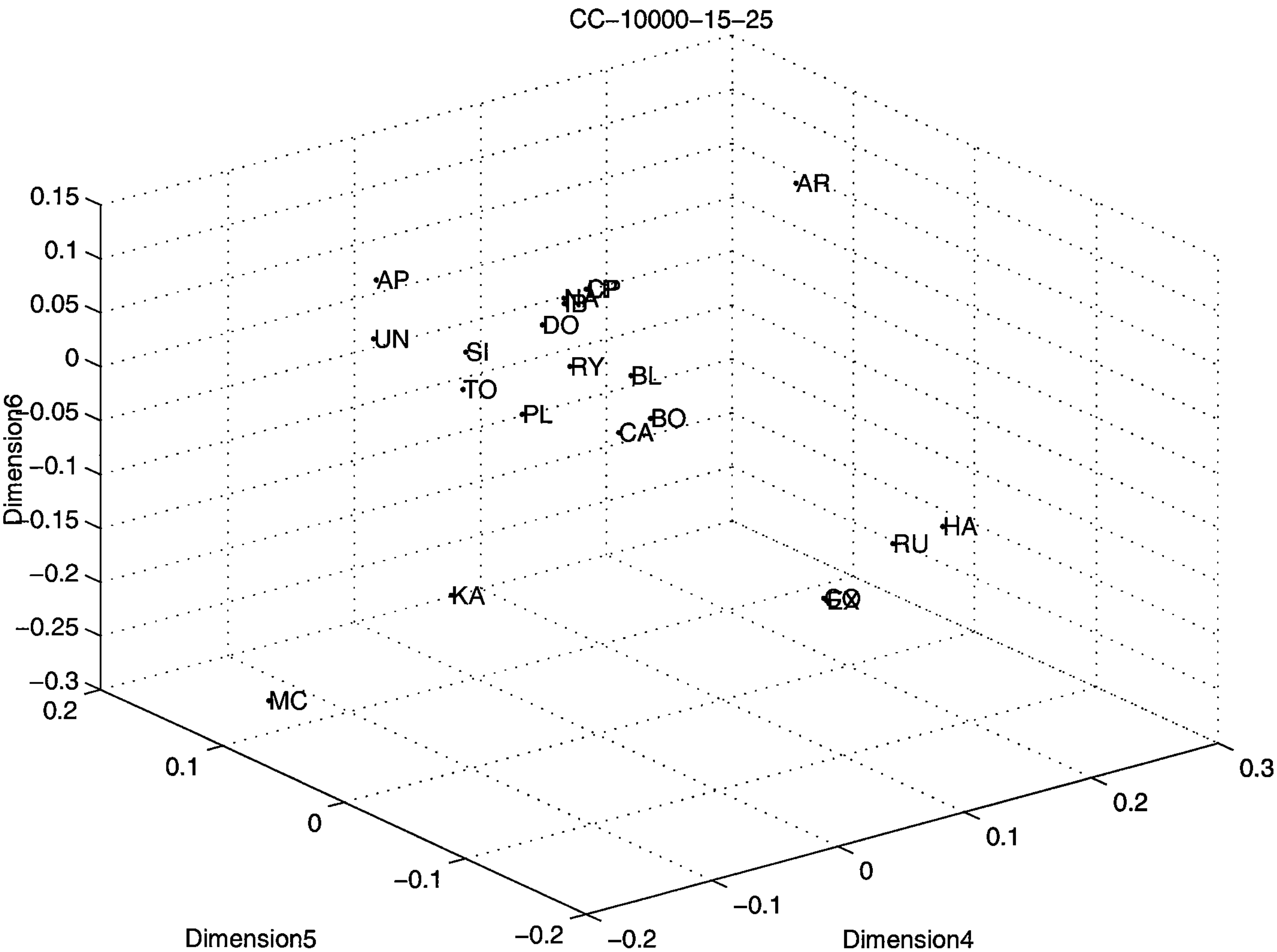
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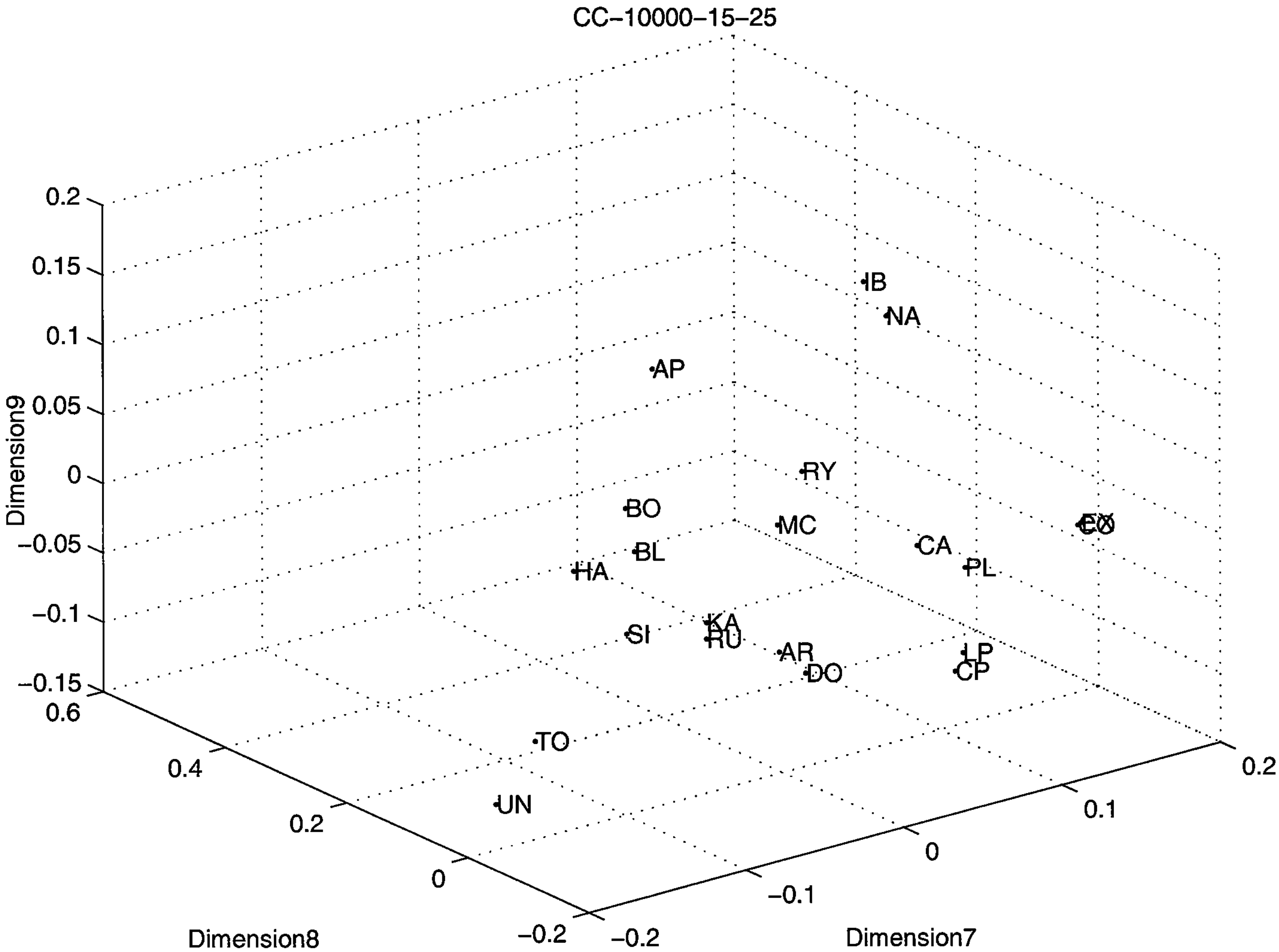

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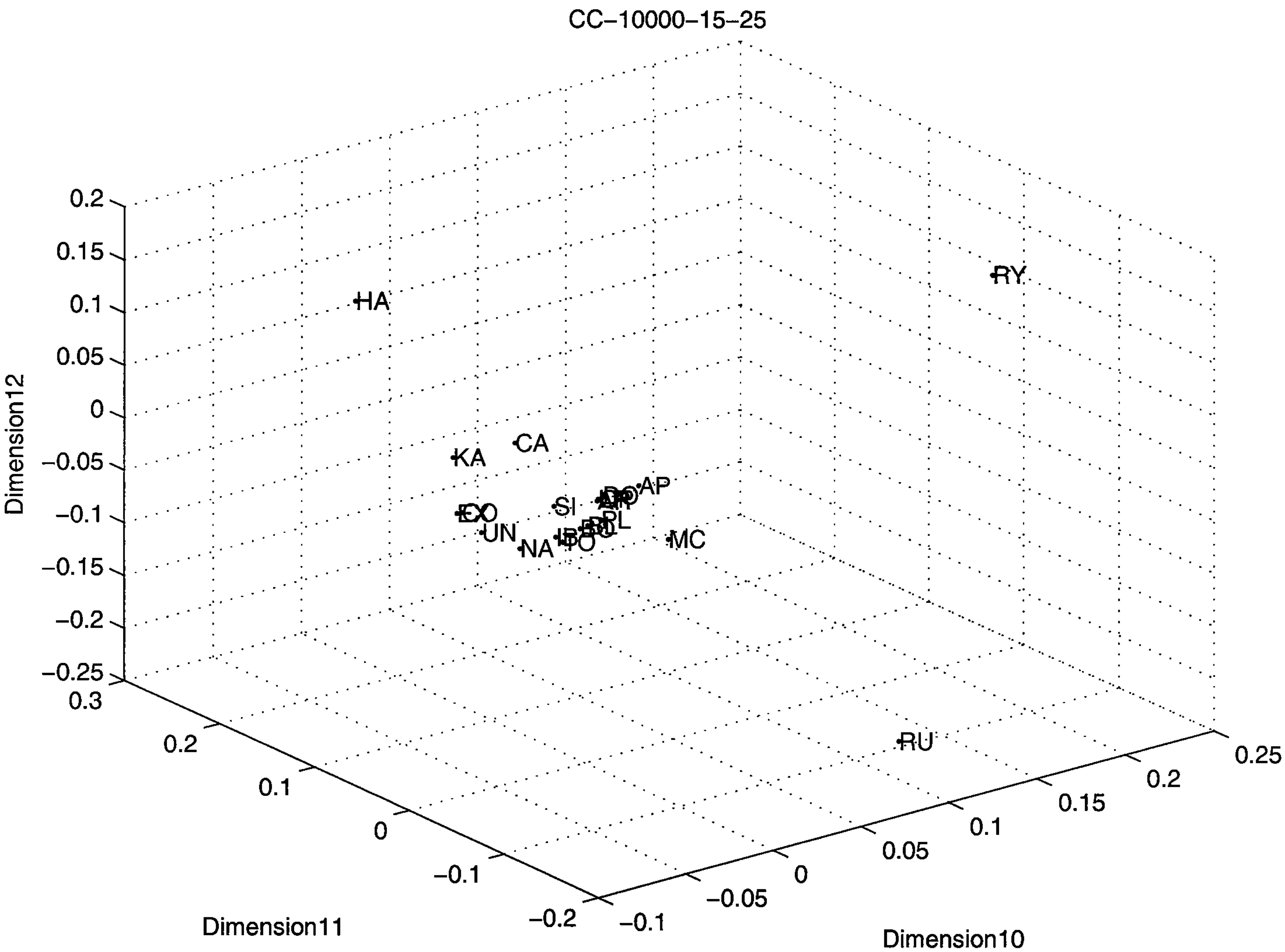

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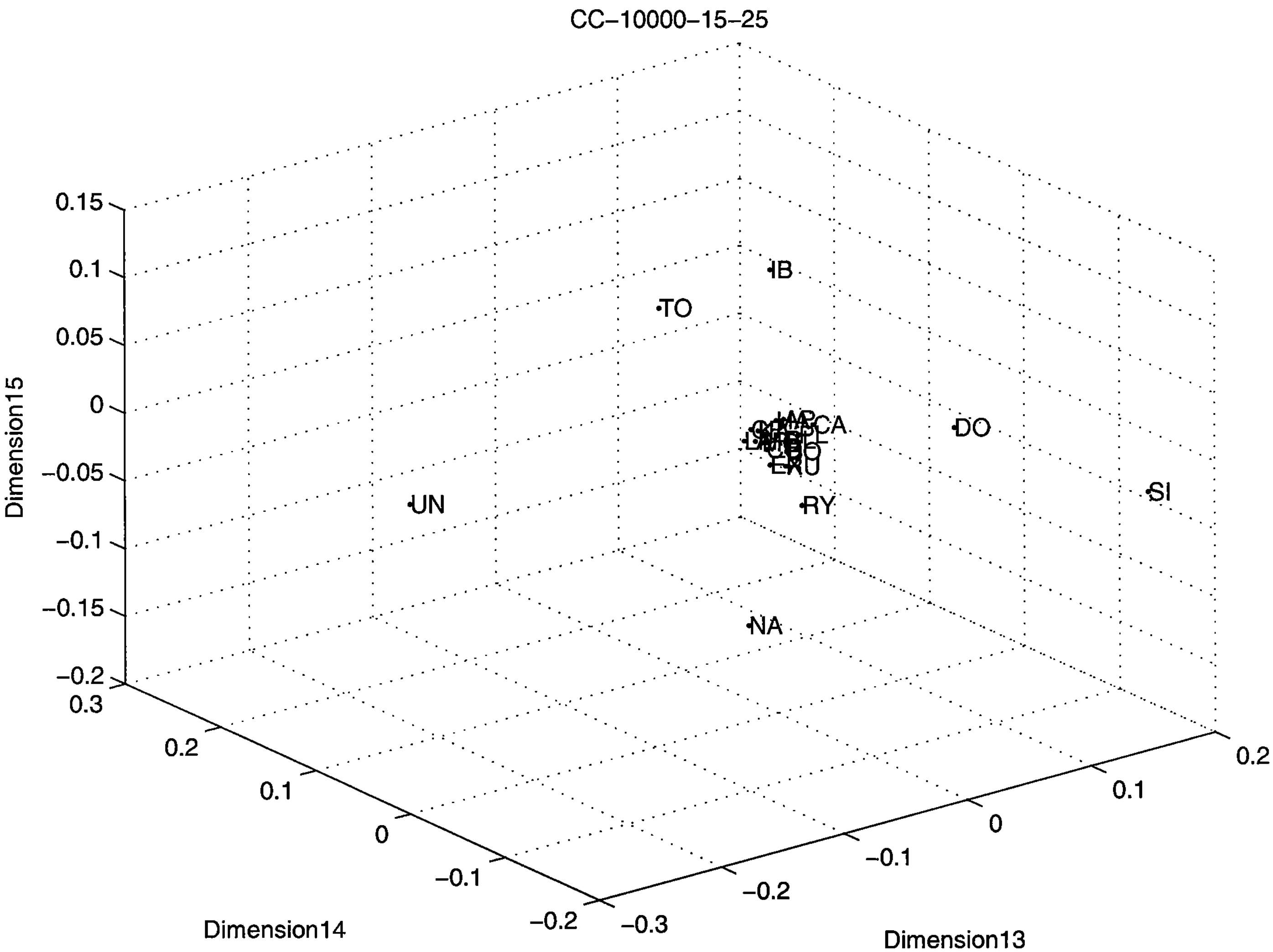

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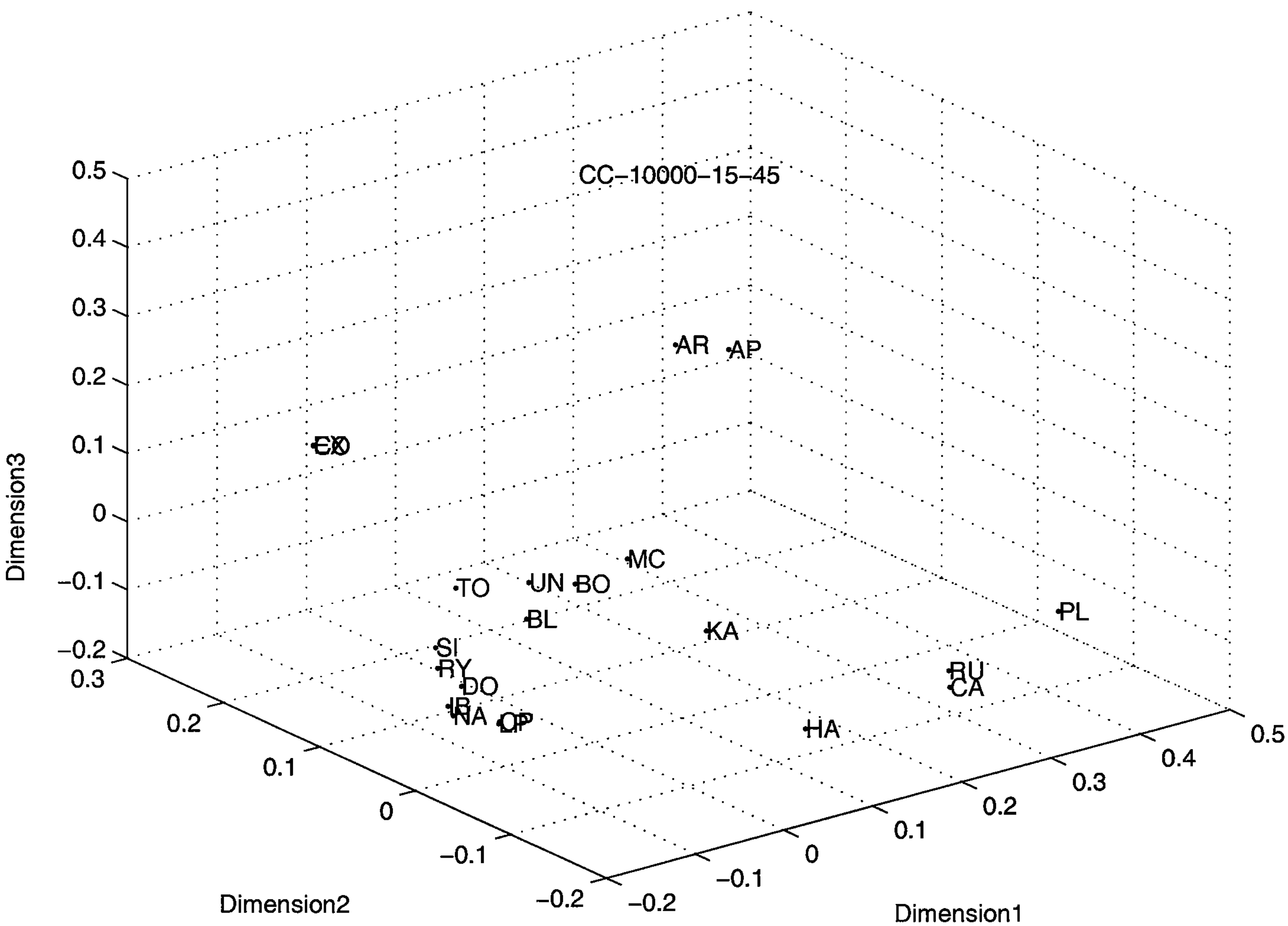

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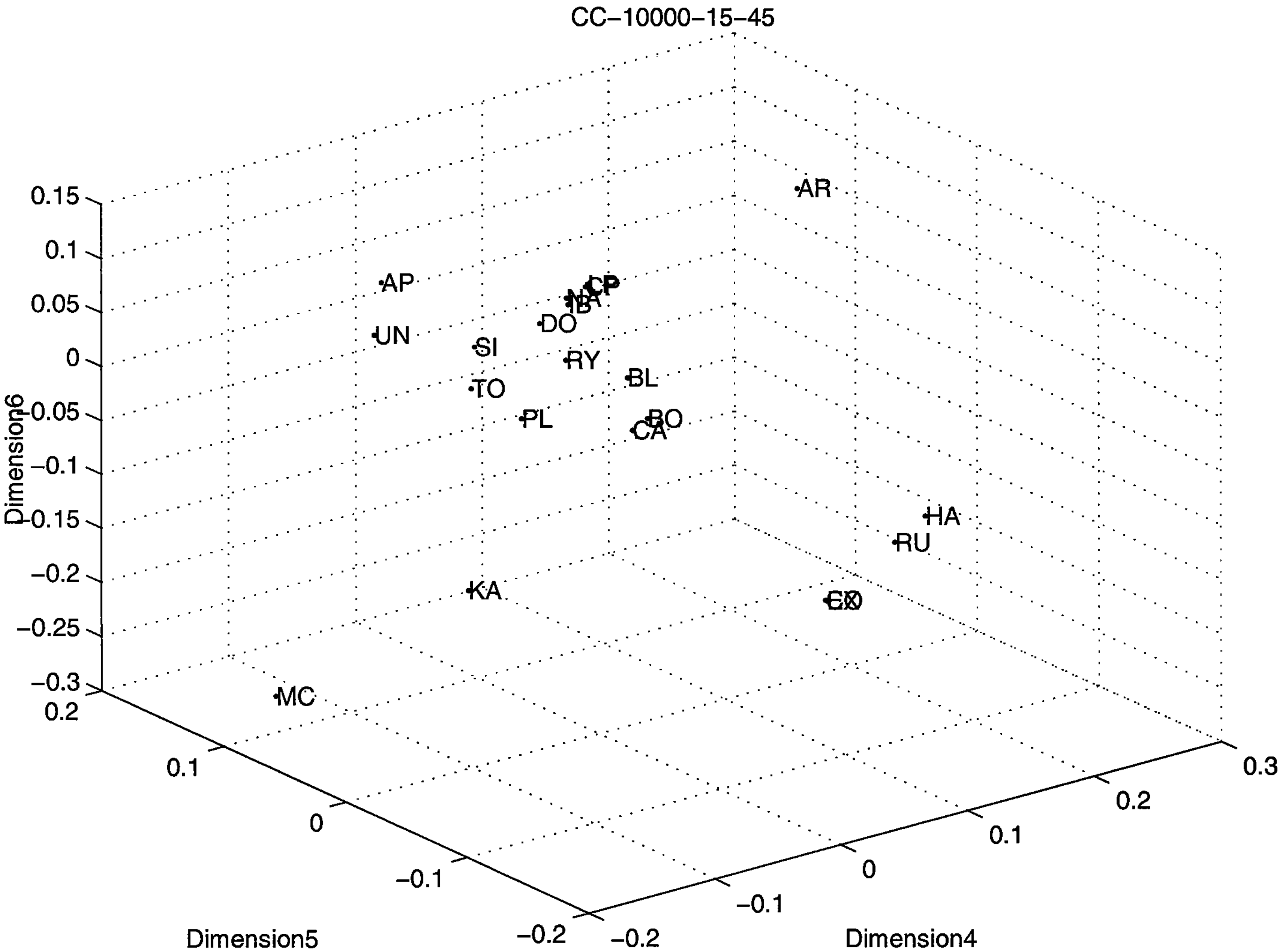

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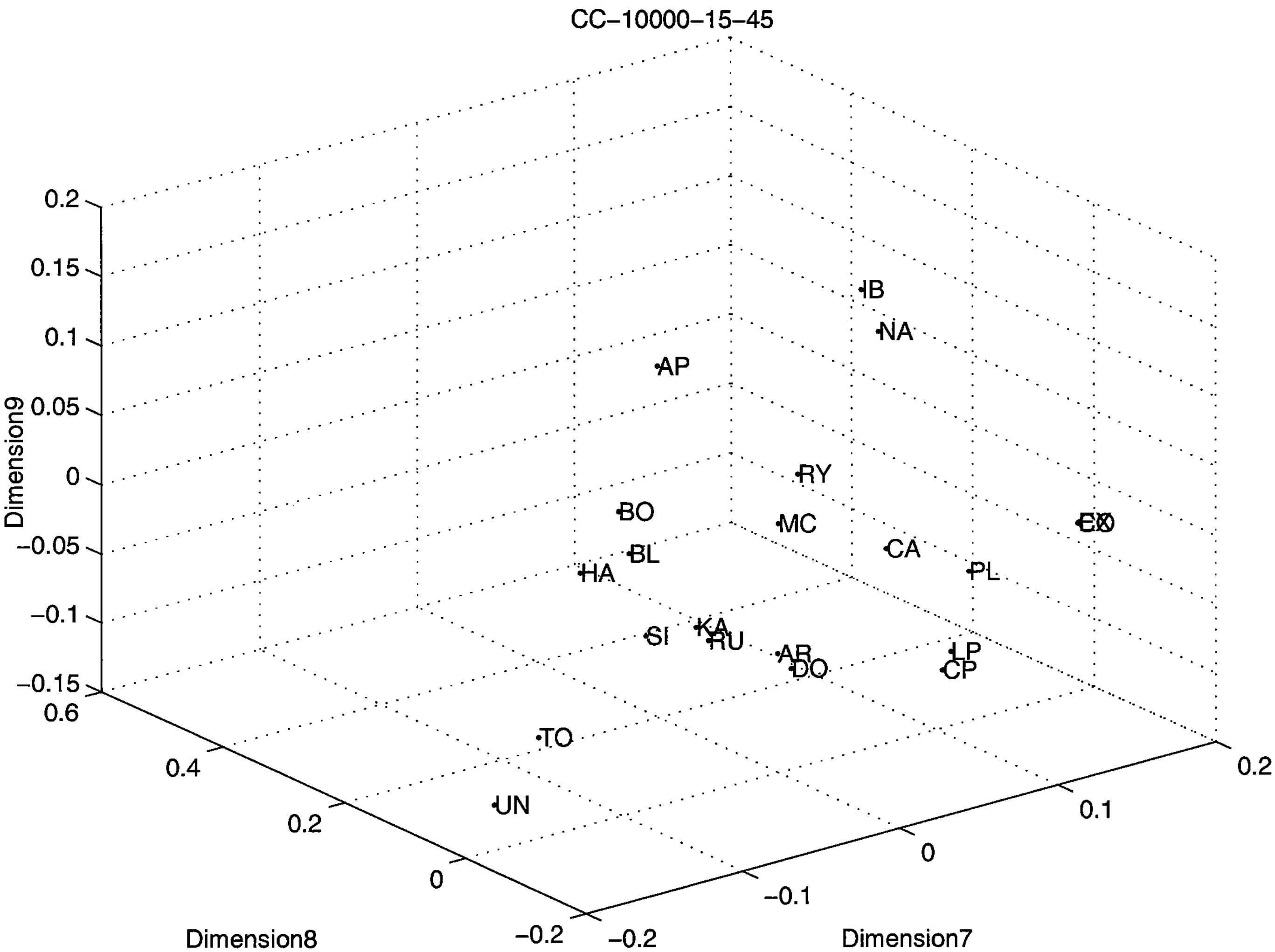
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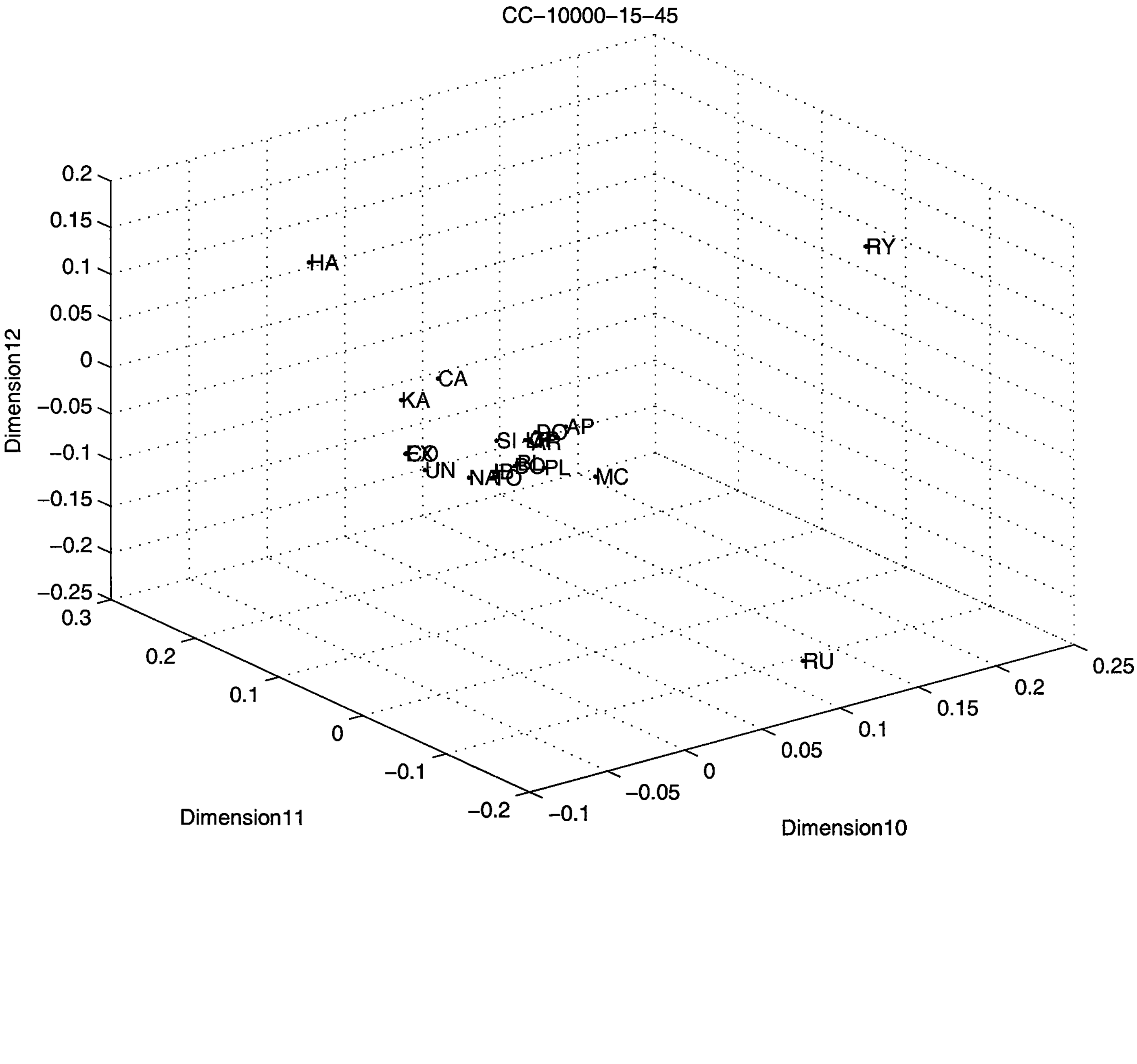
CC−10000−15−45
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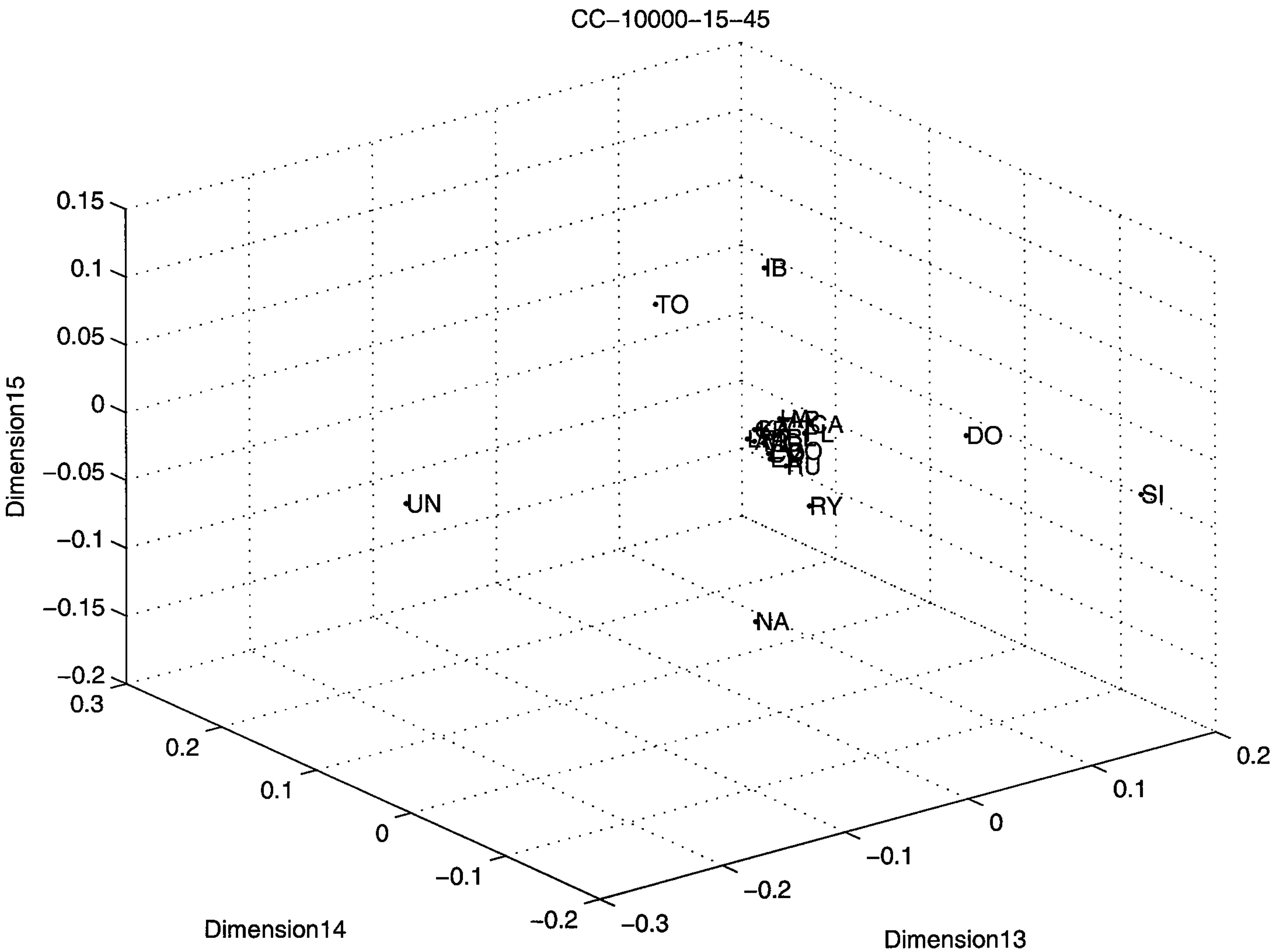

CC–10000–15–45
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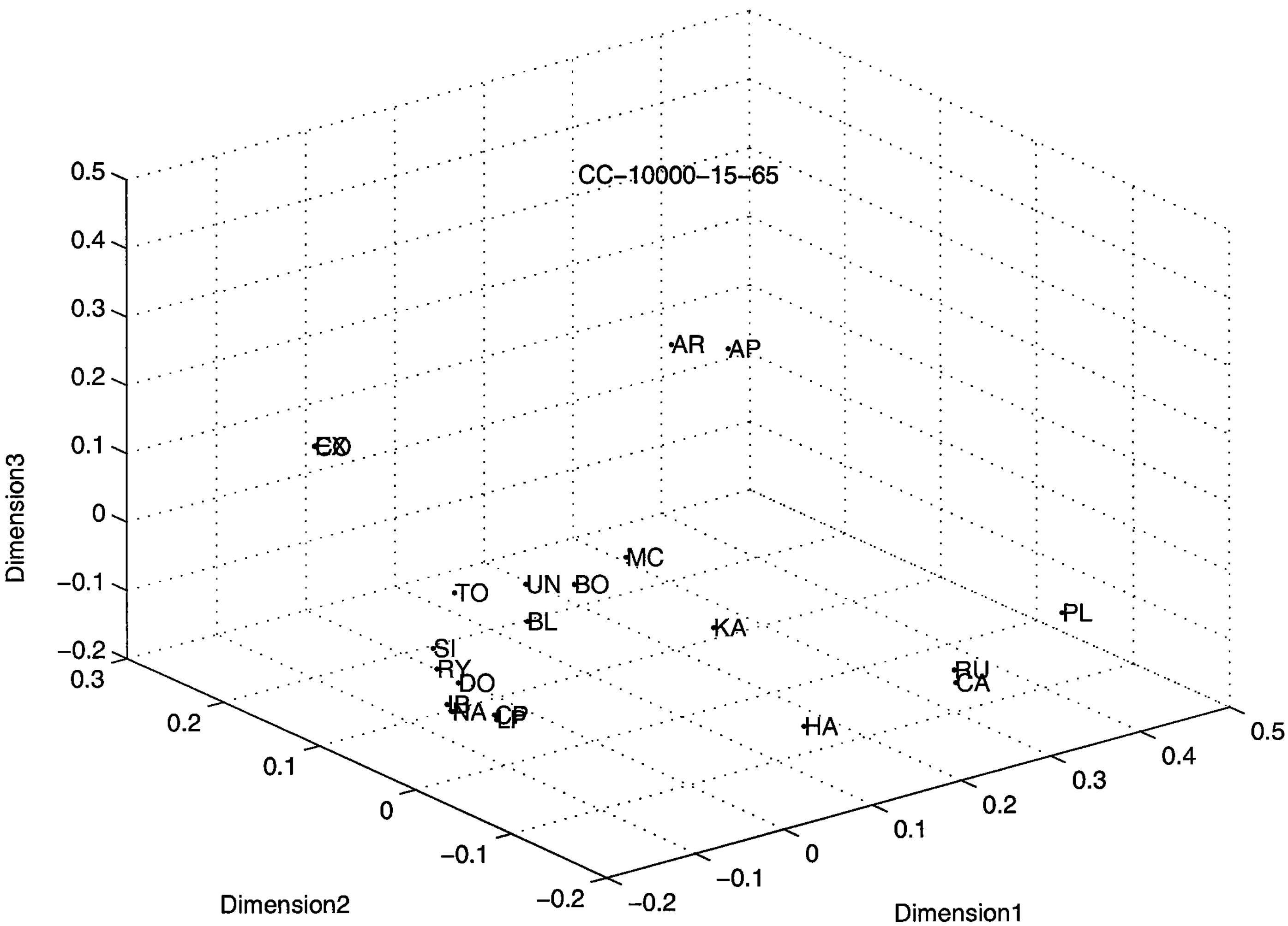

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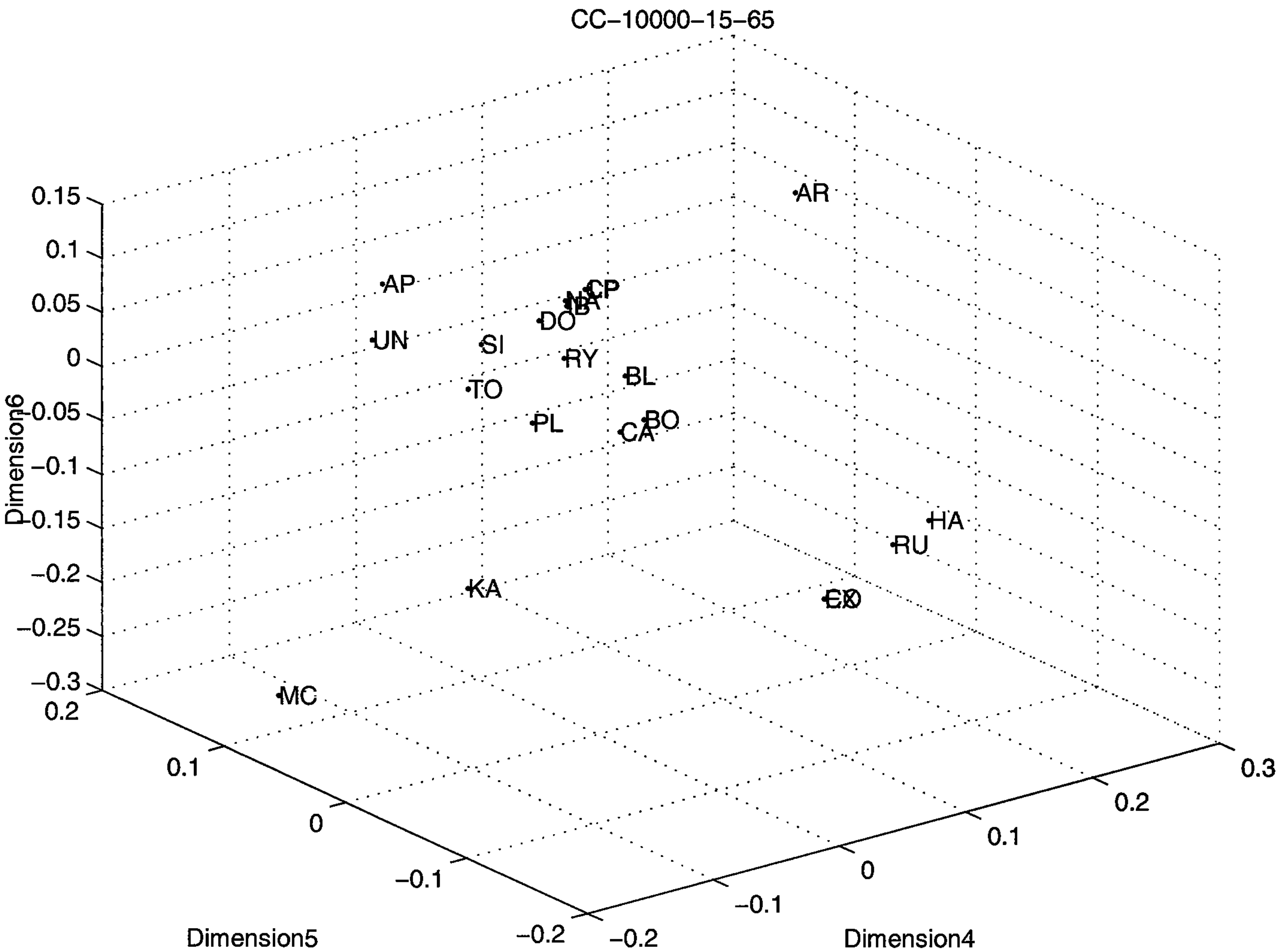

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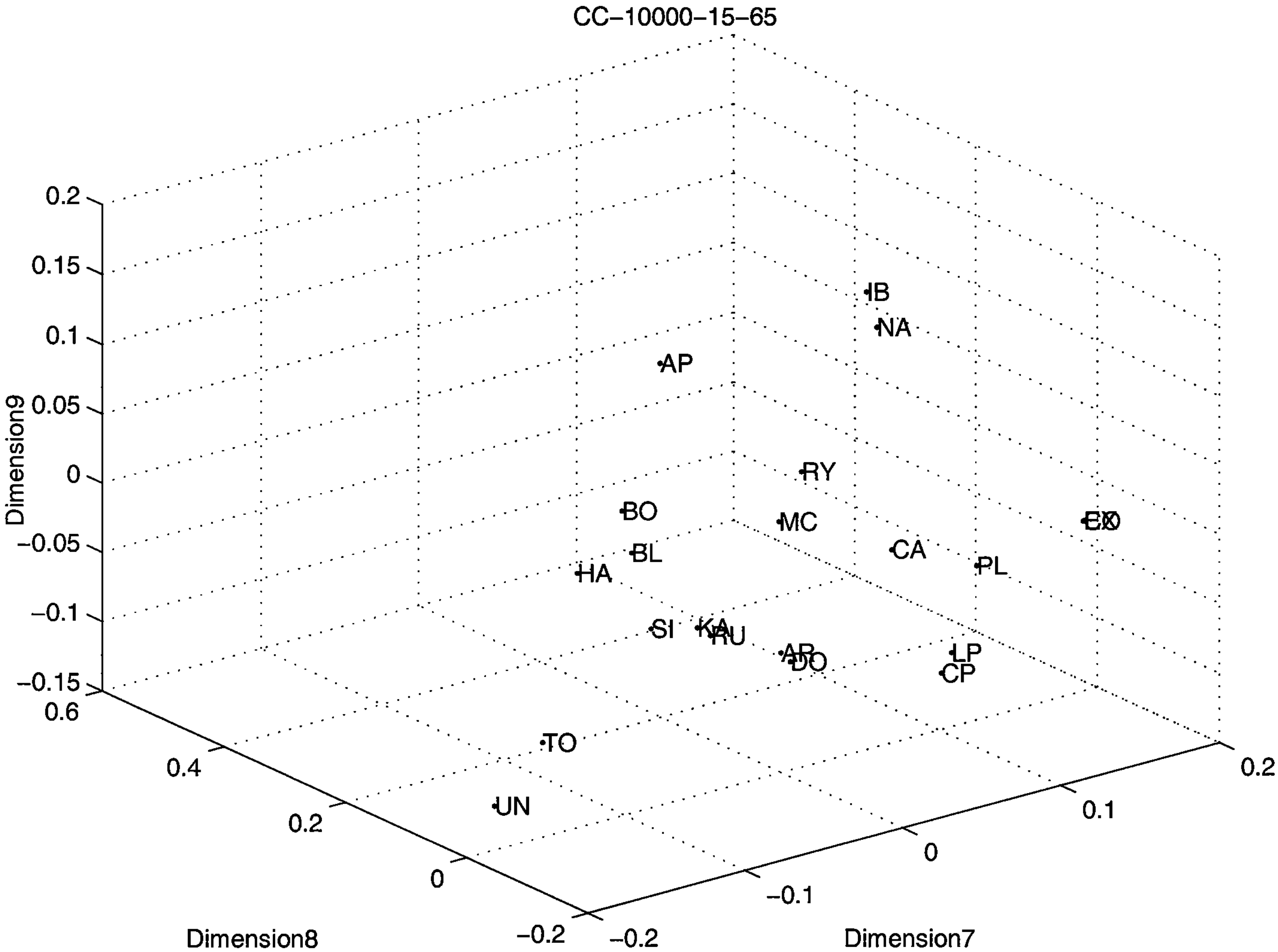
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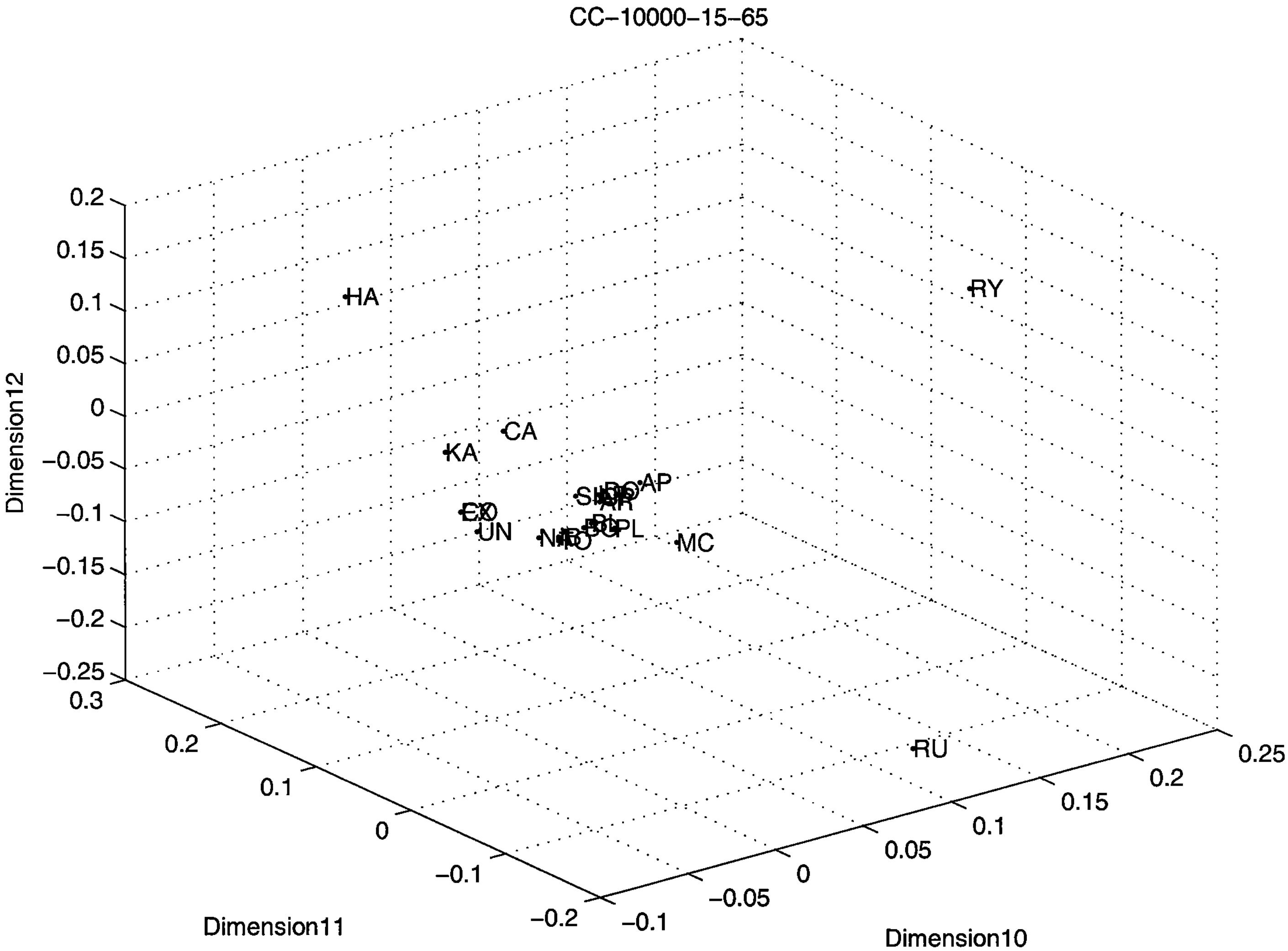

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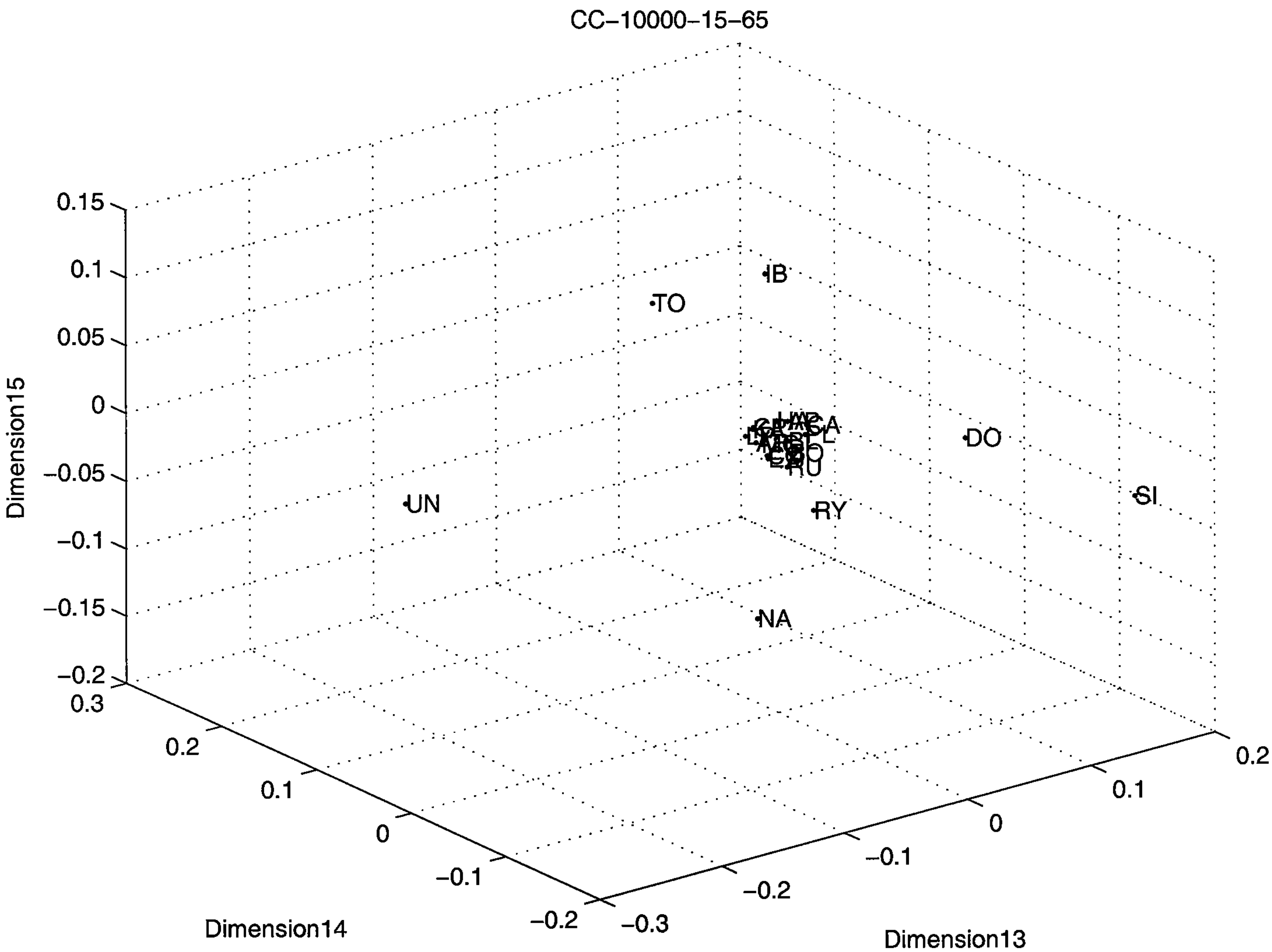
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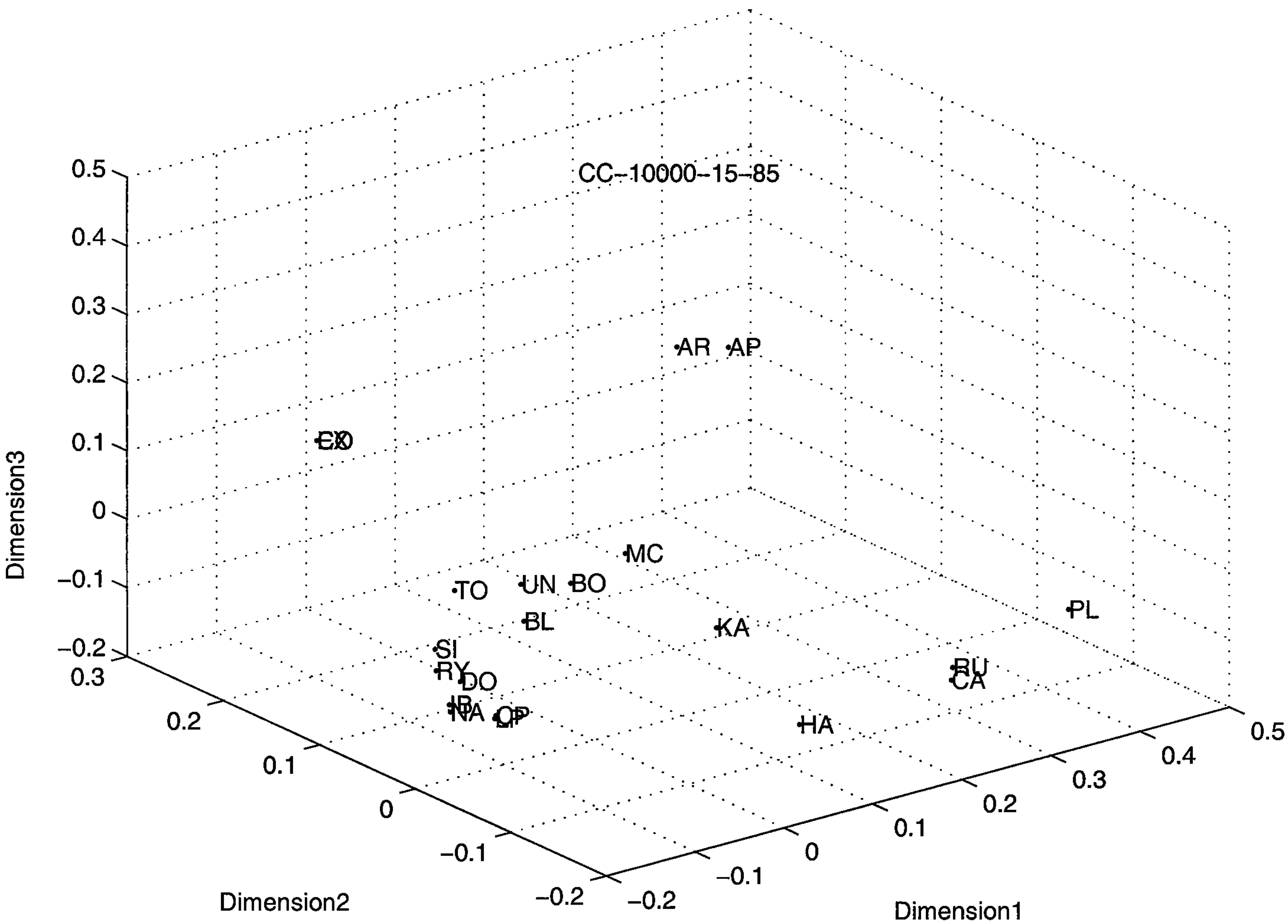

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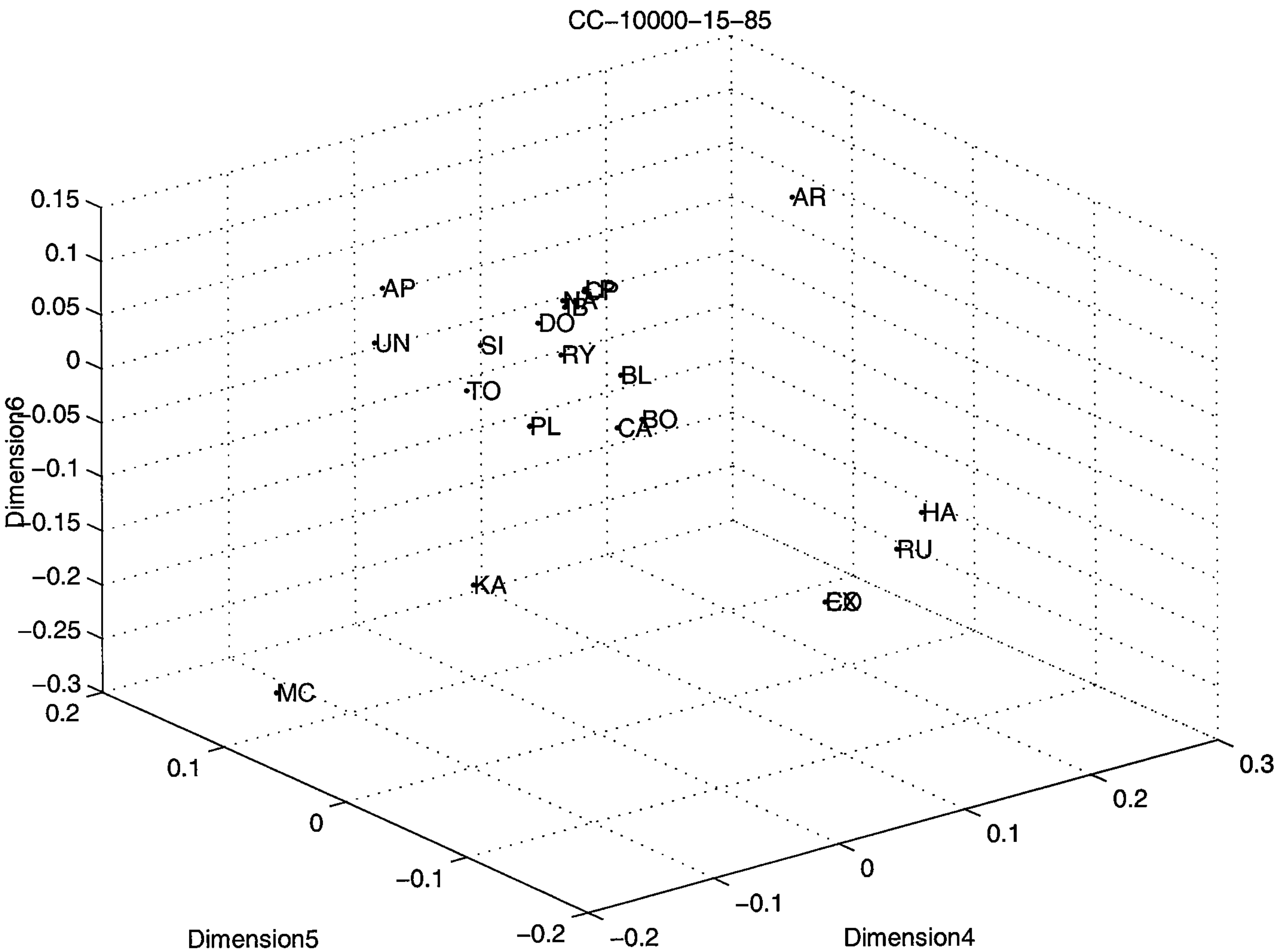
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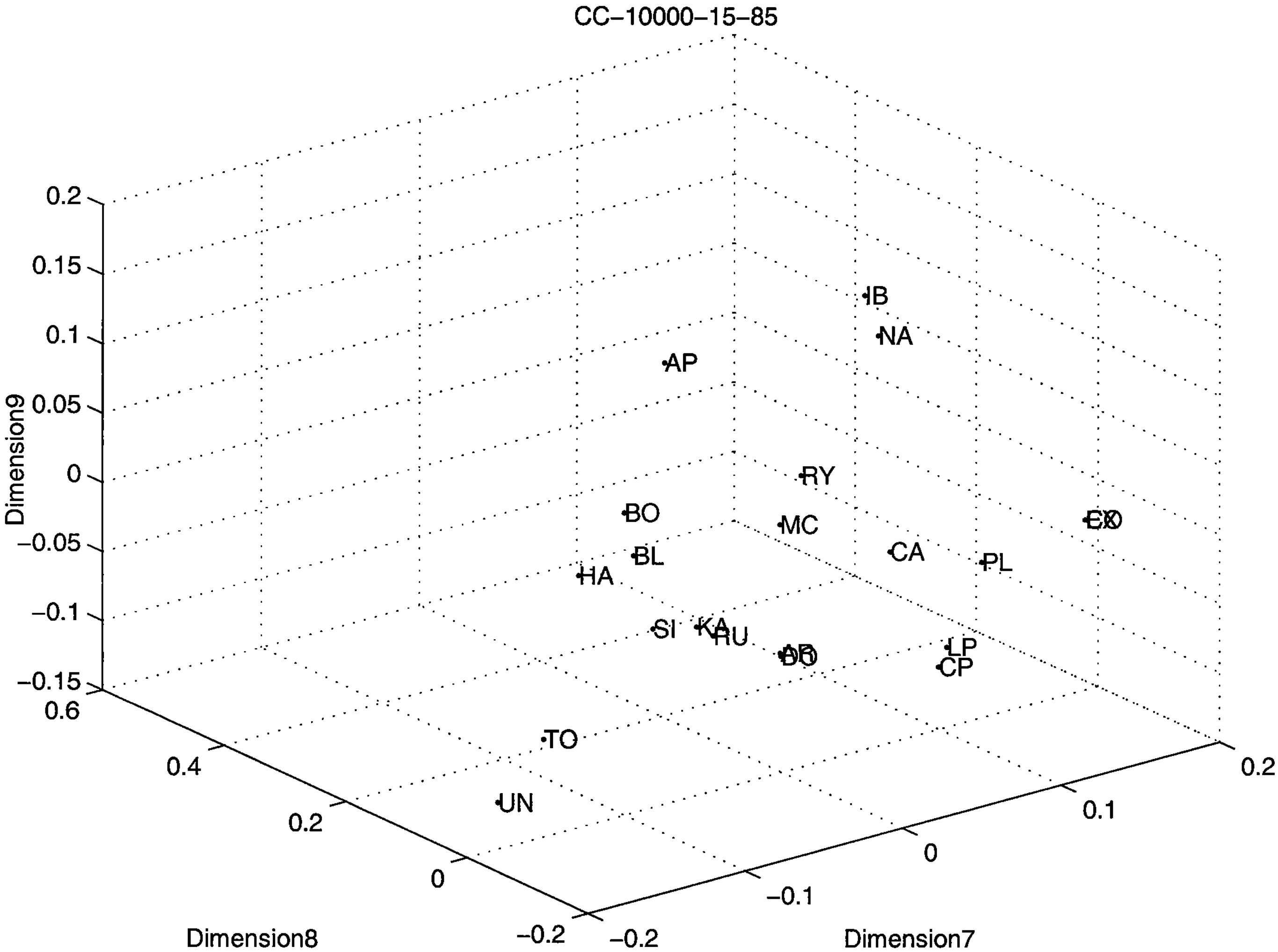

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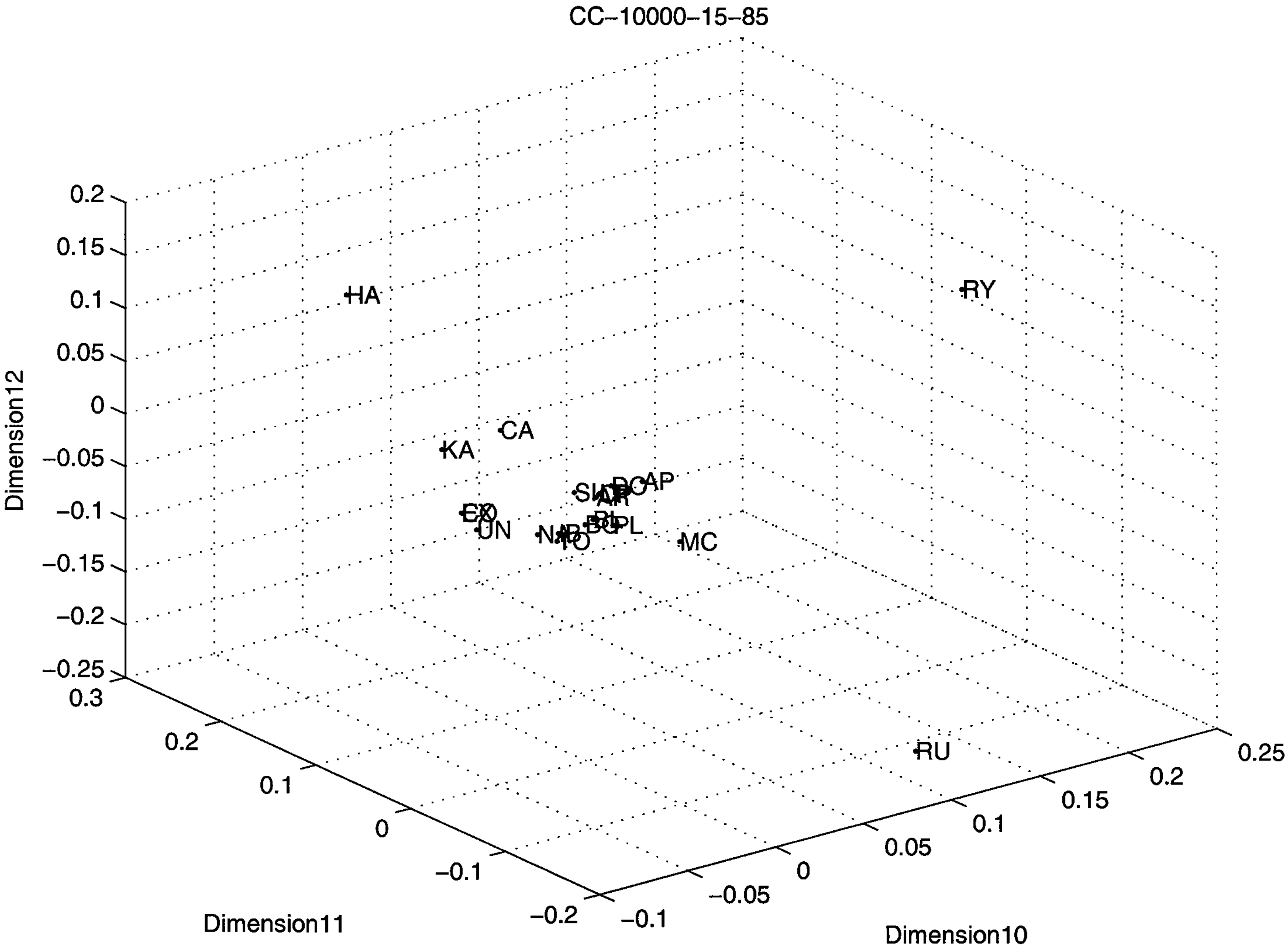
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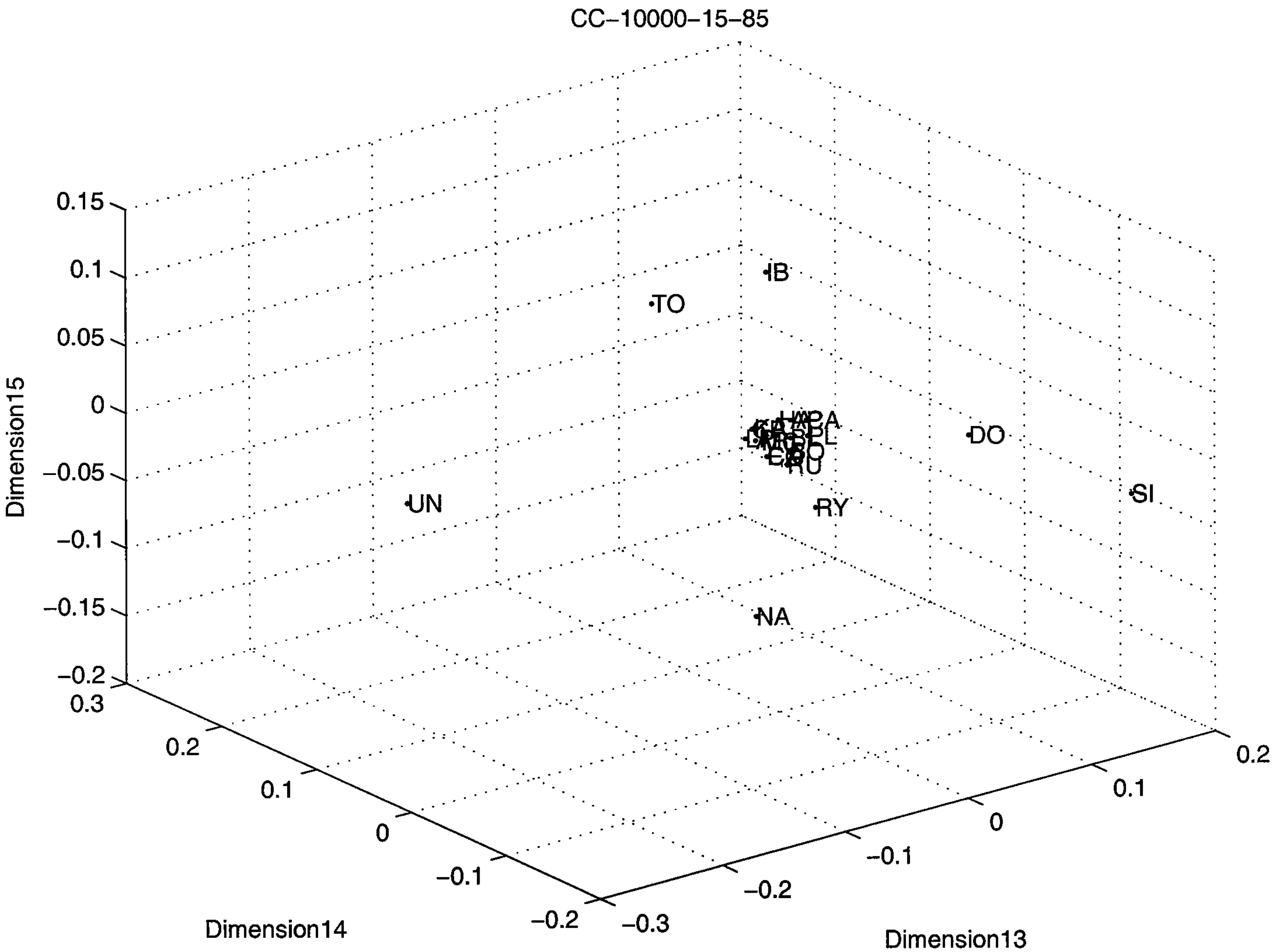
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```
%This file creates 10000 profiles of specified size (culture type is
%hardcoed in lines 23-24). It runs all 21 rules over them, creating a
%similarity matrix, performing MDS, and saving the results

function q = Main2(numalters, numvoters);

N = 10000;
numrules = 21;

        if (mod(numalters,2) ~= 0 && mod(numvoters,2) ~= 0)

            allProfiles = zeros(numalters, numvoters, N);
            allZ = zeros(numrules, N);
            %initialisation
            %%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
            i = 1;
            CumSimTotals = zeros(numrules,numrules);
            SimMatrix = zeros(numrules,numrules); %% <- SHAH: added this
            %%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%%%%%%

            while i < N+1
                    profmatrix = profiles(numalters,numvoters); %IC
                %profmatrix = ClusteredCulture(numalters,numvoters); %CC
                allProfiles(:,:,i) = profmatrix;
                z(1) = antiplurality(profmatrix,numalters,numvoters);%rule 1
                a = kapprovalRevised(profmatrix,numalters,numvoters);
                z(2) = a(floor(numalters/2));
                z(3) = approval(profmatrix,numalters,numvoters);
                z(4) = black(profmatrix,numalters,numvoters);   %rule 4
                z(5) = borda(profmatrix,numalters,numvoters);   %rule 5
                z(6) = exhaustive(profmatrix,numalters,numvoters); %rule 6
                z(7) = copeland(profmatrix,numalters,numvoters); %rule 7
                z(8) = hareRevised(profmatrix,numalters,numvoters); %rule 8
                z(9) = inverseborda(profmatrix,numalters,numvoters);%rule 9
                z(10) = longpath(profmatrix,numalters,numvoters); %rule 10
                z(11) = majorcompromise(profmatrix,numalters,numvoters);
                z(12) = DodgsonRevised(profmatrix,numalters,numvoters);
                % <- SHAH: commented this out
                %z(12) = 1; %% <- SHAH: added this
                z(13) = nansonRevised(profmatrix,numalters,numvoters);%rule 13
                z(14) = plurality(profmatrix,numalters,numvoters); %rule 14
                z(15) = runoff(profmatrix,numalters,numvoters); %rule 15
                z(16) = simpsons(profmatrix,numalters,numvoters); %rule 16
                z(17) = topcycle(profmatrix,numalters,numvoters);%rule 17 &
                %<- SHAH: commented this out
                %z(17) = 1; %% <-SHAH: added this
                z(18) = uncoveredset(profmatrix,numalters,numvoters);%rule 18
                z(19) = RaynaudRevised(profmatrix,numalters,numvoters);
                z(20) = coombsRevised(profmatrix,numalters,numvoters);
                %z(21) = Bucklin(profmatrix,numalters,numvoters);
                z(21) = Carey(profmatrix,numalters,numvoters);
                %z(23) = DodgsonRevised(profmatrix,numalters,numvoters);
                %z(24) = Baldwin(profmatrix,numalters,numvoters);

                allZ(:,i) = z';

                %% <- SHAH: added this next chunk
                for m = 1 : length(z)
                    for n = 1 : length(z)
                        if(z(m) == z(n))
                            %if(CumSimTotals(m,n) == 1)
                            %    print('here');
```

```
                        %end
                        CumSimTotals(m,n) = CumSimTotals(m,n) + 1;
                        %if(CumSimTotals(m,n) == 1)
                        %    print('here');
                        %end
                    end
                end
            end
            i = i + 1;


        end
        SimMatrix = CumSimTotals/N;  %% <- SHAH: added this

        %BigSimMatrix = BigSimMatrix + SimMatrix;
        %BigCount = BigCount + 1;
        [Y,e] = cmdscale(SimMatrix);
        fname = strcat('IC-', int2str(N), '-', int2str(numalters), '-', int2
str(numvoters));
        dataPathName = strcat('../Output/FinalIC/Data/', fname);
        %graphsPathName = strcat('../Output/FinalIIC/Graphs/', fname);

        save(dataPathName);
    end
```

```
%This function file enables us to find out the Antiplurality's Winner
function a = antiplurality(profmatrix,numalters,numvoters);

score = numalters - 1;

%to generate the score matrix for each voter indicating
%the antiplurality score of each alternative = (1,...,1,0)
for a = 1 : numvoters
    for b = 1 : score
        scorematrix(b,a) = 1;
    end
    for c = score+1 : numalters
        scorematrix(c,a) = 0;
    end
end

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%initialisations
for a = 1 : numalters   %total score for each alternative
    totalscore(a) = 0;  %(ie. totalscore(1) = score for alternative 1)
end
currentscore = 0;
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

for a = 1 : numalters   %testing each alternative (ie. 1 to numalters)
    for b = 1 : numvoters
       for c = 1 : numalters
           if profmatrix(c,b) == a;
               if scorematrix(c,b) == 1;
                  currentscore = 1;
               end
           end
        totalscore(a) = totalscore(a) + currentscore;
        currentscore = 0;
       end
    end
end

winnercount = max(totalscore);  %to find the maximum score
win = checktie(numalters,totalscore,winnercount);  %to check if there is a tie
vote = defineposvoter1(profmatrix,numalters,win);  %to define the
                            %position of winners from voter_1's profile

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%to find out the antiplurality winner
for n = 1 : numalters
    if vote(n) == 1;
        winner = profmatrix(n,1);
    break;
    end
end
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%scorematrix
%totalscore
a = winner;
```

```
%This function file enables us to find out the Winner under Approval Voting
%Procedure with k approvals. It returns a vector in which the ith element
%is the winner when k=i.

function f = kapprovalRevised(profmatrix,numalters,numvoters);

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%initialisations
score = 1;
currentscore = 0;
z = 1;
for a = 1 : numalters   %total score for each alternative
        totalscore(a) = 0;  %(ie. totalscore(1) = score for alternative 1)
end
for b = 1 : numalters
        winner(b) = 0;
end
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%to find the winners for 1 > k > m-1 alternatives approved by the voters
while score < numalters+1
        for a = 1 : numvoters   %to generate the matrix of fixed number of
                                %approvals for each voter
                for b = 1 : score
                        scorematrix(b,a) = 1;
                end
                for c = score+1 : numalters
                scorematrix(c,a) = 0;
                end
     end
    %scorematrix
        for a = 1 : numalters   %testing each alternative (ie. 1 to numalters)
                for b = 1 : numvoters
                for c = 1 : numalters
                        if profmatrix(c,b) == a;
                        if scorematrix(c,b) == 1;
                                        currentscore = 1;
                        end
                        end
                                totalscore(a) = totalscore(a) + currentscore;
                                currentscore = 0;
                end
                end
     end
    %totalscore
        winnercount = max(totalscore);  %to find the maximum score
        win = checktie(numalters,totalscore,winnercount);  %to check for tie
        vote = defineposvoter1(profmatrix,numalters,win);  %consult v1
        %to find out the winner in approval voting procedure
        for a = 1 : numalters
                if vote(a) == 1;
                        winner(z) = profmatrix(a,1);
                break;
                end
        end
        score = score + 1;
        z = z + 1;
end

f = winner;
```

```
%This function file enables us to find out the Winner under Approval Voting
%with random number of approvals
function r = approval(profmatrix,numalters,numvoters);

%The following codes generate a randomised approval matrix,
%presenting the number of approved alternatives for each voter
for c = 1 : numvoters
    approvalscore = randperm(numalters+1);
    score = approvalscore(1);
        if score == 1;
            for d = 1 : numalters
                scorematrix(d,c) = 0;
            end
        else
            for e = 1 : score-1
                scorematrix(e,c) = 1;
            end
            for f = score : numalters
                scorematrix(f,c) = 0;
            end
        end
end

currentscore = 0;

for b = 1 : numalters   %total score for each alternative
    totalscore(b) = 0;  %(ie. totalscore(1) = score for alternative 1)
end

for g = 1 : numalters   %testing each alternative (ie. 1 to numalters)
    for h = 1 : numvoters
       for i = 1 : numalters
           if profmatrix(i,h) == g;
               if scorematrix(i,h) == 1;
                  currentscore = 1;
               end
           end
        totalscore(g) = totalscore(g) + currentscore;
        currentscore = 0;
       end
    end
end

winnercount = max(totalscore);  %to find the maximum score
win = checktie(numalters,totalscore,winnercount);  %to check for tie
vote = defineposvoter1(profmatrix,numalters,win);  %consult v1

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%to find out the winner in approval voting procedure
for n = 1 : numalters
    if vote(n) == 1;
        winner = profmatrix(n,1);
    break;
    end
end
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%scorematrix
%totalscore
r = winner;
```

```
%This function file enables us to find out the Winner under the Black's Rule
function b = black(profmatrix,numalters,numvoters);

%to determind the matrix of the majority relation
majorrelat = majorityrelation(profmatrix,numalters,numvoters);

for a = 1 : numalters   %calculate the score under 1st order copeland rule
        count = 0;
        s(a) = 0;
        for b = 1 : numalters
                count = majorrelat(a,b);
                s(a) = s(a) + count;
                end
end

winnercount = max(s);   %to find the maximum score under 1st order copeland rule
win = checktie(numalters,s,winnercount);        %to check if there is a tie
wincount = counttie(numalters,win);     %to count the number of ties
vote = defineposvoter1(profmatrix,numalters,win);       %consult v1

if wincount == 1 & winnercount == numalters-1   %to find the winner
                                        %under 1st copeland rule
        for a = 1 : numalters
        if win(a) == 1
                winner = a;     %determind the condorcet winner
                                %under 1st copeland rule
                end
        end
elseif wincount ~= 1 & winnercount == numalters-1       %tie occurs,
                             %to find the winner from voter_1's profile
        for b = 1 : numalters
            %'here'
                if vote(b) == 1;
                        winner = profmatrix(b,1);       %determind the condorcet
 winner
                break;
                end
        end
else
        totalscore = bordascore(profmatrix,numalters,numvoters);
        bordawinnercount = max(totalscore);  %to find the maximum borda's score
        bordawin = checktie(numalters,totalscore,bordawinnercount);
        bordavote = defineposvoter1(profmatrix,numalters,bordawin);%consult v1
        %to find out the borda's winner
        for c = 1 : numalters
                if bordavote(c) == 1;
                winner = profmatrix(c,1);
                break;
                end
        end
end

%majorrelat
%s
%totalscore
%bordavote
b = winner;
```

```
%This function file enables us to find out the Borda's Winner
function b = borda(profmatrix,numalters,numvoters);

%to calculate the borda's score for each alternative
totalscore = bordascore(profmatrix,numalters,numvoters);
winnercount = max(totalscore);  %to find the maximum borda's score
win = checktie(numalters,totalscore,winnercount);   %to check if there is a tie
vote = defineposvoter1(profmatrix,numalters,win);   %to define the position of w
inners from voter_1's profile

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%to find out the borda's winner
for j = 1 : numalters
    if vote(j) == 1;
        winner = profmatrix(j,1);
    break;
    end
end
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%totalscore
%win
%vote
b = winner;
```

```
function c = exhaustive(profmatrix,numalters,numvoters);
%different from coombs because it eliminates alternatives until there is
%one left - doesn't matter if there is ever a majority winner

totalscore = antipluralityscore(profmatrix,numalters,numvoters);
losercount = min(totalscore);  %to find the smallest score
%totalscore

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%initialisations
newnumalters = 1;
discount = 0;
count = 1:1:numalters;
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%decide the winner under exhaustive voting
while newnumalters < numalters
        lose = checktie(numalters,totalscore,losercount);   %check for tie
        score = counttie(numalters,lose);   %to count the number of ties

        if score == 1;
        for a = 1 : numalters
                        if lose(a) == 1;
                    discount = a;
                    count(a) = 0;
                end
                end
        elseif score >= 2
                for a = 1 : numalters   %to find out the two best alternatives
                        losevecter(a) = 0;  %initialistion
                if lose(a) == 1;
                        for b = 1 : numalters
                                if profmatrix(b,1) == a;
                                losevecter(a) = b;
                        end
                   end
                end
                end
                cut = max(losevecter);
                for c = 1 : numalters,
                        if losevecter(c) == cut;
                        discount = c;
                        count(c) = 0;
                end
                end
        end
        for a = 1 : numvoters
                for b = 1 : numalters
                if profmatrix(b,a) == discount;
                        profmatrix(b,a) = 0;
                end
                end
        end
        %profmatrix
        totalscore = antipluralityscore(profmatrix,numalters,numvoters);
        for a = 1 : numalters
                if count(a) == 0;
                totalscore(a) = numvoters + 1;
                end
     end
        %totalscore
        losercount = min(totalscore);
     newnumalters = newnumalters + 1;
```

```
end
for a = 1 : numalters
        if count(a) ~= 0;
                winner = a;
        end
end

%score
%losevecter
%count
%totalscore
%lose
c = winner;
```

```
%This function file enables us to find out the Winner under the Copeland Rule
function c = copeland(profmatrix,numalters,numvoters);

%to determind the matrix of the majority relation
majorrelat = majorityrelation(profmatrix,numalters,numvoters);

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%find the copeland winner
for a = 1 : numalters   %calculate the score under 1st order copeland rule
    count = 0;
    s(a) = 0;
        for b = 1 : numalters
            count = majorrelat(a,b);
            s(a) = s(a) + count;
        end
end

winnercount = max(s);   %to find the maximum score under 1st order copeland rule
win = checktie(numalters,s,winnercount);   %to check if there is a tie
wincount = counttie(numalters,win); %to count the number of ties

if wincount == 1    %to find the winner under 1st copeland rule
    for d = 1 : numalters
        if win(d) == 1
            winner = d;     %determind the winner under 1st copeland rule
        end
    end
else                %tie occurs, to find the winner under 2nd copeland rule
    for e = 1 : numalters
        s2(e) = 0;
            if win(e) == 1;
                for f = 1 : numalters
                    if majorrelat(e,f) == 1
                        s2(e) = s2(e) + s(f);   %calculate the score under
                                                %2nd copeland rule
                    end
                end
            end
    end

    winnercount2 = max(s2); %to find the maximum score under
                            %2nd order copeland rule
    win2 = checktie(numalters,s2,winnercount2); %to check if there is a tie
    wincount2 = counttie(numalters,win2);   %to count the number of ties

    if wincount2 == 1
        for h = 1 : numalters
            if win2(h) == 1
                winner = h;     %determind the winner under 2nd copeland rule
            end
        end
    else    %tie occurs again, the winner is determinded by the 1st voter
        for i = 1 : numalters
            if win2(i) == 1;
                for j = 1 : numalters
                    if profmatrix(j,1) == i
                        vote(j) = 1;
                    end
                end
            end
        end
        for k = 1 : numalters   %determind the winner
            if vote(k) == 1;
```

```
                winner = profmatrix(k,1);
            break;
            end
        end
    end
end
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%majorrelat
%s
%s2
%win2
%vote
c = winner;
```

```
%This function file enables us to find out the Winner under the Hare's Rule
function h = hareRevised(profmatrix,numalters,numvoters);

totalscore = pluralityscore(profmatrix,numalters,numvoters);
losercount = min(totalscore);  %to find the smallest score
lose = checktie(numalters,totalscore,losercount);%to check if there is a tie
vote = defineposvoter1(profmatrix,numalters,lose);%consult v1
%totalscore

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%initialisations

fiftypercent = numvoters/2;
newnumalters = 1;
discount = 0;
count = 1:1:numalters;
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

if max(totalscore) > fiftypercent   %decide the plurality winner which gain
    %more than 50% of first preferences
    [maximum, index] = max(totalscore);
    winner = index;
%    for a = 1 : numalters
%        if vote(a) == 1;
%            winner = profmatrix(a,1);   %to find out the plurality winner
%            break;
%        end
%    end
else    %decide the winner under hare's rule
    while newnumalters < numalters
        lose = checktie(numalters,totalscore,losercount);
        score = counttie(numalters,lose);   %to count the number of ties

            if score == 1;
                for a = 1 : numalters
                    if lose(a) == 1;
                        discount = a;
                        count(a) = 0;
                    end
                end
            elseif score >= 2
                for a = 1 : numalters  %to find out the two best alternatives
                    losevecter(a) = 0; %initialistion
                        if lose(a) == 1;
                            for b = 1 : numalters
                                if profmatrix(b,1) == a;
                                    losevecter(a) = b;
                                end
                            end
                        end
                end
                %losevecter contains voter 1's rankings of each of the
                %losing alternatives (if alternative 2 is a loser,
                %losevecter(2) == the rank that voter 1 assigns alternative
                %2
                cut = max(losevecter);
                %cut == the position in voter 1's rankings of the losing
                %alternative ranked lowest by voter 1
                for c = 1 : numalters,
                    if losevecter(c) == cut;
                        discount = c; %discount is the alternative to be removed
                        count(c) = 0;
                    end
```

```
                end
            end
            for a = 1 : numvoters
                for b = 1 : numalters
                    if profmatrix(b,a) == discount;
                        profmatrix(b,a) = 0; %replace the removed
                                                    %alternative with a '0'
                    end
                end
             end
        %profmatrix
        totalscore = pluralityscore(profmatrix,numalters,numvoters);
        for a = 1 : numalters
            if count(a) == 0;
                totalscore(a) = numvoters + 1;
            end
        end
        %totalscore
        losercount = min(totalscore);
        newnumalters = newnumalters + 1;
    end


    for a = 1 : numalters
        if count(a) ~= 0;
            winner = a;
        end
    end
end
%score
%losevecter
%count
%totalscore
%lose
h = winner;
```

```
%This function file enables us to find out the Winner under the Inverse Borda's
procedure
function i = inverseborda(profmatrix,numalters,numvoters);

totalscore = bordascore(profmatrix,numalters,numvoters);
losercount = min(totalscore);  %to find the smallest score
lose = checktie(numalters,totalscore,losercount);   %to check if there is a tie
%totalscore

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%initialisations
fiftypercent = numvoters/2;
newnumalters = 1;
discount = 0;
count = 1:1:numalters;
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%decide the plurality winner which gain more than 50% of first preferences
pscore = pluralityscore(profmatrix,numalters,numvoters);
wincount = max(pscore);
win = checktie(numalters,pscore,wincount);      %to check if there is a tie
vote = defineposvoter1(profmatrix,numalters,win);%consult v1
if max(pscore) > fiftypercent
        for a = 1 : numalters
                if vote(a) == 1;
                winner = profmatrix(a,1);   %to find out the plurality winner

                        break;
                end
        end
else
%decide the winner under inverse borda's procedure
        while newnumalters < numalters %continue until only one alternative left
                lose = checktie(numalters,totalscore,losercount);
                score = counttie(numalters,lose);   %to count the number of ties

                        if score == 1;
                        for a = 1 : numalters
                                if lose(a) == 1;
                                        discount = a;
                                count(a) = 0;
                                end
                        end
                elseif score >= 2
                        for a = 1 : numalters
                                losevecter(a) = 0;  %initialistion
                                if lose(a) == 1;
                                        for b = 1 : numalters
                                                if profmatrix(b,1) == a;
                                                        losevecter(a) = b;
                                                end
                                        end
                                end
                        end
                        cut = max(losevecter); %cut the alternative with
                                    %the lowest borda score
                        for c = 1 : numalters,
                                if losevecter(c) == cut;
                                discount = c;
                                count(c) = 0;
                                end
                        end
                        end
```

```
                for a = 1 : numvoters
                        for b = 1 : numalters
                        if profmatrix(b,a) == discount;
                                profmatrix(b,a) = 0;
                        end
                        end
                end
                totalscore = bordascore(profmatrix,numalters,numvoters);
                for a = 1 : numalters
                        if count(a) == 0;
                        totalscore(a) = (numalters-1)*numvoters + 1;
                        end
        end
            %profmatrix
                %totalscore
                losercount = min(totalscore);
                newnumalters = newnumalters + 1;
        end
        for a = 1 : numalters
                if count(a) ~= 0;
                        winner = a;
                end
        end
end

%score
%losevecter
%count
%totalscore
%lose
i = winner;
```

```
%This function file enables us to find out the Long Path Winner
function l = longpath(profmatrix,numalters,numvoters);

%to determind the matrix of the majority relation
majorrelat = majorityrelation(profmatrix,numalters,numvoters);
%majorrelat

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%Method One:
[v,d] = eig(majorrelat);    %find the eigenvalue and eigenvector of the matrix
eigenvalue = eig(majorrelat);   %eigenvalue vector
%v
%eigenvalue
%d
maxeigenvalue = max(eigenvalue);
for a = 1 : numalters
    if eigenvalue(a) == maxeigenvalue;
        check = a;
    end
end
eigenvector = v(:,check);
lp = (1/sum(eigenvector))*eigenvector;
winnercount = max(lp);  %to find the maximum long path score
win = checktie(numalters,lp,winnercount);   %to check if there is a tie
vote = defineposvoter1(profmatrix,numalters,win);   %to define the position of w
inners from voter_1's profile
for a = 1 : numalters   %to find out the long path winner
    if vote(a) == 1;
        winner = profmatrix(a,1);
    break;
    end
end
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%Method Two:
%A = majorrelat
%iden = eye(numalters,numalters);
%x = iden(:,1)
%a = 1;
%while a <= numalters
%    a
%    newx = (A*x)/sqrt(sum((A*x).^2))
%    x = newx;
%    a = a + 1;
%end
%y = A*newx
%lp = (1/sum(y))*y
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

l = winner;
```

```
%Returns Winner under Majoritarian Compromise Procedure
function m = majorcompromise(profmatrix,numalters,numvoters);

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%initialisations
score = 1; %indicates how many of the top rows we consider
currentscore = 0;
z = 1;
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%to find the winner under majoritarian compromise
while score < numalters+1
    for a = 1 : numalters   %total score for each alternative
            totalscore(a) = 0;  %(ie. totalscore(1) = score for alternative 1)
    end
        for a = 1 : numvoters   %get votes for every rank in the top 'score' row
s
                for b = 1 : score
                        scorematrix(b,a) = 1;
                end
                for c = score+1 : numalters
                scorematrix(c,a) = 0;
                end
     end
    %scorematrix
        for a = 1 : numalters   %testing each alternative (ie. 1 to numalters)
        for b = 1 : numvoters
                for c = 1 : numalters
                        if profmatrix(c,b) == a;
                        if scorematrix(c,b) == 1;
                                currentscore = 1;
                        end
                        end
                        totalscore(a) = totalscore(a) + currentscore;
                        currentscore = 0;
                end
        end
     end
    %totalscore
        winnercount = max(totalscore);  %to find the maximum score
        if winnercount >= numvoters/2;
        win = checktie(numalters,totalscore,winnercount); %check for tie
            vote = defineposvoter1(profmatrix,numalters,win);  %consult v1
        for a = 1 : numalters
                if vote(a) == 1;
                        winner = profmatrix(a,1);
                break;
                end
            end
        break;
    else
            score = score + 1;
    end
end

m = winner;
```

```
function y = DodgsonRevised(profmatrix, numalters, numvoters);

%Returns the simplified dodgson winner (i.e. sum each alternative’s margins
%of defeat - choose the alternative with the smallest such sum)

N = Nmatrix(profmatrix, numalters, numvoters);

for i=1:numalters
    totalscore(i) = 0;
    for j=1:numalters
        if(N(i,j) - N(j,i) < 0)
            totalscore(i) = totalscore(i) + N(i,j) - N(j,i);
        end
    end
end

%totalscore

winners = checktie(numalters, totalscore, max(totalscore));

vote = defineposvoter1(profmatrix,numalters,winners);   %to define the position
of winners from voter_1’s profile

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
for j = 1 : numalters
    if vote(j) == 1;
        winner = profmatrix(j,1);
    break;
    end
end

y = winner;
```

```
function y = nansonRevised(profmatrix, numalters, numvoters);

%Returns the nanson winner - eliminates all alternatives with below average
%borda scores until only one remains

count = 1:1:numalters;

while(length(find(count) > 1))
    loseVector = zeros(1,numalters);
    bordaScore = bordascore(profmatrix, numalters, numvoters);
    numCurAlters = length(find(count));
    averagescore = sum(0:1:numCurAlters-1)*numvoters/numCurAlters;
    %averageborda(profmatrix, numalters, numvoters);
    for j=1:numalters
        if((count(j) ~= 0) && (bordaScore(j) < averagescore))
            loseVector(j) = 1;
%            count(j) = 0;
        end
    end

    if(length(find(loseVector)) >= length(find(count)))
        winners = loseVector;
        break;
    end

    for i=1:numalters
        if(loseVector(i) == 1)
            count(i) = 0;
        end
    end

    for i=1:numalters
        for j=1:numvoters
            if(profmatrix(i,j) ~= 0)
                if(loseVector(profmatrix(i,j)) == 1)
                    profmatrix(i,j) = 0;
                end
            end
        end
    end
    winners = count;
    if(length(find(loseVector)) == 0)
        break;
    end

%     if(length(find(count)) == 1)
%         winners = count;
%         break;
%     elseif(length(find(count)) == 0)
%        winners = loseVector;
%         break;
%     elseif(length(find(loseVector)) == 0)
%         winners = count;
%         break;
%     end
end

%winners = count;
%if(length(find(count) == 0))
%    winners = loseVector;
%end

%profmatrix
```

```
%This function file enables us to find out the Plurality's Winner
function p = plurality(profmatrix,numalters,numvoters);

%to calculate the plurality score for each alternative
totalscore = pluralityscore(profmatrix,numalters,numvoters);
winnercount = max(totalscore);  %to find a maximum plurality score
win = checktie(numalters,totalscore,winnercount);  %to check if there is a tie
vote = defineposvoter1(profmatrix,numalters,win);  %to define the position of wi
nners from voter_1's profile

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%to find out the plurality winner
for h = 1 : numalters
    if vote(h) == 1;
        winner = profmatrix(h,1);
    break;
    end
end
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%totalscore
%win
%vote
p = winner;
```

```
%This function file enables us to find out the Winner under the Run-Off Procedur
e

function r = runoff(profmatrix,numalters,numvoters);

%calculate the total score for each alternative under the plurality rule
totalscore = pluralityscore(profmatrix,numalters,numvoters);
winnercount = max(totalscore);  %to find the highest score
fiftypercent = numvoters/2; %50% of total voters

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
win = checktie(numalters,totalscore,winnercount);   %to check if there is a tie
score = counttie(numalters,win);    %to count the number of ties
vote = defineposvoter1(profmatrix,numalters,win);    %to define the position of
winner(s) from voter(1)'s profile
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%


%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
if max(totalscore) > fiftypercent   %decide the plurality winner which gain
                                    %more than 50% of first preferences
    for h = 1 : numalters
        if vote(h) == 1;
            winner = profmatrix(h,1);   %to find out the plurality winner
        break;
        end
    end
else    %decide the winner under run-off procedure
    if score >= 2
        for i = 1 : numalters   %to find out the two best alternatives
            if vote(i) == 1;
                bestalt1 = profmatrix(i,1);
                    for j = i+1 : numalters
                        if vote(j)== 1;
                            bestalt2 = profmatrix(j,1);
                            break;
                        end
                    end
                break;
            end
        end
        winner = runoffwinner(profmatrix,numvoters,numalters,bestalt1,bestalt2);
 %to decide the winner under runoff procedure
    elseif score == 1
        for k = 1 : numalters   %to find out the two best alternatives
            if win(k) == 1;
                bestalt1 = k;
                count = k;
                break;
            end
        end
        for l = 1 : numalters
            best2score(l) = 0;
            best2score(count) = 0;
                if l ~= count;
                    best2score(l) = totalscore(l);
                end
        end
        winnercount2 = max(best2score); %to find the maximum score
        win2 = checktie(numalters,totalscore,winnercount2);   %to check if there
 is a tie
        vote2 = defineposvoter1(profmatrix,numalters,win2);    %to define the po
sition of winner(s) from voter(1)'s profile
```

```
%This function file enables us to find out the Winner under the Simpson's Proced
ure
function s = simpsons(profmatrix,numalters,numvoters)

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%to find a matrix N
for a = 1 : numalters
    for b = 1 : numalters
        if b >= a;
            N(a,b) = 0;
            if a == b;
                N(a,b) = numvoters + 1;
            else
                check1 = 0;
                check2 = 0;
                for c = 1 : numvoters
                    for d = 1 : numalters
                        if profmatrix(d,c) == a;
                            check1 = d;
                        elseif profmatrix(d,c) == b;
                            check2 = d;
                        end
                    end
                    if check1 < check2;
                        N(a,b) = N(a,b) + 1;
                    end
                end
                N(b,a) = numvoters - N(a,b);
            end
        end
    end
end

%N(a,b) == number of voters who rank a ahead of b
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%to find the winner under the simpson's procedure
for a = 1 : numalters
    S(a) = 0;
    for b = 1 : numalters
        test(b) = N(a,b);
    end
    S(a) = min(test); %returns the maximum defeat of each candidate
                                %equivalent to minumum win, when wins can be negativ
e
end
%N
%S
winnercount = max(S);  %to find the smallest maximum defeat, or biggest min win
win = checktie(numalters,S,winnercount);   %to check if there is a tie
vote = defineposvoter1(profmatrix,numalters,win);   %to define the position of w
inners from voter_1's profile
for c = 1 : numalters
    if vote(c) == 1;
        winner = profmatrix(c,1);
    break;
    end
end
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

s = winner;
```

```
%This function file enables us to find out the Top Cycle Winner
function t = topcycle(profmatrix,numalters,numvoters);

%initialisation
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
count = 2;
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%to determind the matrix of the majority relation
majorrelat = majorityrelation(profmatrix,numalters,numvoters);

I = ones(numalters,1);  %matrix of ones (ie. 1m, m = number of alternatives
s = majorrelat * I;     %calculate the copeland score
winnercount = max(s);   %to find the maximum copeland score
win = checktie(numalters,s,winnercount);        %to check if there is a tie
wincount = counttie(numalters,win);     %to count the number of ties
vote = defineposvoter1(profmatrix,numalters,win);       %consult v1

if wincount == 1 & winnercount == numalters-1   %to find the condorcet winner
        for a = 1 : numalters
        if win(a) == 1
                winner = a;     %determind the condorcet winner
        end
    end
else  %tie occurs, to find the topcycle winner
    oldM = majorrelat;
    while count < numalters
        M = majorrelat^count;
        for a = 1 : numalters
            for b = 1 : numalters
                if M(a,b) > 1;
                    M(a,b) = 1;
                end
                if M(a,a) ~= 0;
                    M(a,a) = 0;
                end
            end
        end
        %M
        newM = M + oldM;
        for a = 1 : numalters
            for b = 1 : numalters
                if newM(a,b) > 1;
                    newM(a,b) = 1;
                end
                if newM(a,a) ~= 0;
                    newM(a,a) = 0;
                end
            end
        end
        %newM
        s = newM*I;
        winnercount = max(s);   %to find the maximum copeland score for new M
        win = checktie(numalters,s,winnercount);        %to check if there is a
tie
        wincount = counttie(numalters,win);     %to count the number of ties
        vote = defineposvoter1(profmatrix,numalters,win);       %consult v1
        if winnercount == numalters-1   %to check there is a winner
                                        %has full copeland score
            if wincount == 1    %if there is no tie
                for a = 1 : numalters
                    if win(a) == 1
                        winner = a;     %determind the topcycle winner
```

```
                end
            end
        elseif wincount ~=1 %if there is a tie
            for a = 1 : numalters
                if vote(a) == 1;
                    winner = profmatrix(a,1);%determind the topcycle
                                              %winner from voter_1's profile
                break;
                end
            end
        end
        break;
    else
        count = count + 1;
    end
    oldM = newM;
  end
end

t = winner;
```

```
function u = uncoveredset(profmatrix,numalters,numvoters);

%initialisation
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
for a = 1 : numalters
    for b = 1 : numalters
        covers(a,b) = 0;
        uncovered(b) = 1;
    end
end
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%to determind the matrix of the majority relation
majorrelat = majorityrelation(profmatrix,numalters,numvoters);

I = ones(numalters,1);  %matrix of ones (ie. 1m, m = number of alternatives
s = majorrelat * I;     %calculate the copeland score
winnercount = max(s);   %to find the maximum copeland score
win = checktie(numalters,s,winnercount);        %to check if there is a tie
wincount = counttie(numalters,win);     %to count the number of ties
vote = defineposvoter1(profmatrix,numalters,win);       %consult v1

if wincount == 1 & winnercount == numalters-1   %to find the condorcet winner
        for a = 1 : numalters
        if win(a) == 1
                winner = a;     %determind the condorcet winner
        end
    end
else  %tie occurs, to find the uncovered set winner
    for a = 1 : numalters
        for b = 1 : numalters-1
            if b+1 > a
                for c = 1 : numalters
                    test1(c) = 0;
                    test2(c) = 0;
                    test1(c) = majorrelat(a,c);
                    test2(c) = majorrelat(b+1,c);
                end
                score = 0;
                care = 0;
                for d = 1 : numalters
                    if test1(d) == test2(d);
                        score = score + 1;
                    else
                        care = d;
                    end
                end
                if score == numalters-1;
                    if care == a | care == b+1;
                        if test1(care) == 1;
                            covers(a,b+1) = 1;
                        elseif test2(care) == 1;
                            covers(b+1,a) = 1;
                        end
                    end
                end
            end
        end
    end
    %covers
    for e = 1 : numalters
        for f = 1 : numalters
            if covers(e,f) == 1;
```

```
                uncovered(f) = 0;
            end
        end
    end
    %uncovered
    vote = defineposvoter1(profmatrix,numalters,uncovered);     %consult v1
    for g = 1 : numalters
        if vote(g) == 1;
            winner = profmatrix(g,1);    %to find the uncovered set winner
            break;
        end
    end
end

u = winner;
```

```
function y = RaynaudRevised(profmatrix, numalters, numvoters);

%Finds maximum of each row of the N matrix. Eliminates the alternative with
%the minumum max. Continues until there is one left. N tells us how many
%voters prefer x to each of the other alternatives.

count = 1:1:numalters;
N = Nmatrix(profmatrix, numalters, numvoters);
for i=1:numalters
    N(i,i) = 0;
end
for k=1:numalters-1
    maxVector = max(N');
    for i=1:numalters
        if(count(i) == 0)
            %i
            maxVector(i) = numvoters+1;
        end
    end

    %simpScore = simpsonsScore(profmatrix, numalters, numvoters);

    loseVector = checktie(numalters, maxVector, min(maxVector));
    for i=numalters:-1:1
        %        if(profmatrix(i,1) ~= 0)
        %        if(count(i) ~= 0)
        if(loseVector(profmatrix(i,1)) == 1)
            cutAlternative = profmatrix(i,1);
            break;
        end
        %       end
    end

    count(cutAlternative) = 0;

    N(cutAlternative,:) = 0;
    N(:,cutAlternative) = 0;
        %    for i=1:numalters
%       for j=1:numvoters
%            if(profmatrix(i,j) == cutAlternative)
%                profmatrix(i,j) = 0;
%            end
%        end
%    end
end

[maximum, index] = max(count);

y = index;
```

```
function y = coombsRevised(profmatrix, numalters, numvoters);
%returns the coombs winner - eliminates the candidate who receives the most
%last place votes until one candidate has a majority of first place votes

totalscore = pluralityscore(profmatrix,numalters,numvoters);    %to find the plu
ralityscore for each alters

[maximum, index] = max(totalscore);

count = 1:1:numalters;

while(maximum <= numvoters/2)
    antiscore = antipluralityscore(profmatrix, numalters, numvoters);
    for i=1:numalters
        if count(i) == 0
            antiscore(i) = numvoters + 1;
        end
    end
    loseVector = checktie(numalters, antiscore, min(antiscore));
    for i=numalters:-1:1
        if(profmatrix(i,1) ~= 0)
            if(loseVector(profmatrix(i,1)) == 1)
                cutAlternative = profmatrix(i,1);
                break;
            end
        end
    end

    count(cutAlternative) = 0;
    for i=1:numalters
        for j=1:numvoters
            if(profmatrix(i,j) == cutAlternative)
                profmatrix(i,j) = 0;
            end
        end
    end
%    profmatrix

    totalscore = pluralityscore(profmatrix,numalters,numvoters);    %to find the
 pluralityscore for each alters
    [maximum, index] = max(totalscore);
end

y = index;
```

```
function y = Carey(profmatrix, numalters, numvoters);

%Returns the Carey winner - eliminates all alternatives with below average
%plurality scores. continues until there is one left.

count = 1:1:numalters;

while(length(find(count) > 1))
    loseVector = zeros(1,numalters);
    plurScore = pluralityscore(profmatrix, numalters, numvoters);
    averagePlur = numvoters/length(find(count));
    for j=1:numalters
        if((count(j) ~= 0) && (plurScore(j) < averagePlur))
            loseVector(j) = 1;
%            count(j) = 0;
        end
    end

    if(length(find(loseVector)) >= length(find(count)))
        winners = loseVector;
        break;
    end

    for i=1:numalters
        if(loseVector(i) == 1)
            count(i) = 0;
        end
    end

    for i=1:numalters
        for j=1:numvoters
            if(profmatrix(i,j) ~= 0)
                if(loseVector(profmatrix(i,j)) == 1)
                    profmatrix(i,j) = 0;
                end
            end
        end
    end
    winners = count;
    if(length(find(loseVector)) == 0)
        break;
    end
end

for i=1:numalters
    %if(count(i)~= 0)
    if(profmatrix(i,1) ~= 0)
        if(winners(profmatrix(i,1)) ~= 0)
            winner = profmatrix(i,1);
            break;
        end
    end
    %    end
end
y = winner;
```

```
%This function file enables us to determind the matrix of the majority relation
function m = majorityrelation(profmatrix,numalters,numvoters);

%m(a,b) = 1 means that a beats b in majority contest
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%intialisations of variables
for a = 1 : numalters
    test(a) = 0;
    rankofalter(a) = 0;
    vote(a) = 0;
    for b = 1 : numalters
        matrix(a,b) = 0;
        majorrelat(a,b) = 0;
    end
end
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%determind the matrix of the majority relation
for a = 1 : numalters   %testing for each alternative
    for b = 1 : numvoters
        for c = 1 : numalters
            test(c) = profmatrix(c,b);
        end
        rankofalter = 0;
        for d = 1 : numalters   %solve out the preferences' ranking
            for e = 1 : numalters
                if test(e) == d
                    rankofalter(d) = e;
                end
            end
        end
        for f = 1 : numalters
            if a == f
                matrix(a,f) = 0;
            elseif rankofalter(a) < rankofalter(f)
                matrix(a,f) = matrix(a,f) + 1;
            end
        end
    end
end

average = numvoters/2;

for a = 1 : numalters
    for b = 1 : numalters
        if matrix(a,b) > average
            majorrelat(a,b) = 1;
        else
            majorrelat(a,b) = 0;
        end
    end
end
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%matrix
m = majorrelat;
```

```
%This function file enable us to check if there is a tie
function c = checktie(numalters,totalscore,count);

for e = 1 : numalters
        if totalscore(e) == count;
            winlose(e) = 1;
        elseif totalscore(e) == 0 | totalscore(e) ~= count;
            winlose(e) = 0;
        end
end

c = winlose;
```

```
%This function file enable us to count the number of ties
function c = counttie(numalters,winlose);

score = 0;  %initialisation

for a = 1 : numalters
    if winlose(a) == 1;
        score = score + 1;
    end
end

c = score;
```

```
%This function file enables us to define the position of winners/losers from vot
er_1's profile
function d = defineposvoter1(profmatrix,numalters,win);

%'win' is a vector of 1's and 0's, win(i) = 1 means that alternative i is
%tied for the winning score

for a = 1 : numalters   %initialisation
    vote(a) = 0;
end

for b = 1 : numalters
    if win(b) == 1;
        for c = 1 : numalters
            if profmatrix(c,1) == b
                vote(c) = 1;
            end
        end
    end
end

%Returns a vector d, where d(i) = 1 indicates says that the voter ranked ith by
%voter 1 is a winner (as defined by 'win')
d = vote;
```

```
%This function file enable us to calculate the borda's score for each alternativ
e
function b = bordascore(profmatrix,numalters,numvoters)

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%initialisations
numcount = 0;
count = 0;
currentscore = 0;
for a = 1 : numalters   %total score for each alternative
    totalscore(a) = 0;  %(ie. totalscore(1) = score for alternative 1)
end
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%


while numcount < numalters
        for d = 1 : numvoters
                for e = 1 : numalters-1
                if profmatrix(e,d) == 0
                        profmatrix(e,d) = profmatrix(e+1,d);
                profmatrix(e+1,d) = 0;
                        end
                end
        end
   numcount = numcount + 1;
end
%profmatrix
for f = 1 : numalters
    if profmatrix(f,1) ~= 0;
        count = count + 1;
    end
end
bordascore = count-1 : -1 : 0;  %the bordascore for each alternative
                                %(ie. bordascore(1) = score for alternative bein
g 1st)
for c = 1 : numalters
    for g = 1 : numvoters
        for h = 1 : count
            if profmatrix(h,g) == c;
                currentscore = bordascore(h);
            end
        totalscore(c) = totalscore(c) + currentscore;
        currentscore = 0;
        end
    end
end

profmatrix;
b = totalscore;
```

```
%This function file enable us to calculate the antiplurality score for each alte
rnative
function a = antipluralityscore(profmatrix,numalters,numvoters);

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%initialisations
numcount = 0;
count = 0;
currentscore = 0;
for a = 1 : numalters   %total score for each alternative
   totalscore(a) = 0;  %(ie. totalscore(1) = score for alternative 1)
   antiscore(a) = 0;    %antiplurality score for each alternative
end
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%


while numcount < numalters
        for d = 1 : numvoters
        for e = 1 : numalters-1
        if profmatrix(e,d) == 0
                        profmatrix(e,d) = profmatrix(e+1,d);
                profmatrix(e+1,d) = 0;
                end
        end
        end
   numcount = numcount + 1;
end
%profmatrix
for f = 1 : numalters
    if profmatrix(f,1) ~= 0;
        count = count + 1;
    end
end
for a = 1 : count       %antiplurality score
   antiscore(a) = 1;
        if a == count;
         antiscore(a) = 0;
     end
end
%antiscore
for c = 1 : numalters
    for g = 1 : numvoters
        for h = 1 : count
            if profmatrix(h,g) == c;
                currentscore = antiscore(h);
            end
        totalscore(c) = totalscore(c) + currentscore;
        currentscore = 0;
        end
    end
end

%profmatrix
a = totalscore;
```

```
%This function file enable us to calculate the plurality score for each alternat
ive
function ps = pluralityscore(profmatrix,numalters,numvoters);

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%initialisations
plurscore = 1;      %the plurality score is 1 for the alternative being 1st
currentscore = 0;
current = 0;
for a = 1 : numalters   %total score for each alternative
    totalscore(a) = 0;  %(ie. totalscore(1) = score for alternative 1)
end
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%calculate the total score for each alternative under the plurality rule
for b = 1 : numalters   %testing each alternative (ie. 1 to numalters)
    for c = 1 : numvoters
        if profmatrix(1,c) ~= 0;
            if profmatrix(1,c) == b;
                currentscore = plurscore;
            end
        totalscore(b) = totalscore(b) + currentscore;
        currentscore = 0;
        elseif profmatrix(1,c) == 0;
            for d = 1 : numalters-1
                if profmatrix(1+d,c) == b;
                    for e = 1 : d
                        if profmatrix(1+d-e,c) == 0
                            current = current + 1;
                        end
                    end
                    if current == d;
                        currentscore = plurscore;
                        totalscore(b) = totalscore(b) + currentscore;
                    end
                end
            end
        currentscore = 0;
        current = 0;
        end
   end
end
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

ps = totalscore;
```

```
function y = Nmatrix(profmatrix, numalters, numvoters);
%N(a,b) == number of voters who rank a ahead of b
%N(a,a) == numvoters+1 <- some sort of junk value

for a = 1 : numalters
    for b = 1 : numalters
        if b >= a;
            N(a,b) = 0;
            if a == b;
                N(a,b) = numvoters + 1;
            else
                check1 = 0;
                check2 = 0;
                for c = 1 : numvoters
                    for d = 1 : numalters
                        if profmatrix(d,c) == a;
                            check1 = d;
                        elseif profmatrix(d,c) == b;
                            check2 = d;
                        end
                    end
                    if (check1 < check2 && check1 ~= 0);
                        N(a,b) = N(a,b) + 1;
                    elseif (check1 == 0 || check2 == 0)
                        N(a,b) = numvoters + 1;
                    end
                end
                N(b,a) = numvoters - N(a,b);
                if(check1 == 0 || check2 == 0)
                    N(b,a) = numvoters + 1;
                end
            end
        end
    end
end

y = N;
```

```
%This function file enable us to decide the winner under runoff procedure
function r = runoffwinner(profmatrix,numvoters,numalters,bestalt1,bestalt2);

%determines which of the two alternatives would win a head-to-head matchup

finalscore(1) = 0;  %initialisations
finalscore(2) = 0;

for a = 1 : numvoters   %to decide the winner under runoff procedure
    for b = 1 : numalters
        test(b,a) = 0;
            if profmatrix(b,a) == bestalt1;
                test(b,a) = bestalt1;
            elseif profmatrix(b,a) == bestalt2;
                test(b,a) = bestalt2;
            end
     end
     for c = 1 : numalters
        if test(c,a) == bestalt1;
            finalscore(1) = finalscore(1) + 1;
            bestcount = 1;
            break;
        elseif test(c,a) == bestalt2% & bestcount ~= 0;
            finalscore(2) = finalscore(2) + 1;
            break;
        end
     end
end
finalwinner = max(finalscore);  %to find the maximum score
for d = 1 : 2;
    if finalscore(d) == finalwinner;
        virwinner = d;
    end
end
if virwinner == 1;
    winner = bestalt1;
else
    winner = bestalt2;
end

%test
%finalscore
r = winner;
```

```
%This function file creates a matrix of random preference's profiles for the vot
ers,
%where row = alternative and column = voters - IC Culture

function p = profiles(numalters, numvoters)

%numalters = The total number of alternatives
%numvoters = The total number of voters

profmatrix = [];

for x = 1 : numvoters
    ran = randperm(numalters);
    for y = 1 : numalters
        profmatrix(y,x) = ran(y);
    end
end

p = profmatrix;
```

```
function y = ClusteredCulture(numalters, numvoters);
%generates profiles according to CC hypothesis.
%4 blocs, (3 parties, 1 independent)
%3 parties randomize over the mode by swapping n pairs of preferences for
%each voter

numParties = 3;

partyPercents = zeros(numParties,1);

partyPercents(1) = .35;
partyPercents(2) = .30;
partyPercents(3) = .15;

partySizes = zeros(numParties,1);
modes = zeros(numalters, numParties);
profile = zeros(numalters,numvoters);

numSwaps = numalters;
%numSwaps = round(numalters*log(numalters)/4);
%numSwaps = 0;
count = 1;
for i=1:numParties
    partySizes(i) = round(numvoters*partyPercents(i));
    modes(:,i) = randperm(numalters)';
    for j=1:partySizes(i)
        profile(:,count) = modes(:,i);
        for k=1:numSwaps
            firstSwap = RandomInt(numalters);
            secondSwap = RandomInt(numalters);
            while(firstSwap == secondSwap)
                secondSwap = RandomInt(numalters);
            end
            temp = profile(firstSwap, count);
            profile(firstSwap,count) = profile(secondSwap,count);
            profile(secondSwap,count) = temp;
        end

        count = count + 1;

    end
end
independentSize = numvoters - sum(partySizes);

for i=count:numvoters
    profile(:,i) = randperm(numalters)';
end

y = profile;
```