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Impact of structure space continuity on protein fold classification

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Protein structure classification hierarchically clusters domain structures based on structure and/or sequence similarities and plays important roles in the study of protein structure-function relationship and protein evolution. Among many classifications, SCOP and CATH are widely viewed as the gold standards. Fold classification is of special interest because this is the lowest level of classification that does not depend on protein sequence similarity. The current fold classifications such as those in SCOP and CATH are controversial because they implicitly assume that folds are discrete islands in the structure space, whereas increasing evidence suggests significant similarities among folds and supports a continuous fold space. Although this problem is widely recognized, its impact on fold classification has not been quantitatively evaluated. Here we develop a likelihood method to classify a domain into the existing folds of CATH or SCOP using both query-fold structure similarities and within-fold structure heterogeneities. The new classification differs from the original classification for 3.4–12% of domains, depending on factors such as the structure similarity score and original classification scheme used. Because these factors differ for different biological purposes, our results indicate that the importance of considering structure space continuity in fold classification depends on the specific question asked.

Since the 1970s, classification of protein domain structures has gained wide popularity because of its utility in predicting protein function and studying protein evolution¹. Many hierarchical classifications of domain structures have been developed^{2–6}. Among them, SCOP⁵ and CATH^{3,4,7} databases are commonly regarded as the gold standards because of their substantial manual inspections. The hierarchical levels of SCOP from bottom to top are family, superfamily, fold, and class. In general, families and superfamilies consist of domains that are homologous or structurally very similar. Folds comprise superfamilies of domains with similar secondary structure compositions, orientations, and connection orders. Classes, as the top level, include folds with similar secondary structure compositions. In CATH, the hierarchies are homology superfamily (H), topology (T), architecture (A), and class (C). The H, T, and C levels in CATH are respectively equivalent to the superfamily, fold, and class levels in SCOP. Fold in SCOP or T in CATH is of special interest to structural biologists because members of a fold are structurally similar yet usually have no detectable protein sequence similarity^{8–11}. Thus, fold classification can provide significant insights into protein function and evolution that are beyond the realm of sequence analysis.

The current fold classification in SCOP and CATH implicitly assumes that different folds represent isolated islands in the structure space. This assumption was based on early visual observations from a small number of folds that are structurally highly dissimilar. With the explosion of the number of solved domain structures and the use of structure similarity metrics, increasing evidence supports the concept of a continuous fold space where domains from different folds have significant structural similarities^{12–15}. This discovery prompted multiple authors to question the current fold hierarchy¹⁴ and propose alternative representations such as structure similarity networks¹⁶ and maps^{17,18}. In a network, domains are connected if their structure similarity exceeds an arbitrary threshold, whereas in a map, domains are points in a plane or space reduced from a pairwise structure similarity matrix of all domains. However, none of these new representations are intuitive due to the lack of obvious fold boundaries. As a result, the conventional fold representation still dominates the literature in the study of protein structure-function relationship and protein evolution. Given the wide use of fold classification in many studies¹⁹, examining the impact of structure continuity on fold classification is important.

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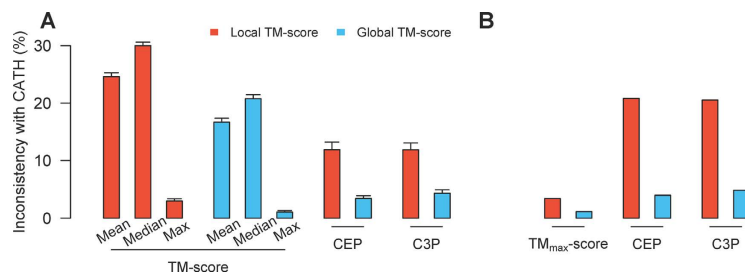


Figure 1. Fractions of fold-level domain structure classifications by various TM-scores, CEP, and C3P that are inconsistent with the CATH classification for (A) 30 sets of 10% randomly chosen domains from CATH v3.5.0 and (B) 8280 newly added domains in CATH v4.0.0 since v3.5.0. Error bars show one standard deviation.

Various automatic pipelines have been developed to classify domain structures into folds, and they can be generally divided into two types. The first type directly classifies domains according to their structure and/or sequence similarities with existing folds^{20–27}. The second type uses a machine learning approach^{28–31}. It first collects positive samples from domain pairs in the same folds and negative samples from randomly paired domains across folds, then trains classifiers on these domain pairs. These classifiers are subsequently used to predict whether a query domain is in the same fold as another domain. To our knowledge, none of the current classification methods explicitly consider fold space continuity. As a result, it is unclear to what degree fold space continuity affects protein structure classification and whether it is legitimate to ignore this continuity in classification.

To answer these questions, we propose and implement a strategy to classify domain structures to existing folds by considering fold space continuity. Briefly, we calculate the likelihood that a structure belongs to a fold by considering the similarity between the structure and the fold as well as the similarities among the structures already classified into the fold. By comparing our new classification with the current CATH and SCOP classifications, we assess the importance of considering the fold space continuity in fold classification.

Results

Fold classification without considering within-fold structure heterogeneity. To classify domain structures, we need an objective quantity to measure structure similarities between two domains. TM-score^{32,33}, calculated by the software TM-align³⁴, is chosen for this purpose. High TM-score indicates short average spatial distance between aligned residues in a structure alignment (see Materials and Methods). Unlike many other similarity scores^{35–38}, TM-scores of different domain pairs are directly comparable^{32–34} due to the normalization using either the average sequence length of the two domains under comparison or the length of the shorter domain. The former normalization penalizes the length difference between the two domains, which is appropriate when both domains are complete and comparable (i.e., one is not a subunit of the other). This normalization emphasizes the global structure similarity between domains, and the obtained TM-score is referred to as the global TM-score. By contrast, the latter normalization is appropriate when one domain corresponds to a subunit of the other or when one or both domains are incomplete. We refer to such normalized TM-scores as local TM-scores. Both global and local TM-scores are used in our analyses. After normalization, TM-scores are between 0 and 1. Larger TM-scores indicate higher structural similarities.

We focus primarily on the CATH database in this study because it is updated regularly and contains more recently solved domain structures than other databases. We refer to the T level in CATH as fold, because it is equivalent to the fold level in SCOP. We collected from CATH (version 3.5.0) 21,309 representative domains whose mutual sequence identities are $\leq 60\%$ and sequence lengths are ≥ 40 residues. These domains are from 1,158 folds in the CATH classification. Of these folds, 141 comprise at least 25 representative domains each. We used these large folds in subsequent analysis, because smaller folds provide insufficient information for statistical analysis. In spite of the relatively low fraction of folds analyzed here, for two reasons, these large folds are highly likely to cover most continuous regions of the fold space. First, these large folds include 17,043 or 82% of all representative domains. Second, the large folds are closer to one another than they are to the 1017 small folds ($P < 1.5e-18$; Wilcoxon signed-rank test), where the closeness between two folds is measured by the highest TM-score of all domain pairs across the two folds.

We randomly choose 10% of domains from each of the large folds as our query domains, whereas the rest of the domains stay in their originally classified folds. To classify a query, TM-scores are calculated between the query and all domains in a fold. The maximum TM-score observed represents the query-fold similarity, and is referred to as query-fold TM_{max}-score. The query is assigned to the fold with the highest query-fold TM_{max}-score. We repeat this entire process 30 times to estimate the frequency of inconsistency between the TM_{max}-based classification and the CATH classification.

Our local TM_{max}-score-based classification is inconsistent with the current CATH fold classification for an average of 2.9% of queries (Fig. 1). This value decreases to 1.1% under the global TM_{max}-score-based classification (Fig. 1). We also tried using either the mean or median TM-score instead of TM_{max}-score to define domain-fold similarity, but the frequency of inconsistency rises to 17–30% (Fig. 1). These results indicate that the CATH fold classification is primarily based on the information contained in TM_{max}-scores, especially in terms of the global structural similarity. Thus, TM_{max}-score-based fold classification, which can be fully automated, may be used as a proxy for CATH classification.

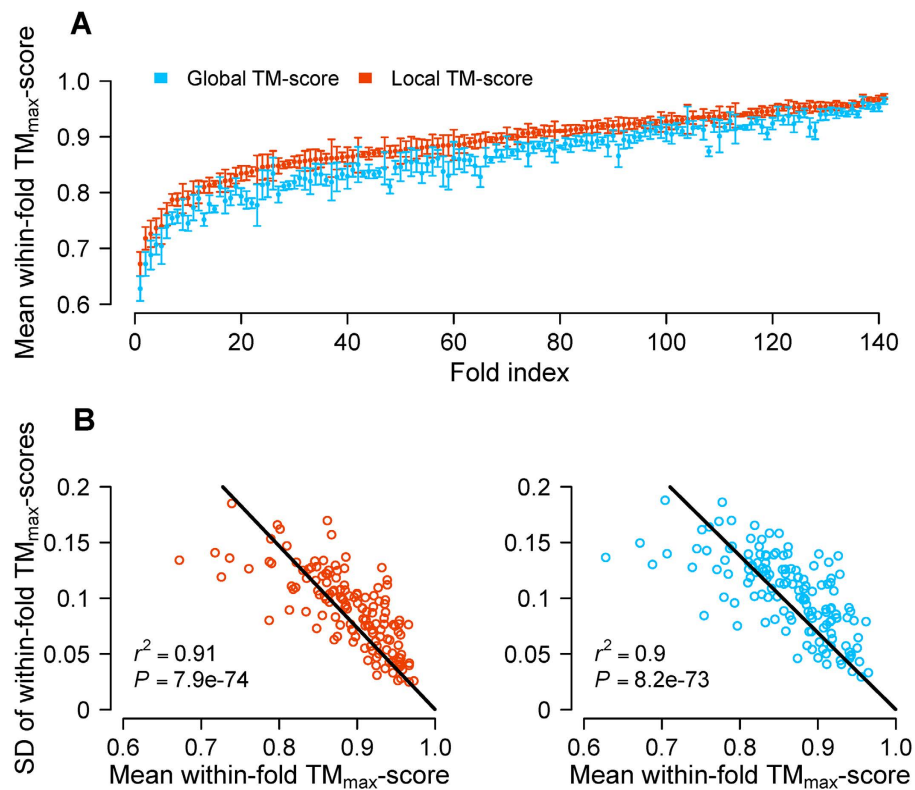


Figure 2. Within-fold structural heterogeneities of the 141 large folds in CATH version 3.5.0. (A) Mean within-fold TM_{\max} -score of each fold. A whisker indicates the standard deviation (SD) of the within-fold TM_{\max} -scores. (B) Correlation between the mean and SD of within-fold TM_{\max} -scores across folds.

Within-fold structure heterogeneity varies among folds. Different folds in the current CATH classification may have different levels of structure heterogeneity. To measure structure heterogeneity within a fold, we first calculated the (local or global) TM_{\max} -score for each domain in the fold, which is defined by the highest TM -score between the focal domain and all other domains in the fold. We then calculated the mean and standard deviation of the TM_{\max} -scores of all domains in the fold. The mean within-fold TM_{\max} -score is a measure of structure homogeneity within a fold, because the higher the mean within-fold TM_{\max} -score, the higher the structure homogeneity within the fold. Our analysis reveals that some folds are highly homogenous with the mean within-fold TM_{\max} -score approaching 1, whereas some other folds are highly heterogeneous with the mean within-fold TM_{\max} -score as low as 0.6–0.7 (Fig. 2A). Furthermore, the standard deviation of within-fold TM_{\max} -scores also varies greatly among folds and a very strong negative correlation exists between the mean and standard deviation of within-fold TM_{\max} -scores (Fig. 2B). This latter observation indicates that, when a fold has a low mean TM_{\max} -score, it is typically because some of the within-fold TM_{\max} -scores are very low rather than all within-fold TM_{\max} -scores are low.

A likelihood method for fold classification considering within-fold structure heterogeneity.

How well a query fits a fold should not only be determined by the query-fold TM_{\max} -score, but also the distribution of within-fold TM_{\max} -scores; folds with wider distributions of within-fold TM_{\max} -scores are more accommodating to a query than those with narrower distributions. The likelihood that a query belongs to a particular fold can be measured by the fraction of within-fold TM_{\max} -scores equal to or smaller than the query-fold TM_{\max} -score. We refer to this fraction as the cumulative empirical probability (CEP). Note that CEP is a measure of the fit of a query-fold TM_{\max} -score to the TM_{\max} -scores of all members already classified to the fold. CEP is not the posterior probability that a query belongs to a fold, and the sum of CEPs for all folds is not necessarily 1. Figure 3 shows a hypothetical example where CEP classifies a query into fold2 despite that the query-fold2 TM_{\max} -score is lower than the query-fold1 TM_{\max} -score (Fig. 3A). This occurs because the fraction of within-fold TM_{\max} -scores that are equal to or smaller than the corresponding query-fold TM_{\max} -score is smaller for fold1 (Fig. 3B) than for fold2 (Fig. 3C). Note, however, that classifications by CEP and TM_{\max} -score would always be consistent if the fold space is completely discrete, because then the TM_{\max} -scores of a query with fold1 and fold2 would be extremely different.

Estimating CEP requires the information on the empirical distribution of within-fold TM_{\max} -scores. When the number of domains in a fold is not very large, CEP estimates may be inaccurate. For example, when the query-fold TM_{\max} -score is lower than all observed within-fold TM_{\max} -scores, one assigns $CEP = 0$, although the true CEP must be > 0 . To minimize this problem, we can fit the observed within-fold TM_{\max} -scores (\mathbf{x}) by a Gaussian mixture model (GMM) and then estimate CEP using the fitted continuous distribution (see Materials and Methods).

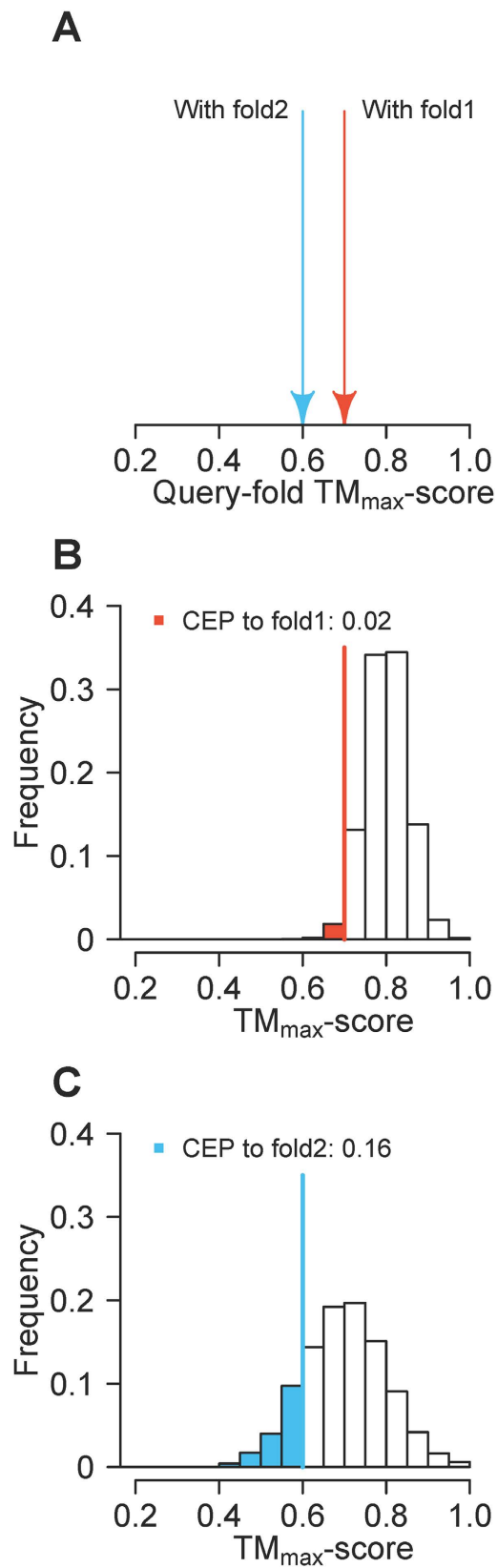


Figure 3. A hypothetical example contrasting fold classifications by TM_{\max} -score and CEP. (A) query-fold TM_{\max} -scores of a query to two folds. **(B)** Frequency distribution of within-fold1 TM_{\max} -scores. **(C)** Frequency distribution of within-fold2 TM_{\max} -scores. In **(B,C)**, CEP is the area left to the vertical line under the distribution.

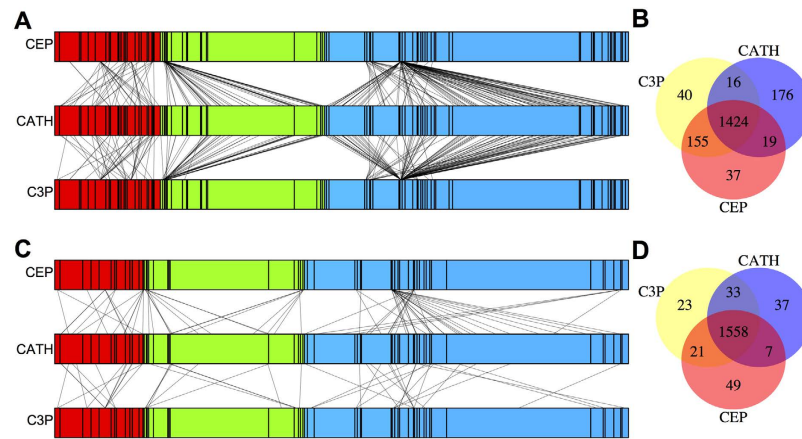


Figure 4. CEP and C3P classifications of 10% of randomly picked domains from large folds in CATH. (A) Reclassifications by local TM_{max} -score-based CEP and C3P. A vertical bar corresponds to a fold, and its width is proportional to the number of domains in the fold. Domains within a fold are sorted by length ascending. The red, green, and blue colors represent folds from α , β and $\alpha\beta$ classes in CATH, respectively. A line linking vertical bars of two horizontal bars connects the same domain that is classified into different folds by the two different methods, although a vertical bar with the same width of a line denotes 20 domains. This discrepancy is introduced for clearer visualization. (B) Venn diagram of classifications by CATH and local TM_{max} -score-based CEP and C3P. (C) Reclassifications by global TM_{max} -score-based CEP and C3P. (D) Venn diagram of classifications by CATH and global TM_{max} -score-based CEP and C3P. In (A,C), results from the first of the 30 sets of queries are presented. In (B,D), average results from the 30 sets of queries are presented.

The use of GMM is inspired by the fact that (i) the distribution of within-fold TM_{max} -scores usually has multiple modes presumably due to the existence of multiple superfamilies in the fold and (ii) that GMM is highly flexible and fits almost any distribution. The parameters of the GMM are inferred under the Bayesian framework with model settings proposed by Richardson and Green³⁹. With the posterior distributions of the parameters, the posterior predictive distribution of TM_{max} -scores $f(\tilde{x}|\mathbf{x})$ is estimated using a Monte Carlo method, where $f(\tilde{x}|\mathbf{x})$ denotes the probability density of a potentially observed TM_{max} -score (\tilde{x}) given the observed TM_{max} -scores (\mathbf{x}). CEP is then determined using $f(\tilde{x}|\mathbf{x})$ as if the potentially observed TM_{max} -scores are actually observed. We refer to this CEP estimate as the cumulative posterior predictive probability (C3P).

Domain classification using CEP and C3P with local TM_{max} -scores. In this section, we use CEP and C3P with local TM_{max} -scores for classification. This treatment is consistent with the focus on substructure similarity between domains in the study of fold space continuity. For the same 30 random sets of queries previously used, the CEP classification differs from the CATH classification in 12% of cases on average (Fig. 1). We refer to the query domains that have different classifications by CEP and CATH as reclassified domains. The majority of these domains are attracted to a small number of folds in CEP classification (Fig. 4A). These folds tend to have large structure heterogeneities (i.e., with low averages and high standard deviations of within-fold TM_{max} -scores). In fact, the structure heterogeneity of a fold and the number of reclassified domains attracted to the fold are significantly correlated (Fig. 5A,B). By contrast, there is no significant correlation between the number of reclassified domains attracted to a fold and the fold size (Fig. 5C).

On average, C3P classification differs from the CATH classification in 12% of cases (Fig. 1), and the reclassified queries by C3P are also attracted to a small number of folds (Fig. 4A). As expected, the general patterns of C3P reclassifications are similar to what was observed in CEP reclassifications (Fig. S1A–C). Averaged over the 30 query sets, 97% of the queries are classified consistently by CEP and C3P (Fig. 4B). Moreover, 81% of the reclassifications by CEP are reclassified the same way by C3P, and 79% of the reclassifications by C3P are reclassified the same way by CEP (Fig. 4B).

Domain classification using CEP and C3P with global TM_{max} -scores. Let us now use global TM_{max} -scores in CEP and C3P classifications. For the 30 sets of queries, CEP and C3P classifications differ from CATH classification for 3.4% and 4.3% of cases (Fig. 1), suggesting that the impact of fold space continuity on fold classification is substantially reduced if global structure similarity is considered. Similar to what was observed in the previous section, the number of domains reclassified into a fold correlates with measures of the fold's structure heterogeneity (Fig. 5D,E; Fig. S1D,E), but is uncorrelated with the number of domains in the fold (Fig. 5F; Fig. S1F). CEP and C3P classifications are consistent with each other for 97% of cases (Fig. 4D). Thirty percent of the reclassifications by CEP are reclassified the same way by C3P, while 48% of the reclassifications by C3P are reclassified the same way by CEP (Fig. 4D).

Why the reclassification rate is lower under global than under local TM_{max} -scores. Considering structure space continuity leads to reclassifications of only ~4% of domains under global TM_{max} -scores, compared with ~12% under local TM_{max} -scores. This increased reclassification rate under local TM_{max} -scores is potentially

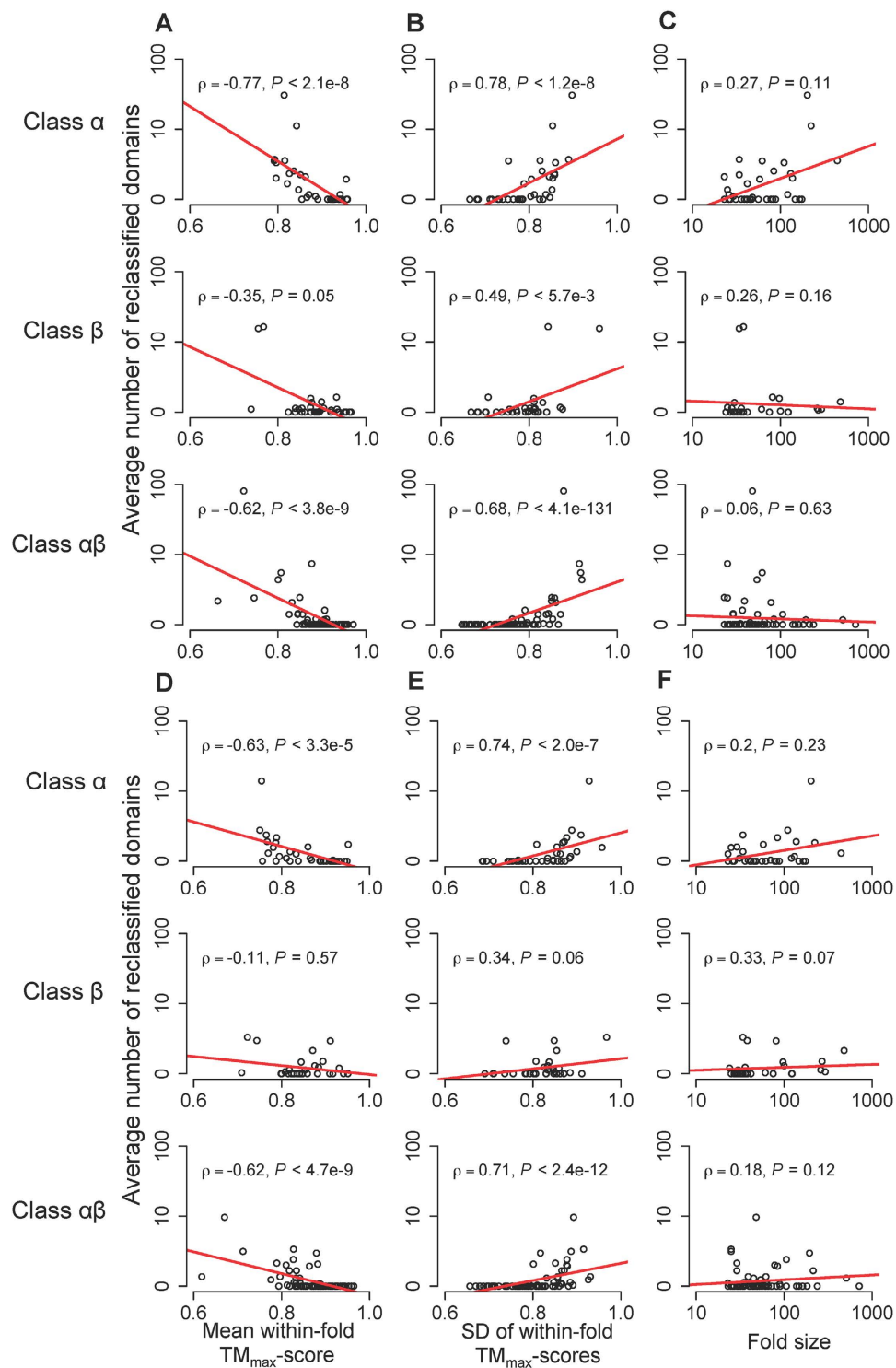


Figure 5. Rank correlations between various properties of a fold and the number of domains reclassified into the fold by (A–C) local TM_{\max} -score-based CEP and (D–F) global TM_{\max} -score-based CEP. The lines show linear regressions. ρ , Spearman's rank correlation coefficient.

due to the Russian doll effect³, which refers to the phenomenon that one domain resembles a substructure of another domain across folds. For example, domain 1lq7A00 (CATH Id) is classified into fold 1.20.1270 by CATH. However, this query domain has a local TM_{\max} -score of 0.73 with both folds 1.20.1270 (Fig. 6A) and 1.20.120 (Fig. 6B), because the query is highly similar to part of the domain structures in fold 1.20.120 (Fig. 6B). As a result, the query is classified by both CEP and C3P into fold 1.20.120, which is more heterogeneous in structure (mean within-fold TM_{\max} -score = 0.82) than fold 1.20.1270 (mean within-fold TM_{\max} -score = 0.87). By contrast,

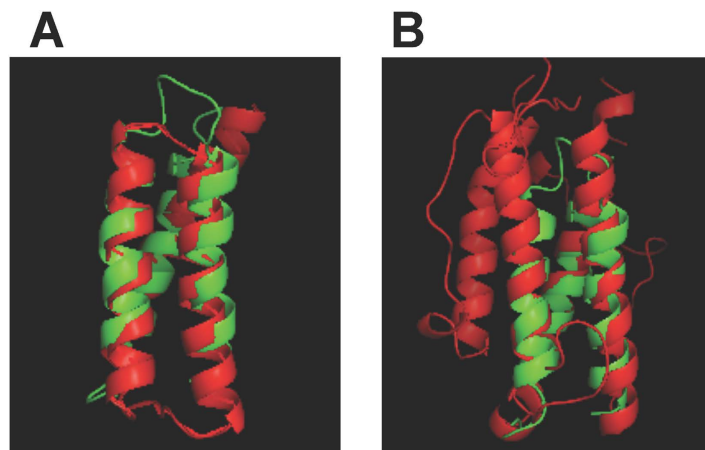


Figure 6. Structure alignments of a CATH domain based on local TM_{\max} -scores. The green structure shows the query domain (CATH id = 1lq7A00). The query is reclassified into fold 1.20.120 from 1.20.1270 by CEP based on local TM_{\max} -scores. (A) Structure alignment with 2oo2A00 (red) of fold 1.20.1270 (query-fold TM_{\max} -score = 0.73). (B) Structure alignment with 2qe9A01 (red) of fold 1.20.120 (query-fold TM_{\max} -score = 0.73).

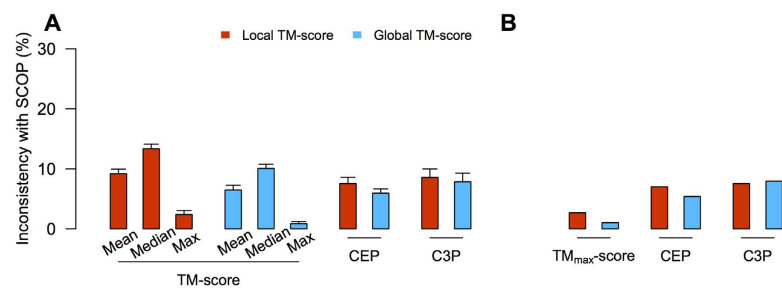


Figure 7. Fractions of fold-level domain structure classifications by various TM -scores, CEP, and C3P that are inconsistent with the SCOP classification for (A) 30 sets of 10% randomly chosen domains from CATH v3.5.0 and (B) 7050 newly added domains in SCOP v1.75 since v1.73. Error bars show one standard deviation.

the query has a much smaller global TM_{\max} -score with fold 1.20.120 (0.48) than fold 1.20.1270 (0.70), and thus is classified into fold 1.20.1270 by CEP/C3P, consistently with the CATH classification.

Classification of newly solved domain structures in CATH by CEP and C3P. The query domains used in previous sections were randomly chosen from the 17,043 representative domains in CATH v3.5.0. These queries are unbiased samples and their reclassification results by CEP and C3P represent the overall impact of structure space continuity on fold classification. However, if we need to classify a newly solved domain structure into the current CATH fold hierarchy, how big of an impact would the use of CEP or C3P have? To address this question, we took the 17,043 representative domains from the 141 large folds in CATH v3.5.0 (available from Sept., 2011) as the initial classification. In CATH v4.0.0 (available from March 2013), these large folds contain 8,280 representative domains that did not exist in CATH v3.5.0. We now use these 8,280 newly added domains as queries. When the local TM_{\max} -score is used, CEP (or C3P) classifications differ from CATH classifications for 20.8% (or 20.5%) of these 8,280 domains (Fig. 1B). When the global TM -score is used, CEP (or C3P) classifications differ from CATH classifications for 4.0% (or 4.8%) of these domains (Fig. 1B). These values are higher than the corresponding numbers for the 30 sets of randomly picked domains. This is potentially because folds were initially defined by some of the 17,043 domains, whereas a large fraction of the newly solved 8,280 domains may exist in uncharted regions between the initially defined folds. Consequently, such domains were assigned as boundary members of various folds by CATH, and thus tend to be reclassified by CEP/C3P.

Classification of domains in the SCOP database. We next examined the fold classification in SCOP, another widely used protein classification system. Using the same criteria as used for CATH, we generated 30 sets of 606 representative queries from 89 large folds in SCOP version 1.73. Local TM_{\max} -score-based fold classification is largely consistent with the SCOP classification, with only 2.4% of inconsistent cases (Fig. 7). This number decreases further to 0.9% under global TM_{\max} -score-based classification. The frequency of inconsistent classification is much greater when the query-fold similarity is measured by either the mean or median TM -score instead of TM_{\max} -score (Fig. 7). These results indicate that, similar to CATH, SCOP fold classification can be automated using query-fold TM_{\max} -scores.

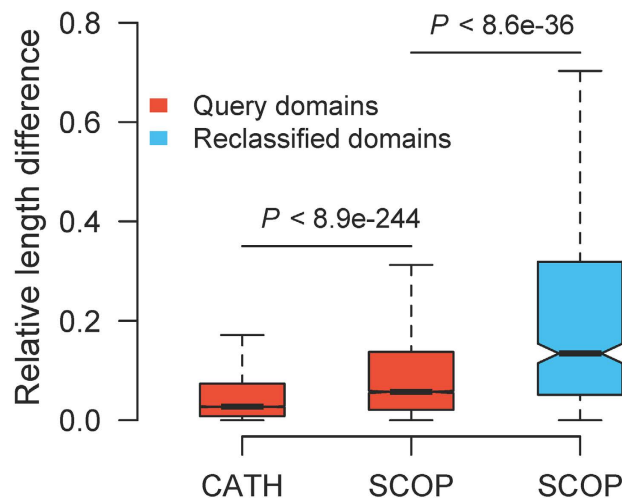


Figure 8. Relative length difference between domains within folds. The relative length difference is defined as the absolute length difference between a query from a fold and its best-matched domain (i.e., with the highest TM-score) in the fold, divided by the length of the shorter of the two. Domains included in the CATH bar are 16,173 nonredundant domains from the 30 sets of random queries in CATH v3.5.0. Domains included in the red SCOP bar are 6,134 nonredundant domains from the 30 sets of random queries in SCOP v1.73. Domains included in the blue SCOP bar are 456 queries reclassified by global TM_{\max} -score-based CEP. In this bar plot, the notch indicates the median and the bar corresponds to the interquartile range (IQR), covering from the first quartile to the third quartile of the sample. The two whiskers of the bar show the minimum value not smaller than the 1st quartile minus 1.5 times IQR and the maximum value not greater than the 3rd quartile plus 1.5 times IQR, respectively. *P* values are from Mann-Whitney *U* tests.

For the same 30 random sets of queries, the local TM_{\max} -score-based and global TM_{\max} -score-based CEP classifications differ from the SCOP classification for an average of 7.6% and 5.9% of queries, respectively (Fig. 7). These numbers become 8.6% and 7.8%, respectively, for local and global TM_{\max} -score-based C3P classifications, respectively (Fig. 7).

By comparing SCOP versions 1.73 (available from Nov. 2007) and 1.75 (available from June 2009 and the most updated version), we found that 7050 representative domains were added into the 89 large folds in version 1.75 since version 1.73. These most recent additions to SCOP were subject to CEP and C3P classifications. The local and global TM_{\max} -score-based CEP classifications of these domains are inconsistent with the SCOP classification for 7.0% and 5.4% of the cases, respectively. These numbers become 7.5% and 8.0%, respectively, under C3P.

Reclassifications are rarer for SCOP than for CATH except under global TM_{\max} -score-based CEP and C3P (Figs 1 and 7). The SCOP data used here comprise 89 large folds and 65% of the total 9,964 representative domains in v1.73, whereas the CATH data consist of 141 large folds and 82% of the total 21,309 representative domains in v3.5.0. The sparser SCOP data than CATH data may render the classification more straightforward for the former than the latter. Intriguingly, however, global TM_{\max} -score-based CEP and C3P classifications are less consistent with SCOP than CATH classifications. To identify the underlying reason, we focus on the CEP classifications of the 6,134 non-redundant queries in the 30 SCOP sets. Each query has an original fold assigned by SCOP. The domain used to calculate query-original fold TM_{\max} -score is referred to as the partner domain. The relative length difference between the query and the partner domain is defined by the absolute value of their length difference divided by the shorter length. We found the relative length difference significantly greater for SCOP than CATH queries (Fig. 8). Because length difference reduces global TM_{\max} -scores, query-original fold global TM_{\max} -scores are reduced more drastically for SCOP than CATH queries, resulting in more reclassifications for the former than the latter. Indeed, reclassified SCOP queries tend to have larger relative length differences with their partner domains than average SCOP queries (Fig. 8).

Domain classification using CEP with HHsuite. HHsuite package^{40,41} is widely used to predict protein fold from sequences⁴². Therefore, it is important to examine its sensitivity to fold space continuity. To this end, we used HHsuite to classify the new CATH domains into the existing folds. HHsuite first generates a hidden Markov model (HMM) for each protein sequence, and then aligns HMMs with two alternative dynamic programming algorithms that are derived respectively from Smith-Waterman⁴³ and Needleman-Wunsch⁴⁴ algorithms. For each alignment, three quantities, Probability, *P*-value, and Raw score, may be used for fold classification. The Raw score measures the sequence similarity of two proteins. The *P*-value is the probability that an alignment of non-homologous proteins will score at least the observed Raw score. The Probability measures the probability that the aligned proteins are homologous, by considering both the Raw score and the similarity of the predicted secondary structures of the proteins. For the newly solved CATH domains, the classifications based on the six quantities (i.e., two alignments each with three scores) differ from the CATH classification in only 2–3% of cases (Fig. S2). These numbers increase to 10–14% when CEP is used with the six quantities (Fig. S2). Thus, fold space continuity affects HHsuite-based fold classification.

Discussion

In this work, we first showed that the fold classification in CATH is highly similar to the classification by the query-fold TM_{\max} -score, especially the global TM_{\max} -score. Considering fold space continuity, we developed the CEP and C3P methods to classify domain structures into existing folds using both query-fold TM_{\max} -scores and within-fold TM_{\max} -scores. When substructure similarity is concerned, fold classification is substantially influenced by the structure space continuity (12–20.8%). This conclusion also holds when the CEP uses HHsuite scores instead of TM-scores. Therefore, it is generally not legitimate to ignore this continuity under such scenarios. By contrast, when overall structure similarity is concerned, fold space continuity has only minor impacts on fold classification (3.4–4.8%) and thus may be ignored. The above results may have important implications for protein function prediction using structure similarity, because similar functions may require substructure similarity but not necessary global structure similarity. In other words, considering fold structure continuity may improve protein function prediction.

Under the global TM_{\max} -score, considering fold space continuity leads to the reclassification of 5–8% SCOP domains, compared to 3–4% of CATH domains. This increased reclassification rate for SCOP domains is potentially due to the stronger Russian doll effect within SCOP folds than CATH folds, indicated by the higher within-fold length heterogeneity in SCOP than CATH (Fig. 8). This renders the global query-original fold TM_{\max} -score lower for SCOP queries than CATH queries, prompting more reclassifications for the former than the latter. The higher length heterogeneity in SCOP than in CATH may be due to different protocols and tools used in their classifications.

We found that the classification using global query-fold TM_{\max} -scores is inconsistent with CATH classification for only 1% of cases, confirming that CATH classifies a new domain based on its best match to existing members of various folds. It is clear that this way of classification will result in the problem that some domains of the same fold are less similar to one another than to domains from other folds, which is observed in CATH³³. For example, domains A and B with low similarity to each other may be classified into the same fold because of their respective high similarities to some existing members in the fold. Non-transitive domain pairs such as A and B were observed previously^{3,13}, but its prevalence and impact on classification in CATH were unclear. Unlike the query-fold TM_{\max} -score, the query-fold TM_{mean} -score is influenced by the non-transitive domain pairs within a fold. The classification using TM_{mean} -score differs from CATH for ~20% of cases. The substantial rise in inconsistency suggests that non-transitive domain pairs within a fold are quite common in CATH.

As mentioned, two types of methods have been developed to classify domain structures into folds. The first type is similar to TM_{\max} -score and does not consider the impact of fold space continuity^{20–27}. The second type is based on the machine learning approach^{28–31} and is trained with within-fold domain pairs from multiple folds. However, pooling domain pairs from many folds for training ignores the among-fold variation in within-fold structure heterogeneity, by which fold space continuity affects current classifications. One might think that training the classifiers with individual folds can solve this problem, but it is infeasible because of small samples of most folds that cause overfitting of the classifiers with large numbers of parameters. Interestingly, although the classifiers neglect fold space continuity, their classification results are still substantially (~20%) different from current fold classifications. This is likely due to the uses of non-transitive domain pairs to train the classifiers. Overall, CEP and C3P are unique in that they explicitly consider structure space continuity in fold classification. In addition, C3P is based on Bayesian hierarchical models that alleviate overfitting.

In summary, we have developed CEP and C3P to estimate the impact of fold space continuity on current fold classifications. The inconsistencies between CEP/C3P and current hierarchical classifications in CATH and SCOP demonstrate a substantial impact of structure continuity on fold classification when local structure similarity is considered. By contrast, for questions that concern global structure similarities, the current fold classifications are largely valid. In our analysis, we classified query domains into existing folds, which were established without considering fold space continuity. In the future, it would be interesting to develop model-based clustering of all domains where the number of folds and memberships in each fold are both probabilistic.

Methods

Protein structure similarity score. TM-score defined below is used to assess the structural similarity between two protein structures. $TM\text{-score} = \frac{1}{L} \left[\sum_{i=1}^{L_{\text{ali}}} \frac{1}{1 + d_i^2 / d_0^2} \right]_{\text{max}}$, where L is the length of the shorter protein (local TM-score) or mean length of the two proteins being compared (global TM-score), L_{ali} is the number of equivalent residues in the two proteins, d_i is the distance of the i th pair of the equivalent residues between the two superposed structures, $d_0 = 1.24^3 / L - 15 - 1.8$ is used to normalize the TM-score so that the average magnitude of the TM-score for random protein pairs is independent of the size of the proteins, and “max” indicates the highest value among all possible superpositions. TM-score ranges in (0, 1] with a higher value indicating a higher similarity. TM-scores between two domains are calculated using the TM-align software³⁴.

Fold recognition using HHsuite. The HHsuite package was used to measure structure similarity between two protein sequences. For each protein alignment, Probability, P -value, and Raw score calculated by HHsuite were respectively used to measure structure similarity. HHsuite provides two alternative algorithms of dynamic programming, derived from Smith-Waterman and Needleman-Wunsch algorithms, respectively. We considered each of these two algorithms, coupled with default values for all other parameters except that realignment was not allowed due to its high computational cost.

Initial classifications and query domains. From CATH v4.0.0, we collected 23,682 representative single domains with mutual sequence identities $\leq 60\%$ and lengths ≥ 40 residues using CD-Hit⁴⁵. Among them, 21,309 representative domains existed in an older version of CATH (v3.5.0). These 21,309 domains are from 1,158 folds

in CATH v3.5.0. A total of 141 of these folds each have at least 25 domains. From each of these 141 large folds, we randomly sampled 10% of domains; these 1,635 queries sampled were subjected to classification by other methods. The remaining 15,408 domains in the 141 folds constitute the initial fold classification. This procedure was repeated 30 times, generating 30 random sets of queries. To examine the CATH classifications of newly solved domain structures, representative domains of the 141 large folds in CATH v3.5.0 were used as the initial classification, whereas the 8,280 domains newly added to the 141 folds in CATH v4.0.0 were queries. With the same criterion, 6,476 representative domains in 89 large folds were collected from SCOP v1.73. Using only the large folds, 30 sets of query domains were randomly picked. Each of the sets contained 606 queries, and the other 5,870 domains in large folds were treated as the initial classifications. A total of 7,050 domains newly added to the 89 folds in SCOP v1.74 since v.1.73 were identified as newly solved queries.

Gaussian mixture model and posterior predictive distribution. The observed within-fold TM_{\max} -scores for a fold are denoted as $\mathbf{x} = (x_1, \dots, x_N)$, which are assumed to have been independently drawn from a mixture of k Gaussian components. N is the number of representative domains in the fold. The probability of observing an x is

$$p(x|k, \pi, \mu, \sigma^2) = \sum_{i=1}^k \pi_i f(x; \mu_i, \sigma_i^2) \quad (1)$$

where μ_i , σ_i^2 , and π_i are the mean, variance, and mixture proportion of component i . Latent allocation data are referred to as $z = (z_1, \dots, z_N)$, in which z_i specifies the mixture component to the observation x_i . Here, z_i 's are independently and identically distributed samples from the following probability mass function (PMF).

$$p(z_i = j|\pi, \mu, \sigma^2) = \pi_j. \quad (2)$$

Conditional on the allocation value z_i , the observed x_i is a random number from the following Gaussian probability density function.

$$p(x_i|z_i = j, \pi, \mu, \sigma^2) = p(x_i; \mu_j, \sigma_j^2) = f(x_i; \mu_j, \sigma_j^2) = \frac{1}{\sqrt{2\pi\sigma_j^2}} e^{-\frac{(x_i - \mu_j)^2}{2\sigma_j^2}} \quad (3)$$

We assume the following priors of the parameters:

$$\pi|k \sim \text{Dirichlet}(\gamma_1, \dots, \gamma_k) \quad (4)$$

$$\mu_j \sim \text{Normal}(\xi, \kappa^{-1}) \quad (5)$$

$$\sigma_j^{-2} \sim \text{Gamma}(\alpha, \beta) \quad (6)$$

$$k \sim \text{Poisson}(\lambda) \quad (7)$$

We set $\gamma_i = 1$, $\xi = \text{median of observed } TM_{\max}\text{-scores of a fold}$, and $\kappa^{-1} = R^2$, where R is the difference between the maximum and minimum of \mathbf{x} . These parameters make the prior distributions of π and μ_j rather flat. We set $\alpha = 2$ and $\beta \sim \Gamma(g, h)$, which is a gamma distribution with the shape parameter $g = 0.2$ and rate parameter h equal to $10/R^2$, to express the belief that the σ_j^{-2} 's are similar. At last, k follows a Poisson distribution with parameter $\lambda = 1$. All the settings together render the priors weakly informative and thus allow observed TM_{\max} -scores to dominate the parameter inference. The joint prior probability can be written as

$$P(k, \pi, \mu, \sigma^{-2}|\alpha, \beta, \gamma, \xi, \kappa^{-1}, \lambda) = P(k|\lambda)P(\pi|k, \gamma)P(\sigma^{-2}|k, \alpha, \beta)P(\mu|k, \xi, \kappa^{-1}) \quad (8)$$

and therefore the joint posterior probability is

$$P(k, \pi, \mu, \sigma^{-2}|\mathbf{x}) \propto P(\mathbf{x}|k, \pi, \mu, \sigma^{-2})P(k, \pi, \mu, \sigma^{-2}|\alpha, \beta, \gamma, \xi, \kappa^{-1}, \lambda) \quad (9)$$

Let $\theta = (k, \pi, \mu, \sigma^{-2})$ and \tilde{x} denote unobserved TM_{\max} -scores of the fold. The posterior predictive distribution is

$$f(\tilde{x}|\mathbf{x}) = \int P(\tilde{x}, \theta|\mathbf{x})d\theta = \int P(\tilde{x}|\theta)P(\theta|\mathbf{x})d\theta \quad (10)$$

which is the probability density function (PDF) of potential query-fold TM_{\max} -scores (\tilde{x}) given the observed within-fold TM_{\max} -scores (\mathbf{x}).

Due to the lack of a closed form, θ 's are sampled from the posterior distribution $P(\theta|\mathbf{x})$ using reversible-jump Markov chain Monte Carlo implemented in the R package of miscF (<https://CRAN.R-project.org/package=miscF>). The simulation had 30,000 iterations, 5000 burn-in steps, and a thinning parameter of 5. Initial values unspecified previously are assigned automatically by the miscF package. Conditional on each θ , \tilde{x} is sampled from the Gaussian mixture $P(\tilde{x}|\theta)$. This model was used to develop the C3P method for fold classifications.

CEP/C3P package and data availability. Both CEP and C3P methods are implemented in the C3P package, which can be obtained at <http://www.umich.edu/~zhanglab/download.htm>. All CEP and C3P classifications analyzed in this work are accessible at the same site.

References

- Kolodny, R., Pereyaslavets, L., Samson, A. O. & Levitt, M. On the universe of protein folds. *Annu Rev Biophys* **42**, 559–582 (2013).
- Swindells, M. B., Orengo, C. A., Jones, D. T., Hutchinson, E. G. & Thornton, J. M. Contemporary approaches to protein structure classification. *Bioessays* **20**, 884–891 (1998).
- Orengo, C. A. *et al.* CATH—a hierarchic classification of protein domain structures. *Structure* **5**, 1093–1108 (1997).
- Cuff, A. L. *et al.* Extending CATH: increasing coverage of the protein structure universe and linking structure with function. *Nucleic Acids Res* **39**, D420–426 (2011).
- Andreeva, A. *et al.* Data growth and its impact on the SCOP database: new developments. *Nucleic Acids Res* **36**, D419–425 (2008).
- Cheng, H. *et al.* ECODE: an evolutionary classification of protein domains. *PLoS Comput. Biol.* **10**, e1003926 (2014).
- Sillitoe, I. *et al.* New functional families (FunFams) in CATH to improve the mapping of conserved functional sites to 3D structures. *Nucleic Acids Res* **41**, D490–498 (2013).
- Caetano-Anolles, G. & Caetano-Anolles, D. An evolutionarily structured universe of protein architecture. *Genome Res.* **13**, 1563–1571 (2003).
- Wang, M. & Caetano-Anolles, G. The evolutionary mechanics of domain organization in proteomes and the rise of modularity in the protein world. *Structure* **17**, 66–78 (2009).
- Grishin, N. V. Fold change in evolution of protein structures. *J Struct Biol* **134**, 167–185 (2001).
- Orengo, C. A. *et al.* The CATH Database provides insights into protein structure/function relationships. *Nucleic Acids Res* **27**, 275–279 (1999).
- Harrison, A., Pearl, F., Mott, R., Thornton, J. & Orengo, C. Quantifying the similarities within fold space. *J Mol Biol* **323**, 909–926 (2002).
- Pascual-Garcia, A., Abia, D., Ortiz, A. R. & Bastolla, U. Cross-over between discrete and continuous protein structure space: insights into automatic classification and networks of protein structures. *PLoS Comput. Biol.* **5**, e1000331 (2009).
- Kolodny, R., Petrey, D. & Honig, B. Protein structure comparison: implications for the nature of ‘fold space’, and structure and function prediction. *Curr. Opin. Struct. Biol.* **16**, 393–398 (2006).
- Shindyalov, I. N. & Bourne, P. E. An alternative view of protein fold space. *Proteins* **38**, 247–260 (2000).
- Nepomnyachiy, S., Ben-Tal, N. & Kolodny, R. Global view of the protein universe. *Proc Natl Acad Sci USA* **111**, 11691–11696 (2014).
- Choi, I. G. & Kim, S. H. Evolution of protein structural classes and protein sequence families. *Proc Natl Acad Sci USA* **103**, 14056–14061 (2006).
- Osadchy, M. & Kolodny, R. Maps of protein structure space reveal a fundamental relationship between protein structure and function. *Proc Natl Acad Sci USA* **108**, 12301–12306 (2011).
- Fox, N. K., Brenner, S. E. & Chandonia, J. M. The value of protein structure classification information—Surveying the scientific literature. *Proteins* **83**, 2025–2038 (2015).
- Taylor, W. R. & Orengo, C. A. Protein structure alignment. *J Mol Biol* **208**, 1–22 (1989).
- Pearl, F. M. *et al.* A rapid classification protocol for the CATH Domain Database to support structural genomics. *Nucleic Acids Res* **29**, 223–227 (2001).
- Getz, G., Vendruscolo, M., Sachs, D. & Domany, E. Automated assignment of SCOP and CATH protein structure classifications from FSSP scores. *Proteins* **46**, 405–415 (2002).
- Rogen, P. & Fain, B. Automatic classification of protein structure by using Gauss integrals. *Proc Natl Acad Sci USA* **100**, 119–124 (2003).
- Harrison, A. *et al.* Recognizing the fold of a protein structure. *Bioinformatics* **19**, 1748–1759 (2003).
- Cheek, S., Qi, Y., Krishna, S. S., Kinch, L. N. & Grishin, N. V. 4SCOPmap: automated assignment of protein structures to evolutionary superfamilies. *BMC Bioinformatics* **5**, 197 (2004).
- Camoglu, O., Can, T., Singh, A. K. & Wang, Y. F. Decision tree based information integration for automated protein classification. *J. Bioinform. Comput. Biol.* **3**, 717–742 (2005).
- Fox, N. K., Brenner, S. E. & Chandonia, J. M. SCOPe: Structural Classification of Proteins—extended, integrating SCOP and ASTRAL data and classification of new structures. *Nucleic Acids Res* **42**, D304–309 (2014).
- Cheng, J. & Baldi, P. A machine learning information retrieval approach to protein fold recognition. *Bioinformatics* **22**, 1456–1463 (2006).
- Kim, Y. J. & Patel, J. M. A framework for protein structure classification and identification of novel protein structures. *BMC Bioinformatics* **7**, 456 (2006).
- Yan, R. X., Si, J. N., Wang, C. & Zhang, Z. DescFold: a web server for protein fold recognition. *BMC Bioinformatics* **10**, 416 (2009).
- Jo, T. & Cheng, J. Improving protein fold recognition by random forest. *BMC Bioinformatics* **15** Suppl 11, S14 (2014).
- Zhang, Y. & Skolnick, J. Scoring function for automated assessment of protein structure template quality. *Proteins* **57**, 702–710 (2004).
- Xu, J. & Zhang, Y. How significant is a protein structure similarity with TM-score = 0.5? *Bioinformatics* **26**, 889–895 (2010).
- Zhang, Y. & Skolnick, J. TM-align: a protein structure alignment algorithm based on the TM-score. *Nucleic Acids Res* **33**, 2302–2309 (2005).
- Kabsch, W. A discussion of the solution for the best rotation to relate two sets of vectors. *Acta Crystallographica Section A: Crystal Physics, Diffraction, Theoretical and General Crystallography* **34**, 827–828 (1978).
- Zemla, A. LGA: A method for finding 3D similarities in protein structures. *Nucleic Acids Res.* **31**, 3370–3374 (2003).
- Siew, N., Elofsson, A., Rychlewski, L. & Fischer, D. MaxSub: an automated measure for the assessment of protein structure prediction quality. *Bioinformatics* **16**, 776–785 (2000).
- Holm, L. & Sander, C. Dali: a network tool for protein structure comparison. *Trends Biochem. Sci.* **20**, 478–480 (1995).
- Richardson, S. & Green, P. J. On Bayesian analysis of mixtures with an unknown number of components (with discussion). *J. Roy. Stat. Soc. Ser. B. (Stat. Method.)* **59**, 731–792 (1997).
- Remmert, M., Biegert, A., Hauser, A. & Soding, J. HHblits: lightning-fast iterative protein sequence searching by HMM-HMM alignment. *Nat. Methods* **9**, 173–175 (2012).
- Soding, J. Protein homology detection by HMM-HMM comparison. *Bioinformatics* **21**, 951–960 (2005).
- Soding, J. & Remmert, M. Protein sequence comparison and fold recognition: progress and good-practice benchmarking. *Curr. Opin. Struct. Biol.* **21**, 404–411 (2011).
- Smith, T. F. & Waterman, M. S. Identification of common molecular subsequences. *J Mol Biol* **147**, 195–197 (1981).
- Needleman, S. B. & Wunsch, C. D. A general method applicable to the search for similarities in the amino acid sequence of two proteins. *J Mol Biol* **48**, 443–453 (1970).
- Fu, L., Niu, B., Zhu, Z., Wu, S. & Li, W. CD-HIT: accelerated for clustering the next-generation sequencing data. *Bioinformatics* **28**, 3150–3152 (2012).

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Author Contributions

J.X. and J.Z. conceived the research, designed the experiments, and wrote the manuscript. J.X. conducted the experiments and analyzed the data.

Additional Information

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