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N. Malod-Dognin — R. Andonov — N. Yanev

N° 7053

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A large, stylized grey 'R' with a horizontal bar underneath it, followed by the text 'apport de recherche' in a serif font.

*Rapport
de recherche*

Maximum Cliques in Protein Structure Comparison

N. Malod-Dognin^{*}, R. Andonov^{*}, N. Yanev^{† ‡}

Thème : Bio
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Abstract: Computing the similarity between two protein structures is a crucial task in molecular biology, and has been extensively investigated. Many protein structure comparison methods can be modeled as maximum clique problems in specific k -partite graphs, referred here as alignment graphs.

In this paper, we propose a new protein structure comparison method based on internal distances (DAST) which is posed as a maximum clique problem in an alignment graph. We also design an algorithm (ACF) for solving such maximum clique problems. ACF is first applied in the context of VAST, a software largely used in the National Center for Biotechnology Information, and then in the context of DAST. The obtained results on real protein alignment instances show that our algorithm is more than 37000 times faster than the original VAST clique solver which is based on Bron & Kerbosch algorithm. We furthermore compare ACF with one of the fastest clique finder, recently conceived by Östergård. On a popular benchmark (the Skolnick set) we observe that ACF is about 20 times faster in average than the Östergård's algorithm.

Key-words: protein structure comparison, maximum clique problem, k -partite graphs, combinatorial optimization.

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Les cliques maximum dans la comparaison des structures protéiques

Résumé : Calculer la similarité entre deux structures de protéines est une tâche cruciale de la biologie moléculaire, et a été étudiée intensément. De nombreuses méthodes de comparaison peuvent être modélisées sous forme de recherches de cliques maximum dans des graphes k -partis spécifiques, que nous appellerons graphes d'alignments.

Dans ce rapport, nous proposons une nouvelle méthode de comparaison de structures protéiques basée sur les distances internes (DAST), qui est formulée comme une recherche de cliques maximum dans un graphe d'alignement. Nous avons également conçu un algorithme (ACF) pour résoudre de tels problèmes de cliques. ACF est dans un premier temps appliqué dans le contexte de VAST, un logiciel largement utilisé au NCBI (National Center for Biotechnology Information), puis il est appliqué dans le contexte de DAST. Les résultats obtenus sur de véritables instances de comparaison de structures de protéines montrent que notre algorithme est plus de 37000 fois plus rapide que le solveur original de VAST, qui est basé sur l'algorithme de Bron et Kerbosch. Nous avons ensuite comparé ACF avec l'un des plus rapides algorithmes de recherche de clique maximum, récemment proposé par Östergård. Sur un jeu de test connu (l'ensemble de Skolnick), nous observons qu'ACF est en moyenne 20 fois plus rapide que l'algorithme d'Östergård.

Mots-clés : Comparaison de structures protéiques, problème de clique maximum, graphes k -partis, optimisation combinatoire.

1 Introduction

A fruitful assumption in molecular biology is that proteins of similar three-dimensional (3D) structures are likely to share a common function and in most cases derive from a same ancestor. Understanding and computing physical similarity of protein structures is one of the keys for developing protein based medical treatments, and thus it has been extensively investigated [8, 14]. Evaluating the similarity of two protein structures can be done by finding an optimal (according to some criterions) order-preserving matching (also called alignment) between their components. We show that finding such alignments is equivalent to solving maximum clique problems in specific k -partite graphs referred here as alignment graphs. These graphs could be very large (more than 25000 vertices and 3×10^7 edges) when comparing real protein structures. We are not aware of any previous specialized algorithm for solving the maximum clique problem in k -partite graphs. Even very recent general clique finders [10, 16] are oriented to notably smaller instances and are not able to solve problems of such size (the available code of [16] is limited to graphs with up to 1000 vertices).

For solving the maximum clique problem in this context we conceive an algorithm, denoted by *ACF* (for Alignment Clique Finder), which profits from the particular structure of the alignment graphs. We furthermore compare *ACF* to an efficient general clique solver [13] and the obtained results clearly demonstrate the usefulness of our dedicated algorithm.

1.1 The maximum clique problem

We usually denote an undirected graph by $G = (V, E)$, where V is the set of vertices and E is the set of edges. Two vertices i and j are said to be adjacent if they are connected by an edge of E . A clique of a graph is a subset of its vertex set, such that any two vertices in it are adjacent.

Definition 1 *The **maximum clique problem** (also called **maximum cardinality clique problem**) is to find a largest, in terms of vertices, clique of an arbitrary undirected graph G , which will be denoted by $MCC(G)$.*

The maximum clique problem is one of the first problem shown to be NP-Complete [9] and it has been studied extensively in literature. Interested readers can refer to [3] for a detailed state of the art about the maximum clique problem.

1.2 Alignment graphs

In this paper, we focus on grid alike graphs, which we define as follows.

Definition 2 *A $m \times n$ **alignment graph** $G = (V, E)$ is a graph in which the vertex set V is depicted by a $(m\text{-rows}) \times (n\text{-columns})$ array T , where each cell $T[i][k]$ contains at most one vertex $i.k$ from V (note that for both arrays and vertices, the first index stands for the row number, and the second for the column number). Two vertices $i.k$ and $j.l$ can be connected by an edge $(i.k, j.l) \in E$ only if $i < j$ and $k < l$. An example of such alignment graph is given in Fig 2a.*

It is easily seen that the m rows form a m -partition of the alignment graph G , and that the n columns also form a n -partition. In the rest of this paper we will

use the following notations. A successor of a vertex $i.k \in V$ is an element of the set $\Gamma^+(i.k) = \{j.l \in V \text{ s.t. } (i.k, j.l) \in E, i < j \text{ and } k < l\}$. $V^{i.k}$ is the subset of V restricted to vertices in rows $j, i \leq j \leq m$, and in columns $l, k \leq l \leq n$. Note that $\Gamma^+(i.k) \subset V^{i+1.k+1}$. $G^{i.k}$ is the subgraph of G induced by the vertices in $V^{i.k}$. The cardinality of a vertex set U is $|U|$.

1.3 Relations with protein structure similarity

From a general point of view, two proteins P_1 and P_2 can be represented by their ordered set of components N_1 and N_2 , and estimating their similarity can be done by finding the longest alignment between the elements of N_1 and N_2 . In our approach, such matchings are represented in a $|N_1| \times |N_2|$ alignment graph $G = (V, E)$, where each row corresponds to an element of N_1 and each column corresponds to an element of N_2 . A vertex $i.k$ is in V (i.e. matching $i \leftrightarrow k$ is possible), only if element $i \in N_1$ and $k \in N_2$ are compatible. An edge $(i.k, j.l)$ is in E if and only if (i) $i < j$ and $k < l$, for order preserving, and (ii) matching $i \leftrightarrow k$ is compatible with matching $j \leftrightarrow l$. A feasible matching of P_1 and P_2 is then a clique in G , and the longest alignment corresponds to a maximum clique in G . There is a multitude of alignment methods and they differ mainly by the nature of the elements of N_1 and N_2 and by the compatibility definitions between elements and between pairs of matched elements. At least two protein structure similarity related problems from the literature can be converted into clique problems in alignment graphs : the secondary structure alignment in VAST[6], and the Contact Map Overlap Maximization problem (CMO)[7].

VAST, or Vector Alignment Search Tool, is a software for aligning protein 3D structures largely used in the National Center for Biotechnology Information ¹. In VAST, N_1 and N_2 contain 3D vectors representing the secondary structure elements (SSE) of P_1 and P_2 . Matching $i \leftrightarrow k$ is possible if vectors i and k have similar norms and correspond either both to α -helices or both to β -strands. Finally, matching $i \leftrightarrow k$ is compatible with matching $j \leftrightarrow l$ only if the couple of vectors (i, j) from P_1 can be well superimposed in 3D-space with the couple of vectors (k, l) from P_2 .

CMO is one of the most reliable and robust measures of protein structure similarity. Comparisons are done by aligning the residues (amino-acids) of two proteins in a way that maximizes the number of common contacts (when two residues that are close in 3D space are matched with two residues that are also close in 3D space). We have already dealt with CMO in [1], but not by using cliques. Note that a maximum clique formulation in alignment graphs was proposed by Strickland et al. in [15], but this formulation differs from ours.

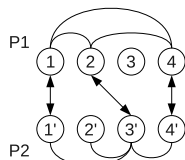
1.4 DAST: an improvement of CMO based on internal distances

One of the main drawback of CMO is that in order to maximize the number of common contacts, it also introduces some “errors” like aligning two residues that are close in 3D space with two residues that are remote, as illustrated in Fig 1. These errors could potentially yield alignments with big root mean square deviations (RMSD) which is not desirable for structures comparison.

¹<http://www.ncbi.nlm.nih.gov/Structure/VAST/vast.shtml>

To avoid such problems we propose DAST (Distance-based Alignment Search

Figure 1: An optimal CMO matching.



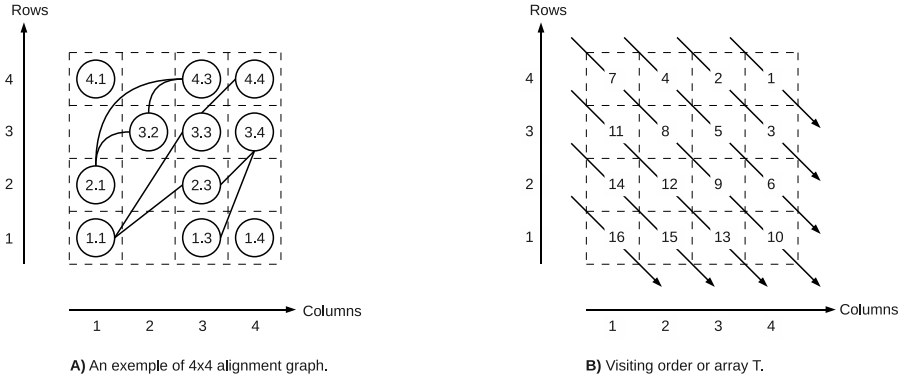
Two proteins (P_1 and P_2) are represented by their contact map graphs where the vertices corresponds to the residues and where edges connect residues in contacts (i.e. close). The matching “ $1 \leftrightarrow 1', 2 \leftrightarrow 3', 4 \leftrightarrow 4'$ ”, represented by the arrows, yields two common contacts which is the maximum for the considered case. However, it also matches residues 1 and 4 from P_1 which are in contacts with residues $1'$ and $4'$ in P_2 which are remote.

Tool), an alignment method based on internal distances which is modeled in an alignment graph. In DAST, the two proteins P_1 and P_2 are represented by their ordered sets of residues N_1 and N_2 . Two residues $i \in N_1$ and $k \in N_2$ are compatible if they come from the same kind of secondary structure elements (i.e. i and k both come from an α -helix, or from a β -strand) or if both come from a loop. Let us denote by d_{ij} (resp. d_{kl}) the euclidean distance between the α -carbons of residues i and j (resp. k and l). Matching $i \leftrightarrow k$ is compatible with matching $j \leftrightarrow l$ only if $|d_{ij} - d_{kl}| \leq \tau$, where τ is a distance threshold. The longest alignment in terms of residues, in which each couple of residues from P_1 is matched with a couple of residues from P_2 having similar distance relations, corresponds to a maximum clique in G . Since $RMSD = \sqrt{\frac{1}{N_m} \times \sum (|d_{ij} - d_{kl}|^2)}$, where N_m is the number of matching pairs “ $i \leftrightarrow k, j \leftrightarrow l$ ”, the alignments given by DAST have a RMSD of internal distances $\leq \tau$.

2 Branch and Bound approach

We have been inspired by [13] to propose our own algorithm which is more suitable for solving the maximum clique problem in the previously defined $m \times n$ alignment graph $G = (V, E)$. Let $Best$ be the biggest clique found so far (first it is set to \emptyset), and $|\overline{MCC}(G)|$ be an over-estimation of $|MCC(G)|$. By definition, $V^{i+1.k+1} \subset V^{i.k+1} \subset V^{i.k}$, and similarly $V^{i+1.k+1} \subset V^{i+1.k} \subset V^{i.k}$. From these inclusions and from definition2, it is easily seen that for any $G^{i.k}$, $MCC(G^{i.k})$ is the biggest clique among $MCC(G^{i+1.k})$, $MCC(G^{i.k+1})$ and $MCC(G^{i+1.k+1}) \cup \{i.k\}$, but for the latter only if vertex $i.k$ is adjacent to all vertices in $MCC(G^{i+1.k+1})$. Let C be a $(m+1) \times (n+1)$ array where $C[i][k] = |\overline{MCC}(G^{i.k})|$ (values in row $m+1$ or column $n+1$ are equal to 0). For reasoning purpose, let assume that the upper-bounds in C are exact. If a vertex $i.k$ is adjacent to all vertices in $MCC(G^{i+1.k+1})$, then $C[i][k] = 1 + C[i+1][k+1]$, else $C[i][k] = \max(C[i][k+1], C[i+1][k])$. We can deduce that a vertex $i.k$ cannot be in a clique in $G^{i.k}$ which is bigger than $Best$ if $C[i+1][k+1] < |Best|$, and this reasoning still holds if values in C are upper estimations. Another important inclusion is $\Gamma^+(i.k) \subset V^{i+1.k+1}$. Even if $C[i+1][k+1] \geq |Best|$, if $|\overline{MCC}(\Gamma^+(i.k))| < |Best|$ then $i.k$ cannot be in a clique in $G^{i.k}$ bigger than $Best$.

Figure 2: A 4×4 alignment graph and the visiting order of its array T



Our main clique cardinality estimator is constructed and used according to these properties. A function, $\text{Find_clique}(G)$, will visit the cells of T according to north-west to south-east diagonals, from diagonal “ $i+k = m+n$ ” to diagonal “ $i+k = 2$ ” as illustrated in Fig 2b. For each cell $T[i][k]$ containing a vertex $i.k \in V$, it may call $\text{Extend_clique}(\{i.k\}, \Gamma^+(i.k))$, a function which tries to extend the clique $\{i.k\}$ with vertices in $\Gamma^+(i.k)$ in order to obtain a clique bigger than $Best$ (which cannot be bigger than $|Best| + 1$). If such a clique is found, $Best$ is updated. However, $\text{Find_clique}()$ will call $\text{Extend_clique}()$ only if two conditions are satisfied : (i) $C[i+1][k+1] = |Best|$ and (ii) $|\overline{MCC}(\Gamma^+(i.k))| \geq |Best|$. After the call to $\text{Extend_clique}()$, $C[i][k]$ is set to $|Best|$. For all other cells $T[i][k]$, $C[i][k]$ is set to $\max(C[i][k+1], C[i+1][k])$ if $i.k \notin V$, or to $1 + C[i+1][k+1]$ if $i.k \in V$. Note that the order used for visiting the cells in T guaranties that

when computing the value of $C[i][k]$, the values of $C[i+1][k]$, $C[i][k+1]$ and $C[i+1][k+1]$ are already computed.

Array C can also be used in function `Extend_clique()` to fasten the maximum clique search. This function is a branch a bound (B&B) search using the following branching rules. Each node of the B&B tree is characterized by a couple $(Cli, Cand)$ where Cli is the clique under construction and $Cand$ is the set of candidate vertices to be added to Cli . Each call to `Extend_clique({i.k}, $\Gamma^+(i.k)$)` create a new B&B tree which root node is $(\{i.k\}, \Gamma^+(i.k))$. The successors of a B&B node $(Cli, Cand)$ are the nodes $(Cli \cup \{i'.k'\}, Cand \cap \Gamma^+(i'.k'))$, for all vertices $i'.k' \in Cand$. Branching follows lexicographic increasing order (row first). According to the branching rules, for any given B&B node $(Cli, Cand)$ the following cutting rules holds : (i) if $|Cli| + |Cand| \leq |Best|$ then the current branch cannot lead to a clique bigger than $|Best|$ and can be fathomed, (ii) if $|\overline{MCC}(Cand)| \leq |Best| - |Cli|$, then the current branch cannot lead to a clique bigger than $|Best|$, and (iii) if $|\overline{MCC}(Cand \cap \Gamma^+(i.k))| \leq |Best| - |Cli| - 1$, then branching on $i.k$ cannot lead to a clique bigger than $|Best|$. For any set $Cand$ and any vertex $i.k$, $Cand \cap \Gamma^+(i.k) \subset \Gamma^+(i.k)$, and $\Gamma^+(i.k) \subset G^{i+1.k+1}$. From these inclusions we can deduce two way of over-estimating $|\overline{MCC}(Cand \cap \Gamma^+(i.k))|$. First, by using $C[i+1][k+1]$ which over-estimate $|\overline{MCC}(G^{i+1.k+1})|$ and second, by over-estimating $|\overline{MCC}(\Gamma^+(i.k))|$. All values $|\overline{MCC}(\Gamma^+(i.k))|$ are computed once for all in `Find_clique()` and thus, only $|\overline{MCC}(Cand)|$ needs to be computed in each B&B node.

3 Maximum clique cardinality estimators

Even if the described functions depend on array C , they also use another upper-estimator of the cardinality of a maximum clique in an alignment graph. By using the properties of alignment graphs, we developed the following estimators.

3.1 Minimum number of rows and columns

Definition 2 implies that there is no edge between vertices from the same row or the same column. This means that in a $m \times n$ alignment graph, $|MCC(G)| \leq \min(m, n)$. If the numbers of rows and columns are not computed at the creation of the alignment graph, they can be computed in $O(|V|)$.

3.2 Longest increasing subset of vertices

Definition 3 An *increasing subset of vertices* in an alignment graph $G = \{V, E\}$ is an ordered subset $\{i_1.k_1, i_2.k_2, \dots, i_t.k_t\}$ of V , such that $\forall j \in [1, t-1]$, $i_j < i_{j+1}$, $k_j < k_{j+1}$. $LIS(G)$ is the longest, in terms of vertices, increasing subset of vertices of G .

Since any two vertices in a clique are adjacent, definition 2 implies that a clique in G is an increasing subset of vertices. However, an increasing subset of vertices is not necessarily a clique (since vertices are not necessarily adjacent), and thus $|MCC(G)| \leq |LIS(G)|$. In a $m \times n$ alignment graph $G = (V, E)$, $LIS(G)$ can be computed in $O(n \times m)$ times by dynamic programming. However, it is possible by using the longest increasing subsequence to solve $LIS(G)$ in $O(|V| \times \ln(|V|))$ times which is more suited in the case of sparse graph like in our protein structure comparison experiments.

Definition 4 The *longest increasing subsequence* of an arbitrary finite sequence of integers $S = "i_1, i_2, \dots, i_n"$ is the longest subsequence $S' = "i'_1, i'_2, \dots, i'_t"$ of S respecting the original order of S , and such that for all $j \in [1, t]$, $i'_j < i'_{j+1}$. By example, the longest increasing subsequence of "1,5,2,3" is "1,2,3".

For any given alignment graph $G = \{V, E\}$, we can easily reorder the vertex set V , first by increasing order of columns, and second by decreasing order of rows. Let's denote by V' this reordered vertex set. Then we can create an integer sequence S corresponding to the row indexes of vertices in V' . For example, by using the alignment graph presented in Fig2a, the reordered vertex set V' is $\{4.1, 2.1, 1.1, 3.2, 4.3, 3.3, 2.3, 1.3, 4.4, 3.4, 1.4\}$, and the corresponding sequence of row indexes S is "4, 2, 1, 3, 4, 3, 2, 1, 4, 3, 1". An increasing subsequence of S will pick at most one number from a column, and thus an increasing subsequence is longest if and only if it covers a maximal number of increasing rows. This proves that solving the longest increasing subsequence in S is equivalent to solving the longest increasing subset of vertices in G . Note that the longest increasing subsequence problem is solvable in time $O(l \times \ln(l))$ [5], where l denotes the length of the input sequence. In our case, this corresponds to $O(|V| \times \ln(|V|))$.

3.3 Longest increasing path

Definition 5 An *increasing path* in an alignment $G = \{V, E\}$ is an increasing subset of vertex $\{i_1.k_1, i_2.k_2, \dots, i_t.k_t\}$ such that $\forall j \in [1, t-1]$, $(i_j.k_j, i_{j+1}.k_{j+1}) \in E$. The longest increasing path in G is denoted by $LIP(G)$

As the increasing path take into account edges between consecutive vertices, $|LIP(G)|$, should better estimate $MCC(G)$. $|LIP(G)|$ can be computed in $O(|V|^2)$ by the following recurrence. Let $DP[i][k]$ be the length of the longest increasing path in $G^{i.k}$ containing vertex $i.k$. $DP[i][k] = 1 + \max_{i'.k' \in \Gamma^+(i.k)} (DP[i'][k'])$. The sum over all $\Gamma^+(i.k)$ is done in $O(|E|)$ time complexity, and finding the maximum over all $DP[i][k]$ is done in $O(|V|)$. This results in a $O(|V| + |E|)$ time complexity for computing $|LIP(G)|$.

Amongst all of the previously defined estimators, the longest increasing subset of vertices (solved using the longest increasing subsequence) exhibits the best performances and is the one we used for obtaining the results presented in the next section.

4 Results

All results presented in this section come from real protein structure comparison instances. Our algorithm, denoted by *ACF* (for Alignment Clique Finder), has been implemented in C and was tested in two different contexts: secondary structure alignments in VAST and residue alignments in DAST. *ACF* will be compared to Östergård’s algorithm[13] (denoted by *Östergård*) and to the original VAST clique solver which is based on Bron and Kerbosch’s algorithm[4] (denoted by *BK*). Note that *BK* is not a maximum clique finder but returns all maximal cliques in a graph.

4.1 Secondary structures alignments

This section illustrates the behavior of *ACF* in the context of secondary structure element (SSE) alignments. For this purpose we integrated *ACF* and *Östergård* (which code is freely available) in VAST. We afterwards compared them with *BK* by selecting few large protein chains having between 80 to 90 SSE’s (for smaller protein chains the running times of both *Östergård* and *ACF* are less than 0.01 sec.). Computations were done on a AMD at 2.4 GHz computer, and the corresponding running times are presented in **table 1**. We observe that *Östergård* is 4053 times faster than *BK*, and that *ACF* is about 9.3 times faster than *Östergård*. Although we have chosen large protein chains, the SSE alignment graphs are relatively small (up to 5423 vertices and 551792 edges). On such graphs the difference between *Östergård* and *ACF* performance is not very visible—it will be better illustrated on larger alignment graphs in the next section.

Table 1: Runing time comparison on secondary structure alignment instances

Instances		BK (sec.)	Östergård (sec.)	ACF (sec.)
1k32B	1n6eI	1591.89	1.42	0.09
1k32B	1n6fB	1546.78	0.01	0.01
1k32B	1n6fF	1584.25	0.14	0.02
1n6dD	1k32B	1373.35	0.06	0.01
1n6dD	1n6eI	1390.27	0.11	0.03
1n6dD	1n6fB	1328.85	0.65	0.06
1n6dD	1n6fF	1398.41	0.13	0.05

Runing time comparison of *BK*, *Östergård* and *ACF* on secondary structure alignment instances for long protein chains (containing from 80 to 90 SSE’s). *BK* is notably slower than the *Östergård*’s algorithm, which is slightly slower than *ACF*.

4.2 Residues alignment

In this section we compare *ACF* to *Östergård* in the context of residue alignments in DAST. Computations were done on a PC with an Intel Core2 processor at 3Ghz, and for both algorithms the computation time was bounded to 5 hours per instance. Secondary structures assignments were done by KAKSI[12], and the threshold distance τ was set to 3Å. The protein structures come from the well known Skolnick set, described in [11]. It contains 40 protein chains having from 90 to 256 residues, classified in SCOP[2] (v1.73) into five families.

Amongst the 780 corresponding alignment instances, 164 align protein chains from the same family and will be called “similar”. The 616 other instances align protein chains from different families and thus will be called “dissimilar”. Characteristics of the corresponding alignment graphs are presented in **table 2**.

Table 2: DAST alignment graphs characteristics

		array size	—V—	—E—	density	—MCC—
similar instances	min	97×97	4018	106373	8.32%	45
	max	256×255	25706	31726150	15.44%	233
dissimilar instances	min	97×104	1581	77164	5.76%	12
	max	256×191	21244	16839653	14.13%	48

All alignment graphs from DAST have small edge density (less than 16%). Similar instances are characterized by bigger maximum cliques than the dissimilar instances.

Table 3 compares the number of instances solved by each algorithm on Skolnick set. *ACF* solved 155 from 164 similar instances, while *Östergård* solved 128 instances. *ACF* was able to solve all 616 dissimilar instances, while *Östergård* solved 545 instances only. Thus, on this popular benchmark set, *ACF* clearly outperformed *Östergård* in terms of number of solved instances.

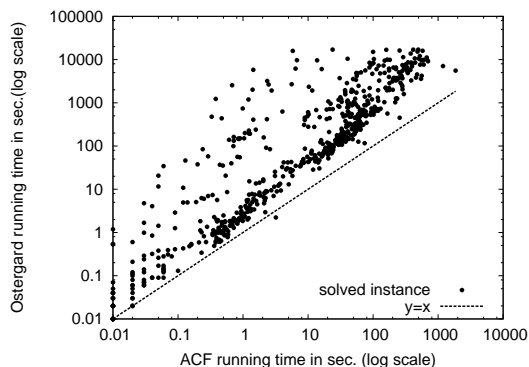
Table 3: Number of solved instances comparison

	Östergård	ACF
Similar instances (164)	128	155
Dissimilar instances (616)	545	616
Total (780)	673	771

Number of solved instances on Skolnick set: *ACF* solves 21% more similar instances and 13% more dissimilar instances than *Östergård*.

Figure 3 compares the running time of *ACF* to the one of *Östergård* on the set of 673 instances solved by both algorithms (all instances solved by *Östergård* were also solved by *ACF*). For all instances except one, *ACF* is significantly faster than *Östergård*. More precisely, *ACF* needed 12 hs. 29 min. 56 sec. to solve all these 673 instances, while *Östergård* needed 260 hs. 10 min. 10 sec. Thus, on the Skolnick set, *ACF* is about 20 times faster in average than *Östergård*, (up to 4029 times for some instances).

Figure 3: Running time comparison on the Skolnick set



ACF versus *Östergård* running time comparison on the set of the 673 Skolnick instances solved by both algorithms. The *ACF* time is presented on the x-axis, while the one of *Östergård* is on the y-axis. For all instances except one, *ACF* is faster than *Östergård*.

5 Conclusion and future work

In this paper we introduce a novel protein structure comparison approach DAST, for Distance-based Alignment Search Tool. For any fixed threshold τ , it finds the longest alignment in which each couple of pairs of matched residues shares the same distance relation ($\pm \tau$), and thus the RMSD of the alignment is $\leq \tau$. This property is not guaranteed by the CMO approach, which inspired initially DAST. From computation standpoint, DAST requires solving the maximum clique problem in a specific k -partite graph. By exploiting the peculiar structure of this graph, we design a new maximum clique solver which significantly outperforms one of the best general maximum clique solver. Our solver was successfully integrated into two protein structure comparison softwares and will be freely available soon. We are currently studying the quality of DAST alignments from practical viewpoint and compare the obtained results with other structure comparison methods.

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