The MAX-CMO problem and its representation Improving an efficiency of the heuristic search

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5th East Midlands Proteomics Workshop

2006-11-15

Outline



Problem definition

- Biological background
- Measure of similarity



Dual representation



Metaheuristic search efficiency

- Search method outline
- Possible improvements



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Protein comparison







- root mean square distance
- difference of distance matrices
- alignment of contact maps

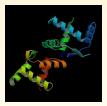
Contact map

Mathematical construct capturing the **proximity relation** between residues.



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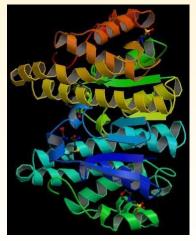
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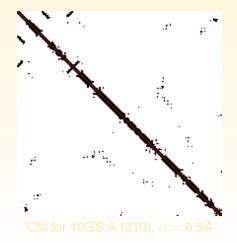


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Proximity relation depicted as 2D binary matrix



10GS (GLUTATHIONE S-TRANSFERASE P1-1)



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Proximity relation depicted as graph



Contact map graph

•
$$r_i \mathbf{R} r_j \Leftrightarrow \delta(r_i, r_j) \leqslant \alpha$$
,
 $\alpha \in [2\mathring{A}, 9\mathring{A}]$

• node \leftrightarrows residue

• edge \leftrightarrows contact

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Proximity relation depicted as graph

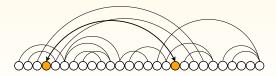


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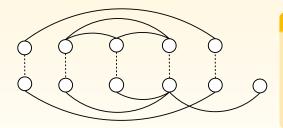




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MAX-CMO problem

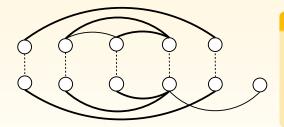


Definition

Maximum contact map overlap is an **alignment** of two proteins that **maximises** the structural **similarity**.

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MAX-CMO problem



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Graph isomorphism

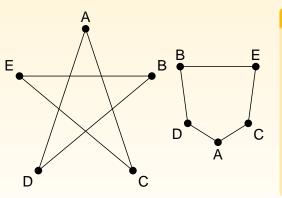


Figure: Isomorphic or not?

Graph isomorphism

Two graphs are isomorphic if there is a one-to-one correspondence between their nodes and there is an edge between two nodes of one graph if and only if there is an edge between the two corresponding nodes in the other graph.

Subgraph isomorphism Is G1 isomorphic to a subgraph of G2?

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Graph isomorphism

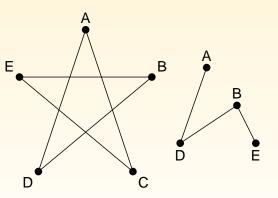


Figure: What about a subgraph?

Graph isomorphism

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Subgraph isomorphism

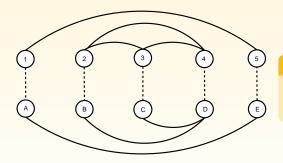
Is G1 isomorphic to a subgraph of G2?

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DUAL REPRESENTATION

Domain of a problem

Classical approach

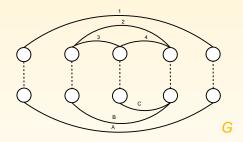


Representation

- protein alignment
- nodes matching

Domain of a solution

Line graph approach



Line graph

- a node of L(G) represents an edge of G
- two nodes of L(G) are adjacent if edges in G share a common node

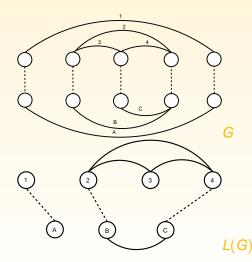
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Line graph approach



Line graph

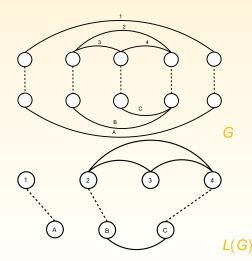
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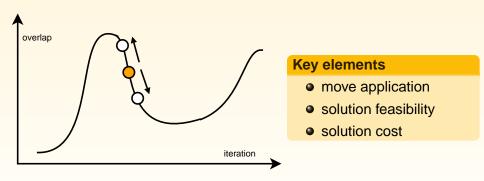
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Representation

- graph isomorphism
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Search strategy

Beyond random walk

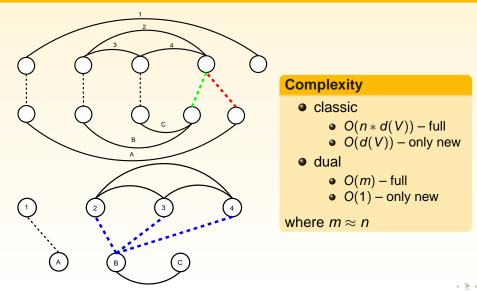


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METAHEURISTIC SEARCH EFFICIENCY POSSIBLE IMPROVEMENTS

How good the move is?

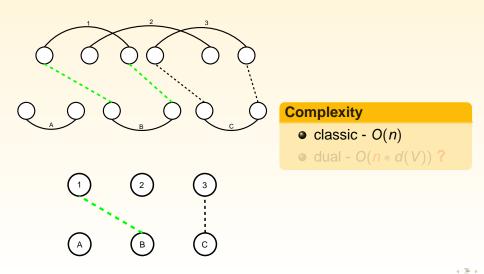
Determining the solution value



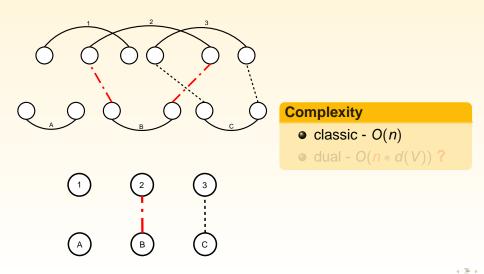
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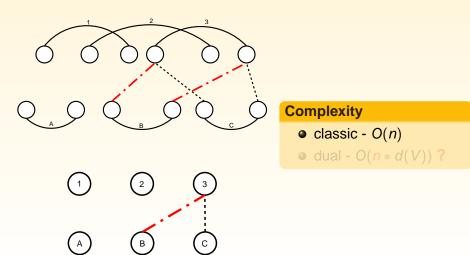
Checking the solution feasibility



Checking the solution feasibility

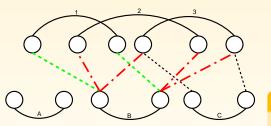


Checking the solution feasibility



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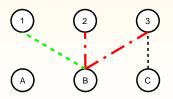
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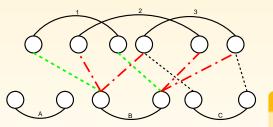
Complexity

• classic - O(n)

• dual - O(n * d(V)) ?

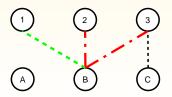


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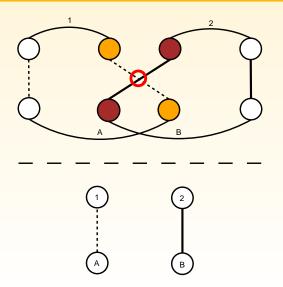
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Crossing conditions

Rules for feasibility checking



Consistent order

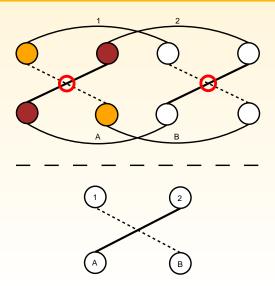
Relation of **succession** between **source** nodes should also hold for assigned **target** nodes.

Crossing rules

- inner crossing
- outer crossing
- empirical prof of correctness

Crossing conditions

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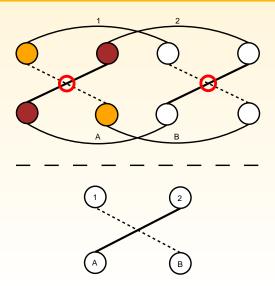
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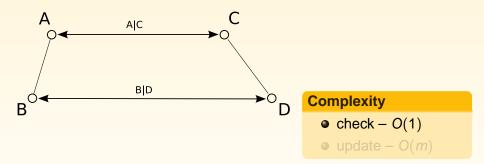
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The concept of limits

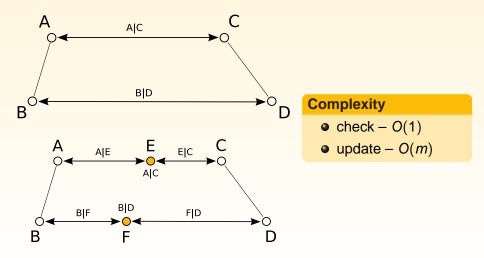
Improving the efficiency



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The concept of limits

Improving the efficiency



SUMMARY

Summary New algorithm vs. classical aproach

Computational complexity comparison

evaluation of solution O(1) vs. O(d(V))

feasibility check $O(m^2 * O(1) + O(m))$ vs. $O(n^2 * O(n))$ overall gain O(n) times faster

Future work

test on reference data sets

• make available in ProCKSi server

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Thank you!

Acknowledgements

This work was supported by **Marie Curie Action** MEST-CT-2004-7597 under the **Sixth Framework Programme** of the European Community.



SIXTH FRAMEWORK PROGRAMME



MARIE CURIE ACTIONS

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