Does inclusion of residue-residue contact information boost protein threading?

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Introduction

"Given an amino acid sequence, what is the protein three-dimensional structure?"

Background

Residue-residue contact map

Protein threading

Query protein

Template

Sequence alignment

ABCDEFGH

ABCDXYZGH

Challenges:

- Fold recognition
- Optimal query-template alignment

Research question?

Does contact map boost protein threading?

Methods

Query Sequence

COEKKCTEMKFKVCE

Hydropathy match

Profile match

Template Library

Pre-defined contact map

Al-eigen

CMO

Native contact map

Final model

F_score = F_domain + (CMO*10)

Results

(1) Performance on Test500 dataset

Target: 2f2ba (245 residues)

This work vs. MUSTER

Our (including contacts) predicted model superimposed to the native

TM-score: 0.33

Our (without contacts) predicted model superimposed to the native

TM-score: 0.28

(2) Performance on PSICOV150 dataset

Target: T0966 (494 residues)

This work vs. This work

Template selected by our work

TM-score: 0.8

Template selected by EigenTHREADER

TM-score: 0.19

(3) Performance on CASP13 dataset

Target: T0966 (494 residues)

This work vs. This work

Our predicted model superimposed to the native

EigenTHREADER predicted model superimposed to the native

Case study:

Challenges:

- Fold recognition
- Optimal query-template alignment

Conclusions

- Test500: contact + threading better than pure threading
- PSICOV150: contact + threading better than contact-assisted ab initio folding method
- Contact boosts threading.

Future works

- Does contact improve query-template alignment?
- Is distance more informative than contact in improving protein threading?

Reference