Role of protein dimerization

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Dimers and oligomers. Are they overrepresented?

R. Love et al. (2009)

W. Humphrey et al. (1996)

J. Thoden et al. (1997)

S. Roh et al. (2017)
The MAIN objective is to understand whether the **oligomeric structure** is **more evolutionary preferable** than monomeric.

General plan of the project is as follows:

1. detect core residues (CR) responsible for structure formation
2. determine how number of CR grows with protein length
3. compare obtained results with dimeric proteins
4. go further for larger oligomers (n-mers) to find the most preferable n

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Тихо-тихо ползи,
Улитка, по склону Фудзи...

Plan

analysis of monomeric protein families with similar structures

for CR in subunits interface
Steps:

1. Start to study related literature
Objectives:

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Steps:

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2. Select database containing information about proteins with similar structures and collect data
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![Diagram showing relationships between databases](Diagram.png)

- pfam
- CDD
- CATH
- SCOP

Evolutionary Classification of Protein Domains (ECOD)
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   ![Database Diagram]

   - pfam
   - CDD
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   **Evolutionary Classification of Protein Domains (ECOD)**

3. Find core residues!

   \[ S_i = - \sum_{j} P(\sigma_j) \log_2 P(\sigma_j) \]

   \[ P(\sigma_j) \] – probability of \( \sigma_j \) residue on \( i^{th} \) position
Steps:

4. Find relationship between number of core residues and length of aa chain
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5. Collect information about protein dimers and residues that form their subunits interface

G. Ackers et al. (2002)
Steps:

4. Find relationship between number of core residues and length of aa chain

5. Collect information about protein dimers and residues that form their subunits interface

6. Analyse the data

G. Ackers et al. (2002)
Thank you for your time!

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GitHub: https://github.com/troublov/BI_project_spring18