Bornberglab
Molecular Evolution and Bioinformatics

Bachelor thesis project

High-Throughput Computational Analysis of Protein Repeats

Incorporation of Modules into DomainWorld Infrastructure

Background: Domains are the evolving units of proteins, changing, re-arranging and being swapped and shared between different genes. Studying these changes requires the use of advanced computational tools. We have collected many of these tools in the Domain World server and are seeking to expand it.

Objectives: Incorporate an existing program suite into an existing website architecture. This will involve adding to an editing an existing web page and some interface with a server- Design and implement an aesthetically pleasing webpage interface. Optimize for efficiency and user experience as best as possible given normal aesthetic (*i.e.* color choices) and utility concerns (*i.e.* arrangement of website materials).

Requirements:

- Adequate skills in computer coding.
- Interest in server and website architecture and code efficiency

Methods:

- Web-page design
- Organization of program suites into existing architecture

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Selected Literature:

1) Dohmen E, Kremer L.P.M., Bornberg-Bauer E., Kemena C., “DOGMA: Domain-based transcriptome and proteome quality assessment” *Bioinformatics* **32,** 2577 (2016)
2) Merski, M. et al. “Self-analysis of repeat proteins reveals evolutionary conserved patterns” *BMC Bioinformatics* **21,** 179 (2020)