



Forschungsmodul

Conservation analysis of domain arrangements

Analyzing expression differences in isoforms with domain composition differences

Background: In the context of DOGMA we make use of different core sets to evaluate new proteomes based on conserved domain arrangements. As well in the domRates program we can see that a lot of domain arrangements are conserved.

Objectives:

- Analyse arrangements to determine their overall conservation between different clades.
- Analyse properties of conserved domain arrangements (e.g. length)
- Identify clades that are sufficiently different so that a specific core set would make sense.

Requirements:

- Python/Bash experience is required

Methods:

- Prepare a set of proteomes to analyse
- Extract domain arrangements and analyse them for conservation along clades

Supervision: Carsten Kemena, Hüfferstr. 1, Raum 17, c.kemena@uni-muenster.de, Molecular Evolution and Bioinformatics Group (<http://bornberglab.org/>).

Selected Literature:

<https://academic.oup.com/bioinformatics/article/32/17/2577/2450731>

<https://bmcevolbiol.biomedcentral.com/articles/10.1186/s12862-020-1591-0>