DomRates v2.0

Upgrading DomRates to increase resolution

Background: Protein domains are building blocks of proteins. The rearrangements of protein domains create new proteins with novel functions, therefore expand the protein repertoire. DomRates (https://domainworld.uni-muenster.de/programs/domrates/) infers these rearrangement events of protein domains for a given phylogeny and calculates the rates of the related events.

Objectives: In the current version, DomRates infers domain rearrangement events by checking six domain rearragenment events in four solutions: exact, ambiguous, non-ambiguous and complex solutions (Fig 1). The goal of this project is to upgrade DomRates to increase the resolution of "Complex solutions" defined by DomRates. To do so, new rearrangement events (eg. Insertion, deletion) can be added to the event set and/or events can be checked in a multistep fashion (i.e new arrangement as a result of two or more consecutive events).
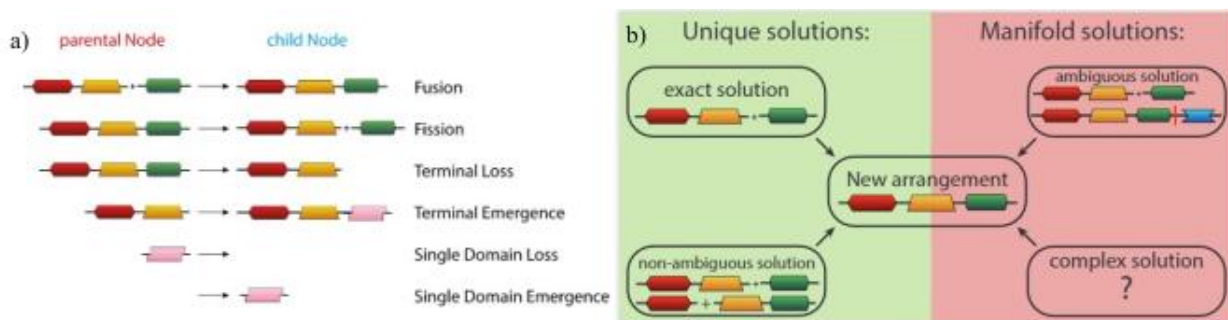

Figure 1: Currently defined domain rearrangement events (a) and solutions (b) by DomRates.

Requirements:

- General interest in protein evolution.
- Experience in C++

Methods:

- Develop and implement new algorithms.

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References:

Dohmen, E., Klasberg, S., Bornberg-Bauer, E., Perrey, S., & Kemena, C. (2020). The modular nature of protein evolution: domain rearrangement rates across eukaryotic life. BMC evolutionary biology, 20(1), 1-13.

Mistry, J., Chuguransky, S., Williams, L., Qureshi, M., Salazar, G. A., Sonnhammer, E. L., ... & Bateman, A. (2021). Pfam: The protein families database in 2021. Nucleic acids research, 49(D1), D412-D419.

Moore, A. D., Björklund, Å. K., Ekman, D., Bornberg-Bauer, E., & Elofsson, A. (2008). Arrangements in the modular evolution of proteins. Trends in biochemical sciences, 33(9), 444-451.