Title: Algorithms for Bioinformatics

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Bioinformatics gives rise to a wealth of computational problems, both fundamental and advanced. In this lecture, we will give a broad overview over typical tasks and computational challenges on the path between generation of biological data sets and their interpretation. Herein, we focus on discrete computational problems on (di-)graphs and sequences, avoiding statistical analysis for the most part. As some problems turn out to be NP-hard, we will employ approximation and parameterized algorithmics. To this end, a range of parameterized algorithmic techniques will be explored.

Pre-requisites: computational complexity basics

Selected Topics:
- sequence generation (sanger, NGS, …)
- read error correction
- assembly and scaffolding
- phylogenetic reconstruction, comparision
- gene-tree/species-tree reconciliation
- phylogenetic networks
- genomic rearrangement: transpositions, reversals
- genomic distances
- parameterized algorithms
- kernels
- parameterized techniques: color-coding, iterative compression, ...

Textbooks:
- Semple, Steel. Phylogenetics.
- Downey, Fellows. Parameterized Complexity
- Fertin, Labarre, Rusu, Tannier, Vialette. Combinatorics of Genome Rearrangements