

## Summary

Course “Discrete Biological Models” (Modelli Biologici Discreti)

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Goals of this course:

- learn about some **discrete models** used in bioinformatics: models that use **strings (= sequences)**, **graphs**, **integer matrices**, **permutations**, ...
- **recognize** situations where similar models can be applied, and **develop** simple models for given phenomena
- improve knowledge of **discrete mathematics** (combinatorics, strings, graphs)

For this we will need to:

- study in detail some **discrete models used in biology**
- study **basic discrete mathematics** (combinatorics, counting, fundamental sequences, strings, graphs, trees)
- understand **NP-completeness**

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## What did we do?

- What is **modeling**?
- Some basic **discrete maths**: basic counting principles, binomial coefficients, graphs
- **NP-completeness**

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## What did we do?

- Biological problem 1 – **Sanger Sequencing** (Fragment Assembly, classical)  
**models/techniques:**
  - SCS (simplistic, **NP-hard**) - **overlap graph** (SCS = **heaviest Hamiltonian path**);  
Greedy algorithm (**efficient, approximate**)
  - Reconstruction (more complex, **NP-hard**)
  - Multicontig (even more complex, **NP-hard**)

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## What did we do?

- Biological problem 2: **SBH (Sequencing by Hybridization)**  
**models/techniques:** de Bruijn graph, Euler path/tour, efficiently solvable (Hierholzer's algorithm)
- Biological problem 3:  
NGS-Sequencing: Fragment Assembly for Short Reads  
**models/techniques:** de Bruijn graph, Euler path/tour, efficiently solvable (Hierholzer's algorithm);  
N.B.: Problem needed adjustment before applying this technique!

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## What did we do?

- Biological problem 4: **Phylogenetic Reconstruction**  
**models/techniques:** phylogenetic trees (different types)
  - distance data: path metric = input distances; for certain inputs efficiently solvable
  - character data: PP, Maximum Parsimony, NP-hard