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#### Introduction

1.1	Α	few	biology	notions
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- 1.1.1 From genome to proteins, the Central Dogma
- 1.1.1.1 ADN, genome
- 1.1.1.2 ARN, transcriptome
- 1.1.1.3 Proteins, peptides, proteome, and interactions
- 1.1.2 Measuring the state of the living, sequencing
- 1.1.2.1 Genome sequencing
- 1.1.2.2 ARN sequencing, expression levels
- 1.1.2.3 ARN levels as a proxy for proteins expression levels
- 1.1.2.4 Differential analysis
- 1.1.3 ??? Phage display ???
- 1.1.4 ??? Mass spectrometry ???

#### 1.2 Some computer science elements

- 1.2.1 String
- 1.2.1.1 suffix tree
- 1.2.1.2 generalized suffix tree
- 1.2.1.3 generalized suffix array
- 1.2.2 Graph
- 1.2.2.1 Connectivity
- 1.2.2.2 Minimum cut
- 1.2.3 Combinatorial optimization
- 1.2.3.1 Dynamic programming
- 1.2.3.2 Decision trees, Branch and bound, Branch and cut
- 1.2.3.3 Linear programming, Mixed integer linear programming
- 1.2.4 Complexity
- 1.2.4.1 APX-difficulty

## String selection

- 2.1 Intro
- 2.1.1 Sequences
- 2.1.1.1 Two sets of sequences (PhD or ?? + proteome)
- 2.1.1.2 Equals two sets of small sequences (kmers)
- 2.1.2 Distance measure of two AA sequences
- 2.2 Algorithm
- 2.2.1 Encoding the two sets as generalized suffix arrays
- 2.2.2 Minimum-Maximum distance over length, and pruning
- 2.2.3 Mappings, profiles, and significance
- 2.3 Analysis
- 2.3.1 Performance
- 2.3.2 Significance
- 2.3.2.1 Pathways test
- 2.4 Biology, pretty please ?!

# Biological module discovery

- 3.1 Module introduction (topological module –connected– vs. aggregation module –stats–)
- 3.2 Mapping biological weights onto PPI networks
- 3.3 Maximum-Weight Connected Subgraph
- 3.3.1 Prize-Collecting Steiner Tree
- 3.3.2 Direct methods (Miranda-Alvarez)

# ??? Multi-modules discovery ???

- 4.1 Some methods find multiple modules
- 4.2 We want exact method
- 4.2.1 Linear program

# Cross-species biological module discovery

- 5.1 Cross-species modules
- 5.2 Maximum-Weight Cross-Connected Subgraph

# Difficulty of the Maximum-Weight Cross-Connected Subgraph

- 6.1 APX-difficulty of the MWCCS problem
- 6.1.1 Frontier of solvability: tree, tree, 1-to-1
- 6.2 An MWCCS subproblem: the Ratio-Bounded MWCS
- 6.2.1 A more general variant of the Budget-Constrained MWCS
- 6.2.2 Producing pseudo-P algorithms for BC-MWCS and RB-MWCS from P algorithms for MWCS

??? Module recognition, cancer classification ???

Conclusion