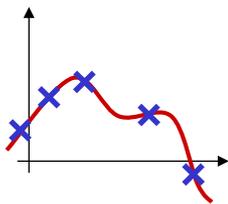


Software Tools for Computational Biology

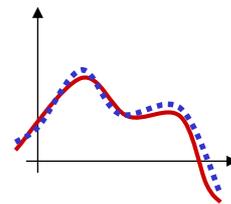
Course introduction

Alessio Bechini

Biology & Computer Science



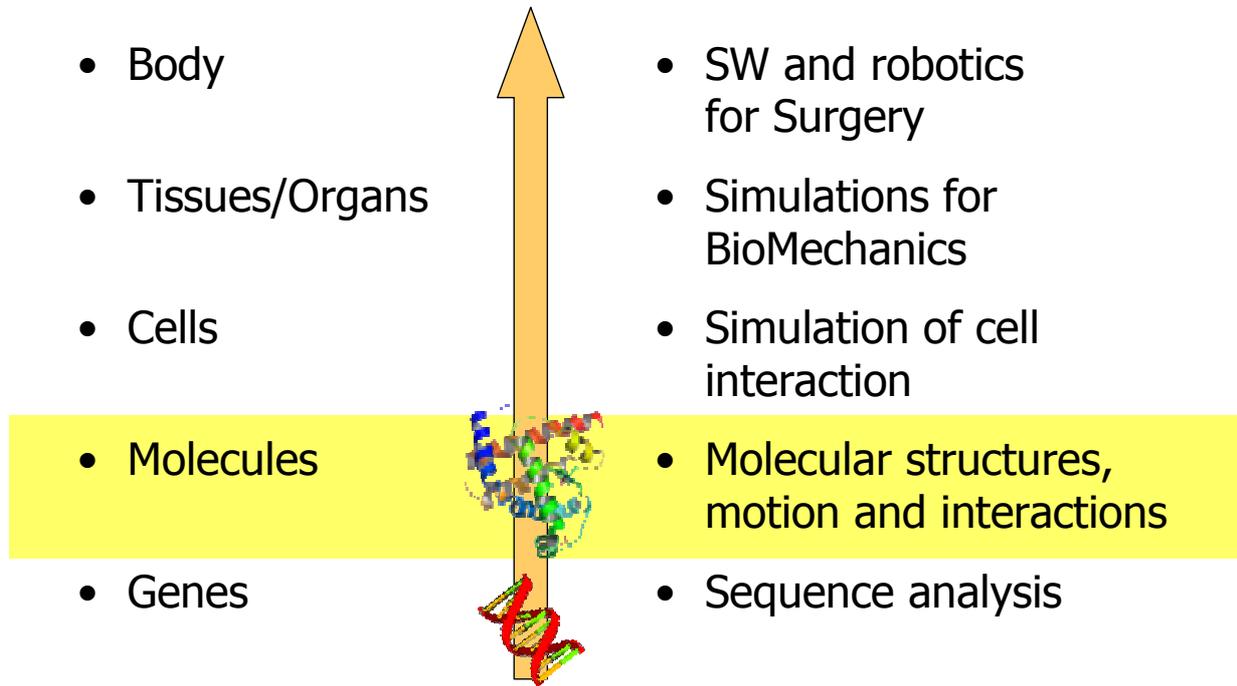
$$y = f(x)$$



- Biologists focus on experiments, specifics and classifications
- In ordinary Biology, research goes through collecting (x_i, y_i) pairs – i.e., facts – and classifying them. What about f ?
- Computer scientists focus on abstract models, algorithms, and tools to work on them
- In Computer Science, interest is towards f (i.e. the overall model in accordance with evidence) and effective/efficient ways to handle-compute it; single pairs (x_i, y_i) are deemed irrelevant

Computational Biology is aimed at investigating biological phenomena by means of tools from Computer Science.

Bio&CS at Different Scales



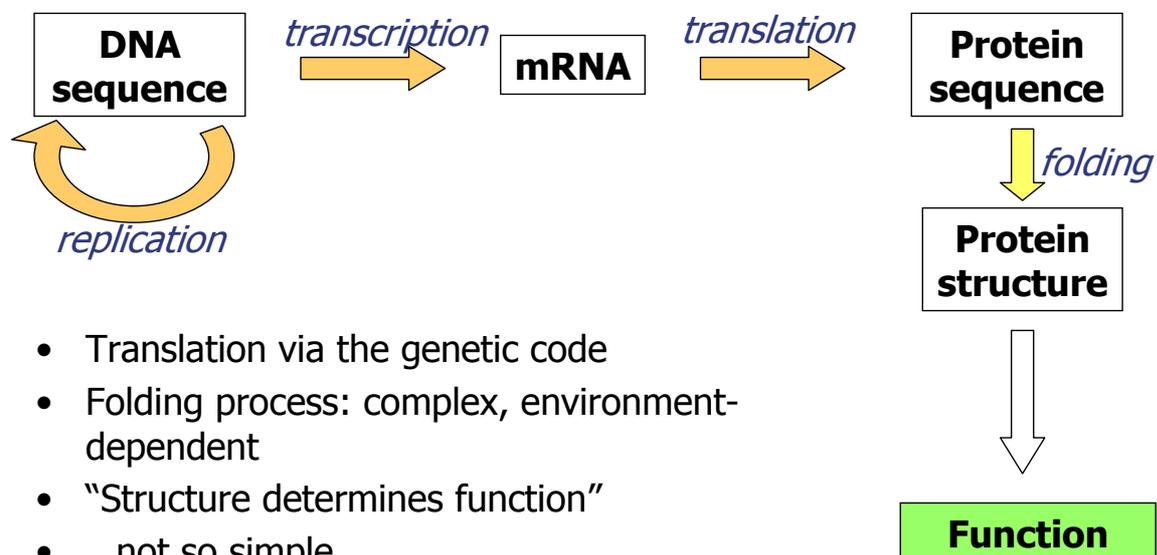
Class Topics

- Scripting in Python
- Molecular modeling
 - Molecular Mechanics
 - Molecular Dynamics
- Structural Computational Biology
 - Proteins
- Docking
- Notes on System Biology

Class Goals

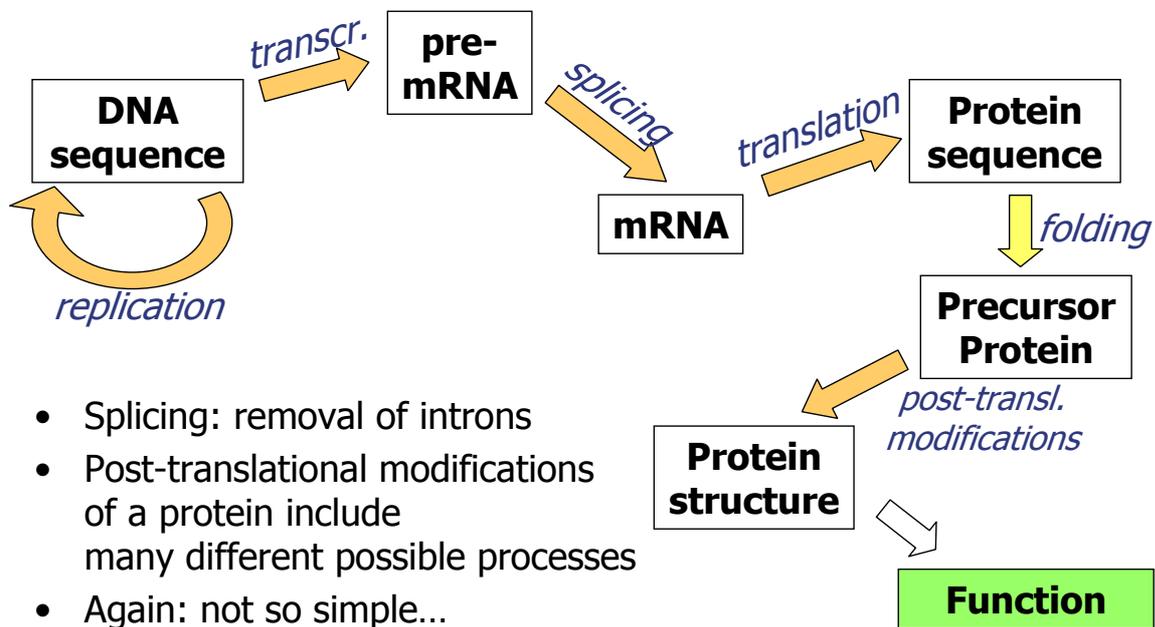
- Overlook of main themes in Computational Biology
- Master current assorted SW tools for working on biological problems
- Integrate different tools to work on a specific problem
- Be able to collaborate in the design and implementation of new tools for Computational Biology

Central Dogma of Molecular Biology

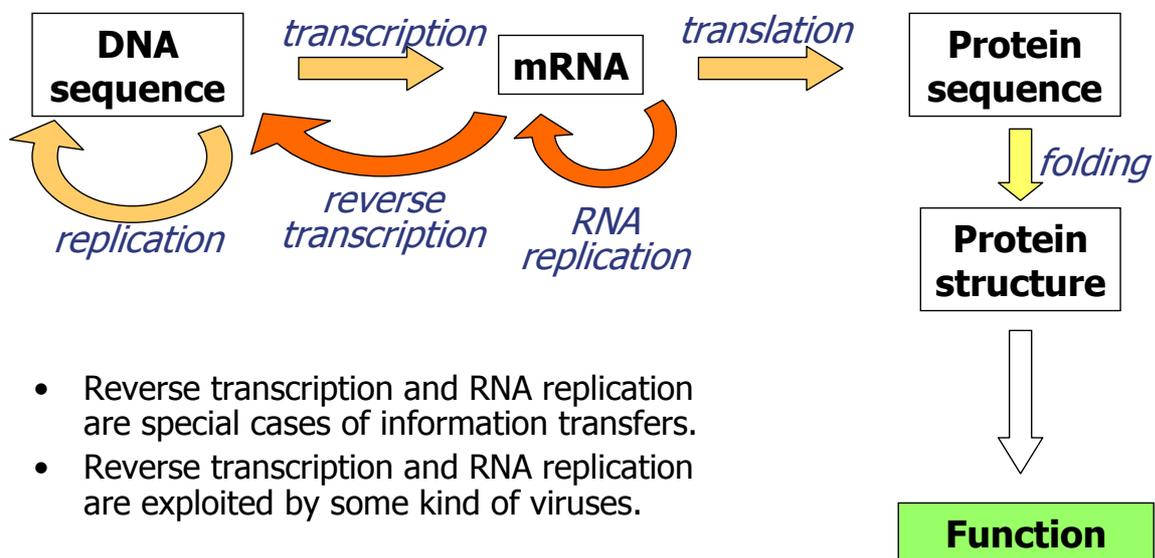


- Translation via the genetic code
- Folding process: complex, environment-dependent
- "Structure determines function"
- ...not so simple...

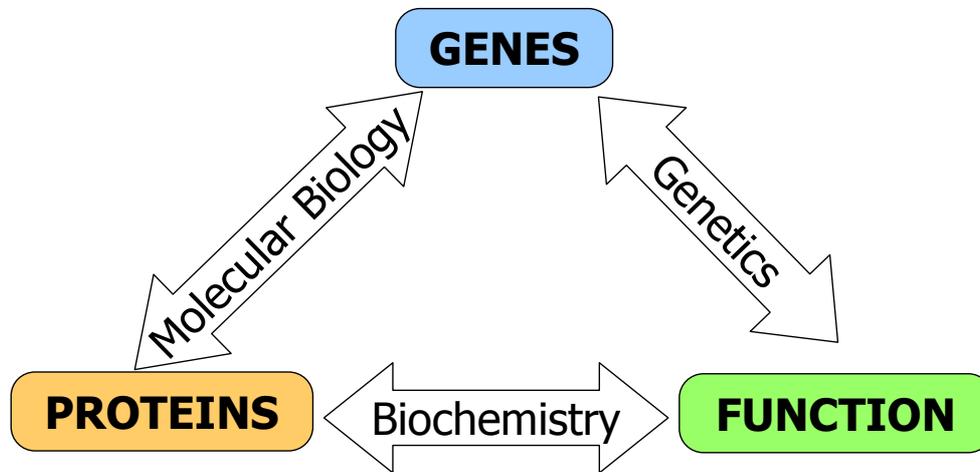
Central Dogma Revisited



Central Dogma "Reversed"



Studying the Scenery



Information from the Sequence downwards...

- Information is coded into gene sequences
 - Sequence → Structure (Shape) → Function
 - Similar sequences → Similar Shapes/Functions?
 - Sequences are evolutionary related (phylogeny)
- Functions depends on movements/bindings of biomolecules
 - Correct function ↔ correctly folded proteins
 - Function can depend on multi-molecule complexes
 - The sequence-to-function paths are extremely complex
- Computational challenges
 - Sequence/structure similarities, interpretation of experimental data, folding/misfolding prediction, shape/function relation, analysis of molecular interactions and networks, etc.

What's Required?

- Reliable models
 - From Physics, Chemistry...
 - From Computer Science...
- Efficient algorithms
 - Depending upon model/process characteristics
- Exploitation of available information
 - Access to data banks, standard data format
 - Data from experiments
- A basic SW tool to work on models, algorithms, data: a scripting language

What Language?

Several languages are used
in the Computational Biology community

- Perl
 - Efficient in dealing with strings (also BioPerl toolkit)
- Python
 - Multiparadigm, flexible, good with sequences
 - Getting more popular (also BioPython modules)
- Ad-hoc languages
 - e.g. BioLisp dialect, Dynamite (for dynamic programming), etc.
- C++ required for speed
- Java (even a BioJava toolkit exists)
- Fortran (old routines)

Why Python?

- It's a free, handy, efficient scripting language
- It can be used both standalone and as an integration glue for other sw tools
- A lot of specific libraries are available, such as

- SciPy
- NumPy
- BioPython



- ...and it can be used in many other fields (not limited to Bioinformatics)!

Final Project

- Final test: presentation of the assigned project + oral discussion
- Project
 - Each project must be developed by X people
 - Each project must address a specific topic in Computational Biology, chosen with the teacher
 - Python + other tools (depending on the project goals) must be used
 - Projects are assigned 2/3 weeks before the class end.
- Final defense: Slide show + program(s) show + questions on class topics