# **VELSERA**

SevenBridges

Applied Bioinformatics



## **Agenda**

- Introductions
- Course overview
- Bioinformatics intro
- Platform registration

## **Applied Bioinformatics**

Introductions: Lecturers

## Different backgrounds - bioinformatics engineers

Bojana Smiljanić, BF



Boris Majić, ETF



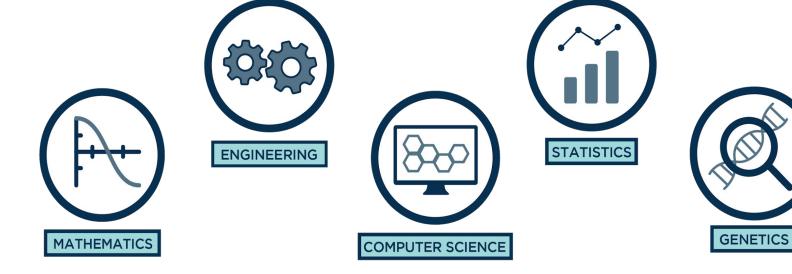
Marko Zečević, ETF



• Milan Kovačević, PMF



## **Bioinformatics analyst**



## **Applied Bioinformatics**

Course overview



### **Course logistics (1/2)**

- 2 classes each week
- A mixture of lectures and hands-on exercises
- Exercises will be done in IPython notebooks on the CGC platform
  - We will provide help with the Python syntax if needed
- The course is not covered by a single textbook
- Lessons are mostly linked

## Course logistics (2/2)

- Attending classes is mandatory and highly recommended
- Practice test in the end of semester
- For all course related questions contact
  - milan.kovacevic@velsera.com

#### **Course topics**

- Introduction to biological background and sequencing (2 weeks)
- DNA analysis (4 weeks)
- RNA analysis (2 weeks)
- Structural variation detection (1 week)
- Cancer genomics (1 week)
- Methylation/epigenetics analysis (1 week)
- Exam practise (1 week)

## **Applied Bioinformatics**

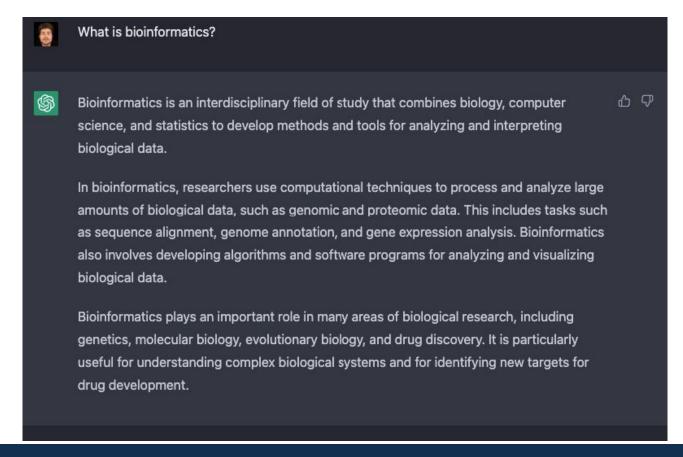
Bioinformatics intro



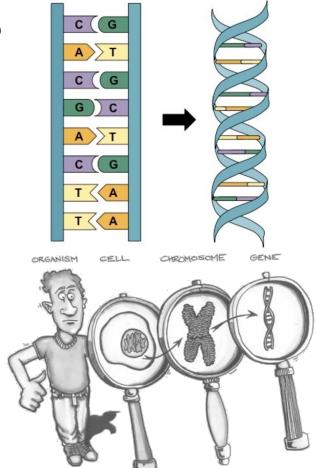
#### During this course you will learn/hear:

- More about
  - Human cells
  - DNA
  - RNA
- Why is the DNA so important?
- What can we find out from the DNA?
- More about certain diseases, like cancer
- Genome digitalisation
- How to analyse genomic data
- Interesting algorithms
- Optimisations for huge data

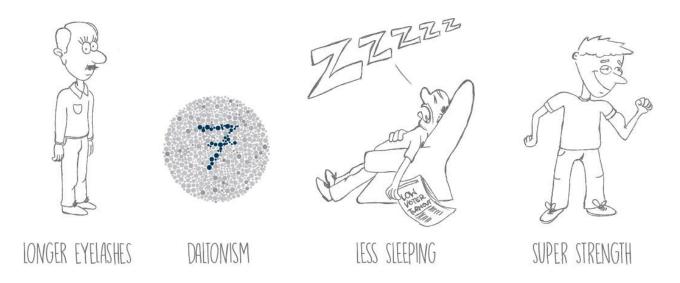
## What is bioinformatics?



- A, T, C, G
- 3.000.000.000 letters in a DNA molecule
- 46 chromosomes
- Almost everything in the body is predefined by the order of those letters



#### Some interesting characteristics:



#### And some not that interesting things:

- Cancer
- Rare diseases

Autoimmune diseases

 Neurological diseases

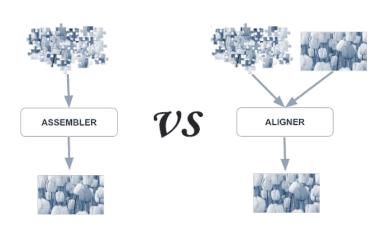
## **DNA** digital representation

- DNA is stored as a string
- Human genome project and reference genome
- 3 billion As, Ts, Cs and Gs translates into ~ 3 GB of data

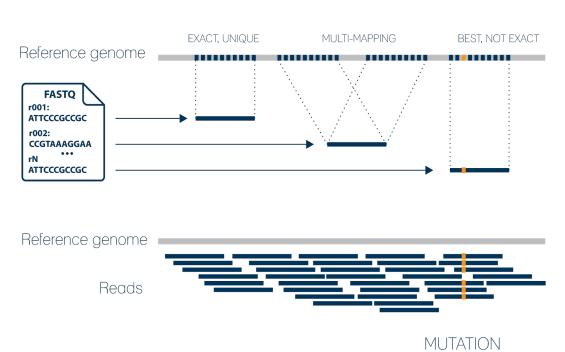
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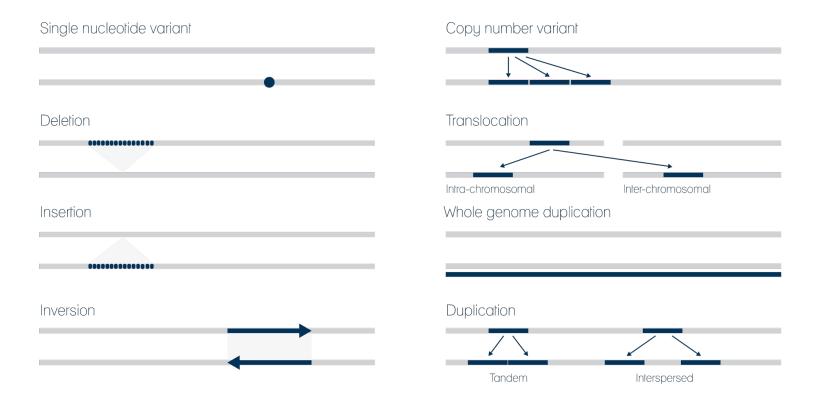


# Common 1st step: Reconstruct personal genome

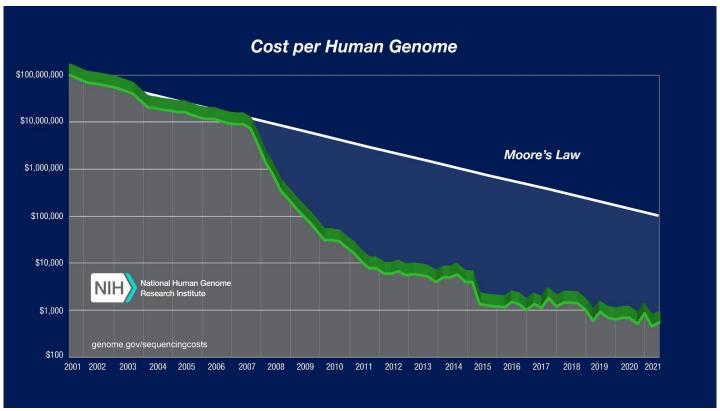


$$\Theta(n^2)$$
 vs  $\Theta(nm)$ 





## Why bioinformatics

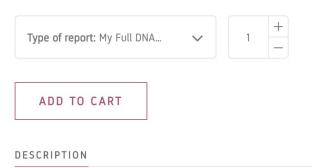


source: https://www.genome.gov/about-genomics/fact-sheets/DNA-Sequencing-Costs-Data

## Why bioinformatics



# My Full DNA: Whole Genome Sequencing with mtDNA



My Full DNA by Dante Labs gives you unparalleled access to your health, your family traits, and predispositions. Having your full genome sequenced means:

## **Applied Bioinformatics**

Platform registration



#### **CGC** registration

- Exercises are going to be done on CGC platform
- cgc.sbgenomics.com
- CGC = Cancer Genomics Cloud
  - Funded by NCI National Cancer Institute (NIH)
  - Powered by Seven Bridges
  - For academic use
  - Many researchers/ institutes / labs are using it for their analysis
- More information about the project available <u>here</u>.
- Registration

#### **Course materials**

https://github.com/milankovacevicsbg/MATF-2023-Primenjena-Bioinformatika

# Thank you!