





# **Deep Learning Project – DNA Sequencing**

Part 1: General presentation

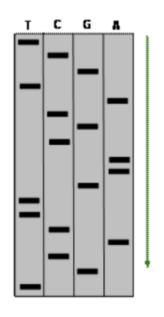
Franco Alexis Kenda Tom Laloux Noé

LBRTI2101(B) – Data Science in Bioscience Engineering





DNA Sequencing: 1980's vs Today







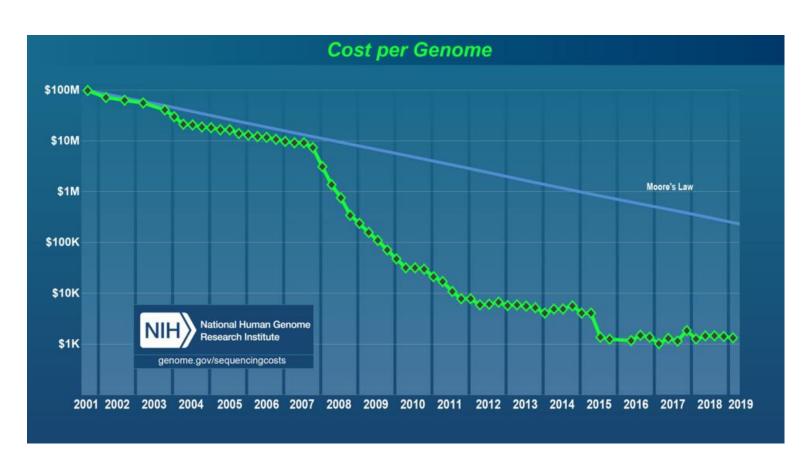
**Source** 











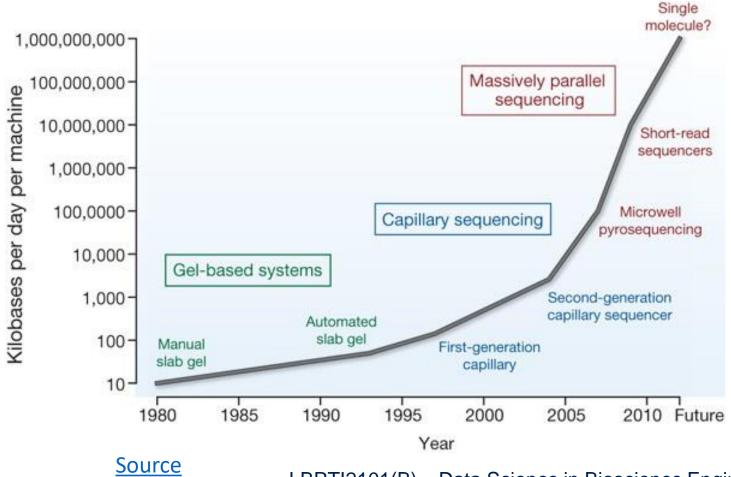
#### **Source**



# LOUVAIN BIOINGÉNIEURS

# Faculté des bioingénieurs

### DNA Sequencing entering the Big Data scene



LBRTI2101(B) – Data Science in Bioscience Engineering





#### Computational tools demand to manage all this data







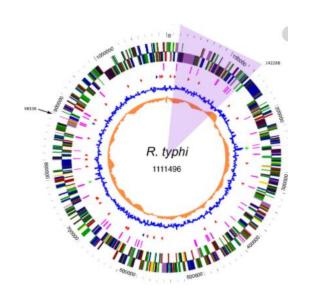
<u>Source</u> <u>Source</u>

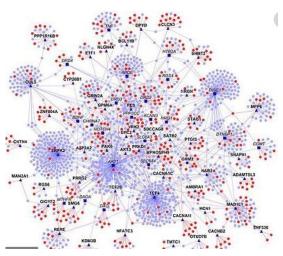
**Source** 

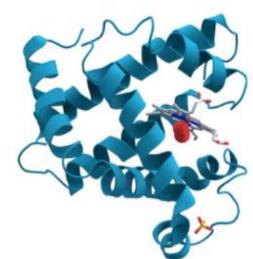




## **Applications of Bioinformatics Tools**







<u>Source</u>

**Source** 

**Source** 





### Real world applications



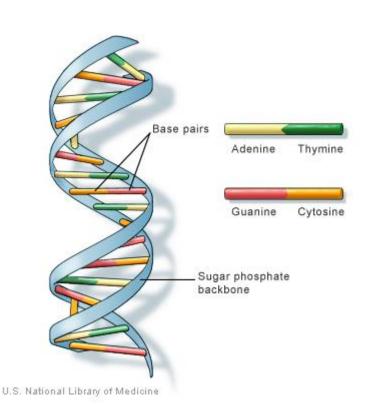
<u>Source</u> <u>Source</u>

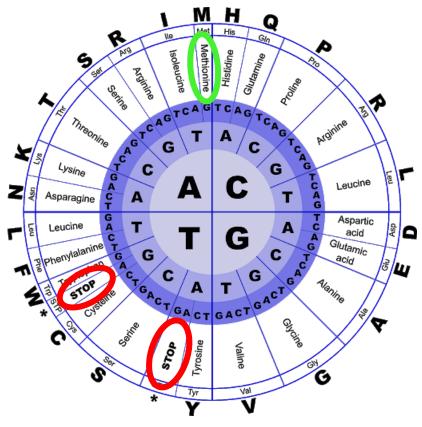
# UCLouvain

# Faculté des bioingénieurs



#### DNA's structure and Protein synthesis





Source: News medical

Source: Firmalis



# LOUVAIN BIOINGÉNIEURS

#### Faculté des bioingénieurs

#### What is the difference between ORFs and genes?

RF: Reading Frame: 3 possibilities to read DNA for each strand

ex: (5'-P) TGGTATAGCAGAATGTCTGAATTTAGTTG (3'-OH)

- -> TGG TAT AGC AGA ATG TCT GAA TTT AGT TG
- -> T GGT ATA GCA GAA TGT CTG AAT TTA GTT G
- -> TG GTA TAG CAG AAT GTC TGA ATT TAG TTG

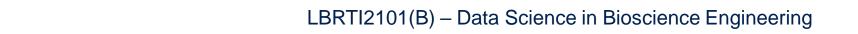
**ORF : Open Reading Frame**: Part of a Reading Frame that starts with an ATG and ends with a STOP codon

ex: ATG TGG TAT AGC AGA ATG TCT GAA TTT AGT TGC TGA

Gene: ORF that corresponds to a real protein that can be expressed by the organism

ex: ATG TGG TAT AGC AGA ATG TCT GAA TTT AGT TGC TGA

- -> Met Trp Tyr Ser Arg Met Ser Glu Phe Ser Cys -STOP
- -> if this polypeptide corresponds to a protein



# UCLouvain



# LOUVAIN BIOINGÉNIEURS

# **Goal of Our Project**

Input: Output:



# LOUVAIN BIOINGÉNIEURS

## Faculté des bioingénieurs

# How can Deep Learning help us?

#### Our hypothesis:

- → It is possible to predict whether or not a DNA sequence is a coding gene
- → A well trained algorithm can do that through Deep Learning

#### Questions we have been facing in the beginning:

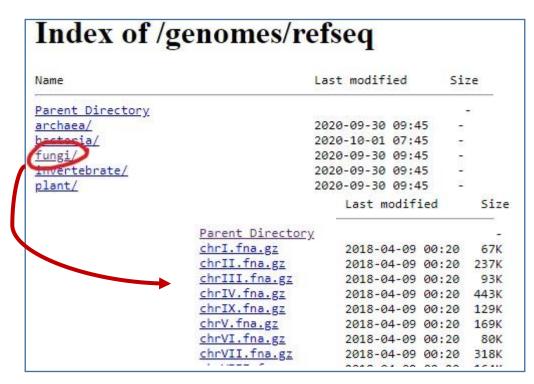
- → Any existing libraries/algorithm doing this?
- → Is Deep Learning relevant for this application?
- → Can we find some data



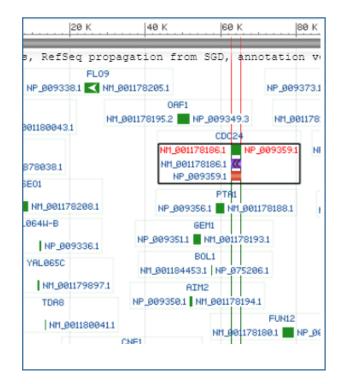


### How to find a data set?

#### 1. Getting the entire genome



#### 2. Getting the coding sequences



Source : ncbi

# Référence et bibliographie

<u>Index of the genome of saccharomyces cerevisiae</u>

<u>Genome data viewer (with all the coding genes) for S. cerevisiae</u>

LBIR1352 : Génétique Générale, Mahillon J.

LBRMC2201 : Bioinformatique : séquences d'ADN et de protéines, Ghislain M.