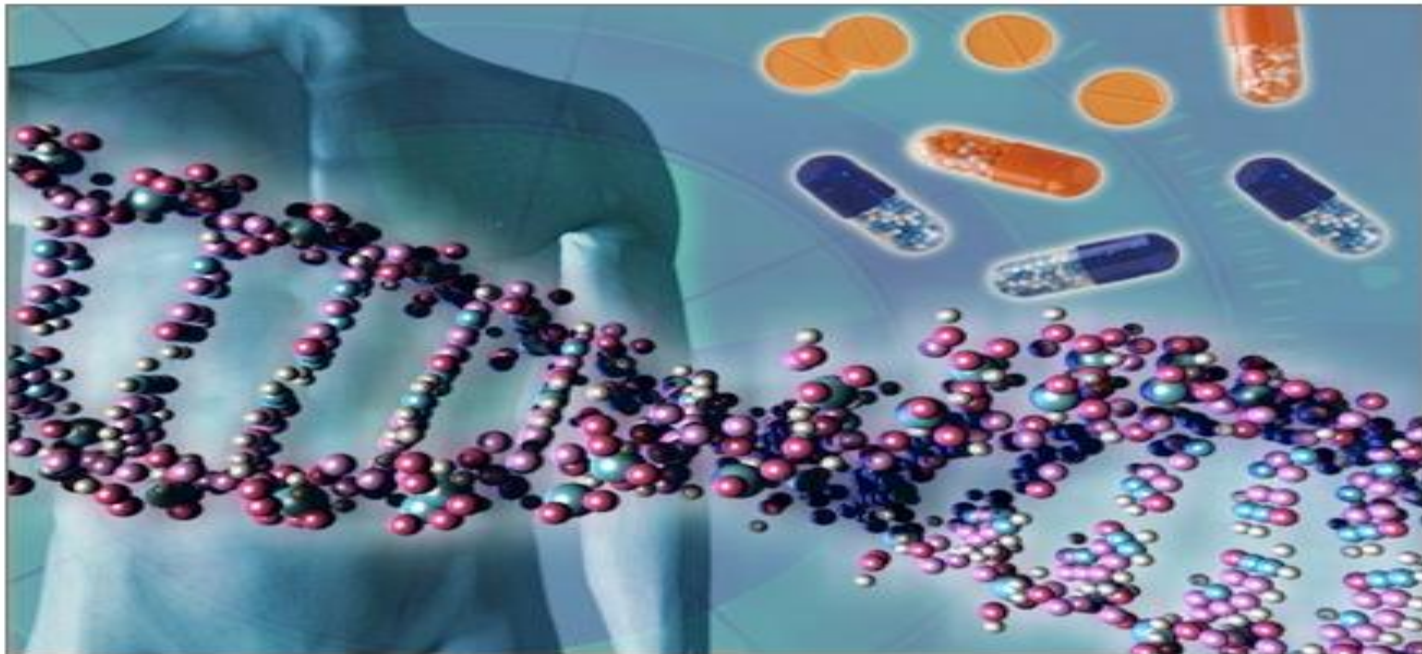
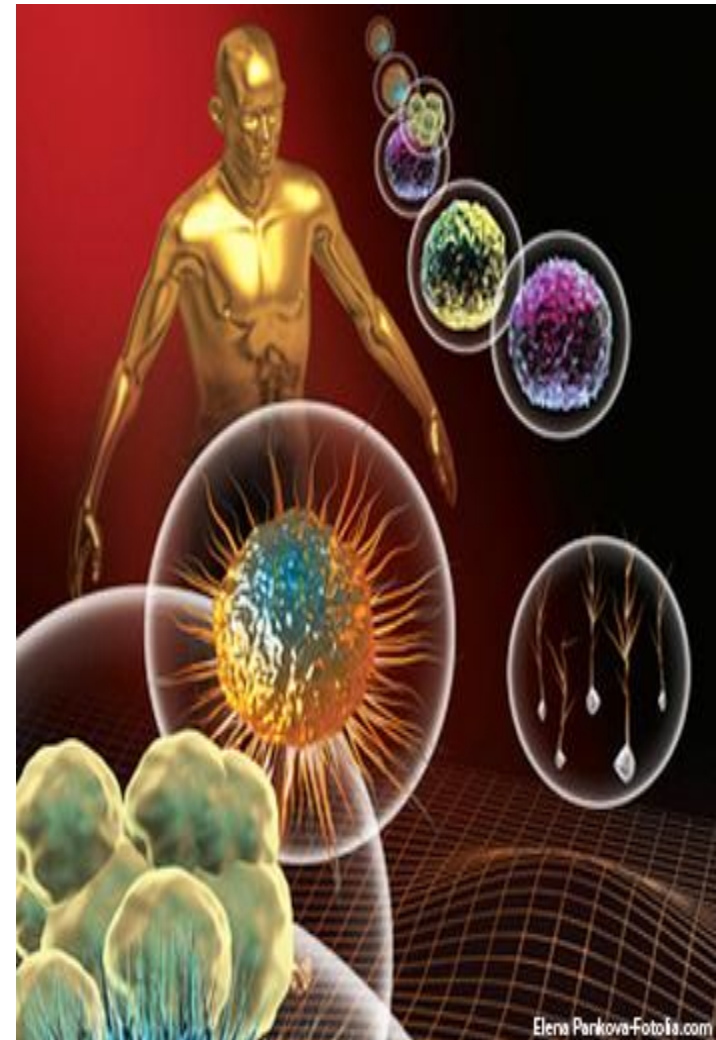


# Genome Sequencing



**Mohamed N. Seleem**

# From Gene to Genome





# •Sequencing of the whole genome of the Organism

## •Sequence must be annotated

- Location of genes (locationofgenes)
- Location of transcribed regions (coding region)
- Location of promoters, start codons and terminators
- Function of other DNA sequences
- Translated Protein and assigned function

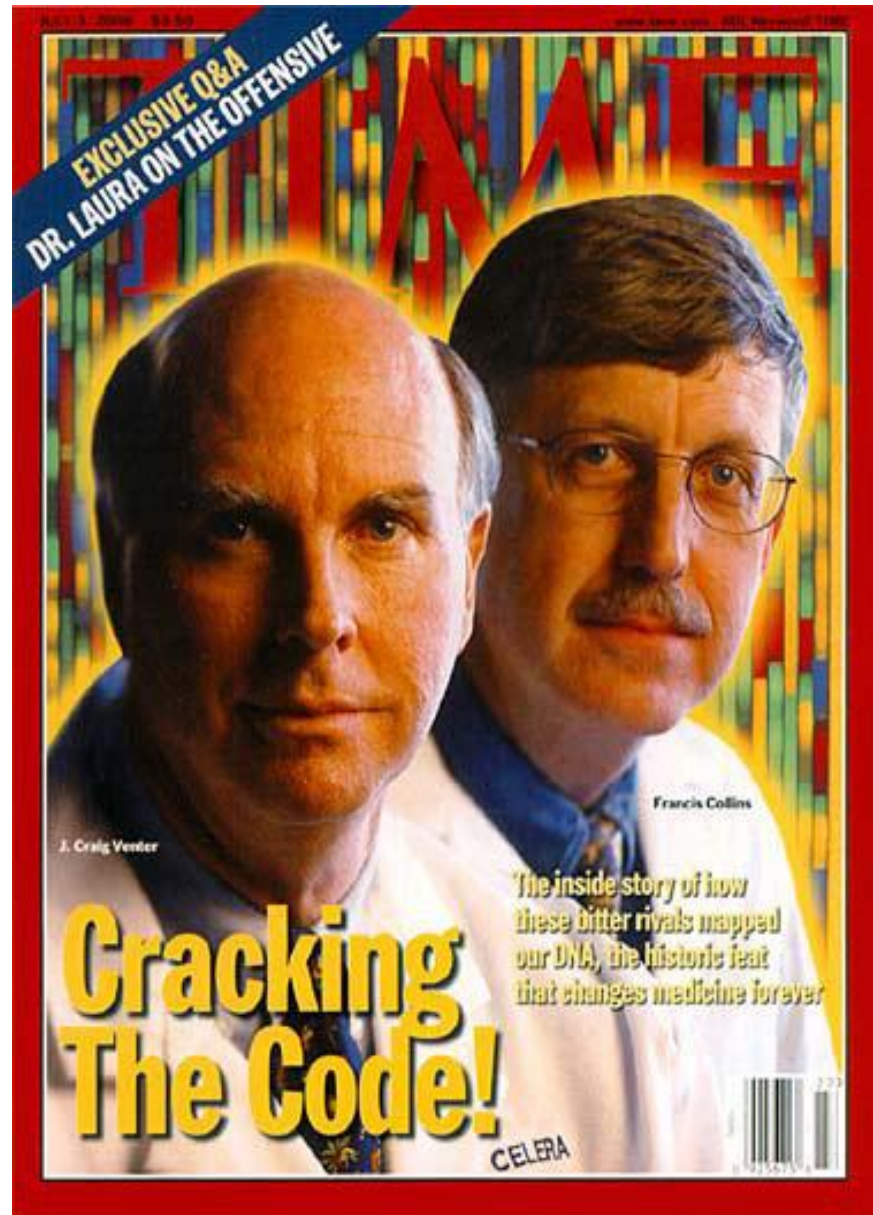
# Human Genome Project

1990–2003

\$3 billion

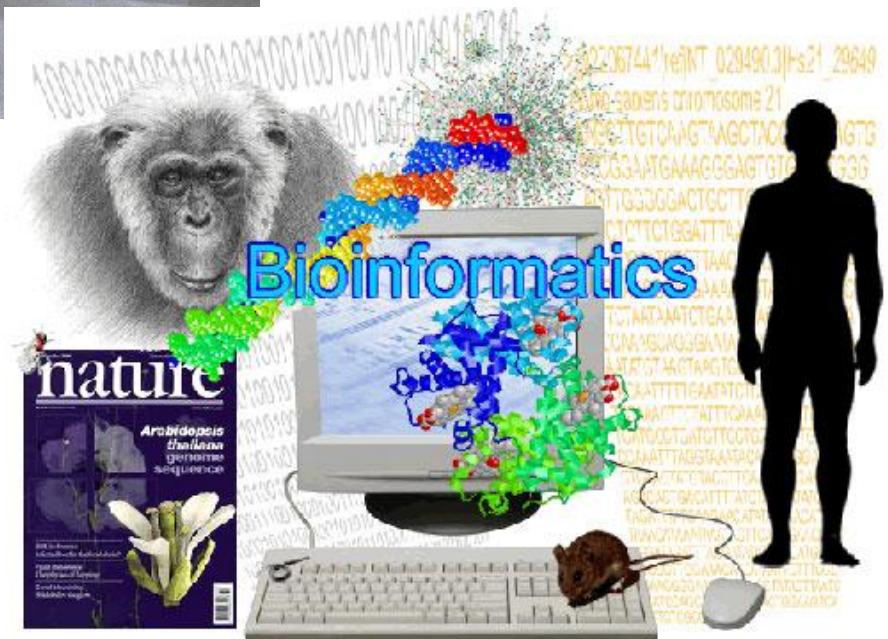


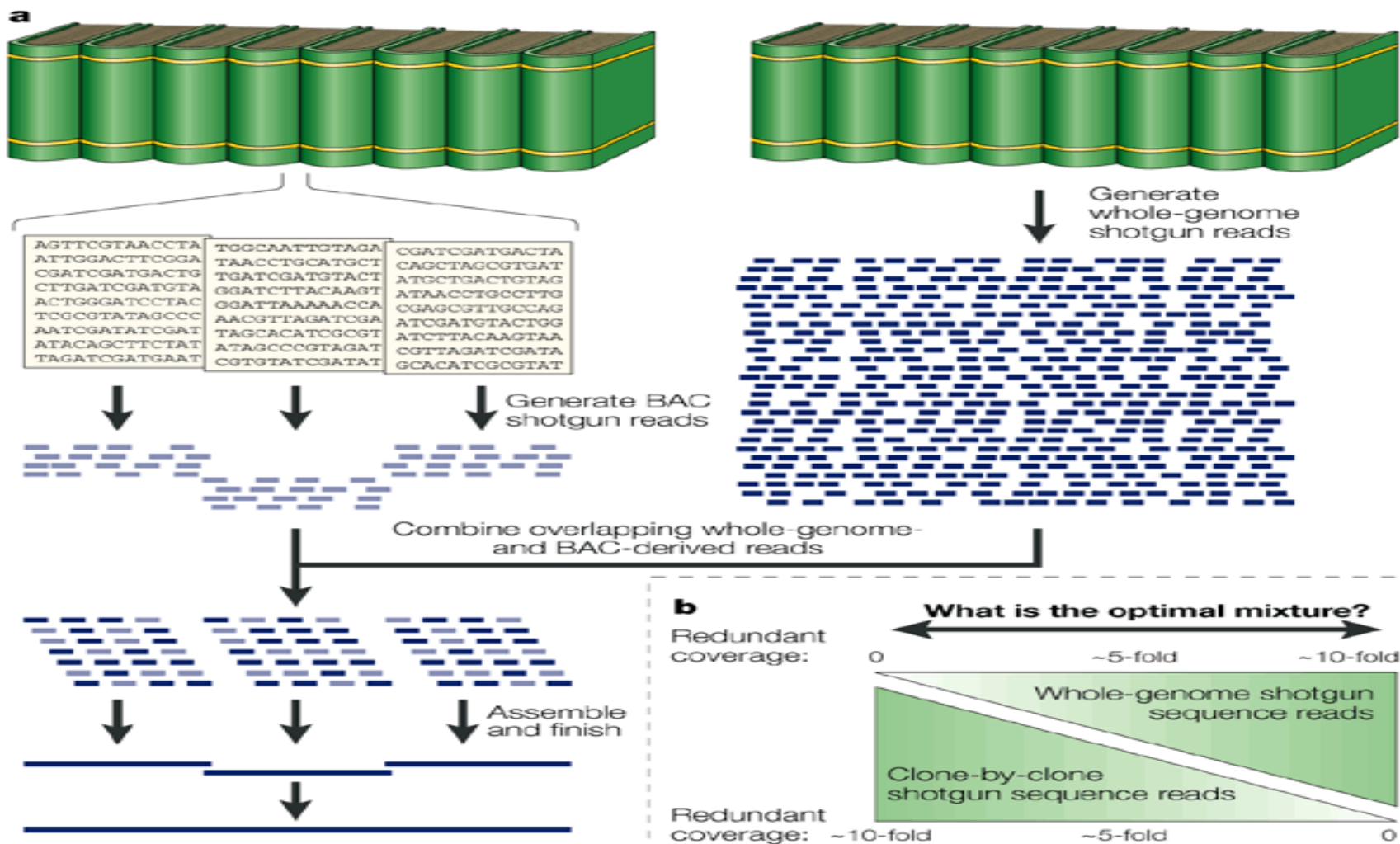
Francis Collins  
J. Craig Venter



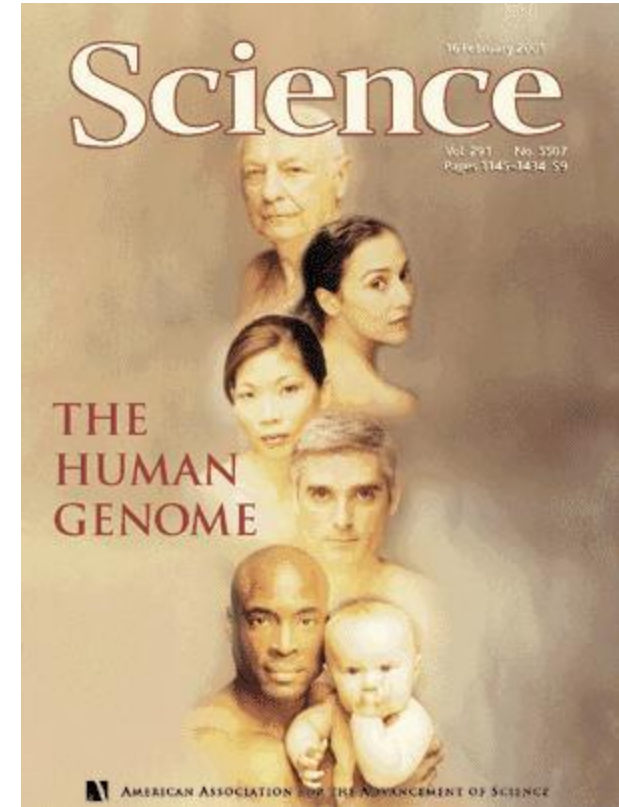


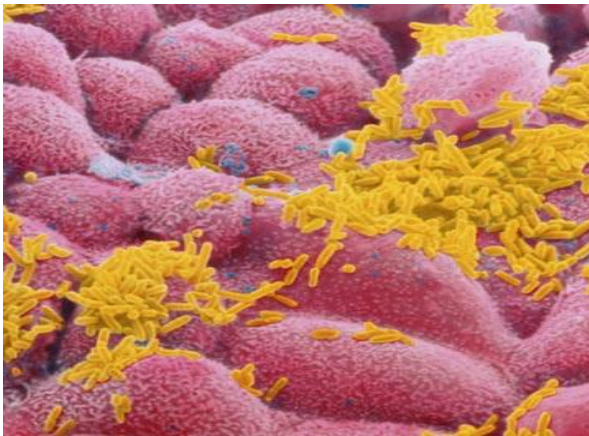
# Supercomputers & Bioinformatics





# Draft 2000 Complete 2003

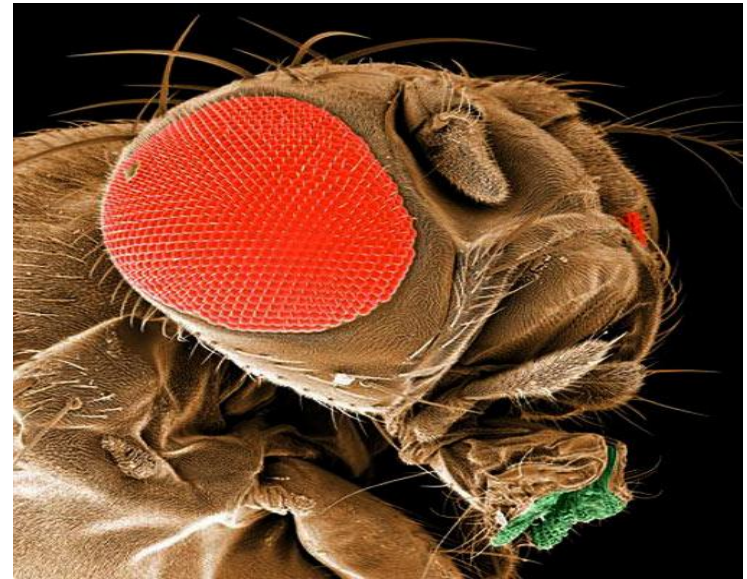




***H. influenzae***

**1.8 million bases**

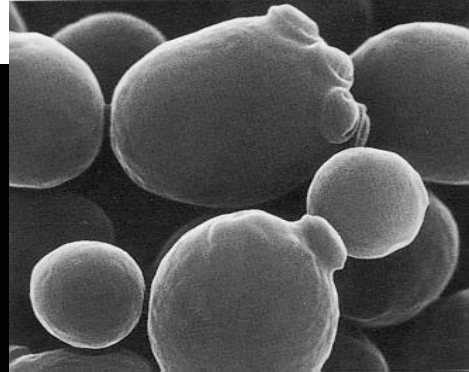
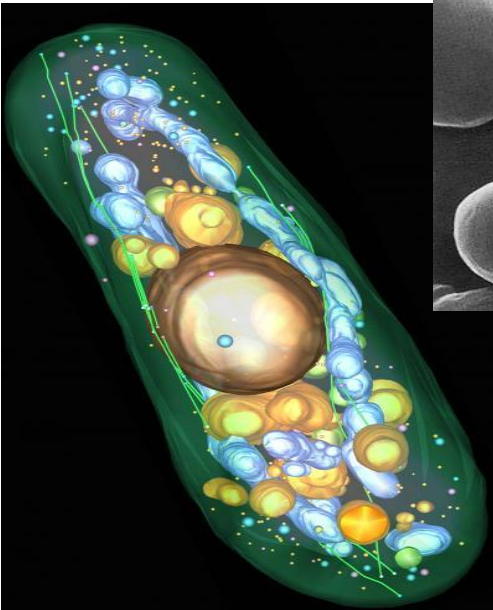
**1700 genes**



***Drosophila melanogaster***

**137 million bases**

**13,700 genes**



***Saccharomyces cerevisiae***

**12.1 million bases**

**5800 genes**

***Caenorhabditis elegans***

**97 million bases**

**19,000 genes**



***Oryza Sativa* (Rice)**

**430 million base**

**60,000 genes**



***Homo sapiens* (human)**

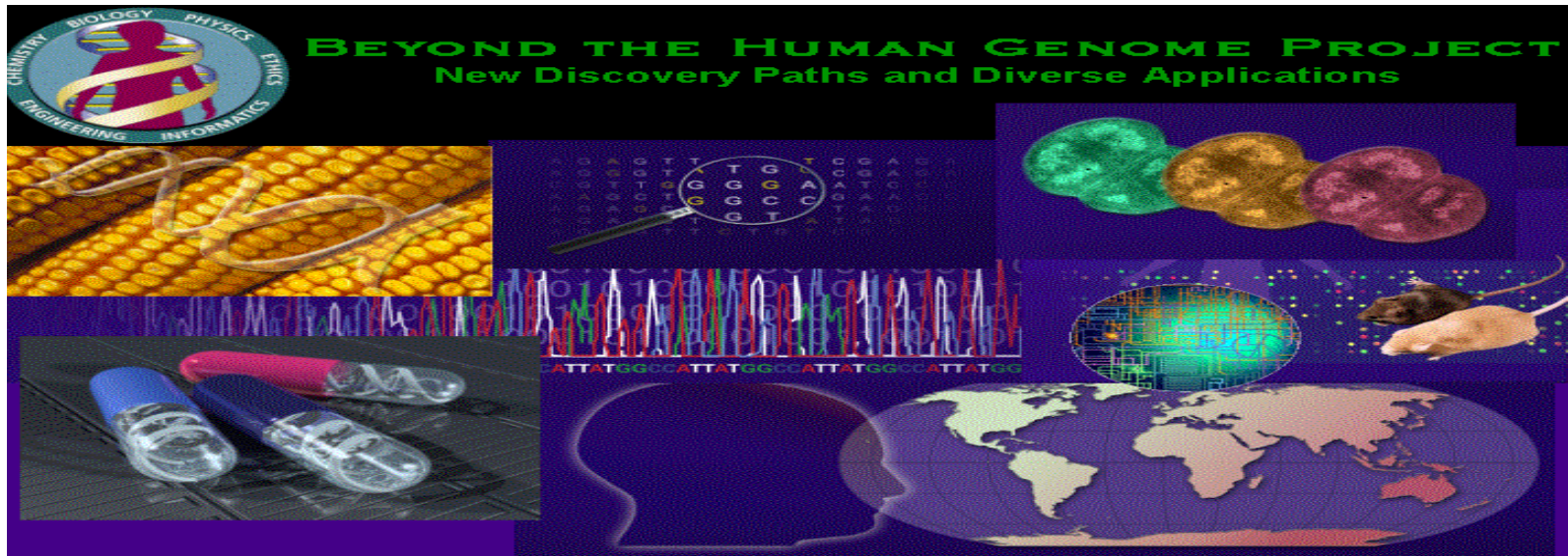
**3.2 billion base**

**~25,000 genes**

2% only code for protein

100,000 proposed earlier

40,000 after first draft

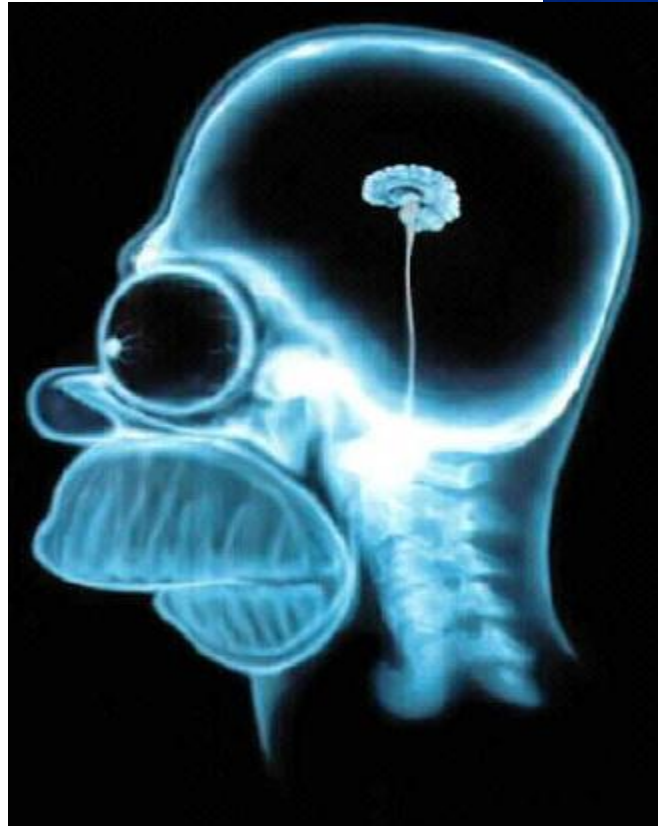


**\$1,000 Genome by 2015-2020**



**Every Child Genome**

# Sequencing is just letters



Reaching Beyond Horizons

## How to use it?