

# CHEM 498Q / 630Q

Molecular modelling of proteins

Fall 2015 Term

**Instructor:**

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## **Syllabus:**

[http://faculty.concordia.ca/glamoure/pdfs/CHEM498Q\\_syllabus\\_2015.pdf](http://faculty.concordia.ca/glamoure/pdfs/CHEM498Q_syllabus_2015.pdf)

## **Course material (tutorials and overheads):**

<http://faculty.concordia.ca/glamoure/teaching.html>

# Bioinformatics *versus* Molecular modelling

Both disciplines are studying biology and biomolecules using computers but...

- **Molecular modelling** is based on “physics”  
(molecules & interaction)
- **Bioinformatics** is based on “information”  
(databases & statistical inference)

# Sources of information

*"A month in the laboratory can often save an hour in the library."*

– F. H. Westheimer

## The (infamous) Wikipedia

- Do not use as your primary source of information
- Use only as a starting point to the original (peer-reviewed) articles

## Google Scholar (<http://scholar.google.com>)

## Web of Science (<http://apps.webofknowledge.com>)

- Indexes most scientific journals
- Better organized than Google Scholar

## PubMed (<http://www.ncbi.nlm.nih.gov/pubmed/>)

- Comprehensive resource for biological and medical information
- Take some time to explore it: It will pay you back a thousand fold.

## The... library!

- There still is nothing like reading textbooks to get an introduction to a new field.
- You may find that books nearby on the shelves are interesting as well.

# Information overload !

## Too many hits?

Learn how to use the advanced search features (e.g. Boolean operators).

## Too much to read?

Start with review articles (the most recent ones) and work your way down.

## Nothing relevant?

Try a different search approach:

- Use MeSH terms (<http://www.ncbi.nlm.nih.gov/mesh>) instead of your own keywords (start from the MeSh Browser: <http://www.nlm.nih.gov/mesh/MBrowser.html>).
- Look for the articles citing a “foundational” article.

**“I had found a bunch of super-relevant articles, but I can’t trace back the exact search that got me there!”**

- In PubMed, save your searches.
- Keep the Digital Object Identifiers (“DOIs”).
- Organize your references with Mendeley or Zotero.

# Do you know your Subject Librarian ?

At Concordia University:

<http://library.concordia.ca/about/staff/artscilib.php>

At Université de Montréal:

<http://www.bib.umontreal.ca/nous-joindre/bibliothecaires.htm>

At McGill University:

<http://www.mcgill.ca/library/contact/askus/liaison>

# Do you know what constitutes plagiarism ?

From Section 17 of the Concordia University Undergraduate calendar:

*plagiarism – the presentation of the work of another person, in whatever form, as one's own or without proper acknowledgement*

- If you can't write the introduction/discussion of a tutorial report in your own words, without including chunks of text from the articles you have consulted, you are not ready to write it yet. (Read more!)
- If you don't know the meaning of a technical term, don't use it.
- Writing takes time and effort. You should (temporarily) accept that your own words may not be as effective/concise/stylish as those from the world experts on the topic.
- In case of doubt about what constitutes plagiarism, or on how to cite a certain element of information, come see me.

# Databases :

## Primary *versus* Derived

### [Protein Data Bank](#) (PDB)

- primary database of atomically resolved protein structures
- structures obtained from x-ray diffraction or NMR

How many structures?  
What other experimental methods?

### [GenBank](#), [Ensembl](#)

- primary databases of DNA sequences
- contain taxonomic and functional information

### SwissProt, [UniProt](#)

- primary databases of protein sequences
- richly annotated and connected to bibliographic databases

How many protein sequences?

### [SCOP](#), [CATH](#), [Dali](#)

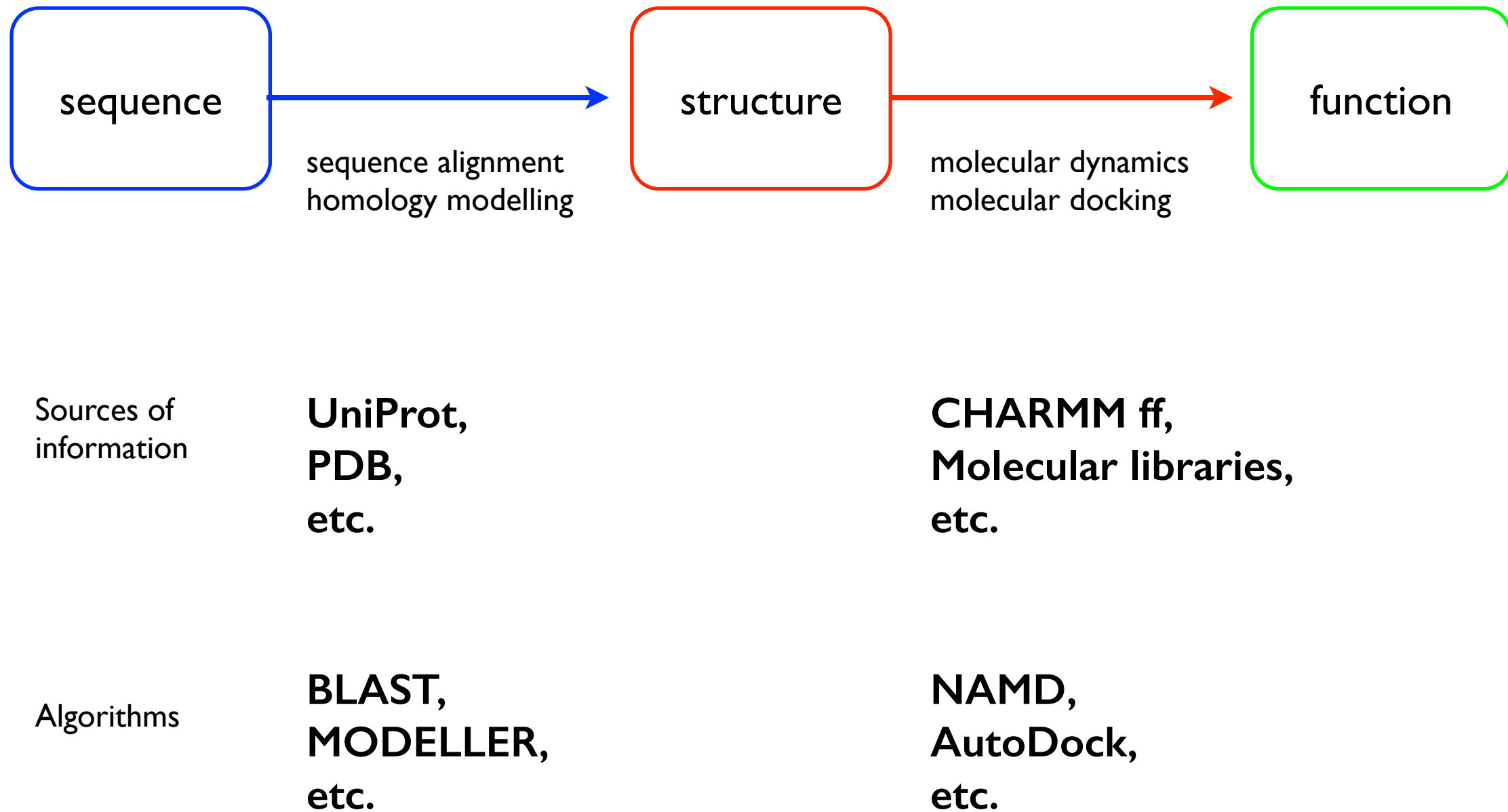
- classifications of proteins in terms of their structure
- derived from the PDB

### [Pfam](#), [CDD](#), [PROSITE](#)

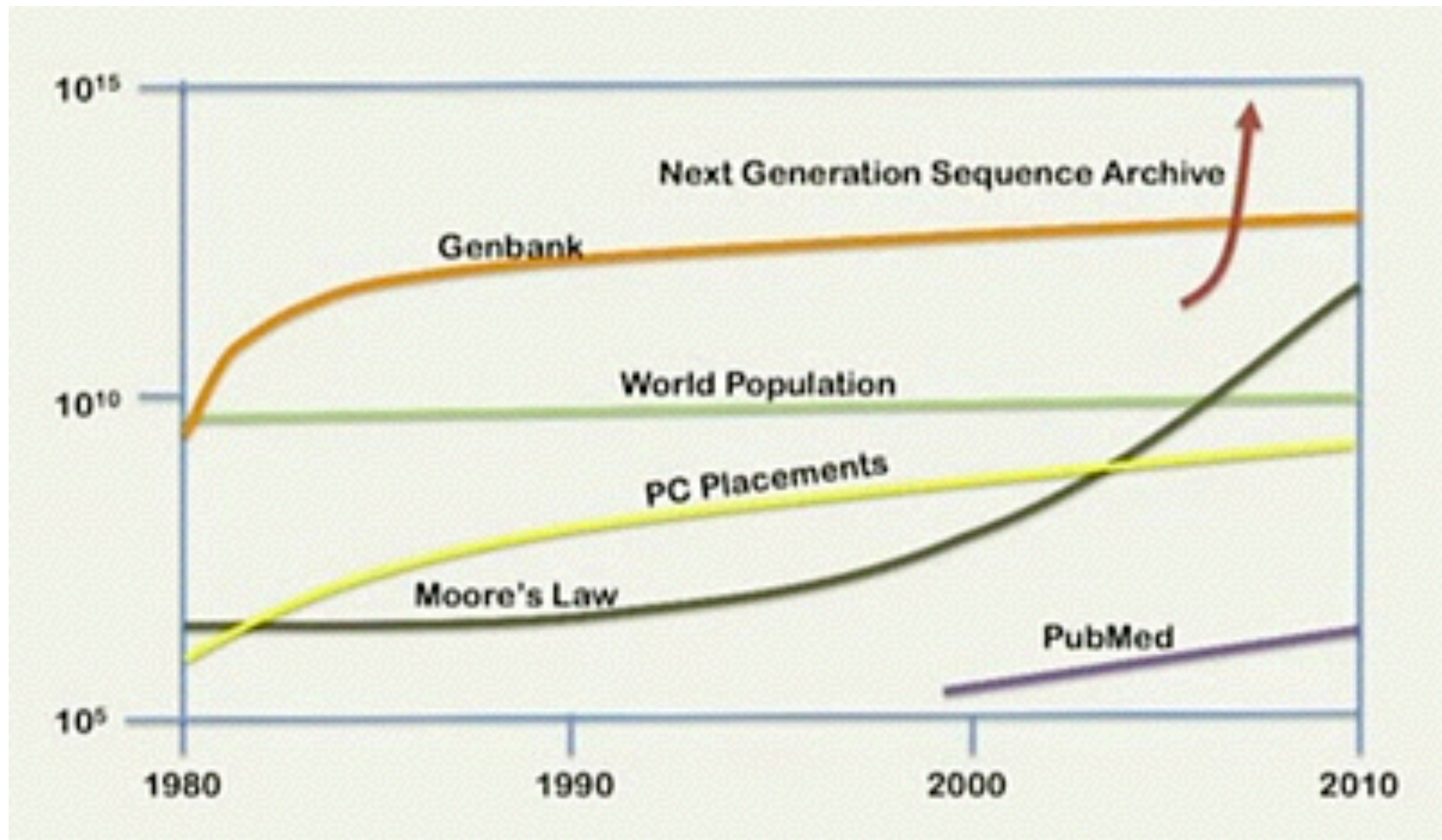
- classification based on protein sequence patterns
- derived from protein sequence databases



# Overview of the course



# Why computer modelling ?

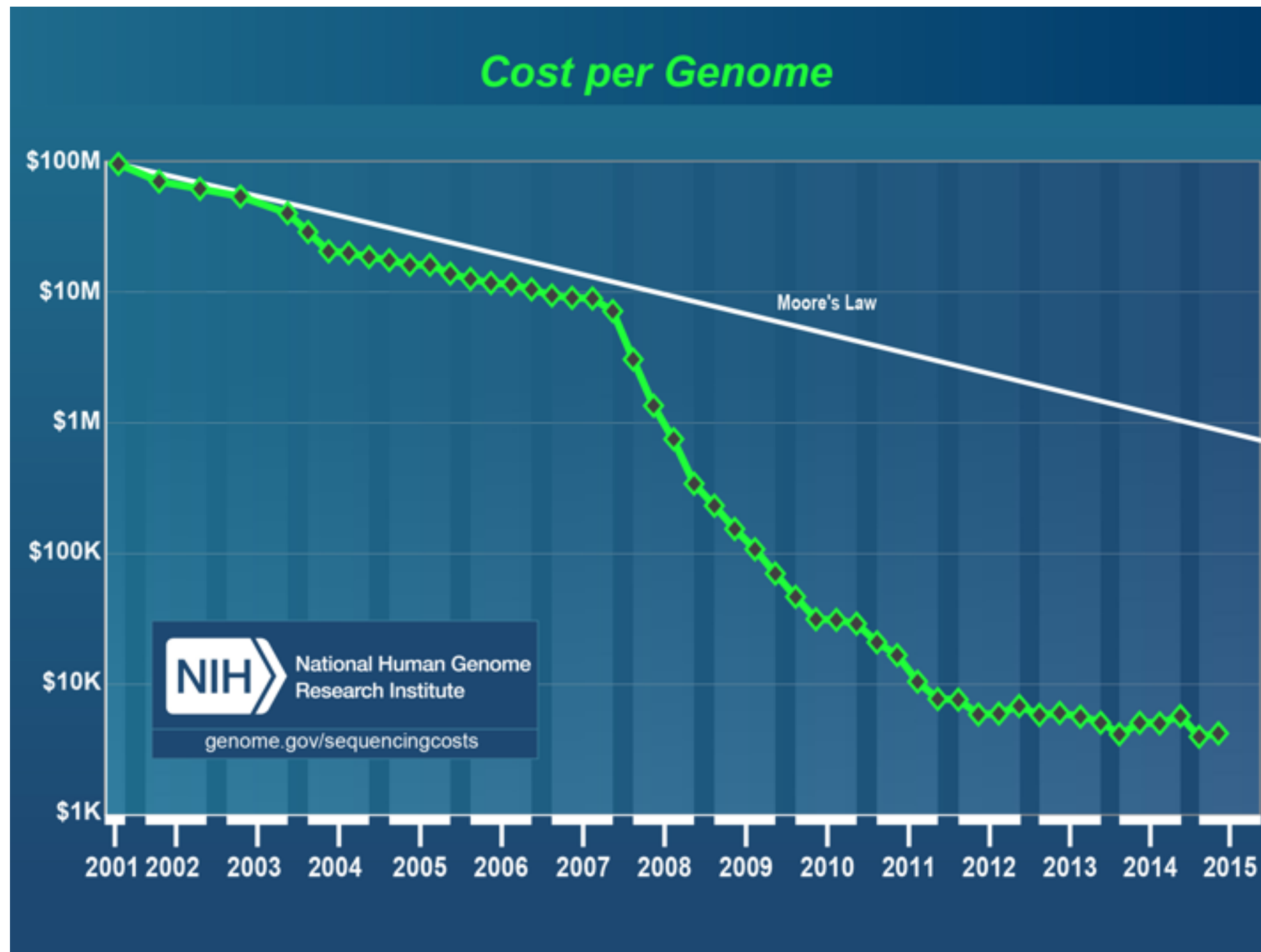


Source:

Richard Resnick, *Welcome to the genomic revolution*, TED Talk (July 2011)

[http://www.ted.com/talks/richard\\_resnick\\_welcome\\_to\\_the\\_genomic\\_revolution.html](http://www.ted.com/talks/richard_resnick_welcome_to_the_genomic_revolution.html)

# Towards personalized biology and medicine ?



Source:

Kris Wetterstrand, *DNA Sequencing Costs: Data from the NHGRI Genome Sequencing Program (GSP)*

<http://www.genome.gov/sequencingcosts/>