Practical Bioinformatics for Biologists (BIOS493/700)

- Course overview

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Spring 2013

MO444

BIOS 643 and 646

- Minimum theoretical intro
- A LOT of practical applications
- Goal: enhance the use of computational tools in molecular biology research

Half day on the web can save you half month in the lab

Questions

- How many have experience in Linux/Unix
- How many working in a research lab
- How many have programming experience of any kind language
- How many have used BLAST
- What bioinfo softwares you have ever used
- What softwares you will be using

Tools

- Two parts

Web-based resources

Stand-alone tools

  Windows-based (have a GUI)
  Linux-based (no GUI, command line)

Class rules:

- Attendance: students are required to attend all classes. Absences without notifying the instructor in advance will result in 5% reduction in final grade.

- Plagiarism: copying materials (figures, tables, sentences) directly from other people, literatures or internet without proper reference are considered as plagiarism and will lead to a fail of this course.

Grading:

- Attendance: 10%
- Home work: 40%
- Final report: 40%

  -Project 1: 20%

  -Project 2: 20%
- Presentation: 10%

Books:

Mainly uses slide notes, but may refer to:

- Building Bioinformatics Solutions with Perl, R and MySQL by Bessamt et al., 2009 Oxford
- Practical Computing for Biologists by Haddock and Dunn, 2011 Sinauer
- Developing Bioinformatics Computer Skills by Gibas and Jambeck, 2001 O’reilly

Class website

http://cys.bios.niu.edu/yyin/teach/PBB/

Slides, homeworks, reading materials, notes, handouts

Expectations

- Be focused inside class
- Spend at least 5 hours outside class per week
- Turn in homework on time
- Use what you learned in your research

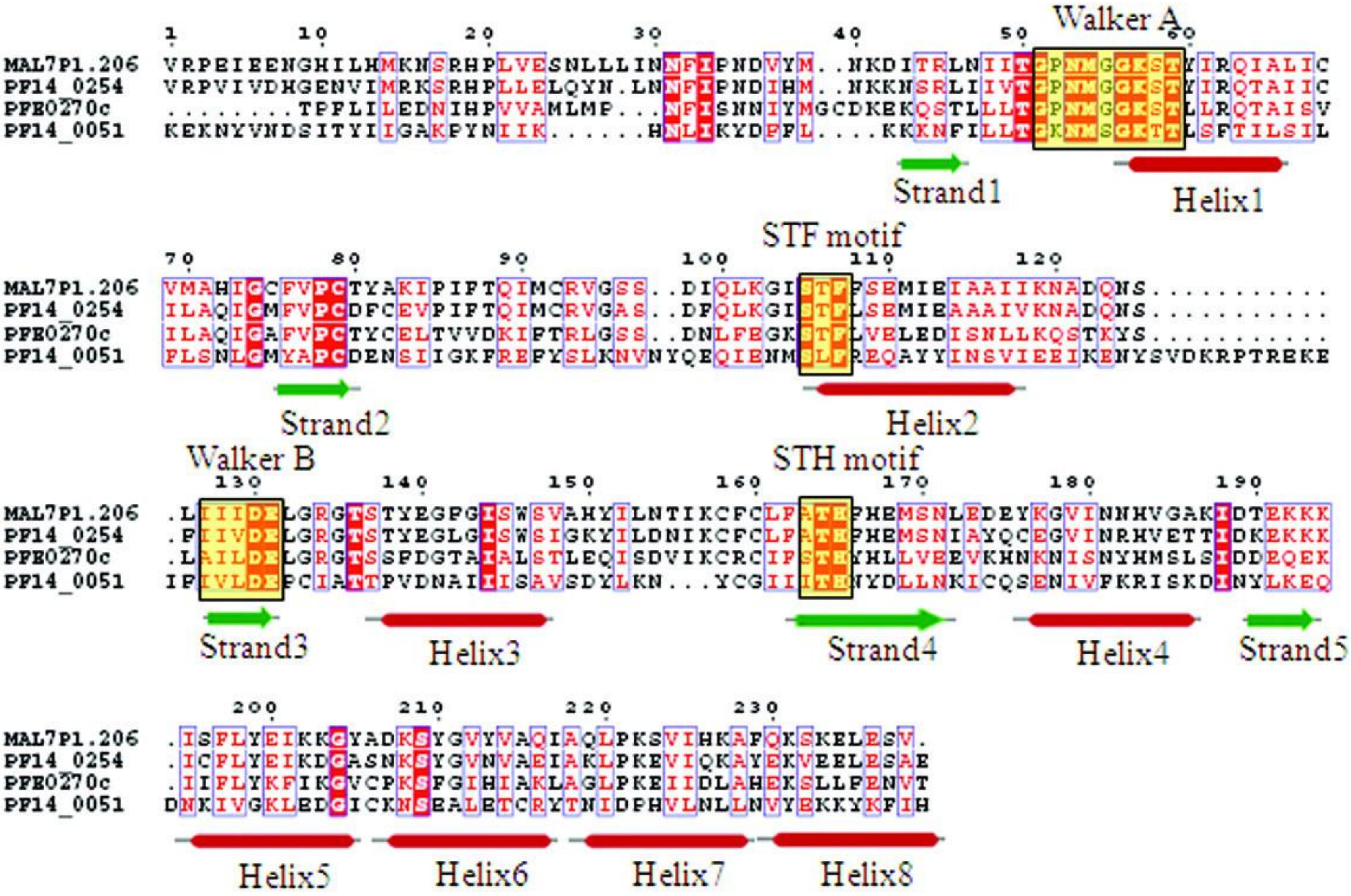
What you can expect from this course

- How to find a particular gene in NCBI?
- How to find the homologs for that gene?
- How to get 100 protein sequences at a time?
- How to predict functions for an uncharacterized gene?
- How to perform a sequence alignment of 100 proteins?
- How to predict the 3D structure of a protein?
- …

What you can expect from this course

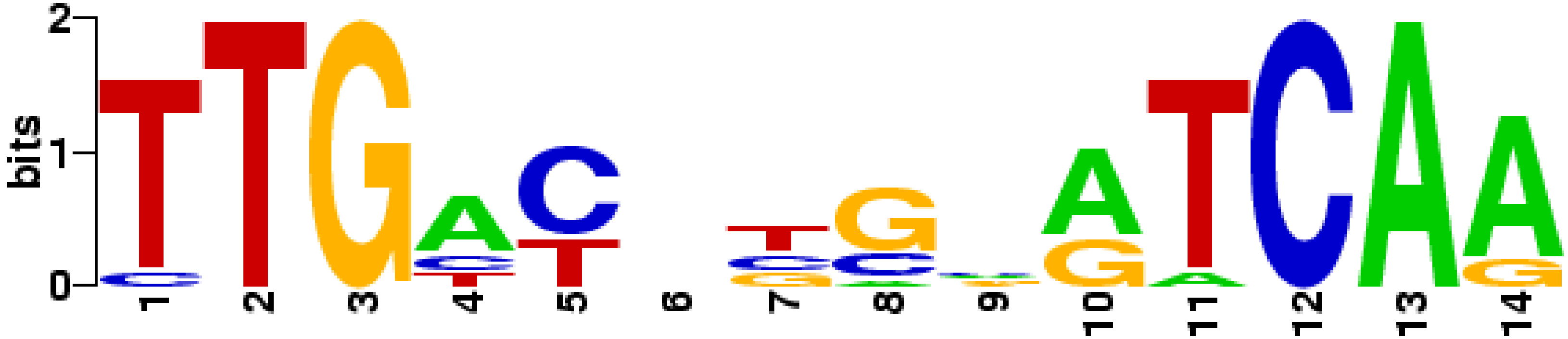
- How to install Ubuntu Linux on a laptop/desktop?
- How to access a remote Linux machine from Windows?
- How to work with Linux terminals?
- How to install bioinformatics softwares using terminals?
- How to run bioinfo tools e.g. BLAST in the Linux terminal?
- How to do basic sequence analysis using bioinfo tools such as EMBOSS commands?
- How to extract 100 protein sequences from a large protein database, given the IDs of the proteins, using a combination of Linux commands and perl one-liner script?
- and many more ...

Multiple sequence alignment

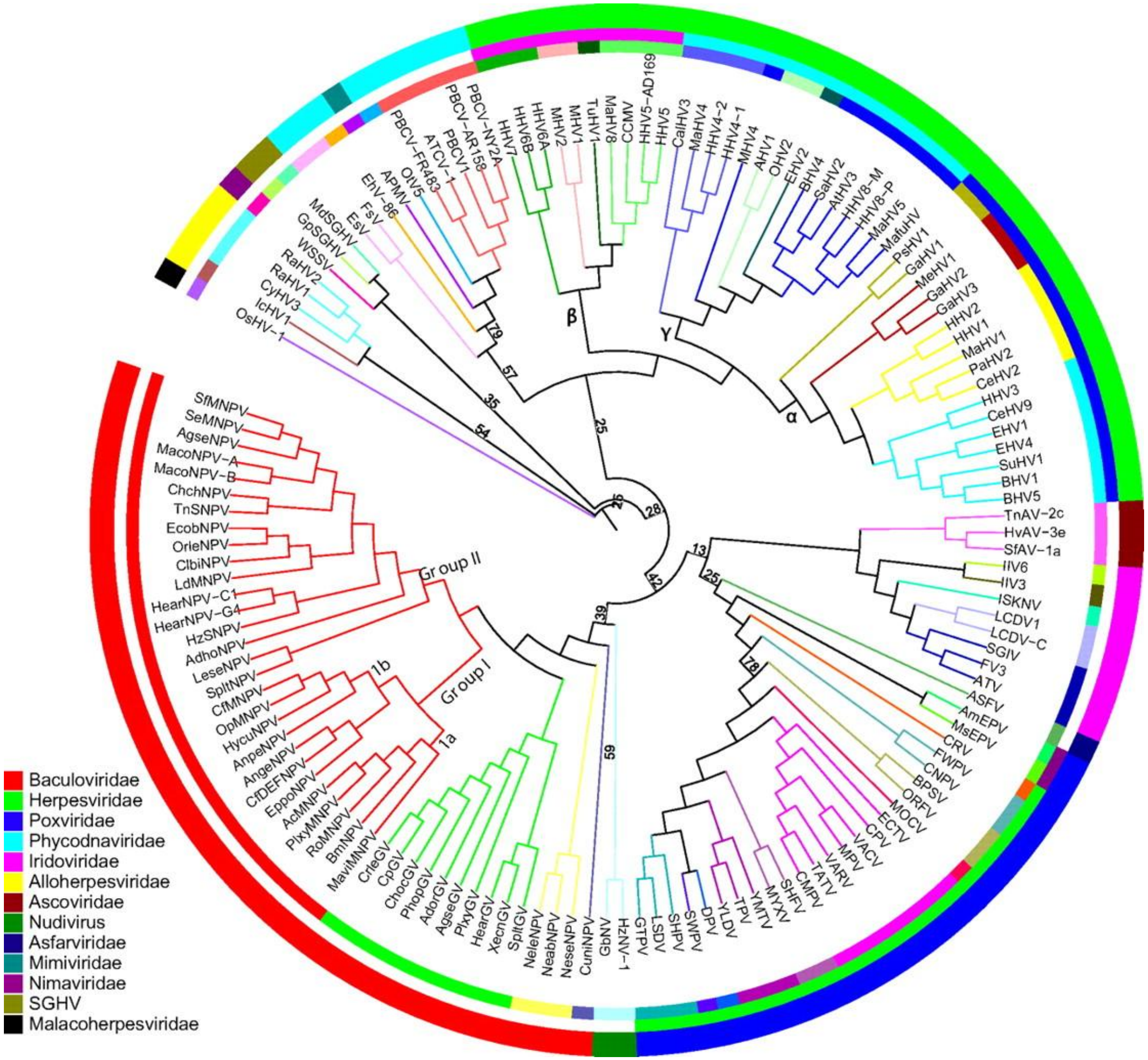


```
            1        10        20        30        40        50        60
MAL7P1.206  VRPEIEENGHILHMKNSRHPLVESNLLLINNFIPNDVYM..NKDITRLNIITGPNMGGKSTYIRQIALIC
PF14_0254   VRPVIVDHGENVIMRKSRHPLLELQYN.LNNFIPNDIHM..NKKNSRLIIVTGPNMGGKSTYIRQTAIIC
PFE0270c    ........TPFLILEDNIHPVVAMLMP...NFISNNIYMGCDKEKQSTLLLTGPNMGGKSTLLRQTAISV
PF14_0051   KEKNYVNDSITYIIGAKPYNIIK......HNLIKYDPFL....KKKNFILLTGKNMSGKTTLSFTILSIL

            70        80        90        100       110       120
MAL7P1.206  VMAHIGCFVPCTYAKIPIFTQIMCRVGSS..DIQLKGISTFPSEMIEIAAIIKNADQNS...........
PF14_0254   ILAQIGMFVPCDFCEVPIFTQIMCRVGAS..DFQLKGISTFLSEMIEAAAIVKNADQNS...........
PFE0270c    ILAQIGAFVPCTYCELTVVDKIPTRLGSS..DNLFEGKSTFLVELEDISNLLKQSTKYS...........
PF14_0051   FLSNLGMYAPCDENSIIGKFREPYSLKNVNYQEQIENMSLFREQAYYINSVIEEIKENYSVDKRPTREKE

            130       140       150       160       170       180       190
MAL7P1.206  .LIIIDELGRGTSTYEGPGISWSVAHYILNTIKCFCLPATHPHEMSNLEDEYKGVINNHVGAKIDTEKKK
PF14_0254   .PIIVDELGRGTSTYEGLGISWSIGKYILDNIKCFCLPATHPHEMSNIAYQCEGVINRHVETTIDKEKKK
PFE0270c    .LAILDELGRGTSSPDGTAIALSTLEQISDVIKCRCIPSTHYHLLVEEVKHNKNISNYHMSLSIDDEQEK
PF14_0051   IPIVLDEPCIATTPVDNAIIISAVSDYLKN...YCGIIITHNYDLLNKICQSENIVFKRISKDINYLKEQ

            200       210       220       230
MAL7P1.206  .ISFLYEIKKGYADKSYGVYVAQIAQLPKSVIHKAFQKSKELESV.
PF14_0254   .ICFLYEIKDGASNKSYGVNVAEIAKLPKEVIQKAYEKVEELESAE
PFE0270c    .IIFLYKFIKGVCPKSFGIHIAKLAGLPKEIIDLAHEKSLLPENVT
PF14_0051   DNKIVGKLEDGICKNSEALETCRYTNIDPHVLNLLNVYEKKYKFIH
```

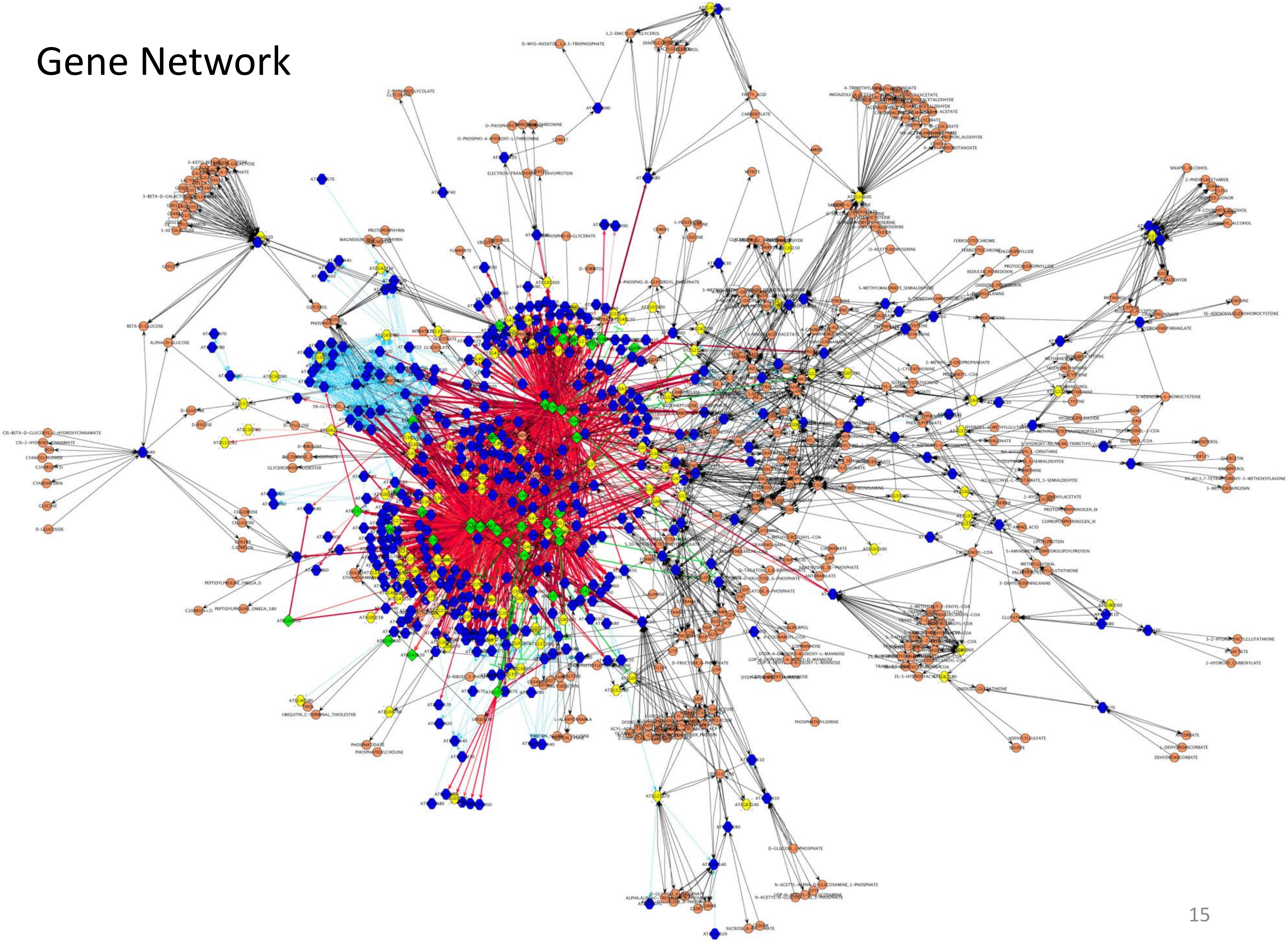
Sequence logo



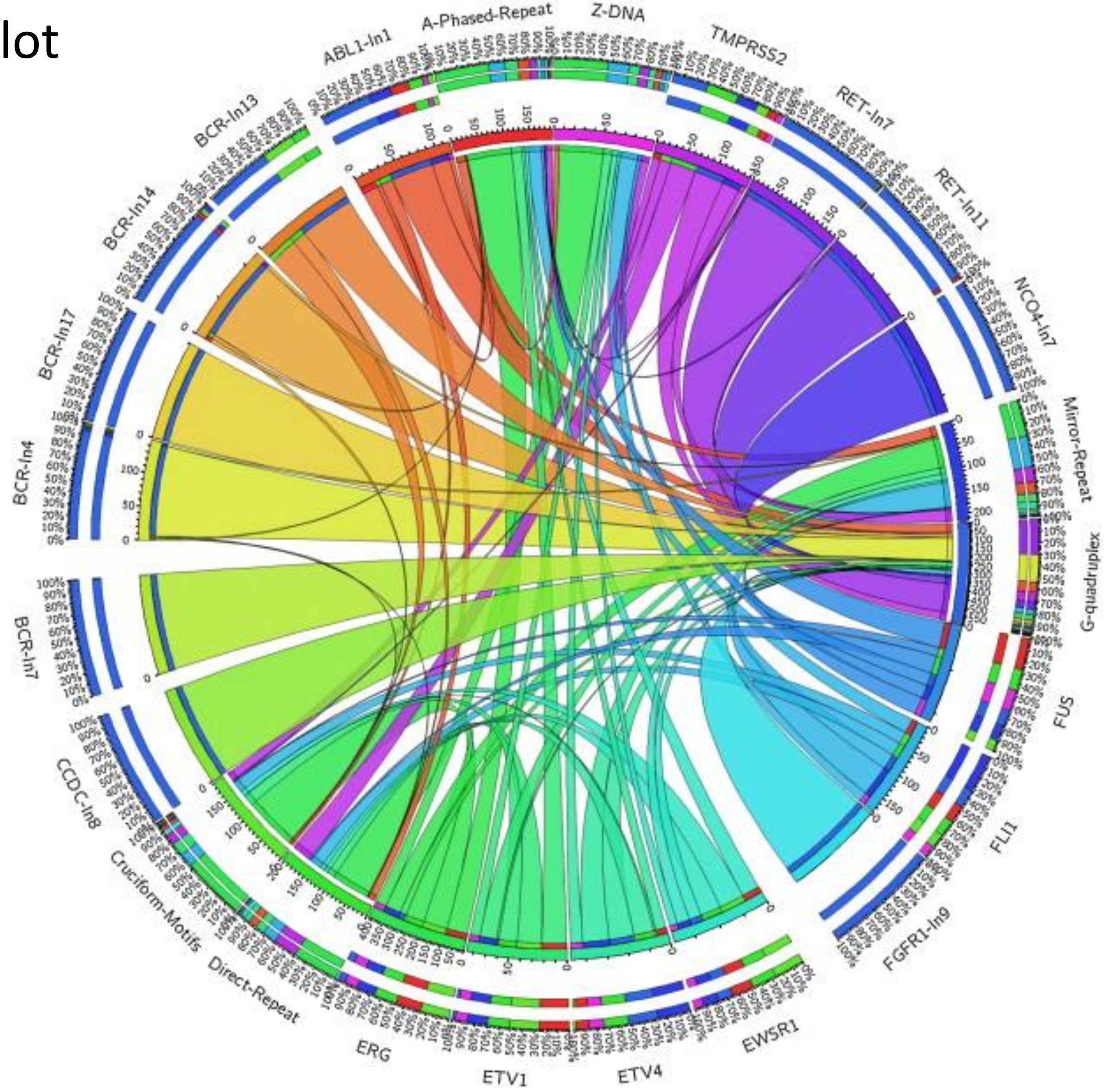
Phylogenetic tree



Gene Network

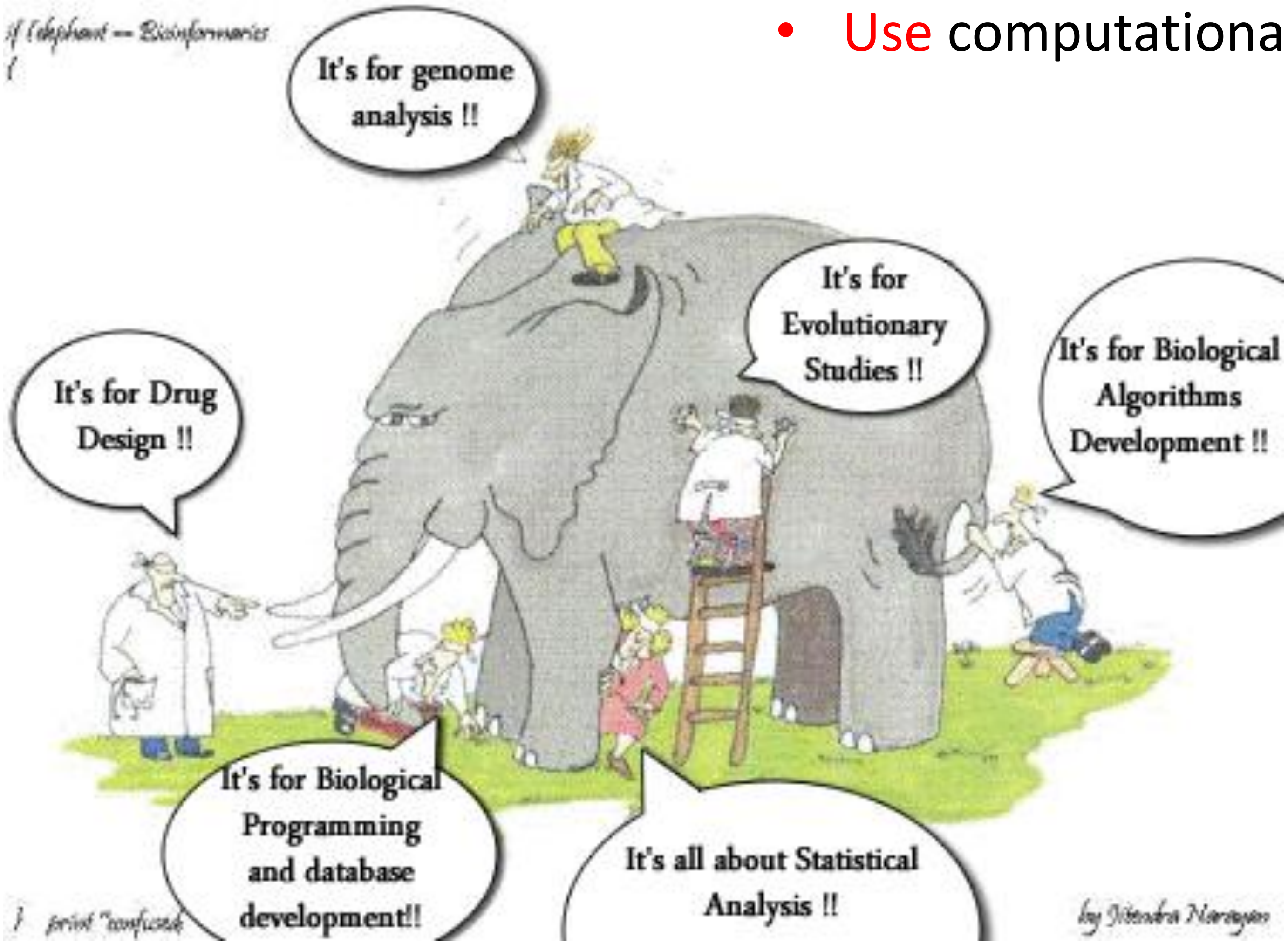


Circos plot


ABL1-In1
A-Phased-Repeat
Z-DNA
TMPRSS2
RET-In7
RET-In11
NCO4-In7
Mirror-Repeat
G-quadruplex
FUS
FLI1
FGFR1-In9
EWSR1
ETV4
ETV1
ERG
Direct-Repeat
Cruciform-Motifs
CCDC-In8
BCR-In7
BCR-In4
BCR-In17
BCR-In14
BCR-In13

What is bioinformatics?

- Develop computational tools
- Use computational tools

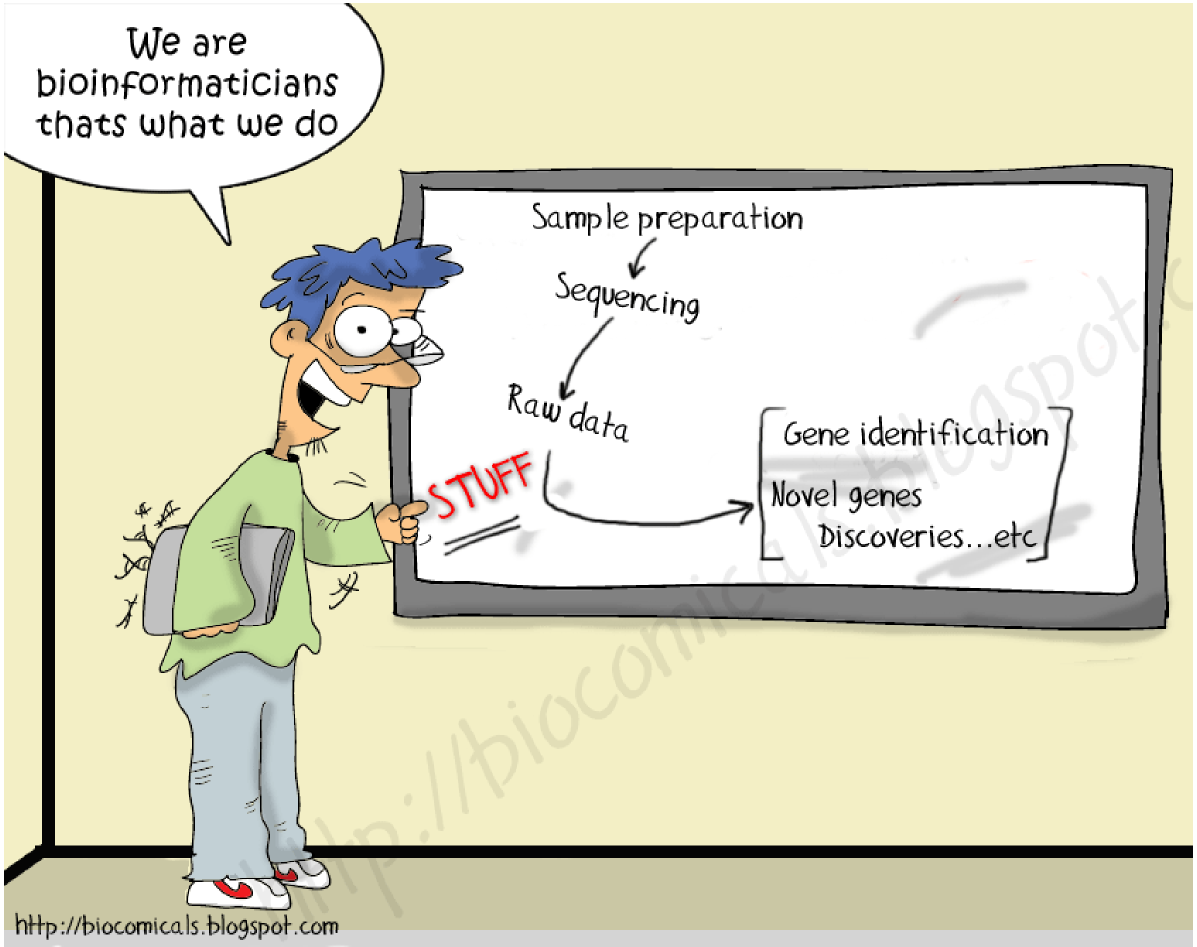


Three themes in molecular biology

- DNA sequence determines protein sequence
- Protein sequence determines protein structure
- Protein structure determines protein function

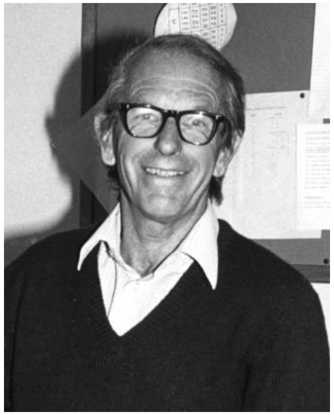
The study of how to represent, store, search, retrieve and analyze DNA/RNA/protein data

What are most bioinformaticians doing?



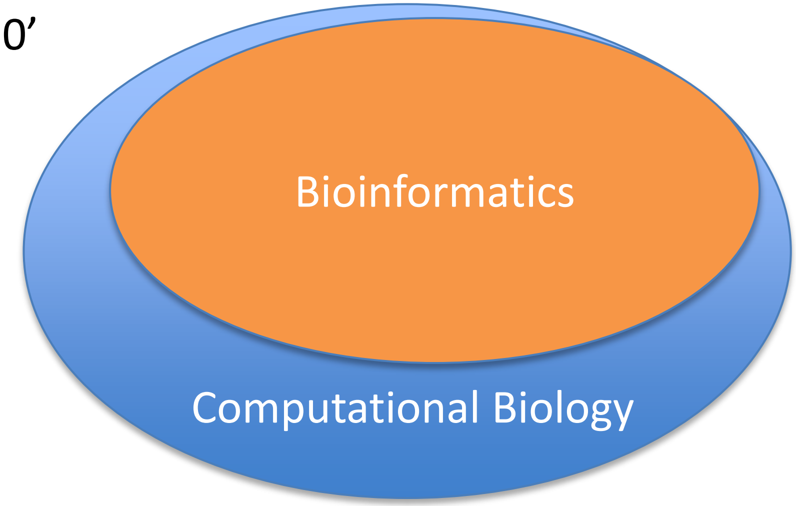
Bioinformatics pioneers

The study of how to represent, store, search, retrieve and analyze biological data



Sanger 50’

Dayhoff 60’



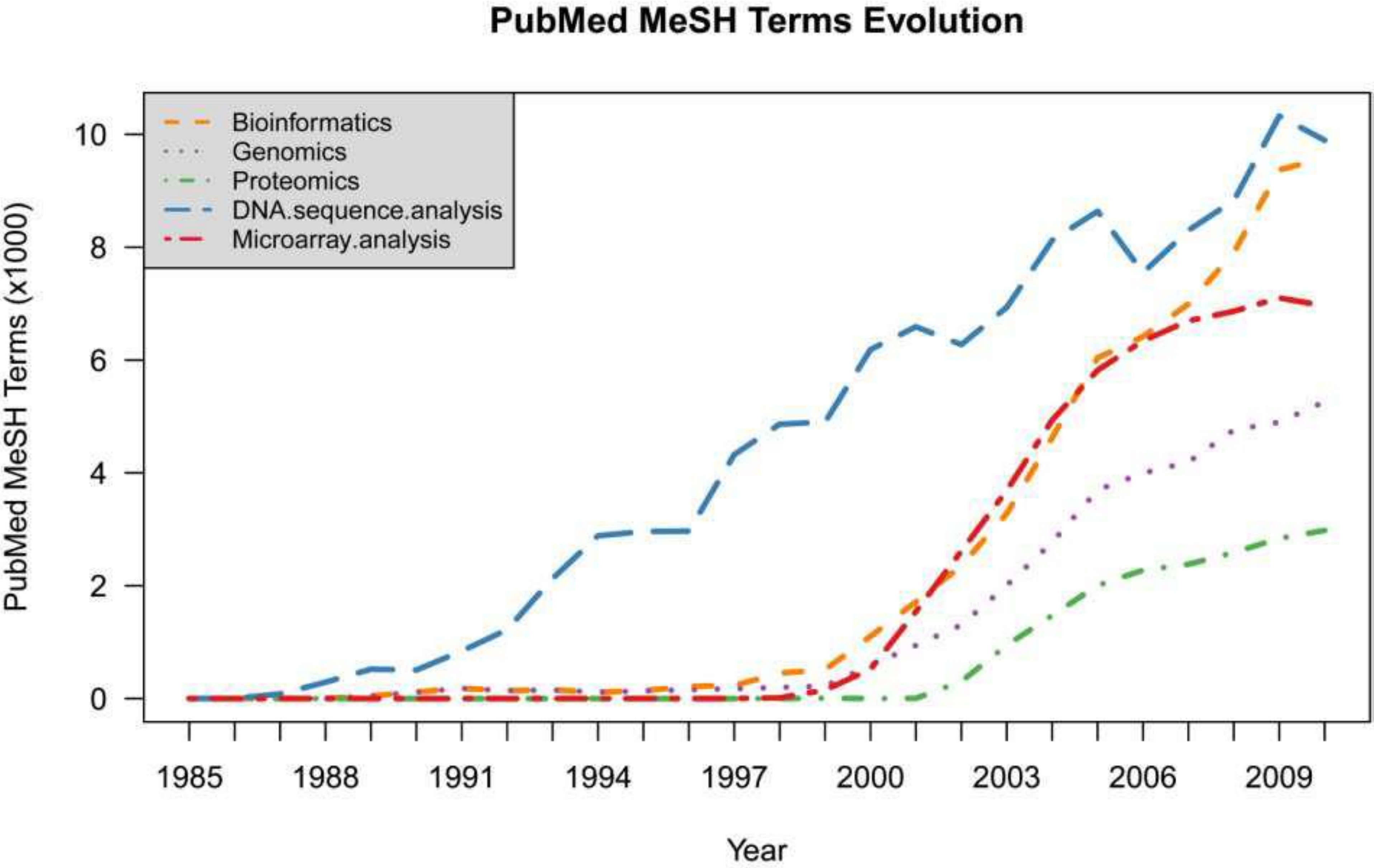
Bioinformatics

Computational Biology

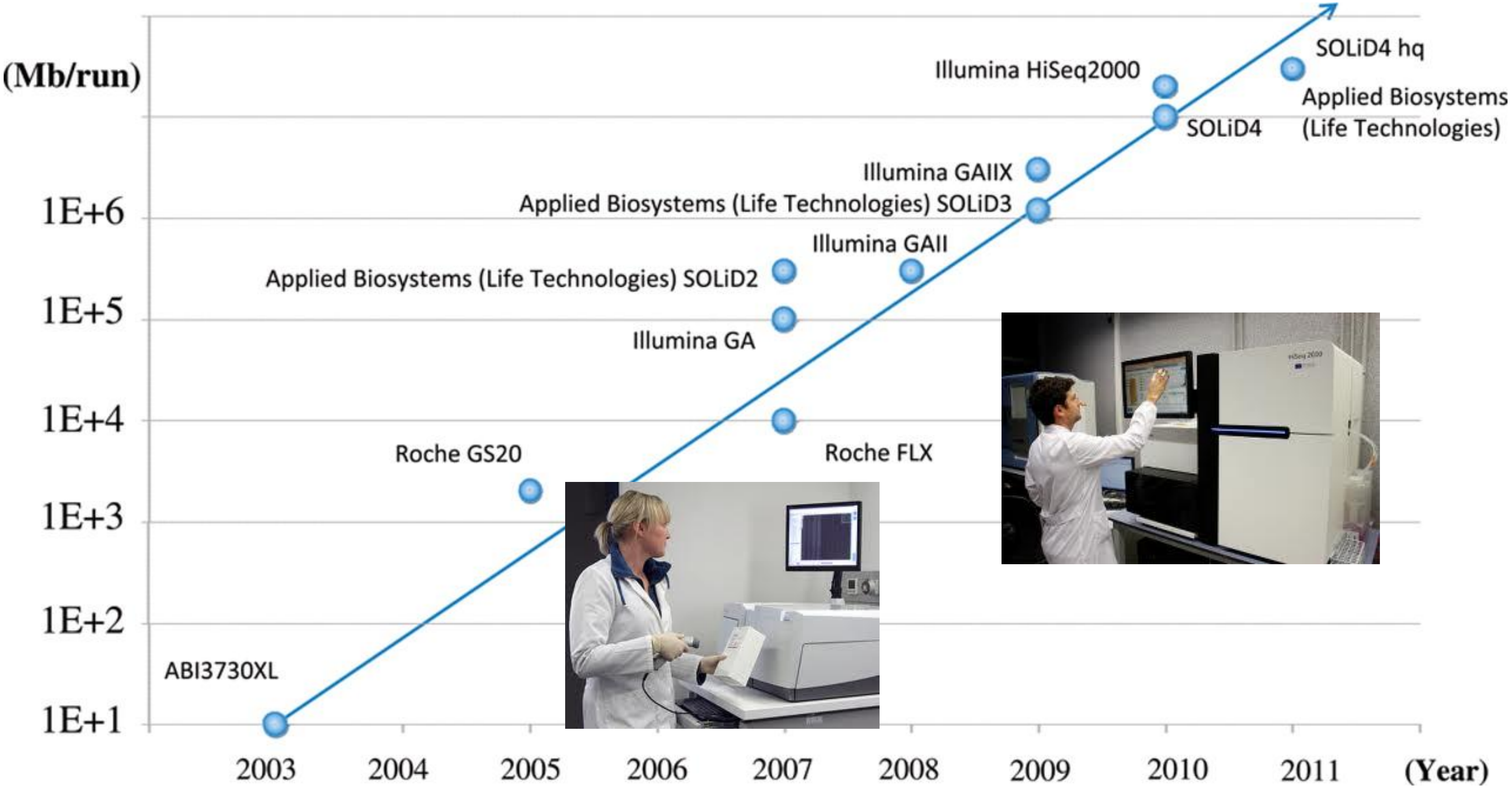
80’
Smith and Waterman

90’
Altschul

Lipman

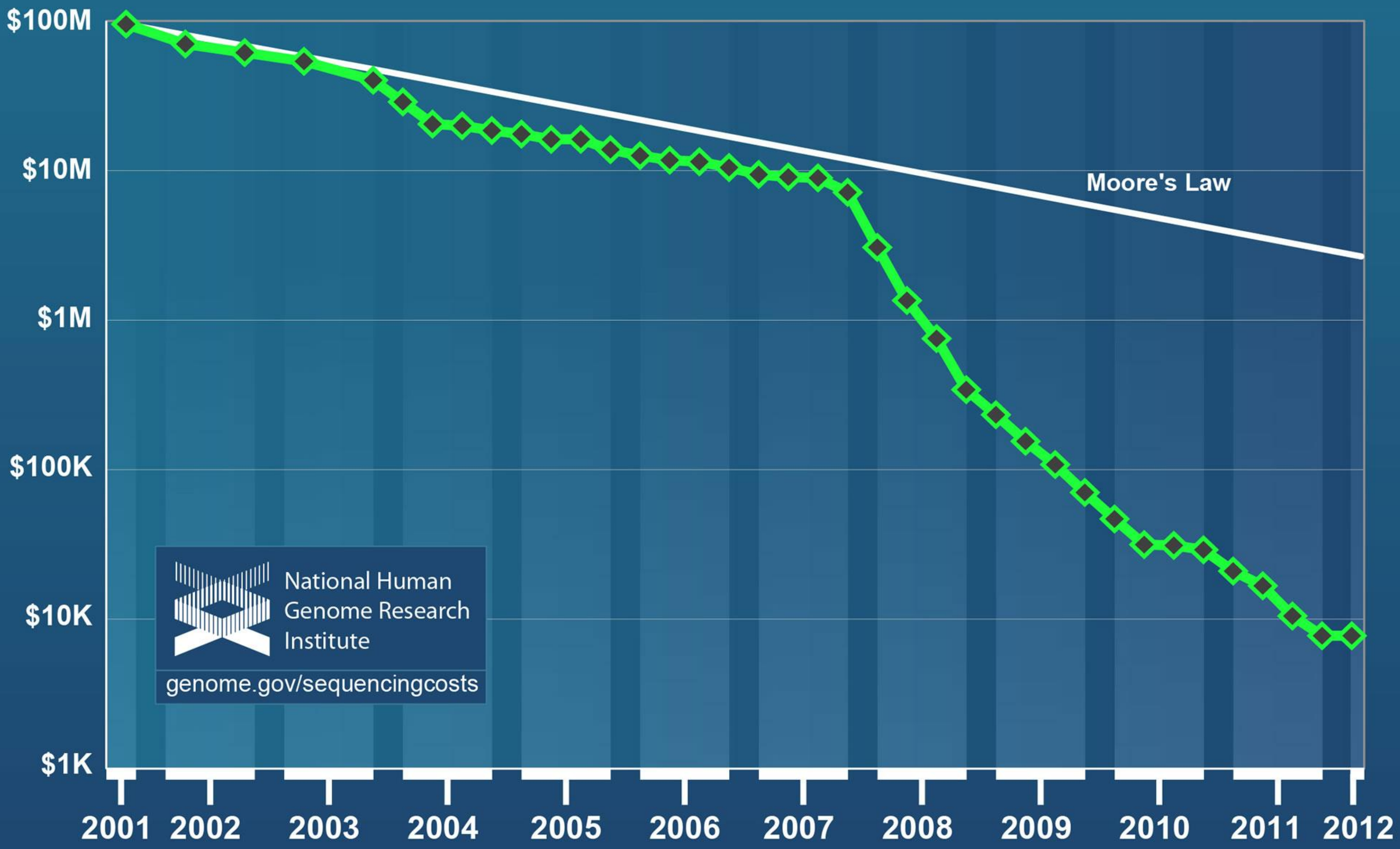

PubMed MeSH Terms Evolution
Bioinformatics
Genomics
Proteomics
DNA.sequence.analysis
Microarray.analysis
PubMed MeSH Terms (x1000)
0
2
4
6
8
10
1985
1988
1991
1994
1997
2000
2003
2006
2009
Year

Driven by big (sequence) data

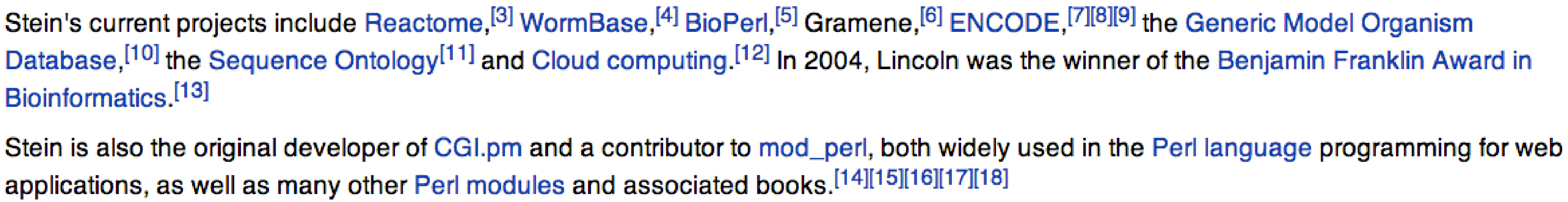


Tsuji S, 2010, Hum. Mol. Genet

Cost per Genome



http://www.genome.gov/images/content/cost_per_genome.jpg



Stein's current projects include Reactome,[3] WormBase,[4] BioPerl,[5] Gramene,[6] ENCODE,[7][8][9] the Generic Model Organism Database,[10] the Sequence Ontology[11] and Cloud computing.[12] In 2004, Lincoln was the winner of the Benjamin Franklin Award in Bioinformatics.[13]

Stein is also the original developer of CGI.pm and a contributor to mod_perl, both widely used in the Perl language programming for web applications, as well as many other Perl modules and associated books.[14][15][16][17][18]

Opinion

Bioinformatics: alive and kicking

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The electronic version of this article is the complete one
found online at http://genomebiology.com/2008/9/12/114

Bioinformaticians: gone by 2012. Bioinformatics: stronger than ever.

Abstract

Bioinformatics has become too central to biology to be left to specialist bioinformaticians. Biologists are all bioinformaticians now.

Bioinformaticians: gone by 2012. Bioinformatics: stronger than ever.

In February 2003 I gave a keynote address for the second annual O’Reilly Bioinformatics Technology Conference called ‘Bioinformatics: Gone in 2012’ in which I predicted that bioinformatics as a discipline separate from mainstream biology would be gone in ten years.

In 2008 as it happens, my predictions were quite wrong.

My prediction was that bioinformatics would become one of a series of core courses taught in undergraduate and graduate biology programs, and that there would be a vanishing market for researchers who focus solely on biological data management.

Example

http://www.iscb.org/iscb-degree-certificate-programs

The graduate programs in bioinformatics are within the Institute of Bioinformatics at University of Georgia, which offer two different focuses of study:

(1) Bioinformatics applications designed for students with background and strengths in the biological sciences; and

(2) Bioinformatics Methods Development is designed for students with background and strengths in the computer science, mathematics, and statistics.

Bioinformaticians: gone by 2012. Bioinformatics: stronger than ever.

So bioinformatics isn’t disappearing. But who is giving these bioinformatics talks, and making and analyzing these large databases? By and large these are not people who call themselves bioinformaticians. Instead, we are witnessing the rise of a new generation of computational biologists who spend part of their time at the bench and part of their time at the computer.

Login info

Windows@MO444

Account: student ID

Password: student ID

Use secure SSH to log in:

IP: 131.156.41.220

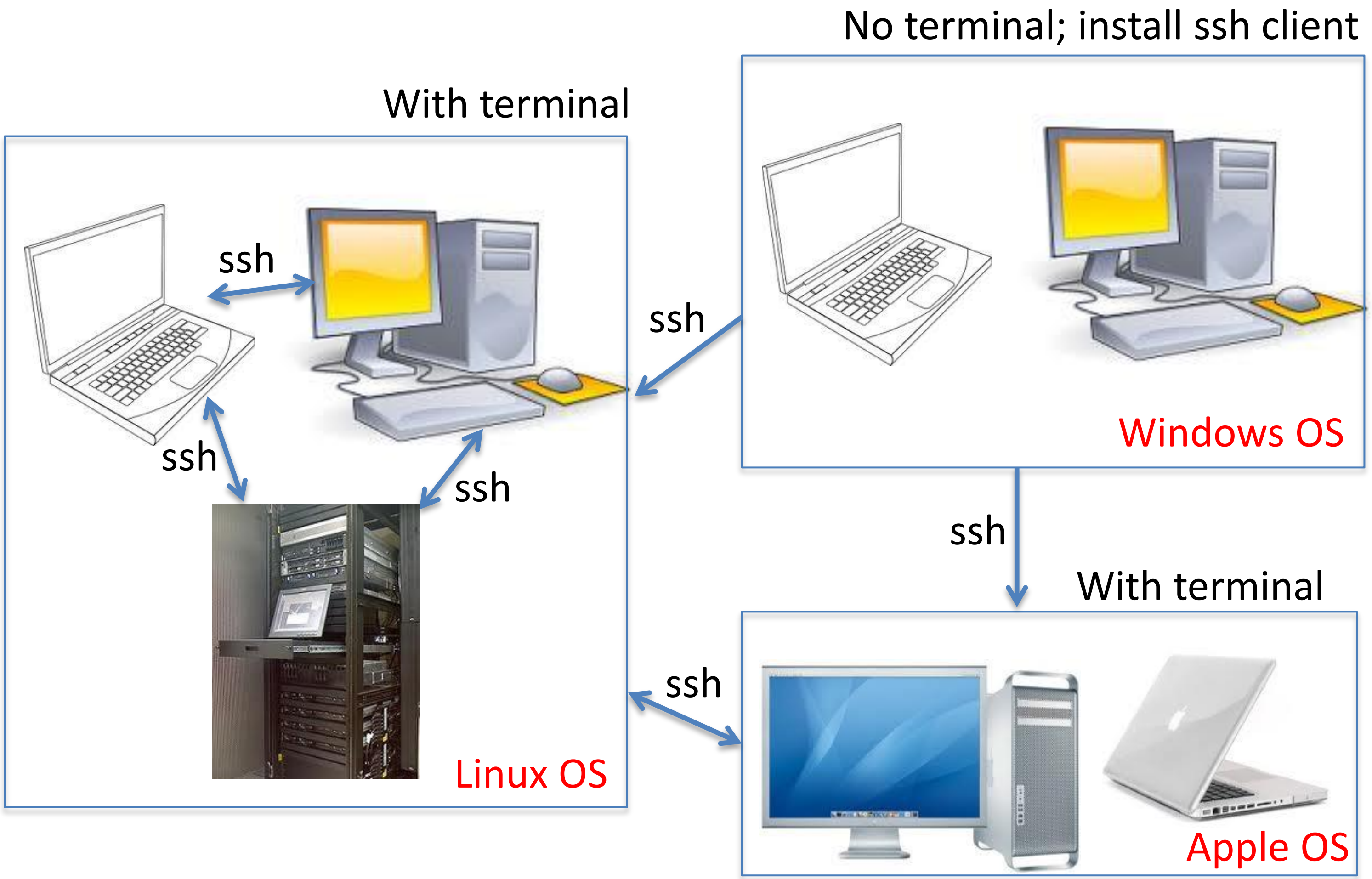
Account: student ID

Password: student ID

Change password right now

Linux@MO429

Linux or Windows?



With terminal

ssh

ssh

ssh

Linux OS

ssh

No terminal; install ssh client

Windows OS

ssh

With terminal

ssh

Apple OS

Next lecture: basic molecular biology and introduction to bioinformatics web resources