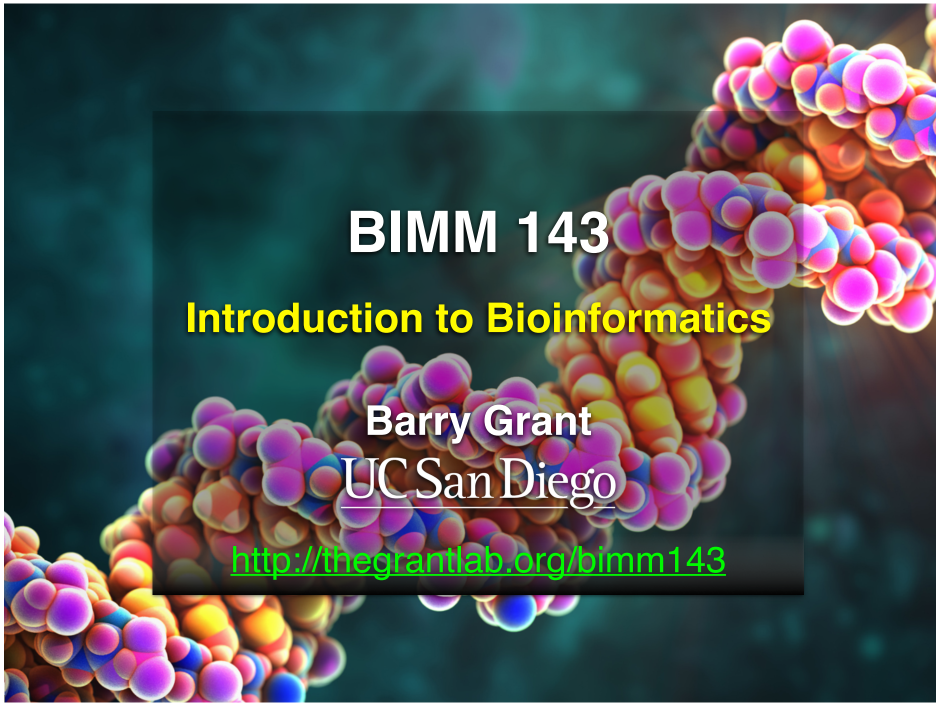


BIMM 143

Introduction to Bioinformatics

Barry Grant

UC San Diego

http://thegrantlab.org/bimm143

HELLO
my name is

BARRY

bjgrant@ucsd.edu

Office Hours:
SignUp

Location:
TATA, #2501

HELLO
HER ~~my~~ name is

YAN

yal069@ucsd.edu

HELLO
HER ~~my~~ name is

NHIEN

n7nguyen@ucsd.edu

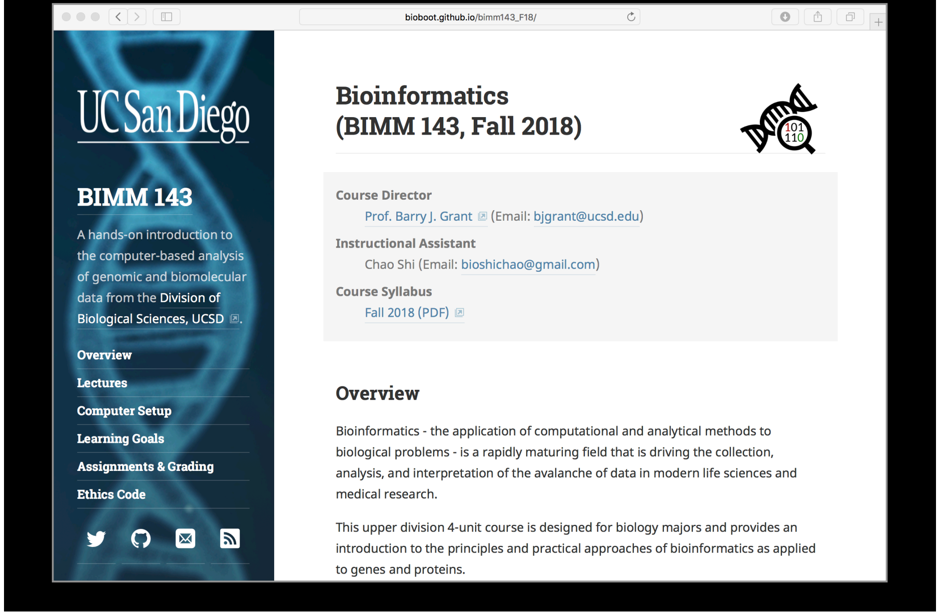
Introduce Yourself!

Your preferred name,
Place you identify with,
Major area of study/research,
Favorite joke (optional)!

Today's Menu

Course Logistics	Website, screencasts, survey, ethics, assessment and grading.
Learning Objectives	What you need to learn to succeed in this course.
Course Structure	Major lecture topics and specific leaning goals.
Introduction to Bioinformatis	**Introducing the *what, why* and *how* of bioinformatics?**
Bioinformatics Database	**Hands-on** exploration of several major databases and their associated tools.

http://thegrantlab.org/bimm143/



UC San Diego

BIMM 143

A hands-on introduction to the computer-based analysis of genomic and biomolecular data from the Division of Biological Sciences, UCSD.

Bioinformatics (BIMM 143, Fall 2018)

Course Director
Prof. Barry J. Grant (Email: bjgrant@ucsd.edu)

Instructional Assistant
Chao Shi (Email: bioshichao@gmail.com)

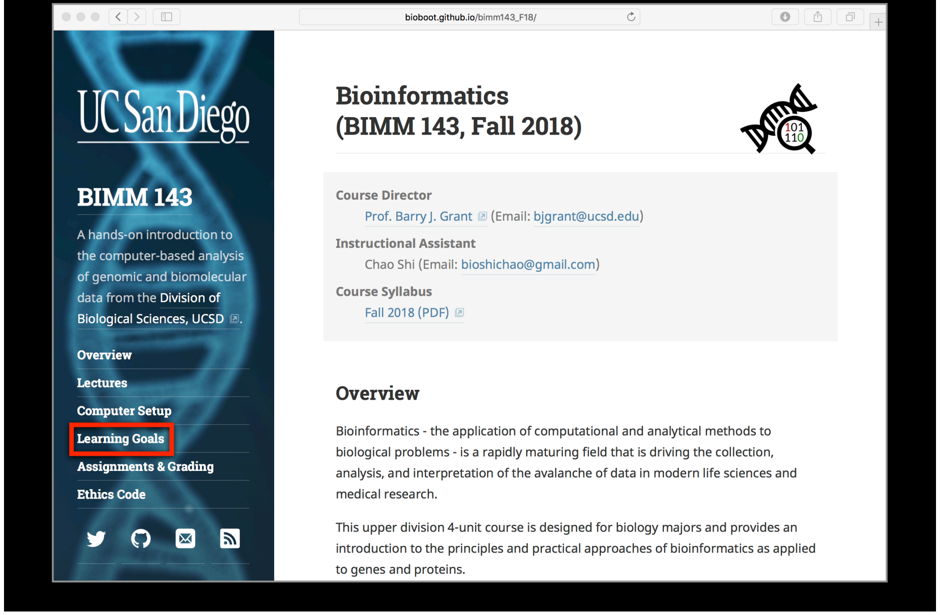
Course Syllabus
Fall 2018 (PDF)

Overview

Bioinformatics - the application of computational and analytical methods to biological problems - is a rapidly maturing field that is driving the collection, analysis, and interpretation of the avalanche of data in modern life sciences and medical research.

This upper division 4-unit course is designed for biology majors and provides an introduction to the principles and practical approaches of bioinformatics as applied to genes and proteins.

http://thegrantlab.org/bimm143/



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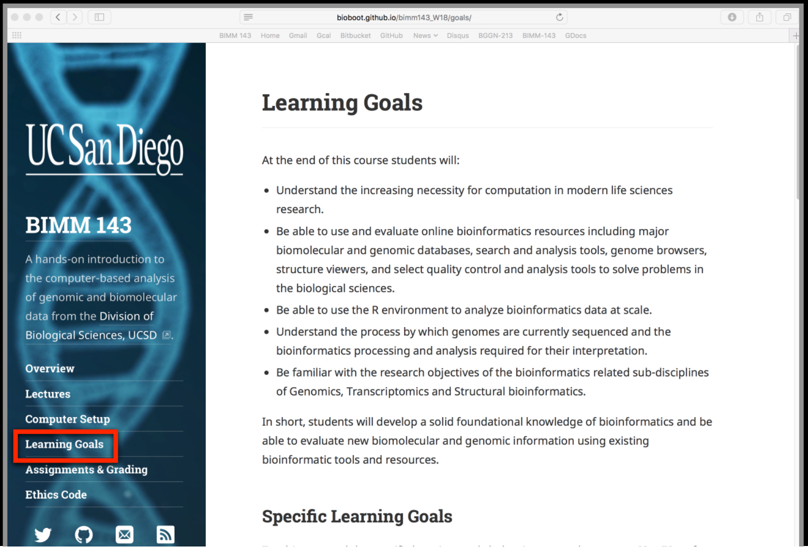
What essential concepts and skills should YOU attain from this course?



UC San Diego

BIMM 143

A hands-on introduction to the computer-based analysis of genomic and biomolecular data from the Division of Biological Sciences, UCSD.

Learning Goals

At the end of this course students will:

- Understand the increasing necessity for computation in modern life sciences research.
- Be able to use and evaluate online bioinformatics resources including major biomolecular and genomic databases, search and analysis tools, genome browsers, structure viewers, and select quality control and analysis tools to solve problems in the biological sciences.
- Be able to use the R environment to analyze bioinformatics data at scale.
- Understand the process by which genomes are currently sequenced and the bioinformatics processing and analysis required for their interpretation.
- Be familiar with the research objectives of the bioinformatics related sub-disciplines of Genomics, Transcriptomics and Structural bioinformatics.

In short, students will develop a solid foundational knowledge of bioinformatics and be able to evaluate new biomolecular and genomic information using existing bioinformatic tools and resources.

Specific Learning Goals

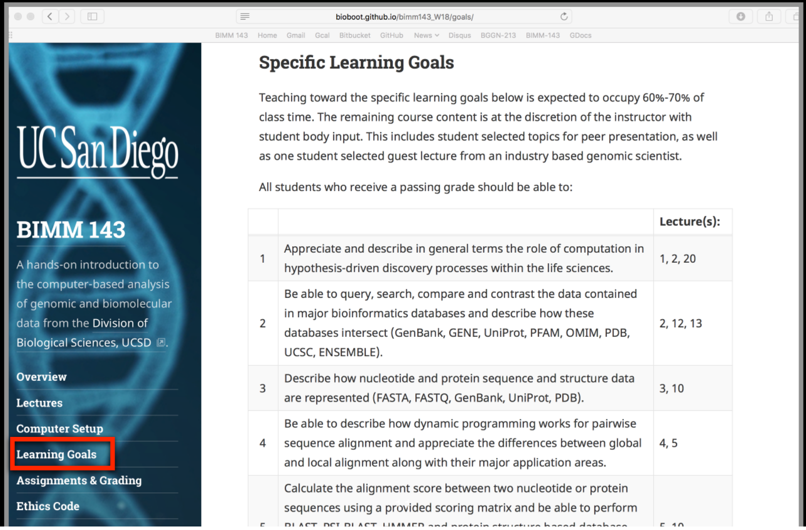
At the end of this course students will:

- Understand the increasing necessity for computation in modern life sciences research.
- Be able to use and evaluate online bioinformatics resources and analysis tools to solve problems in the biological sciences.
- Be able to use the R environment to analyze bioinformatics data at scale.
- Be familiar with the research objectives of the bioinformatics related sub-disciplines of Genome informatics, Transcriptomics and Structural informatics.

In short, you will develop a solid foundational knowledge of **bioinformatics** and be able to evaluate new biomolecular and genomic information using **existing bioinformatic tools and resources**.

Specific Learning Goals….

What I want you to know by course end!



BIMM 143

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Specific Learning Goals

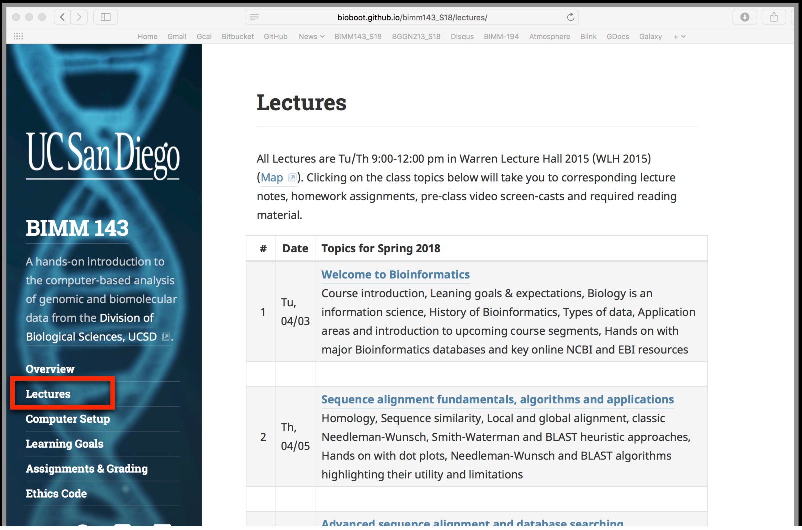
Teaching toward the specific learning goals below is expected to occupy 60%-70% of class time. The remaining course content is at the discretion of the instructor with student body input. This includes student selected topics for peer presentation, as well as one student selected guest lecture from an industry based genomic scientist.

All students who receive a passing grade should be able to:

		Lecture(s):
1	Appreciate and describe in general terms the role of computation in hypothesis-driven discovery processes within the life sciences.	1, 2, 20
2	Be able to query, search, compare and contrast the data contained in major bioinformatics databases and describe how these databases intersect (GenBank, GENE, UniProt, PFAM, OMIM, PDB, UCSC, ENSEMBLE).	2, 12, 13
3	Describe how nucleotide and protein sequence and structure data are represented (FASTA, FASTQ, GenBank, UniProt, PDB).	3, 10
4	Be able to describe how dynamic programming works for pairwise sequence alignment and appreciate the differences between global and local alignment along with their major application areas.	4, 5
5	Calculate the alignment score between two nucleotide or protein sequences using a provided scoring matrix and be able to perform BLAST, PSI-BLAST, HMMER and protein structure based database	5, 10

Course Structure

Derived from specific learning goals



BIMM 143

A hands-on introduction to the computer-based analysis of genomic and biomolecular data from the Division of Biological Sciences, UCSD.

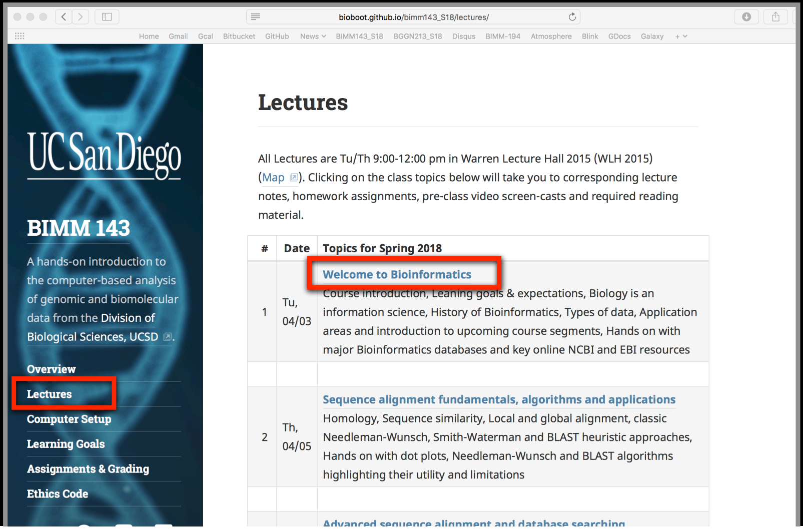
Lectures

All Lectures are Tu/Th 9:00-12:00 pm in Warren Lecture Hall 2015 (WLH 2015) (Map). Clicking on the class topics below will take you to corresponding lecture notes, homework assignments, pre-class video screen-casts and required reading material.

#	Date	Topics for Spring 2018
1	Tu, 04/03	**Welcome to Bioinformatics** Course introduction, Leaning goals & expectations, Biology is an information science, History of Bioinformatics, Types of data, Application areas and introduction to upcoming course segments, Hands on with major Bioinformatics databases and key online NCBI and EBI resources
2	Th, 04/05	**Sequence alignment fundamentals, algorithms and applications** Homology, Sequence similarity, Local and global alignment, classic Needleman-Wunsch, Smith-Waterman and BLAST heuristic approaches, Hands on with dot plots, Needleman-Wunsch and BLAST algorithms highlighting their utility and limitations
		Advanced sequence alignment and database searching

Course Structure

Derived from specific learning goals



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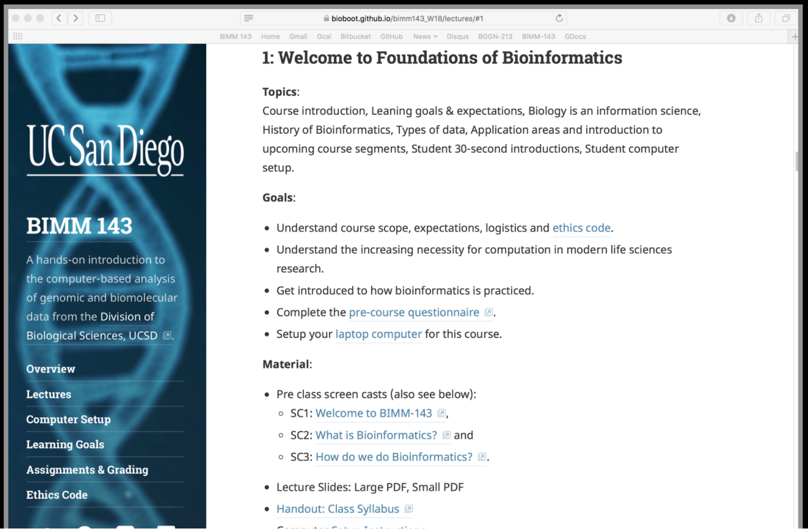
		Advanced sequence alignment and database searching

Class Details

Goals, Class material, Screencasts & **Homework**


bioboot.github.io/bimm143_W18/lectures/#1
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BIMM 143

A hands-on introduction to the computer-based analysis of genomic and biomolecular data from the Division of Biological Sciences, UCSD.

- Overview
- Lectures
- Computer Setup
- Learning Goals
- Assignments & Grading
- Ethics Code

1: Welcome to Foundations of Bioinformatics

Topics:
Course introduction, Leaning goals & expectations, Biology is an information science, History of Bioinformatics, Types of data, Application areas and introduction to upcoming course segments, Student 30-second introductions, Student computer setup.

Goals:

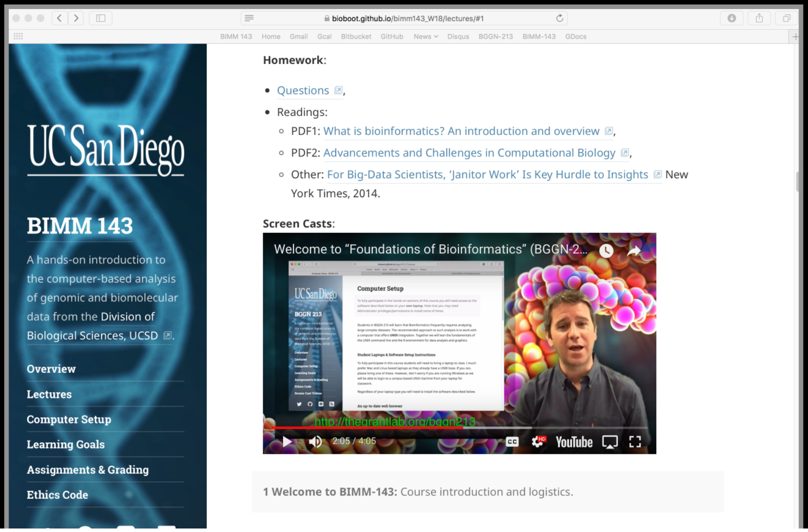
- Understand course scope, expectations, logistics and ethics code.
- Understand the increasing necessity for computation in modern life sciences research.
- Get introduced to how bioinformatics is practiced.
- Complete the pre-course questionnaire.
- Setup your laptop computer for this course.

Material:

- Pre class screen casts (also see below):
  - SC1: Welcome to BIMM-143,
  - SC2: What is Bioinformatics? and
  - SC3: How do we do Bioinformatics?.
- Lecture Slides: Large PDF, Small PDF
- Handout: Class Syllabus

Homework

Goals, Class material, Screencasts & **Homework**


bioboot.github.io/bimm143_W18/lectures/#1
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UC San Diego
Welcome to "Foundations of Bioinformatics" (BGGN-2...
Computer Setup
http://thegrantlab.org/bggn213
2:05 / 4:05
YouTube

BIMM 143

A hands-on introduction to the computer-based analysis of genomic and biomolecular data from the Division of Biological Sciences, UCSD.

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Homework:

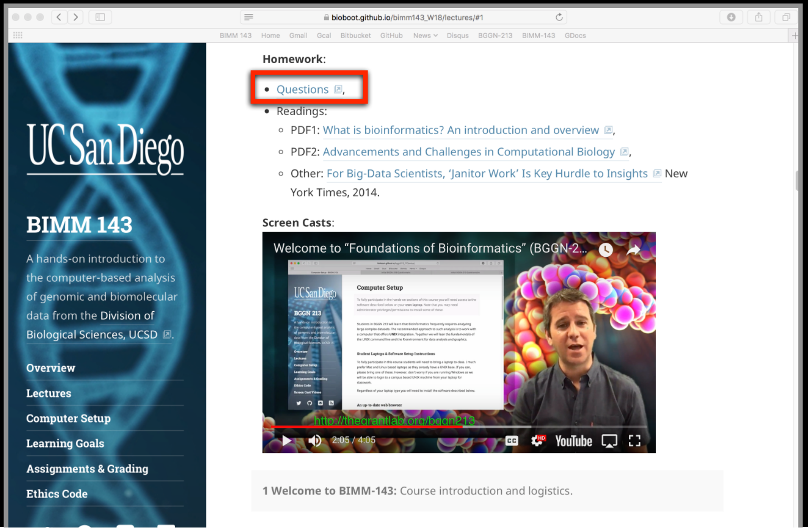
- Questions,
- Readings:
  - PDF1: What is bioinformatics? An introduction and overview,
  - PDF2: Advancements and Challenges in Computational Biology,
  - Other: For Big-Data Scientists, 'Janitor Work' Is Key Hurdle to Insights New York Times, 2014.

Screen Casts:

1 Welcome to BIMM-143: Course introduction and logistics.

Homework

Goals, Class material, Screencasts & **Homework**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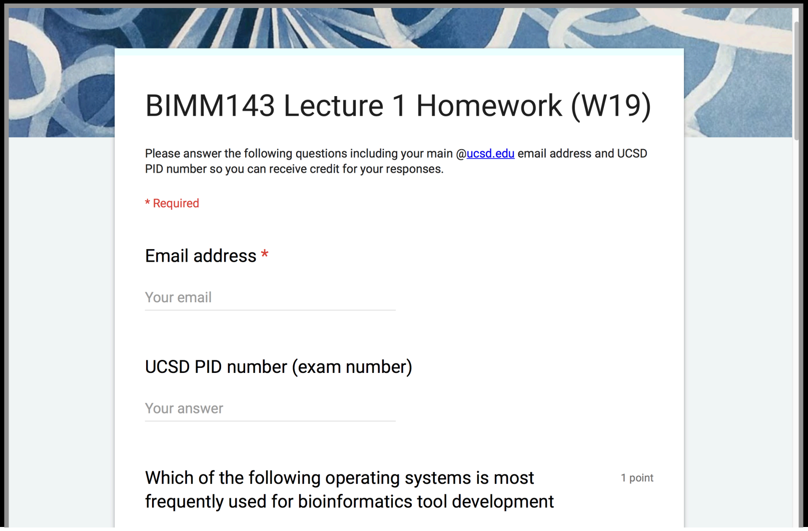


BIMM143 Lecture 1 Homework (W19)

Please answer the following questions including your main @ucsd.edu email address and UCSD PID number so you can receive credit for your responses.

* Required

Email address *

Your email

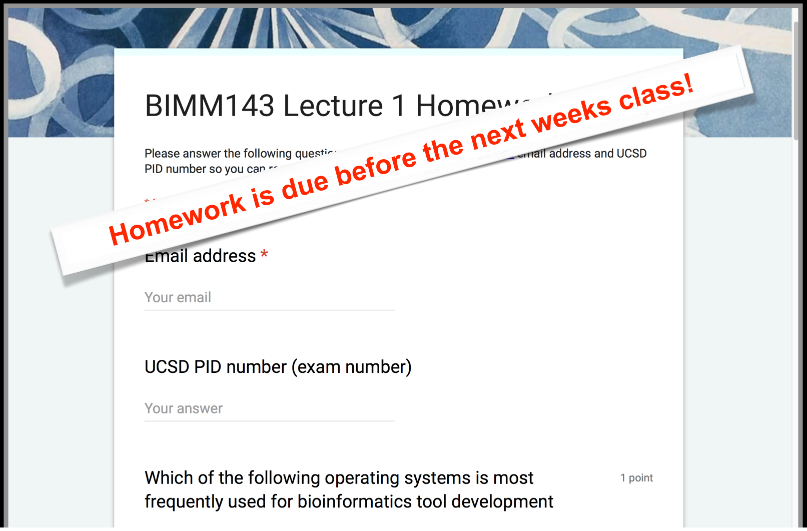
UCSD PID number (exam number)

Your answer

Which of the following operating systems is most frequently used for bioinformatics tool development 1 point

Homework (35% of course grade)

Goals, Class material, Screencasts & **Homework**



BIMM143 Lecture 1 Homew

Please answer the following questi
PID number so you can r

Email address *

Your email

UCSD PID number (exam number)

Your answer

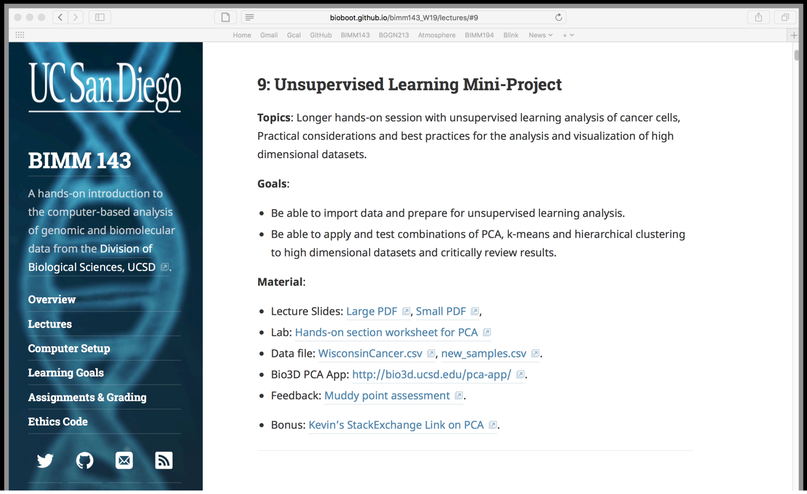
Which of the following operating systems is most frequently used for bioinformatics tool development

1 point

Homework is due before the next weeks class!

Projects

Week long **mini-projects** (x2), and 1 five week main project



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Ethics Code

9: Unsupervised Learning Mini-Project

Topics: Longer hands-on session with unsupervised learning analysis of cancer cells, Practical considerations and best practices for the analysis and visualization of high dimensional datasets.

Goals:

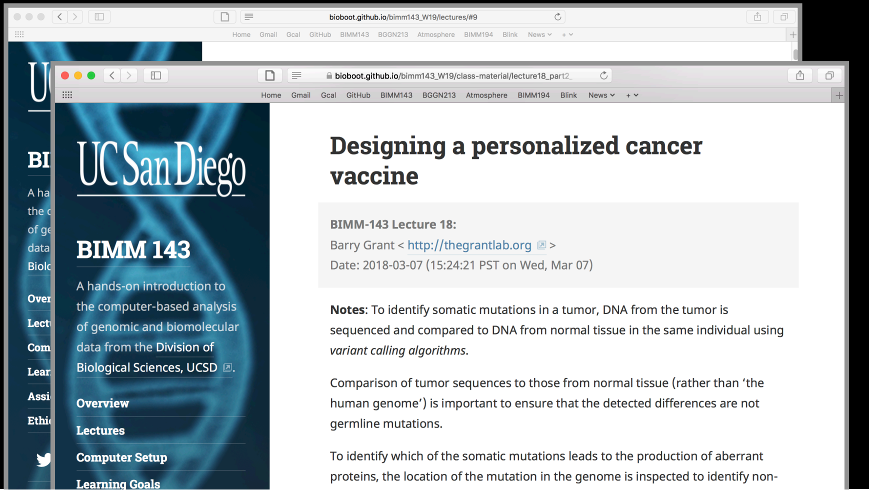
- Be able to import data and prepare for unsupervised learning analysis.
- Be able to apply and test combinations of PCA, k-means and hierarchical clustering to high dimensional datasets and critically review results.

Material:

- Lecture Slides: Large PDF, Small PDF.
- Lab: Hands-on section worksheet for PCA
- Data file: WisconsinCancer.csv, new_samples.csv.
- Bio3D PCA App: http://bio3d.ucsd.edu/pca-app/.
- Feedback: Muddy point assessment.
- Bonus: Kevin's StackExchange Link on PCA.

Projects

Week long **mini-projects** (x2), and 1 five week main project



bioboot.github.io/bimm143_W19/lectures/#9
bioboot.github.io/bimm143_W19/class-material/lecture18_part2
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BIMM 143

A hands-on introduction to the computer-based analysis of genomic and biomolecular data from the Division of Biological Sciences, UCSD.

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Designing a personalized cancer vaccine

BIMM-143 Lecture 18:
Barry Grant < http://thegrantlab.org >
Date: 2018-03-07 (15:24:21 PST on Wed, Mar 07)

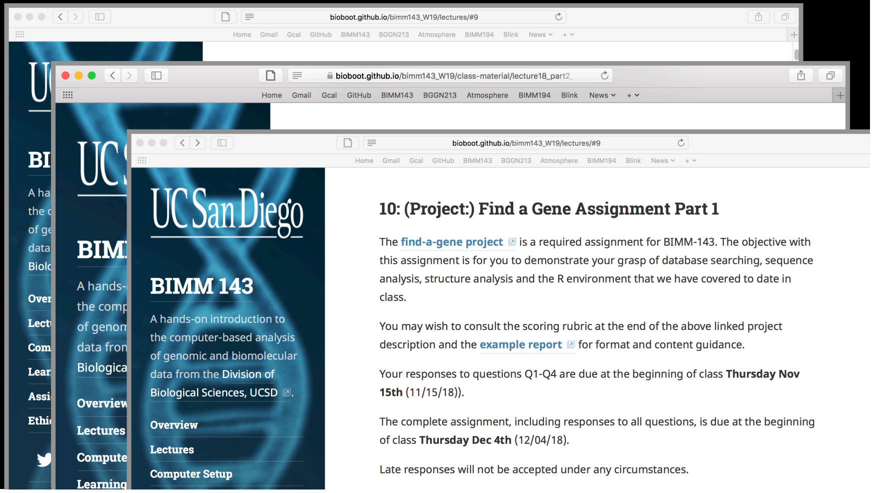
Notes: To identify somatic mutations in a tumor, DNA from the tumor is sequenced and compared to DNA from normal tissue in the same individual using *variant calling algorithms*.

Comparison of tumor sequences to those from normal tissue (rather than 'the human genome') is important to ensure that the detected differences are not germline mutations.

To identify which of the somatic mutations leads to the production of aberrant proteins, the location of the mutation in the genome is inspected to identify non-

Projects (20% of course grade)

Week long mini-projects (x2), and 1 five week **main project**



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10: (Project:) Find a Gene Assignment Part 1

The **find-a-gene project** is a required assignment for BIMM-143. The objective with this assignment is for you to demonstrate your grasp of database searching, sequence analysis, structure analysis and the R environment that we have covered to date in class.

You may wish to consult the scoring rubric at the end of the above linked project description and the **example report** for format and content guidance.

Your responses to questions Q1-Q4 are due at the beginning of class **Thursday Nov 15th** (11/15/18).

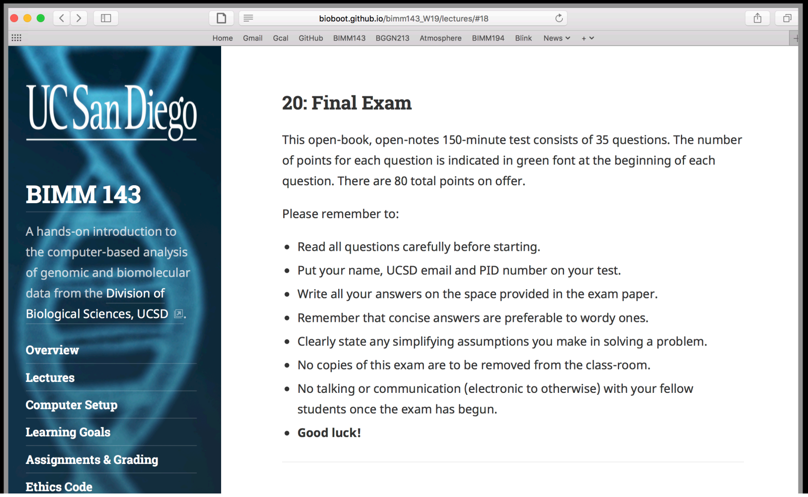
The complete assignment, including responses to all questions, is due at the beginning of class **Thursday Dec 4th** (12/04/18).

Late responses will not be accepted under any circumstances.

Final Exam

Open-book, open-notes 150-minute test

(45% of course grade)



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20: Final Exam

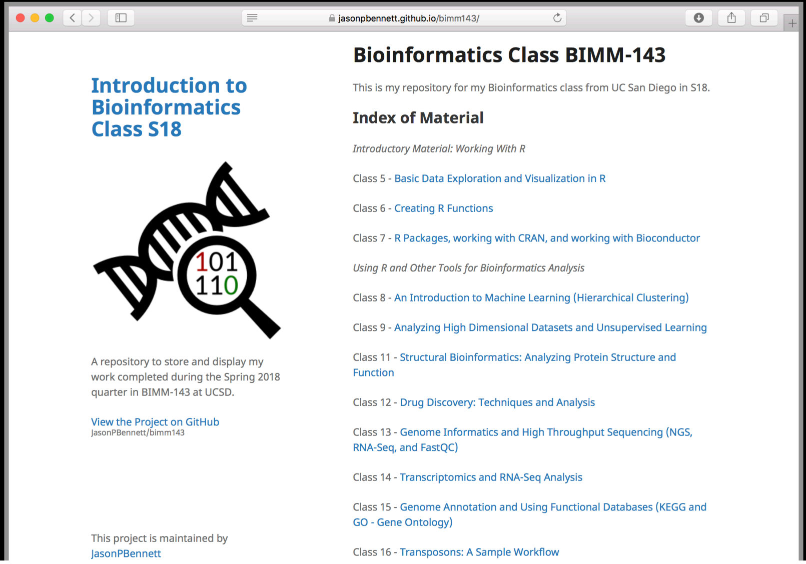
This open-book, open-notes 150-minute test consists of 35 questions. The number of points for each question is indicated in green font at the beginning of each question. There are 80 total points on offer.

Please remember to:

- Read all questions carefully before starting.
- Put your name, UCSD email and PID number on your test.
- Write all your answers on the space provided in the exam paper.
- Remember that concise answers are preferable to wordy ones.
- Clearly state any simplifying assumptions you make in solving a problem.
- No copies of this exam are to be removed from the class-room.
- No talking or communication (electronic to otherwise) with your fellow students once the exam has begun.
- **Good luck!**

Bonus:

Online portfolio of **your** bioinformatics work!



Bioinformatics Class BIMM-143

This is my repository for my Bioinformatics class from UC San Diego in S18.

Introduction to Bioinformatics Class S18

A repository to store and display my work completed during the Spring 2018 quarter in BIMM-143 at UCSD.

View the Project on GitHub
JasonPBennett/bimm143

This project is maintained by JasonPBennett

Index of Material

Introductory Material: Working With R

Class 5 - Basic Data Exploration and Visualization in R

Class 6 - Creating R Functions

Class 7 - R Packages, working with CRAN, and working with Bioconductor

Using R and Other Tools for Bioinformatics Analysis

Class 8 - An Introduction to Machine Learning (Hierarchical Clustering)

Class 9 - Analyzing High Dimensional Datasets and Unsupervised Learning

Class 11 - Structural Bioinformatics: Analyzing Protein Structure and Function

Class 12 - Drug Discovery: Techniques and Analysis

Class 13 - Genome Informatics and High Throughput Sequencing (NGS, RNA-Seq, and FastQC)

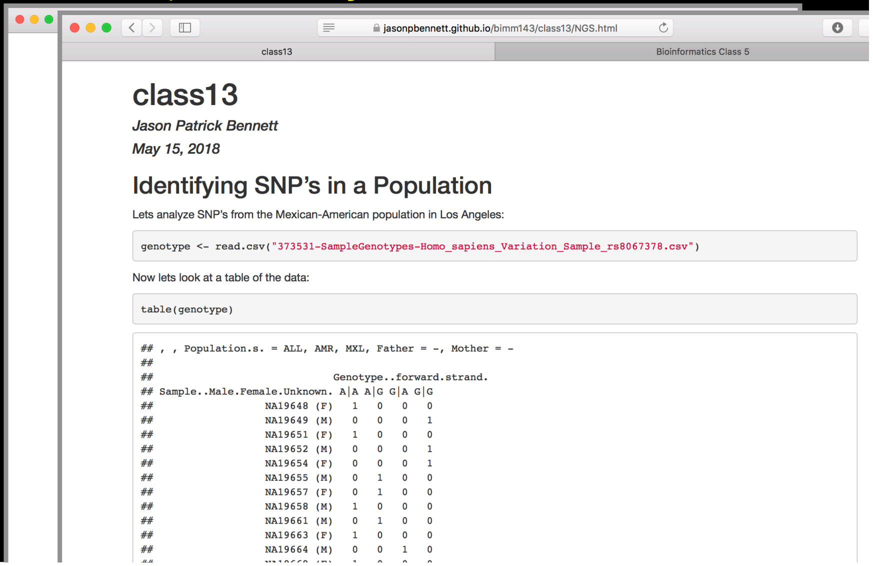
Class 14 - Transcriptomics and RNA-Seq Analysis

Class 15 - Genome Annotation and Using Functional Databases (KEGG and GO - Gene Ontology)

Class 16 - Transposons: A Sample Workflow

Bonus:

Online portfolio of **your** bioinformatics work!



class13

Jason Patrick Bennett

May 15, 2018

Identifying SNP's in a Population

Lets analyze SNP's from the Mexican-American population in Los Angeles:

```
genotype <- read.csv("373531-SampleGenotypes-Homo_sapiens_Variation_Sample_rs8067378.csv")
```

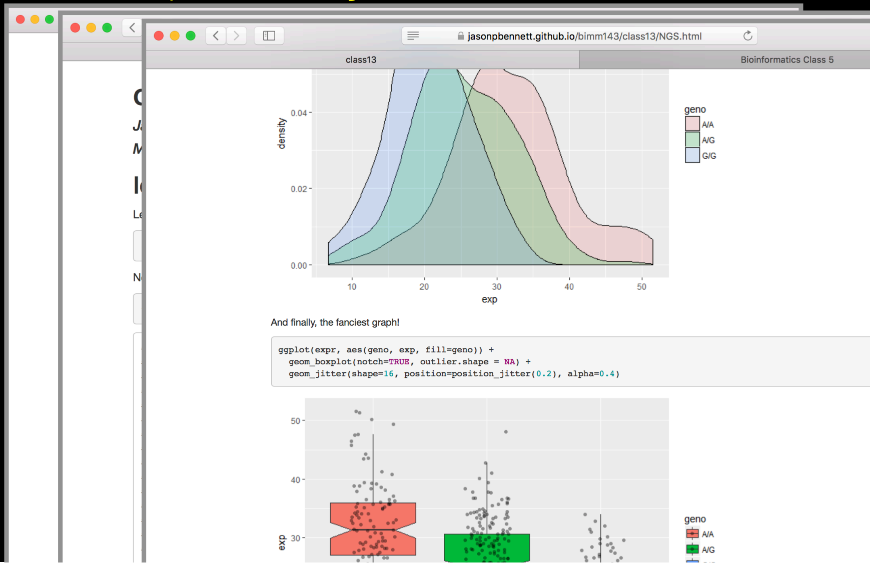
Now lets look at a table of the data:

```
table(genotype)
```

```
## , , Population.s. = ALL, AMR, MXL, Father = -, Mother = -
##
##                               Genotype..forward.strand.
## Sample..Male.Female.Unknown. A|A A|G G|A G|G
##                 NA19648 (F)   1   0   0   0
##                 NA19649 (M)   0   0   0   1
##                 NA19651 (F)   1   0   0   0
##                 NA19652 (M)   0   0   0   1
##                 NA19654 (F)   0   0   0   1
##                 NA19655 (M)   0   1   0   0
##                 NA19657 (F)   0   1   0   0
##                 NA19658 (M)   1   0   0   0
##                 NA19661 (M)   0   1   0   0
##                 NA19663 (F)   1   0   0   0
##                 NA19664 (M)   0   0   1   0
```

Bonus:

Online portfolio of **your** bioinformatics work!



And finally, the fanciest graph!

```
ggplot(expr, aes(geno, exp, fill=geno)) +
  geom_boxplot(notch=TRUE, outlier.shape = NA) +
  geom_jitter(shape=16, position=position_jitter(0.2), alpha=0.4)
```

Side Note: Why stick with this course?

Provides a hands-on practical introduction to major bioinformatics concepts and resources.

Covers modern hot topics and the intimate coupling of informatics with biology - highlighting the impact of computing advances and 'big data' on biology!

Designed for biology majors with no programing experience or high level math skills.

Provides a hook for increasing computational and data science competencies in the biosciences - valuable high demand translational skills!

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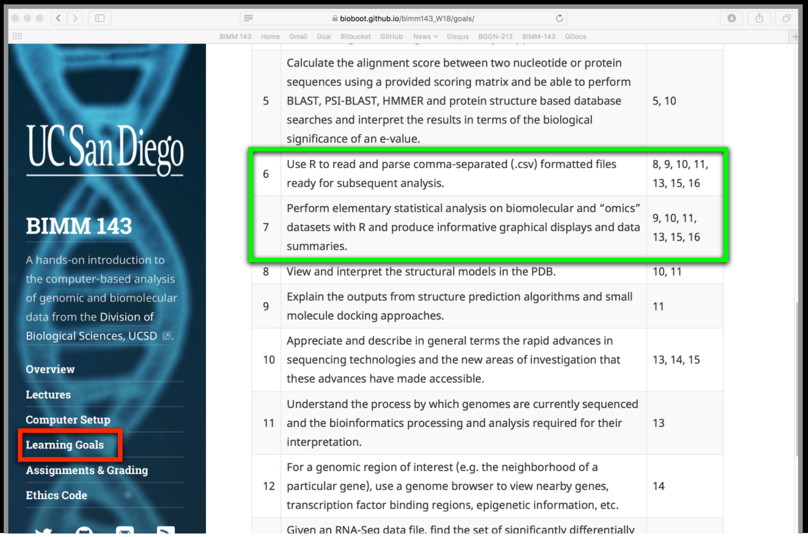
BIMM-143 Learning Goals….

Data science R based learning goals

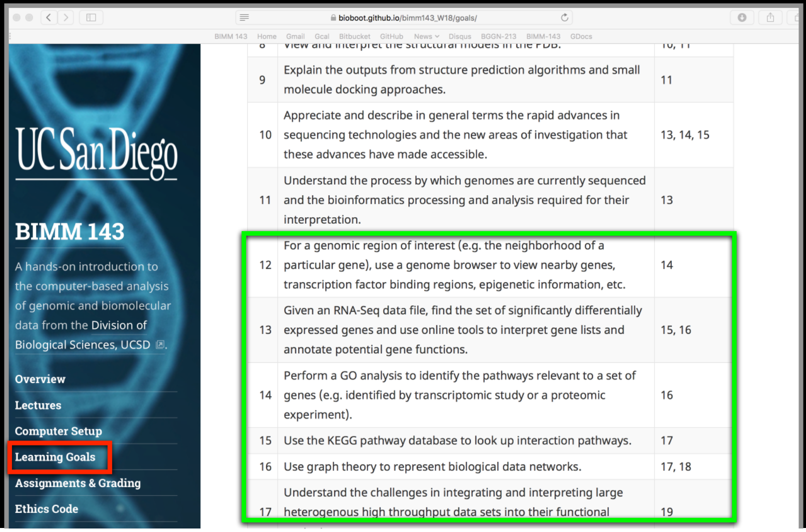


A hands-on introduction to the computer-based analysis of genomic and biomolecular data from the Division of Biological Sciences, UCSD.

5	Calculate the alignment score between two nucleotide or protein sequences using a provided scoring matrix and be able to perform BLAST, PSI-BLAST, HMMER and protein structure based database searches and interpret the results in terms of the biological significance of an e-value.	5, 10
6	Use R to read and parse comma-separated (.csv) formatted files ready for subsequent analysis.	8, 9, 10, 11, 13, 15, 16
7	Perform elementary statistical analysis on biomolecular and "omics" datasets with R and produce informative graphical displays and data summaries.	9, 10, 11, 13, 15, 16
8	View and interpret the structural models in the PDB.	10, 11
9	Explain the outputs from structure prediction algorithms and small molecule docking approaches.	11
10	Appreciate and describe in general terms the rapid advances in sequencing technologies and the new areas of investigation that these advances have made accessible.	13, 14, 15
11	Understand the process by which genomes are currently sequenced and the bioinformatics processing and analysis required for their interpretation.	13
12	For a genomic region of interest (e.g. the neighborhood of a particular gene), use a genome browser to view nearby genes, transcription factor binding regions, epigenetic information, etc.	14
	Given an RNA-Seq data file, find the set of significantly differentially	

BIMM-143 Learning Goals….

Delve deeper into "real-world" bioinformatics



A hands-on introduction to the computer-based analysis of genomic and biomolecular data from the Division of Biological Sciences, UCSD.

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11	Understand the process by which genomes are currently sequenced and the bioinformatics processing and analysis required for their interpretation.	13
12	For a genomic region of interest (e.g. the neighborhood of a particular gene), use a genome browser to view nearby genes, transcription factor binding regions, epigenetic information, etc.	14
13	Given an RNA-Seq data file, find the set of significantly differentially expressed genes and use online tools to interpret gene lists and annotate potential gene functions.	15, 16
14	Perform a GO analysis to identify the pathways relevant to a set of genes (e.g. identified by transcriptomic study or a proteomic experiment).	16
15	Use the KEGG pathway database to look up interaction pathways.	17
16	Use graph theory to represent biological data networks.	17, 18
17	Understand the challenges in integrating and interpreting large heterogenous high throughput data sets into their functional	19

These support a major learning objective

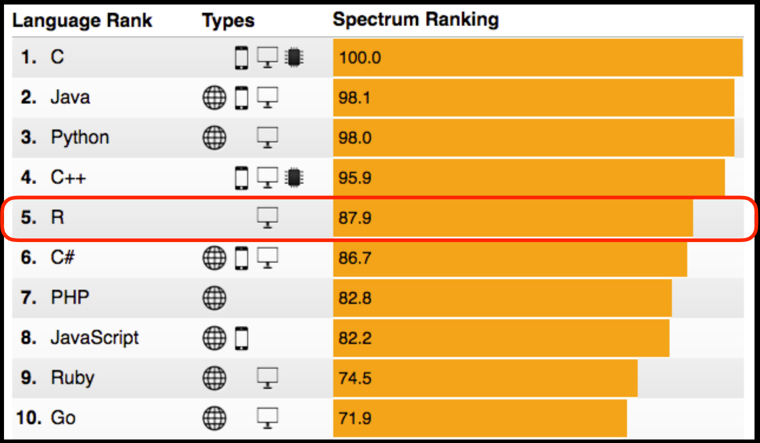
At the end of this course students will:

- Understand the increasing necessity for computation in modern life sciences research.
- Be able to use and evaluate online bioinformatics resources and analysis tools to solve problems in the biological sciences.
- Be able to use the R environment to analyze bioinformatics data at scale.
- Be familiar with the research objectives of the bioinformatics related sub-disciplines of Genome informatics, Transcriptomics and Structural informatics.

Why use R?

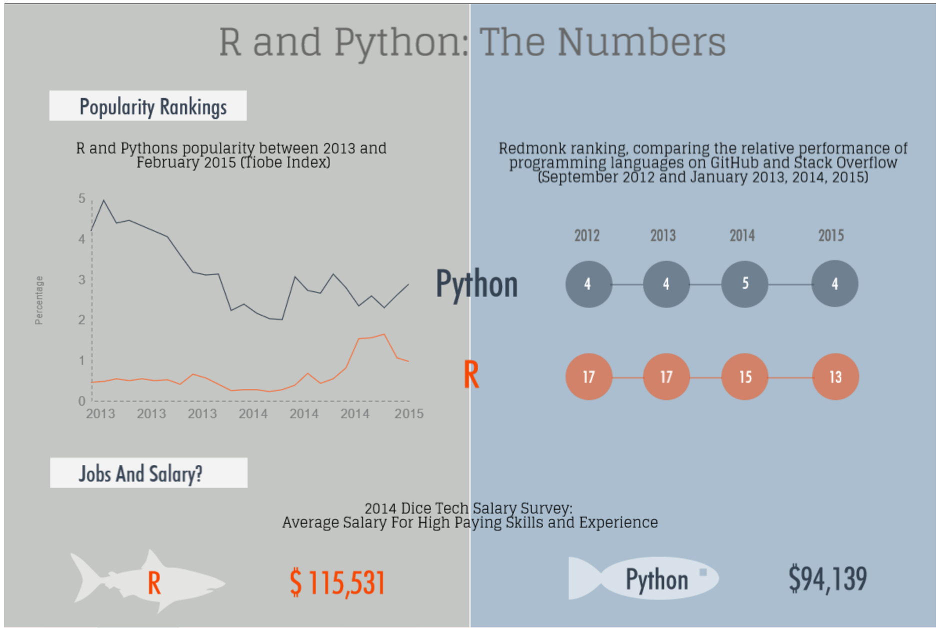
Productivity
Flexibility
Genomic data analysis

IEEE 2016 Top Programming Languages



Language Rank	Types	Spectrum Ranking
1. C	📱 🖥 ▦	100.0
2. Java	🌐 📱 🖥	98.1
3. Python	🌐 🖥	98.0
4. C++	📱 🖥 ▦	95.9
5. R	🖥	87.9
6. C#	🌐 📱 🖥	86.7
7. PHP	🌐	82.8
8. JavaScript	🌐 📱	82.2
9. Ruby	🌐 🖥	74.5
10. Go	🌐 🖥	71.9

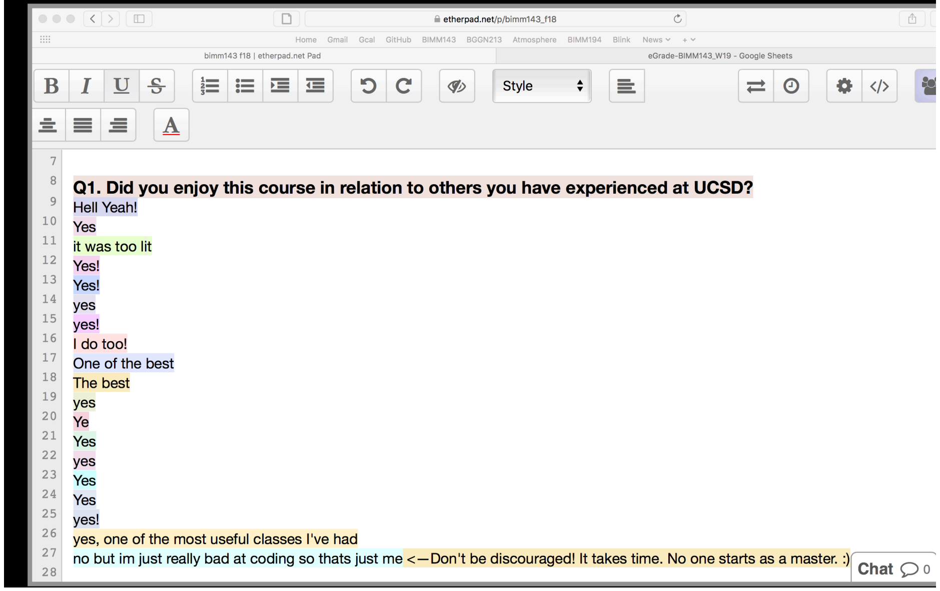
http://spectrum.ieee.org/computing/software/the-2016-top-programming-languages



http://www.kdnuggets.com/2015/05/r-vs-python-data-science.html?utm_medium=email&utm_source=flipboard

- R is the “lingua franca” of data science in industry and academia and was designed specifically for data analysis.
- Large friendly user and developer community.
  - As of Jan 6th 2019 there are 13,645 add on **R packages** on **CRAN** and 1,649 on **Bioconductor** - more on these later!
- Virtually every statistical technique is either already built into R, or available as a free package.
- Unparalleled data analysis environment for **high-throughput genomic data**.

Past Student Opinions...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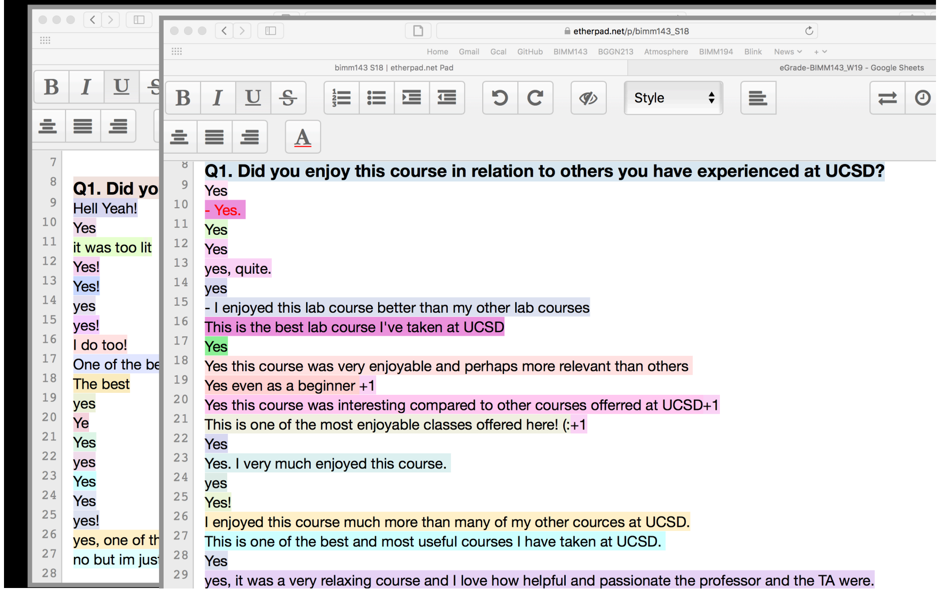
Home Gmail Gcal GitHub BIMM143 BGGN213 Atmosphere BIMM194 Blink News
bimm143 f18 | etherpad.net Pad
eGrade-BIMM143_W19 - Google Sheets
Style
Chat 0

Q1. Did you enjoy this course in relation to others you have experienced at UCSD?
Hell Yeah!
Yes
it was too lit
Yes!
Yes!
yes
yes!
I do too!
One of the best
The best
yes
Ye
Yes
yes
Yes
Yes
yes!
yes, one of the most useful classes I've had
no but im just really bad at coding so thats just me <—Don't be discouraged! It takes time. No one starts as a master. :)

Past Student Opinions...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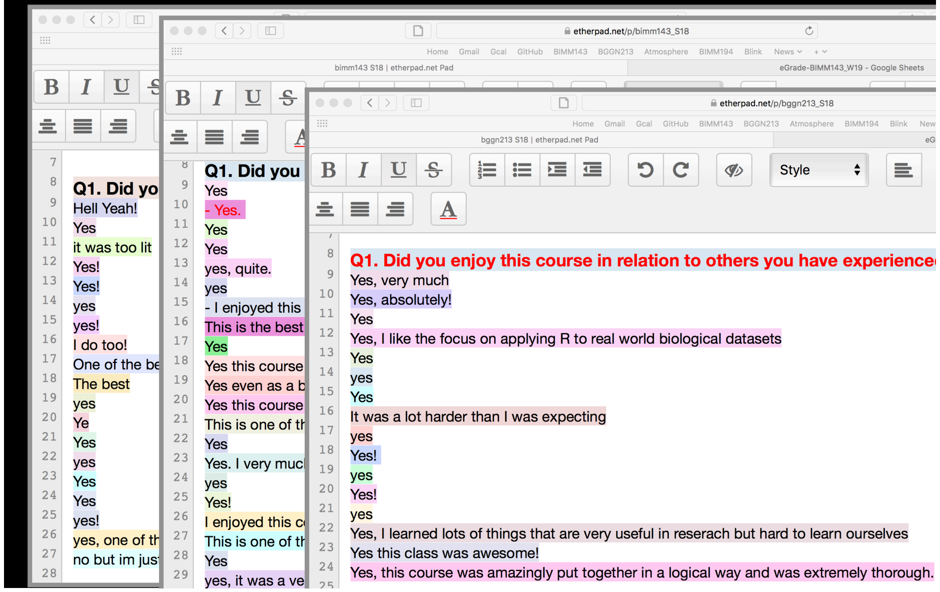
One of the be
The best
yes
Ye
Yes
yes
Yes
Yes
yes!
yes, one of th
no but im jus

Q1. Did you enjoy this course in relation to others you have experienced at UCSD?
Yes
- Yes.
Yes
Yes
yes, quite.
yes
- I enjoyed this lab course better than my other lab courses
This is the best lab course I've taken at UCSD
Yes
Yes this course was very enjoyable and perhaps more relevant than others
Yes even as a beginner +1
Yes this course was interesting compared to other courses offered at UCSD+1
This is one of the most enjoyable classes offered here! (:+1
Yes
Yes. I very much enjoyed this course.
yes
Yes!
I enjoyed this course much more than many of my other cources at UCSD.
This is one of the best and most useful courses I have taken at UCSD.
Yes
yes, it was a very relaxing course and I love how helpful and passionate the professor and the TA were.

Past Student Opinions...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This is the best
Yes
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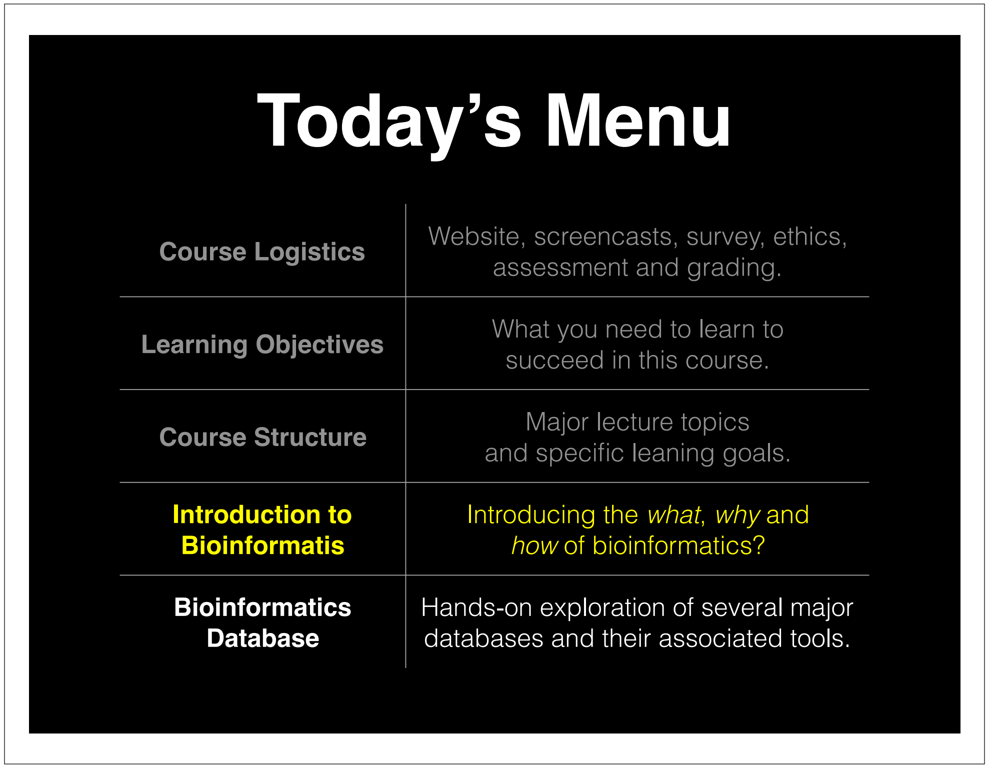
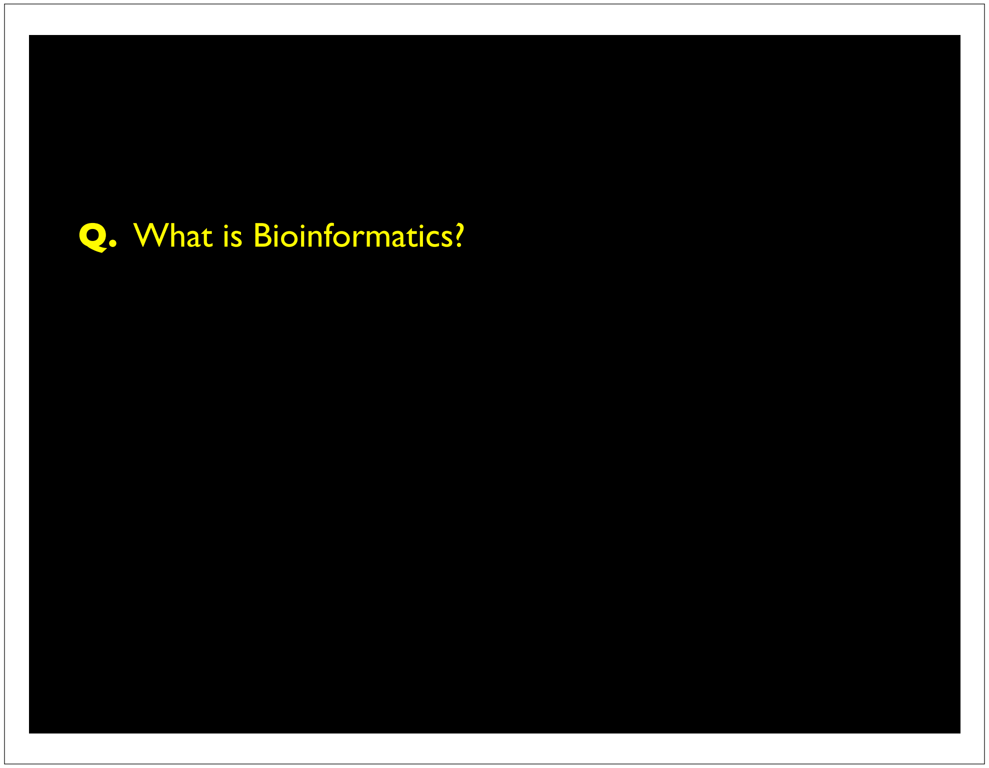
Yes this course
This is one of th
Yes
Yes. I very muc
yes
Yes!
I enjoyed this c
This is one of th
Yes
yes, it was a ve

Q1. Did you enjoy this course in relation to others you have experience
Yes, very much
Yes, absolutely!
Yes
Yes, I like the focus on applying R to real world biological datasets
Yes
yes
Yes
It was a lot harder than I was expecting
yes
Yes!
yes
Yes!
yes
Yes, I learned lots of things that are very useful in reserach but hard to learn ourselves
Yes this class was awesome!
Yes, this course was amazingly put together in a logical way and was extremely thorough.

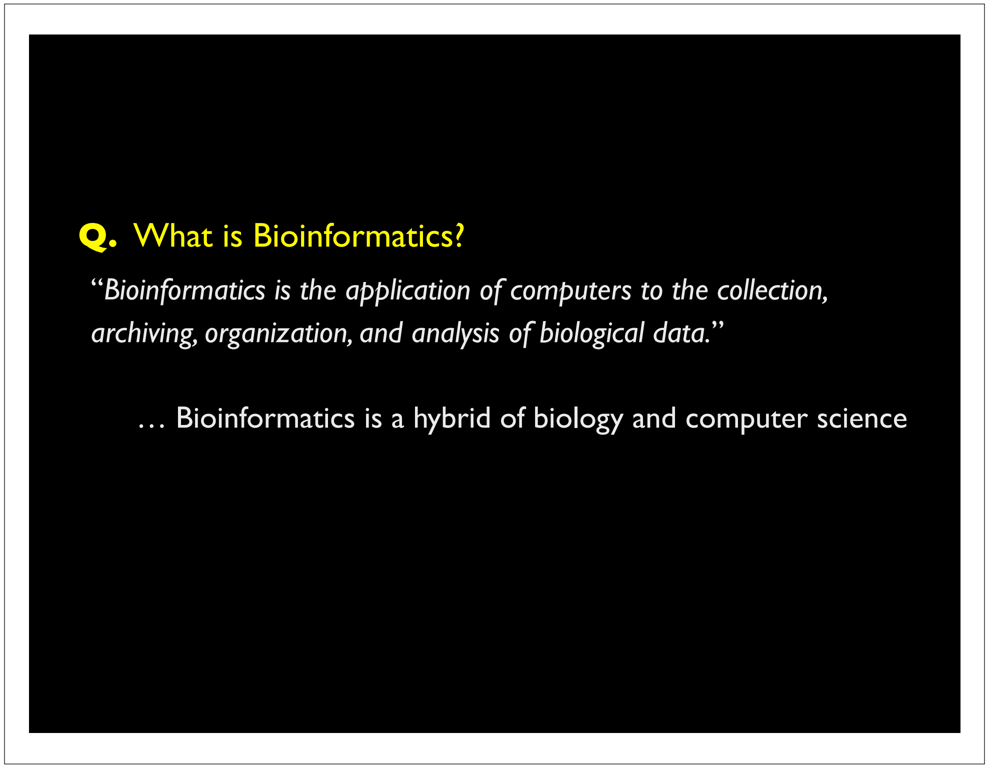


Today’s Menu

Course Logistics	Website, screencasts, survey, ethics, assessment and grading.
Learning Objectives	What you need to learn to succeed in this course.
Course Structure	Major lecture topics and specific leaning goals.
Introduction to Bioinformatis	Introducing the *what*, *why* and *how* of bioinformatics?
Bioinformatics Database	Hands-on exploration of several major databases and their associated tools.



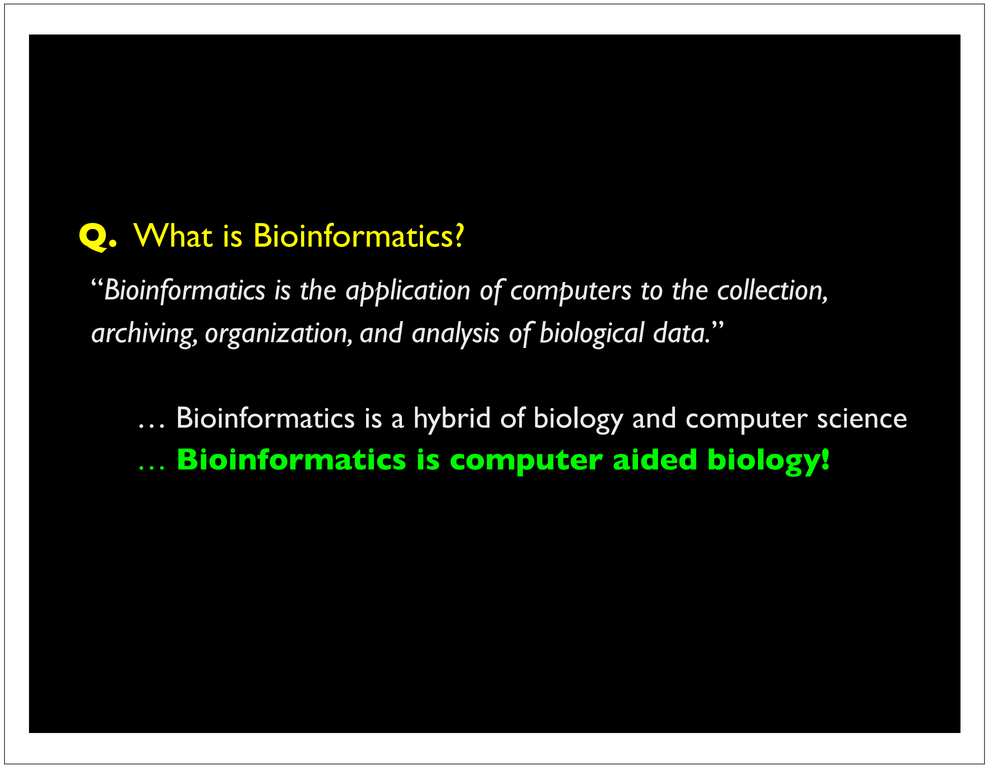
Q. What is Bioinformatics?



Q. What is Bioinformatics?

“Bioinformatics is the application of computers to the collection, archiving, organization, and analysis of biological data.”

… Bioinformatics is a hybrid of biology and computer science



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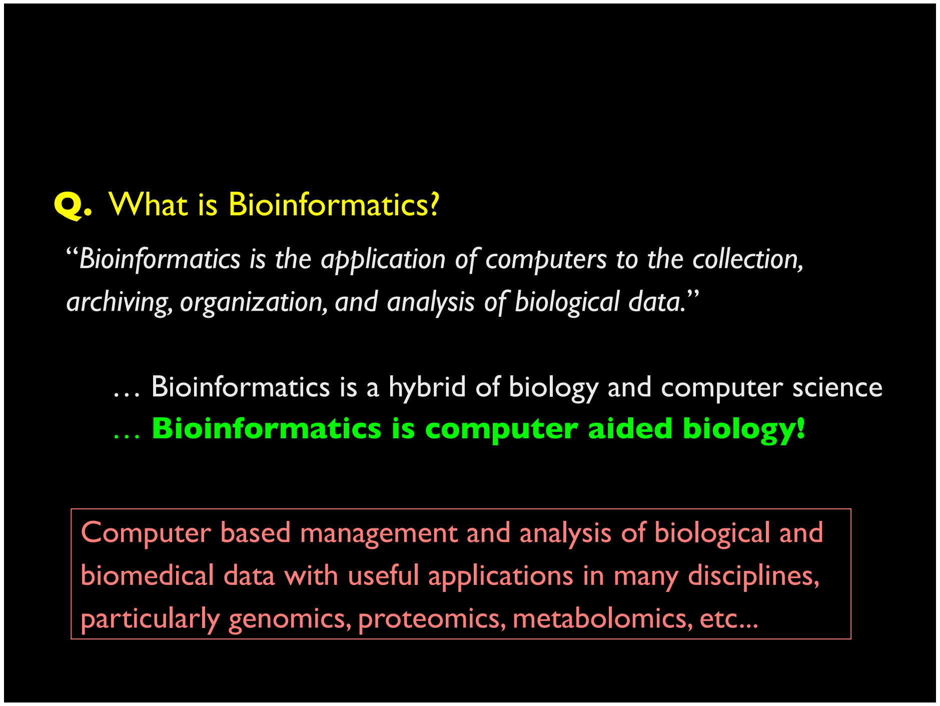
… **Bioinformatics is computer aided biology!**



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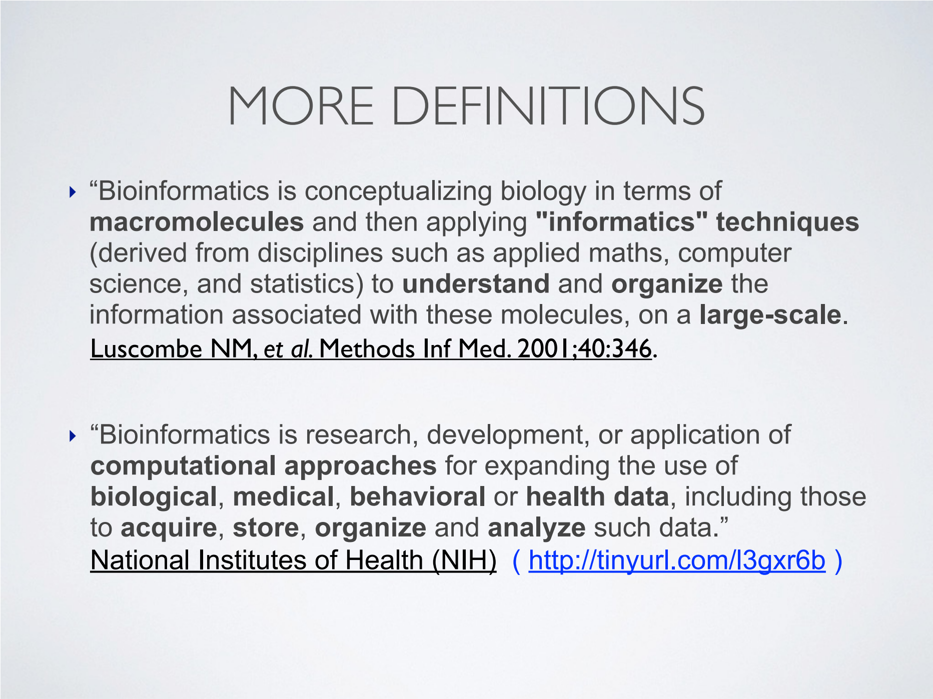
… Bioinformatics is a hybrid of biology and computer science

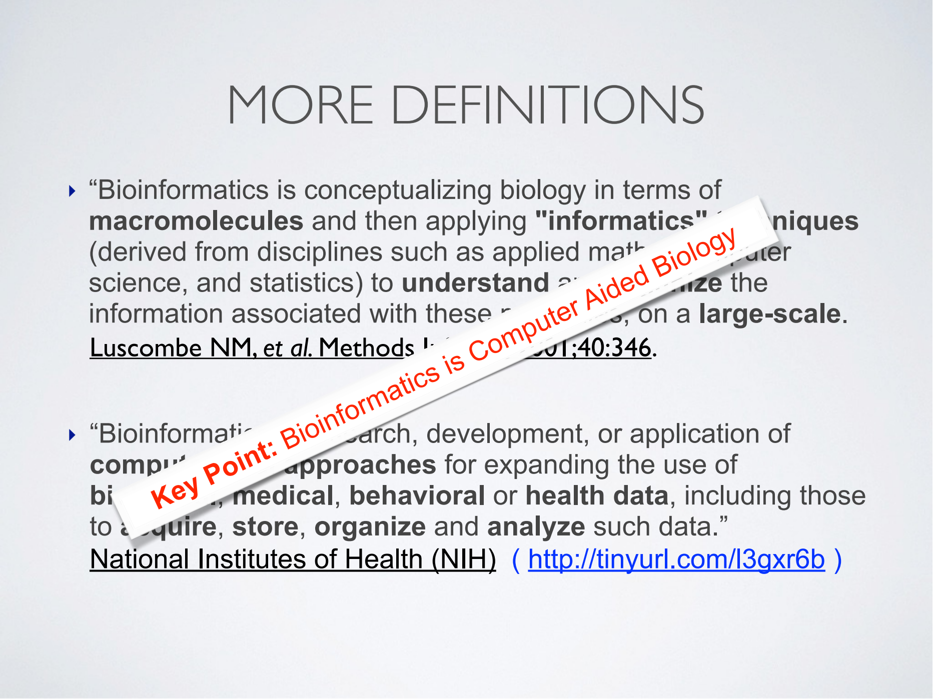
… **Bioinformatics is computer aided biology!**

Computer based management and analysis of biological and biomedical data with useful applications in many disciplines, particularly genomics, proteomics, metabolomics, etc...



MORE DEFINITIONS

- "Bioinformatics is conceptualizing biology in terms of **macromolecules** and then applying **"informatics" techniques** (derived from disciplines such as applied maths, computer science, and statistics) to **understand** and **organize** the information associated with these molecules, on a **large-scale**. Luscombe NM, *et al.* Methods Inf Med. 2001;40:346.
- "Bioinformatics is research, development, or application of **computational approaches** for expanding the use of **biological**, **medical**, **behavioral** or **health data**, including those to **acquire**, **store**, **organize** and **analyze** such data." National Institutes of Health (NIH) (http://tinyurl.com/l3gxr6b)



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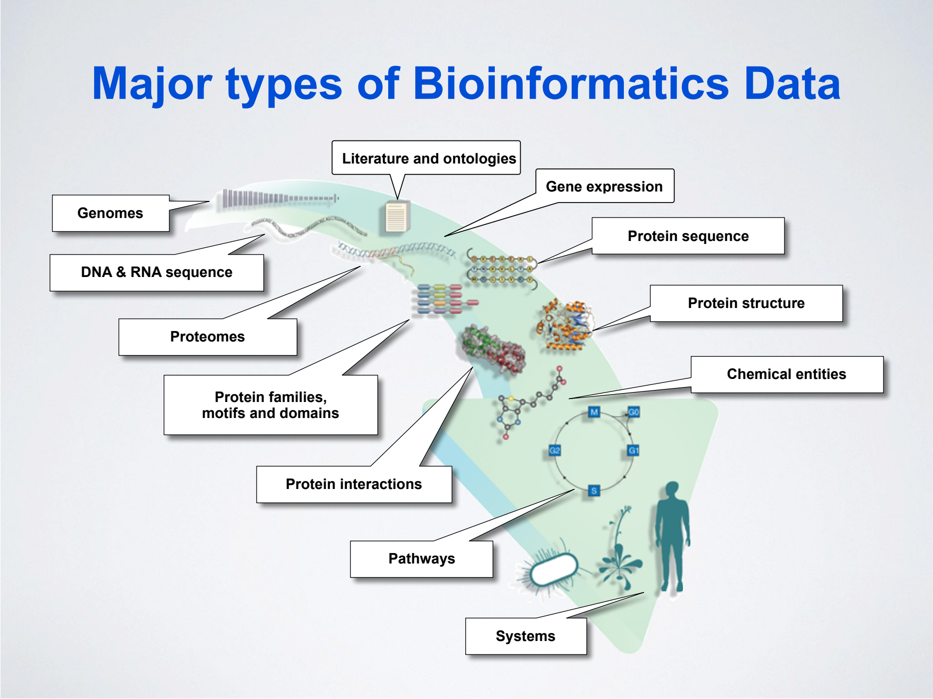
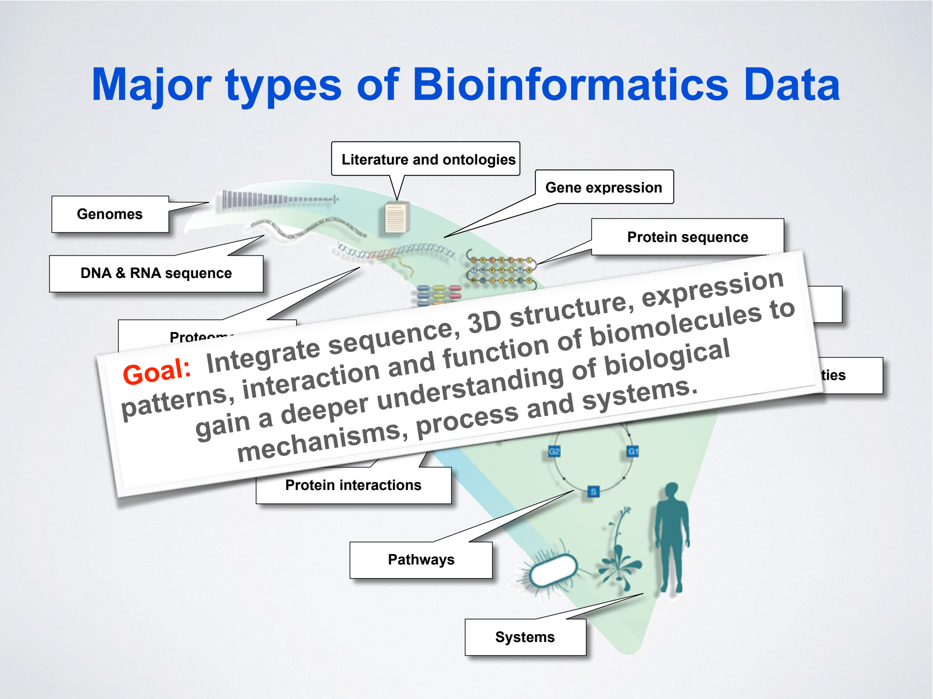
Key Point: Bioinformatics is Computer Aided Biology

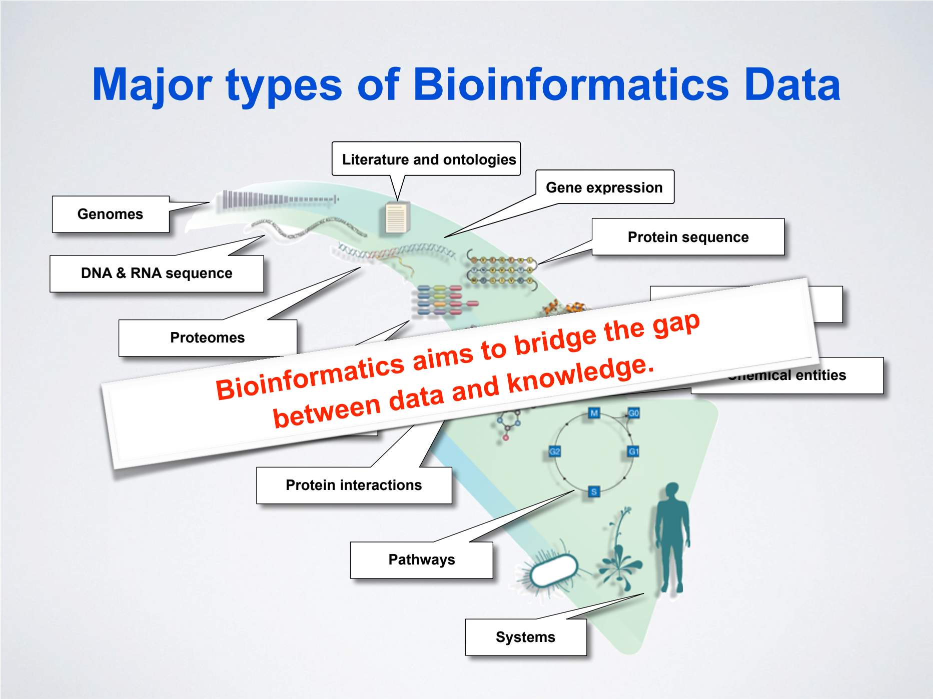


Major types of Bioinformatics Data



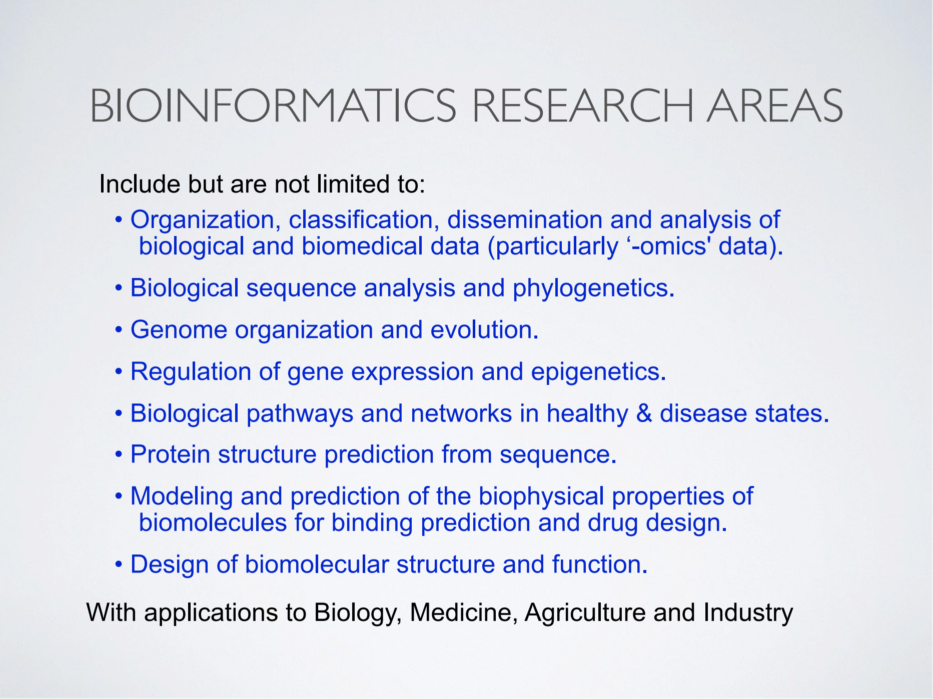
Major types of Bioinformatics Data

Goal: Integrate sequence, 3D structure, expression patterns, interaction and function of biomolecules to gain a deeper understanding of biological mechanisms, process and systems.



Major types of Bioinformatics Data

Bioinformatics aims to bridge the gap between data and knowledge.

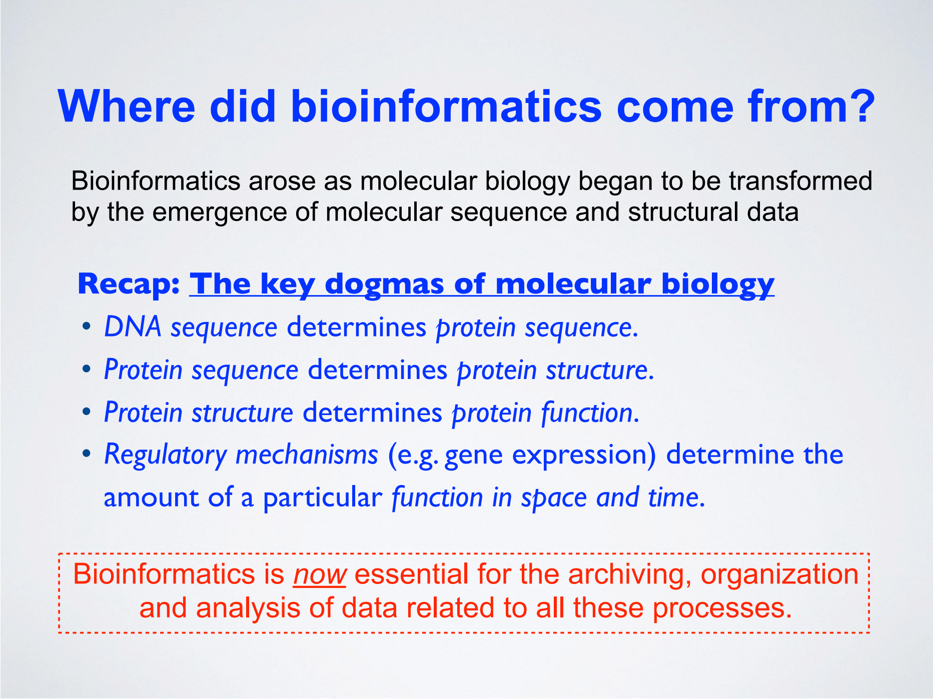


BIOINFORMATICS RESEARCH AREAS

Include but are not limited to:

- Organization, classification, dissemination and analysis of biological and biomedical data (particularly '-omics' data).
- Biological sequence analysis and phylogenetics.
- Genome organization and evolution.
- Regulation of gene expression and epigenetics.
- Biological pathways and networks in healthy & disease states.
- Protein structure prediction from sequence.
- Modeling and prediction of the biophysical properties of biomolecules for binding prediction and drug design.
- Design of biomolecular structure and function.

With applications to Biology, Medicine, Agriculture and Industry



Where did bioinformatics come from?

Bioinformatics arose as molecular biology began to be transformed by the emergence of molecular sequence and structural data

Recap: The key dogmas of molecular biology

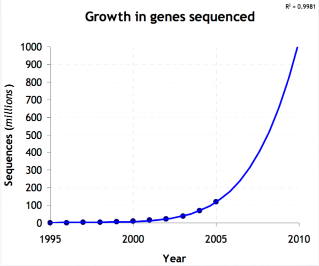
- *DNA sequence* determines *protein sequence.*
- *Protein sequence* determines *protein structure.*
- *Protein structure* determines *protein function.*
- *Regulatory mechanisms* (e.g. gene expression) determine the amount of a particular *function in space and time.*

Bioinformatics is *now* essential for the archiving, organization and analysis of data related to all these processes.

Why do we need Bioinformatics?

Bioinformatics is necessitated by the rapidly expanding quantities and complexity of biomolecular data

- Bioinformatics provides methods for the efficient:
  - **storage**
  - **annotation**
  - **search** and **retrieval**
  - data **integration**
  - data **mining** and **analysis**



E.G. data from sequencing, structural genomics, proteomics, new high throughput assays, *etc…*

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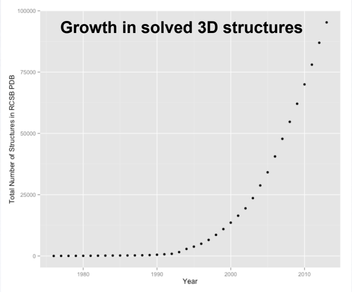
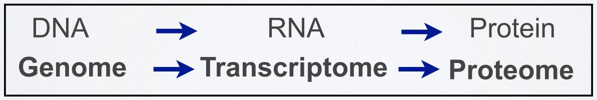


E.G. data from sequencing, structural genomics, proteomics, new high throughput assays, *etc…*

How do we do Bioinformatics?

- A “*bioinformatics approach”* involves the application of **computer algorithms**, **computer models** and **computer databases** with the broad goal of understanding the action of both individual genes, transcripts, proteins and large collections of these entities.



x 1,000

x 100,000

How do we *actually* do Bioinformatics?

Pre-packaged tools and databases

- Many online
- Most are free to use
- Time consuming methods require downloading…

Advanced tool application & development

- Mostly on a UNIX environment
- Knowledge of programing languages frequently required (*e.g.* **R**, Python, Perl, C, Java, Fortran)
- May require specialized high performance computing…

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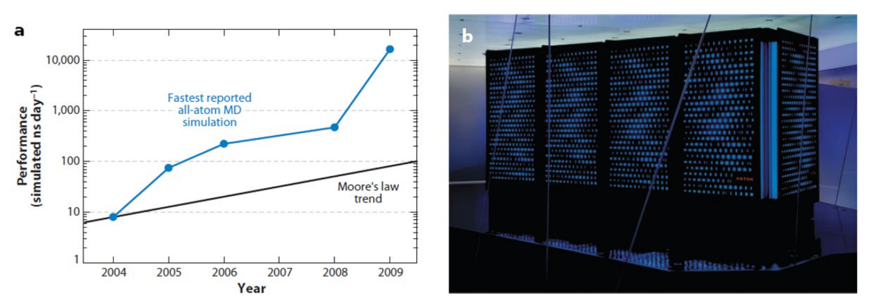
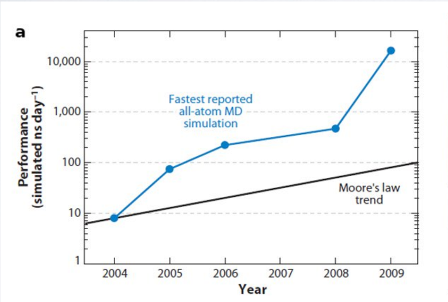
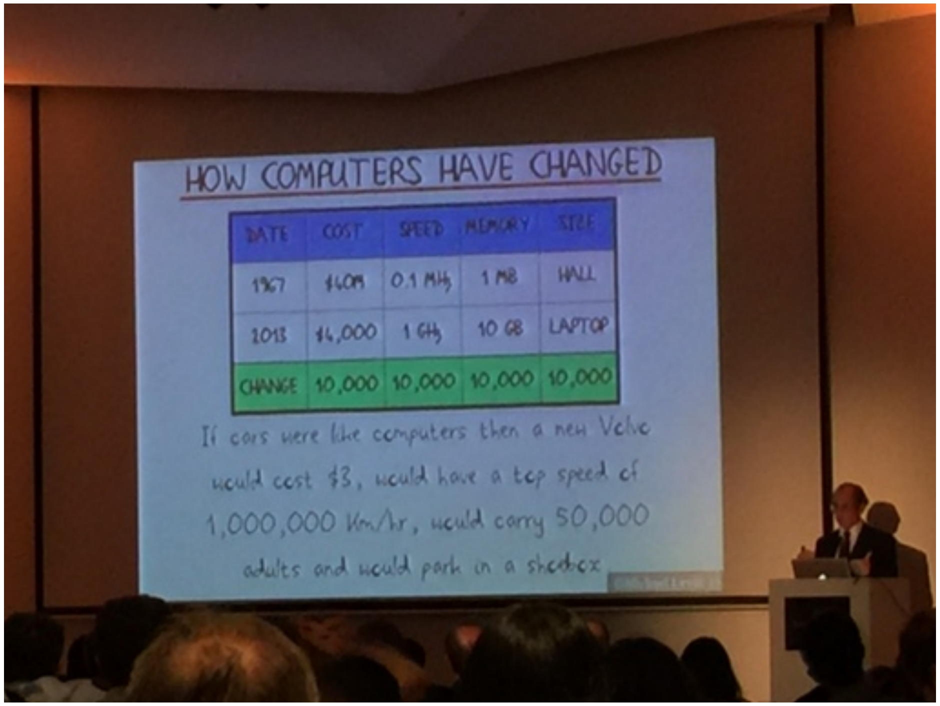
SIDE-NOTE: SUPERCOMPUTERS AND GPUS



SIDE-NOTE: SUPERCOMPUTERS AND GPUS





HOW COMPUTERS HAVE CHANGED

DATE	COST	SPEED	MEMORY	SIZE
1967	$40M	0.1 MHz	1 MB	HALL
2013	$4,000	1 GHz	10 GB	LAPTOP
CHANGE	10,000	10,000	10,000	10,000

If cars were like computers then a new Volvo would cost $3, would have a top speed of 1,000,000 Km/hr, would carry 50,000 adults and would park in a shoebox

Skepticism & Bioinformatics

We have to approach computational results the same way we do wet-lab results:

- Do they make sense?
- Is it what we expected?
- Do we have adequate controls, and how did they come out?
- Modeling is modeling, but biology is different...

  What does this model actually contribute?
- Avoid the miss-use of 'black boxes'

Skepticism & Bioinformatics

Gunnar von Heijne in *"Sequence Analysis in Molecular Biology"* states:

➡"Think about what you're doing; use your knowledge of the molecular system involved to guide both your interpretation of results and your direction of inquiry; use as much information as possible; and do not blindly accept everything the computer offers you".

Key-Point: **Avoid the miss-use of 'black boxes'!**

Common problems with Bioinformatics

Confusing multitude of tools available

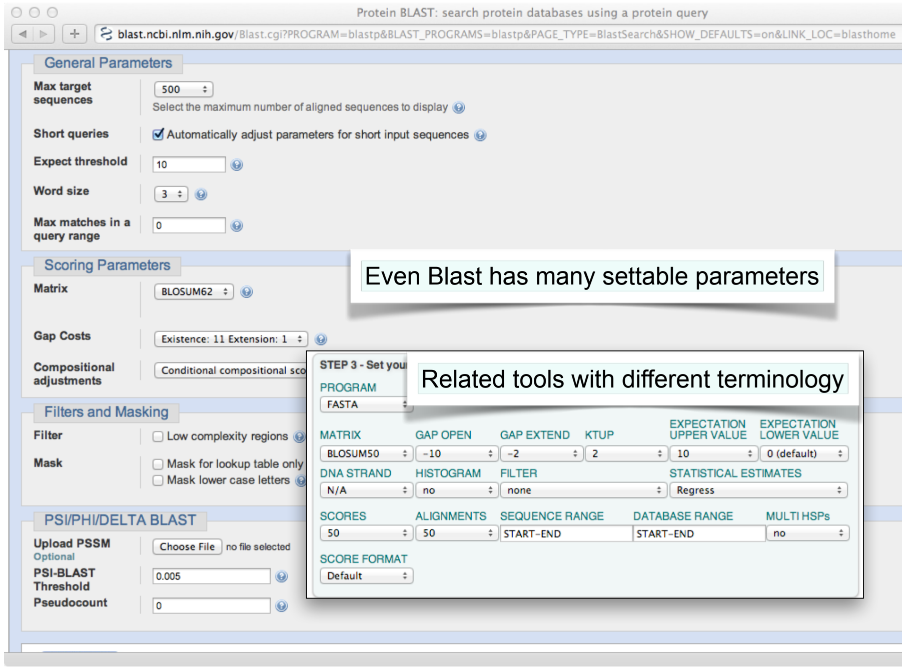
- Each with many options and settable parameters

Most tools and databases are written by and for nerds

- Same is true of documentation - if any exists!

Most are developed independently

Notable exceptions are found at the:
- **EBI** (European Bioinformatics Institute) and
- **NCBI** (National Center for Biotechnology Information)



Protein BLAST: search protein databases using a protein query

blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&BLAST_PROGRAMS=blastp&PAGE_TYPE=BlastSearch&SHOW_DEFAULTS=on&LINK_LOC=blasthome

General Parameters

Max target sequences: 500
Select the maximum number of aligned sequences to display

Short queries: ☑ Automatically adjust parameters for short input sequences

Expect threshold: 10

Word size: 3

Max matches in a query range: 0

Scoring Parameters

Matrix: BLOSUM62

Gap Costs: Existence: 11 Extension: 1

Compositional adjustments: Conditional compositional sco

Filters and Masking

Filter: ☐ Low complexity regions

Mask: ☐ Mask for lookup table only
☐ Mask lower case letters

PSI/PHI/DELTA BLAST

Upload PSSM (Optional): Choose File no file selected

PSI-BLAST Threshold: 0.005

Pseudocount: 0

Even Blast has many settable parameters

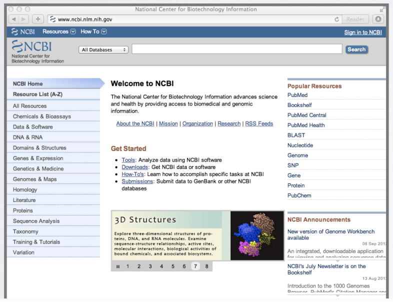
STEP 3 - Set you

Related tools with different terminology

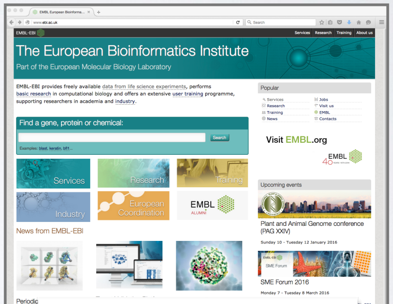
PROGRAM					
FASTA					
MATRIX	GAP OPEN	GAP EXTEND	KTUP	EXPECTATION UPPER VALUE	EXPECTATION LOWER VALUE
BLOSUM50	-10	-2	2	10	0 (default)
DNA STRAND	HISTOGRAM	FILTER		STATISTICAL ESTIMATES	
N/A	no	none		Regress	
SCORES	ALIGNMENTS	SEQUENCE RANGE	DATABASE RANGE	MULTI HSPs	
50	50	START-END	START-END	no	
SCORE FORMAT					
Default					

Key Online Bioinformatics Resources: NCBI & EBI

The NCBI and EBI are invaluable, publicly available resources for biomedical research



http://www.ncbi.nlm.nih.gov



www.ebi.ac.uk

EMBL-EBI | Services | Research | Training | About us

The European Bioinformatics Institute

Part of the European Molecular Biology Laboratory

EMBL-EBI provides freely available data from life science experiments, performs basic research in computational biology and offers an extensive user training programme, supporting researchers in academia and industry.

Find a gene, protein or chemical:

Search

Examples: blast, keratin, bfl1...

Services | Research | Training | Industry | European Coordination | EMBL ALUMNI

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Popular: Services, Jobs, Research, Visit us, Training, EMBL, News, Contacts

Visit EMBL.org

Upcoming events

Plant and Animal Genome conference (PAG XXIV)

Sunday 10 - Tuesday 12 January 2016

SME Forum 2016

Monday 7 - Tuesday 8 March 2016

https://www.ebi.ac.uk

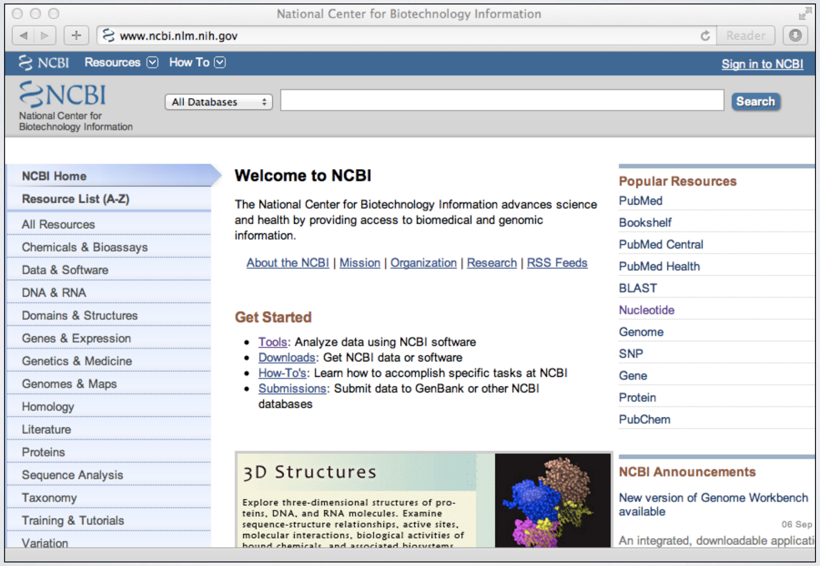
National Center for Biotechnology Information (NCBI)

- Created in 1988 as a part of the National Library of Medicine (NLM) at the National Institutes of Health
- NCBI's mission includes:
  - Establish **public databases**
  - Develop **software tools**
  - **Education** on and dissemination of biomedical information

Bethesda,MD

- We will cover a number of core NCBI databases and software tools in the lecture

http://www.ncbi.nlm.nih.gov



National Center for Biotechnology Information

www.ncbi.nlm.nih.gov

NCBI | Resources | How To | Sign in to NCBI

NCBI National Center for Biotechnology Information

All Databases | Search

NCBI Home
Resource List (A-Z)
All Resources
Chemicals & Bioassays
Data & Software
DNA & RNA
Domains & Structures
Genes & Expression
Genetics & Medicine
Genomes & Maps
Homology
Literature
Proteins
Sequence Analysis
Taxonomy
Training & Tutorials
Variation

Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

About the NCBI | Mission | Organization | Research | RSS Feeds

Get Started

- Tools: Analyze data using NCBI software
- Downloads: Get NCBI data or software
- How-To's: Learn how to accomplish specific tasks at NCBI
- Submissions: Submit data to GenBank or other NCBI databases

3D Structures

Explore three-dimensional structures of proteins, DNA, and RNA molecules. Examine sequence-structure relationships, active sites, molecular interactions, biological activities of bound chemicals, and associated biosystems

Popular Resources
PubMed
Bookshelf
PubMed Central
PubMed Health
BLAST
Nucleotide
Genome
SNP
Gene
Protein
PubChem

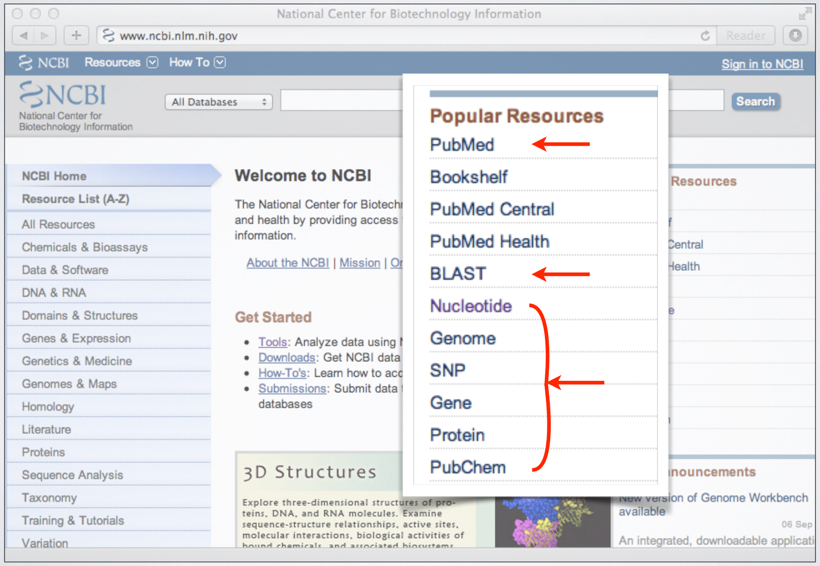
NCBI Announcements

New version of Genome Workbench available

06 Sep

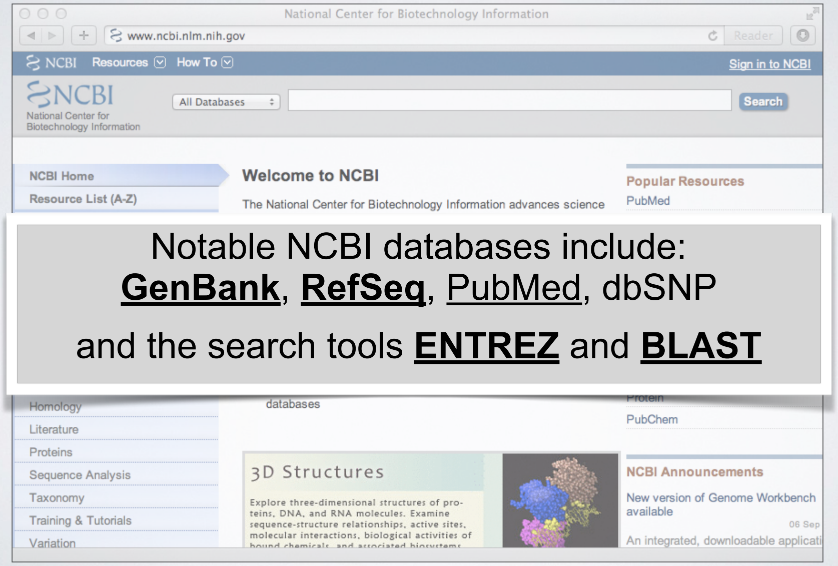
An integrated, downloadable applicati

http://www.ncbi.nlm.nih.gov



Popular Resources
PubMed ←
Bookshelf
PubMed Central
PubMed Health
BLAST ←
Nucleotide
Genome
SNP ←
Gene
Protein
PubChem

http://www.ncbi.nlm.nih.gov



National Center for Biotechnology Information

www.ncbi.nlm.nih.gov

Welcome to NCBI

The National Center for Biotechnology Information advances science

databases

3D Structures

Explore three-dimensional structures of proteins, DNA, and RNA molecules. Examine sequence-structure relationships, active sites, molecular interactions, biological activities of bound chemicals, and associated biosystems.

NCBI Announcements

New version of Genome Workbench available

06 Sep

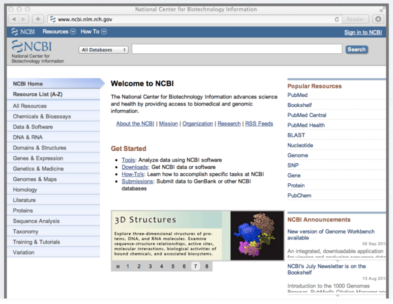
An integrated, downloadable applicati

Notable NCBI databases include:
GenBank, **RefSeq**, PubMed, dbSNP

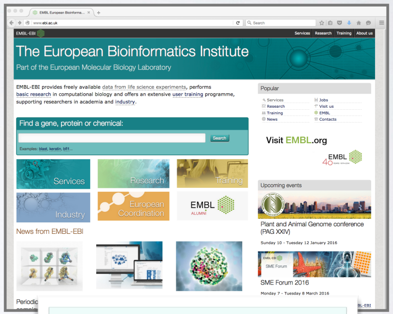
and the search tools **ENTREZ** and **BLAST**

Key Online Bioinformatics Resources: NCBI & EBI

The NCBI and EBI are invaluable, publicly available resources for biomedical research



http://www.ncbi.nlm.nih.gov



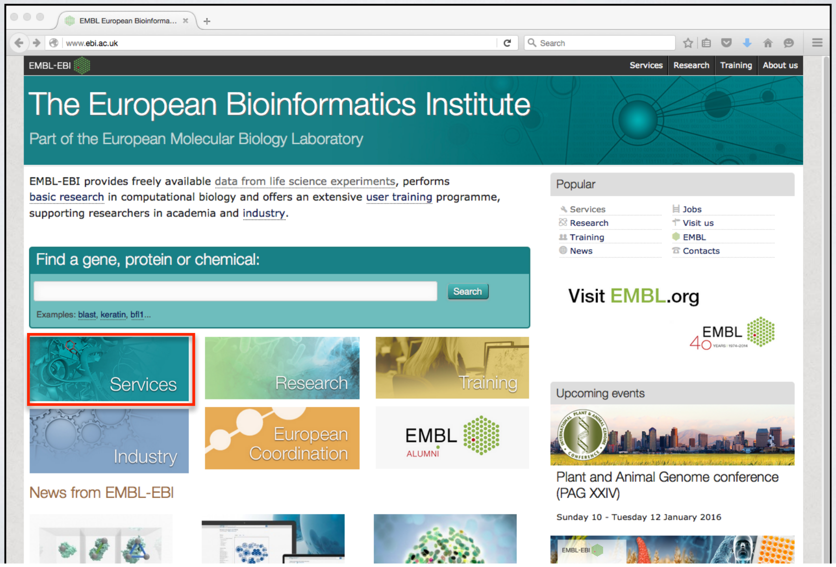
https://www.ebi.ac.uk

European Bioinformatics Institute (EBI)

- Created in 1997 as a part of the European Molecular Biology Laboratory (EMBL)
- EBI's mission includes:
  - providing freely available **data and bioinformatics services**
  - and providing advanced **bioinformatics training**

- We will briefly cover several EBI databases and tools that have advantages over those offered at NCBI

The EBI maintains a number of high quality curated **secondary databases** and associated tools



The European Bioinformatics Institute

Part of the European Molecular Biology Laboratory

EMBL-EBI provides freely available data from life science experiments, performs basic research in computational biology and offers an extensive user training programme, supporting researchers in academia and industry.

Find a gene, protein or chemical:

Examples: blast, keratin, bfl1...

Plant and Animal Genome conference (PAG XXIV)

Sunday 10 - Tuesday 12 January 2016

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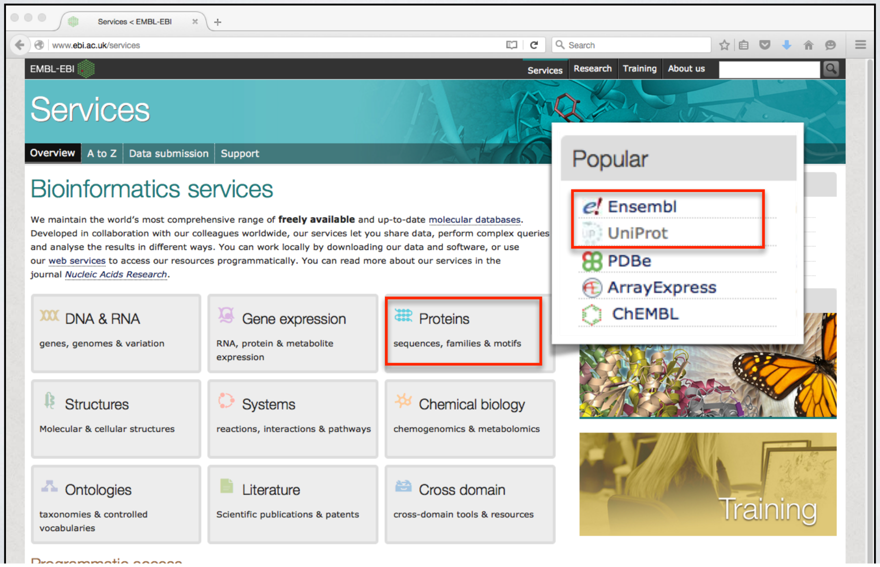


Services

Bioinformatics services

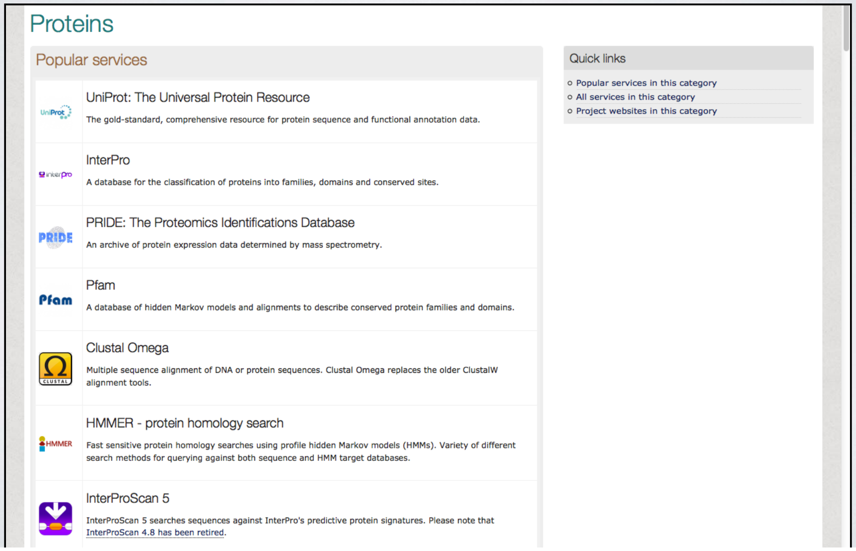
We maintain the world's most comprehensive range of **freely available** and up-to-date molecular databases. Developed in collaboration with our colleagues worldwide, our services let you share data, perform complex queries and analyse the results in different ways. You can work locally by downloading our data and software, or use our web services to access our resources programmatically. You can read more about our services in the journal *Nucleic Acids Research*.

DNA & RNA genes, genomes & variation	Gene expression RNA, protein & metabolite expression	Proteins sequences, families & motifs
Structures Molecular & cellular structures	Systems reactions, interactions & pathways	Chemical biology chemogenomics & metabolomics
Ontologies taxonomies & controlled vocabularies	Literature Scientific publications & patents	Cross domain cross-domain tools & resources

Programmatic access

https://www.ebi.ac.uk

The EBI makes available a wider variety of **online tools** than NCBI



Proteins

Popular services

UniProt: The Universal Protein Resource
The gold-standard, comprehensive resource for protein sequence and functional annotation data.

InterPro
A database for the classification of proteins into families, domains and conserved sites.

PRIDE: The Proteomics Identifications Database
An archive of protein expression data determined by mass spectrometry.

Pfam
A database of hidden Markov models and alignments to describe conserved protein families and domains.

Clustal Omega
Multiple sequence alignment of DNA or protein sequences. Clustal Omega replaces the older ClustalW alignment tools.

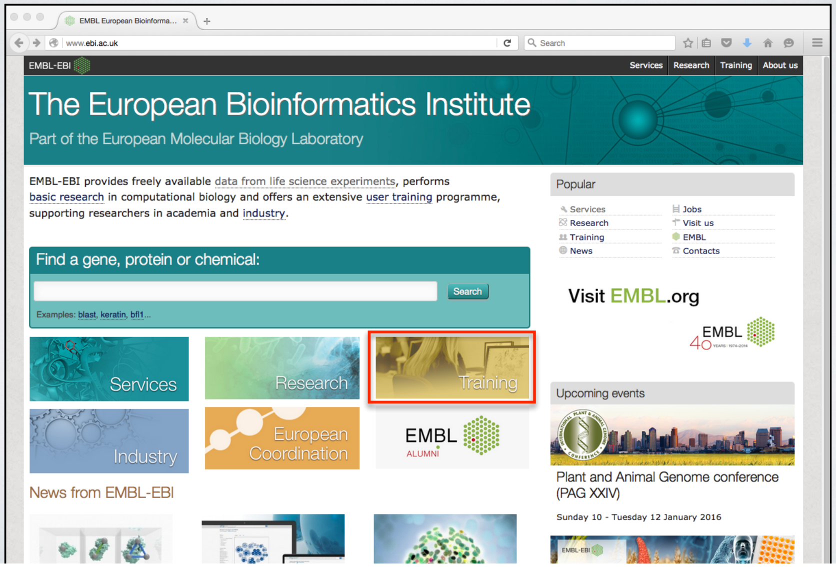
HMMER - protein homology search
Fast sensitive protein homology searches using profile hidden Markov models (HMMs). Variety of different search methods for querying against both sequence and HMM target databases.

InterProScan 5
InterProScan 5 searches sequences against InterPro's predictive protein signatures. Please note that InterProScan 4.8 has been retired.

Quick links

- Popular services in this category
- All services in this category
- Project websites in this category

The EBI also provides a growing selection of **online tutorials** on EBI databases and tools



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News from EMBL-EBI

Upcoming events

Plant and Animal Genome conference (PAG XXIV)

Sunday 10 - Tuesday 12 January 2016

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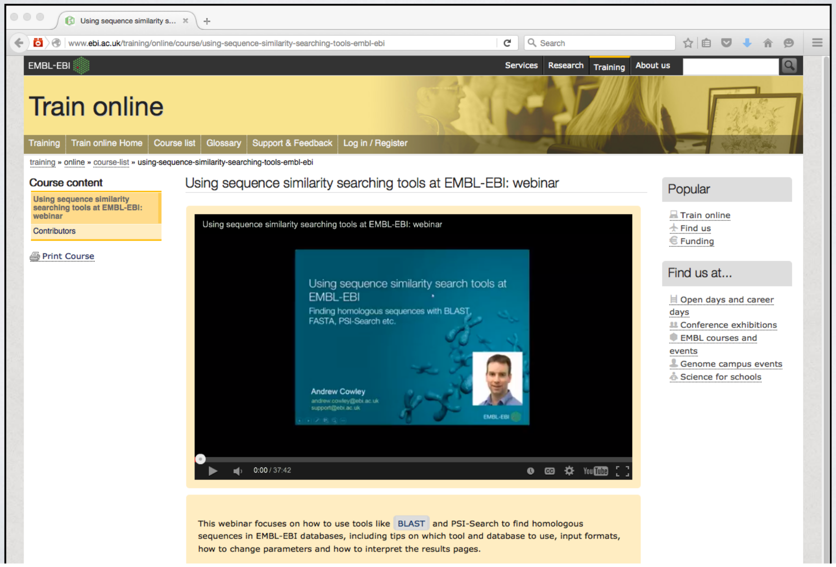


Train online

training » online » course-list » using-sequence-similarity-searching-tools-embl-ebi

Course content

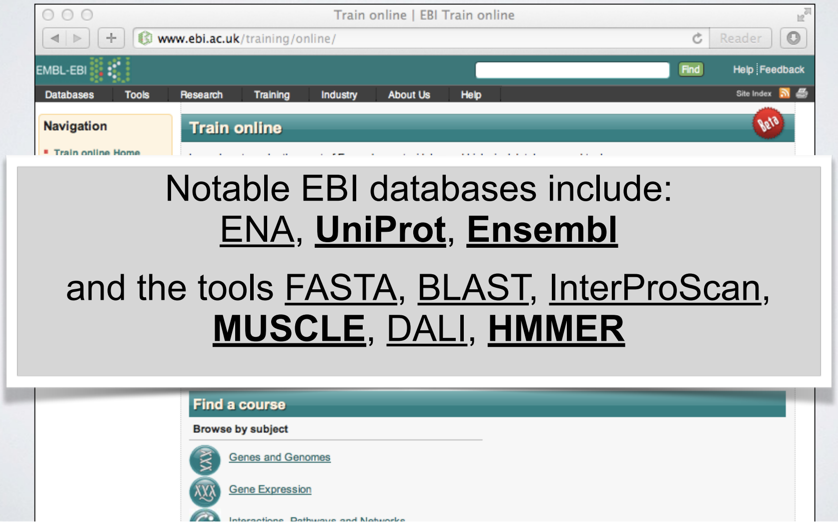
Using sequence similarity searching tools at EMBL-EBI: webinar

Contributors

Using sequence similarity searching tools at EMBL-EBI: webinar

This webinar focuses on how to use tools like BLAST and PSI-Search to find homologous sequences in EMBL-EBI databases, including tips on which tool and database to use, input formats, how to change parameters and how to interpret the results pages.

The EBI also provides a growing selection of **online tutorials** on EBI databases and tools



Notable EBI databases include:
ENA, **UniProt**, **Ensembl**

and the tools FASTA, BLAST, InterProScan, **MUSCLE**, DALI, **HMMER**

Bioinformatics Databases

AATDB, AceDb, ACUTS, ADB, AFDB, AGIS, AMSdb, ARR, AsDb,BBDB, BCGD, Beanref, BioImage, BioMagResBank, BIOMDB, BLOCKS, BovGBASE, BOVMAP, BSORF, BTKbase, CANSITE, CarbBank, CARBHYD, CATH, CAZY, CCDC, CD4OLbase, CGAP, ChickGBASE, Colibri, COPE, CottonDB, CSNDB, CUTG, CyanoBase, dbCFC, dbEST, dbSTS, DDBJ, DGP, DictyDb, Picty_cDB, DIP, DOGS, DOMO, DPD, DPInteract, ECDC, ECGC, EC02DBASE, EcoCyc, EcoGene, EMBL, EMD db, ENZYME, EPD, EpoDB, ESTHER, FlyBase, FlyView, GCRDB, GDB, GENATLAS, Genbank, GeneCards, Genlilesne, GenLink, GENOTK, GenProtEC, GIFTS, GPCRDB, GRAP, GRBase, gRNAsdb, GRR, GSDB, HAEMB, HAMSTERS, HEART-2DPAGE, HEXAdb, HGMD, HIDB, HIDC, HIVdb, HotMolecBase, HOVERGEN, HPDB, HSC-2DPAGE, ICN, ICTVDB, IL2RGbase, IMGT, Kabat, KDNA, KEGG, Klotho, LGIC, MAD, MaizeDb, MDB, Medline, Mendel, MEROPS, MGDB, MGI, MHCPEP5 Micado, MitoDat, MITOMAP, MJDB, MmtDB, Mol-R-Us, MPDB, MRR, MutBase, MycDB, NDB, NRSub, 0-lycBase, OMIA, OMIM, OPD, ORDB, OWL, PAHdb, PatBase, PDB, PDD, Pfam, PhosphoBase, PigBASE, PIR, PKR, PMD, PPDB, PRESAGE, PRINTS, ProDom, Prolysis, PROSITE, PROTOMAP, RatMAP, RDP, REBASE, RGP, SBASE, SCOP, SeqAnaiRef, SGD, SGP, SheepMap, Soybase, SPAD, SRNA db, SRPDB, STACK, StyGene,Sub2D, SubtiList, SWISS-2DPAGE, SWISS-3DIMAGE, SWISS- MODEL Repository, SWISS-PROT, TelDB, TGN, tmRDB, TOPS, TRANSFAC, TRR, UniGene, URNADB, V BASE, VDRR, VectorDB, WDCM, WIT, WormPep, etc .... !!!!

Bioinformatics Databases

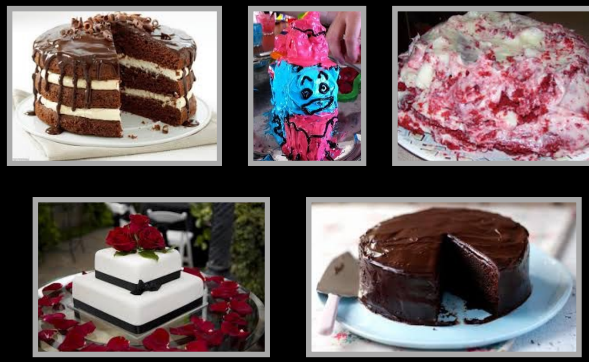
AATDB, AceDb, ACUTS, ADB, AFDB, AGIS, AMSdb, ARR, AsDb,BBDB, Beanref, BioImage, BioMagResBank, BIOMDB, BLOCKS, BovGBASE, TKbase, CANSITE, CarbBank, CARBHYD, CATH, AP, ChickGBASE, Colibri, COPE, bEST, dbSTS, DDBJ, DGP, CDC, ECGC, EC02DBASE, THER, FlyBase, Link, HAEMB, HotMolecBase, IL2RGbase, IMGT, Kabat, KDNA, Medline, Mendel, MEROPS, MGDB, MGI, MJDB, MmtDB, Mol-R-Us, MPDB, MRR, MutBase, 0-lycBase, OMIA, OMIM, OPD, ORDB, OWL, PAHdb, PatBase, Pfam, PhosphoBase, PigBASE, PIR, PKR, PMD, PPDB, PRESAGE, PRINTS, ProDom, Prolysis, PROSITE, PROTOMAP, RatMAP, RDP, REBASE, RGP, SBASE, SCOP, SeqAnaiRef, SGD, SGP, SheepMap, Soybase, SPAD, SRNA db, SRPDB, STACK, StyGene,Sub2D, SubtiList, SWISS-2DPAGE, SWISS-3DIMAGE, SWISS- MODEL Repository, SWISS-PROT, TelDB, TGN, tmRDB, TOPS, TRANSFAC, TRR, UniGene, URNADB, V BASE, VDRR, VectorDB, WDCM, WIT, WormPep, etc .... !!!!

There are lots of Bioinformatics Databases

For a annotated listing of major bioinformatics databases please see the online handout

< Major_Databases.pdf >

Side-note: Databases come in all shapes and sizes



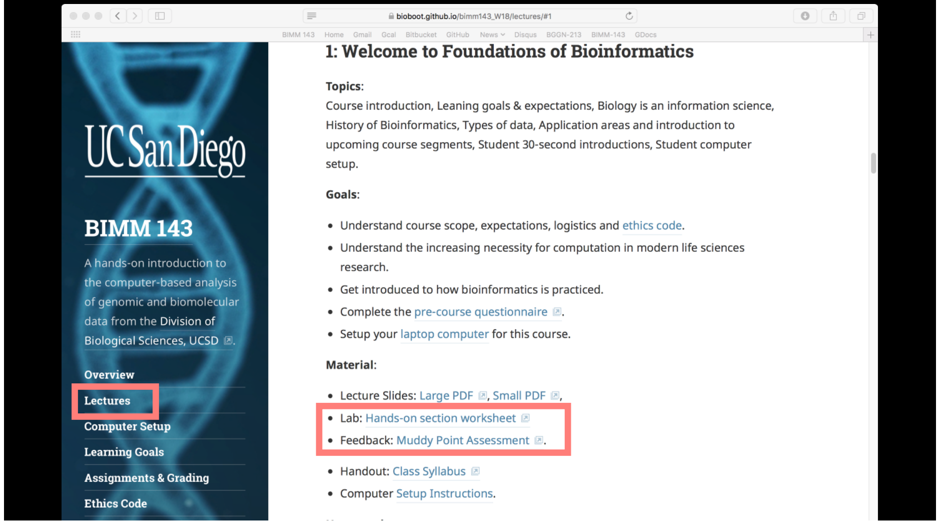
Databases can be of variable quality and often there are multiple databases with overlapping content.

Today’s Menu

Course Logistics	Website, screencasts, survey, ethics, assessment and grading.
Learning Objectives	What you need to learn to succeed in this course.
Course Structure	Major lecture topics and specific leaning goals.
Introduction to Bioinformatis	Introducing the *what*, *why* and *how* of bioinformatics?
Bioinformatics Database	**Hands-on** exploration of several major databases and their associated tools.

Your Turn!

https://bioboot.github.io/bimm143_S19/lectures/#1



BIMM 143

A hands-on introduction to the computer-based analysis of genomic and biomolecular data from the Division of Biological Sciences, UCSD.

- Overview
- Lectures
- Computer Setup
- Learning Goals
- Assignments & Grading
- Ethics Code

1: Welcome to Foundations of Bioinformatics

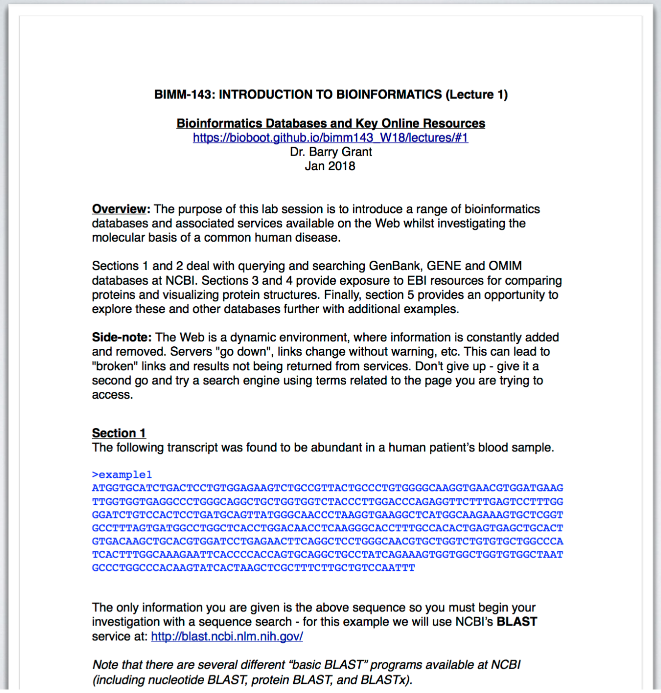
Topics:
Course introduction, Leaning goals & expectations, Biology is an information science, History of Bioinformatics, Types of data, Application areas and introduction to upcoming course segments, Student 30-second introductions, Student computer setup.

Goals:

- Understand course scope, expectations, logistics and ethics code.
- Understand the increasing necessity for computation in modern life sciences research.
- Get introduced to how bioinformatics is practiced.
- Complete the pre-course questionnaire.
- Setup your laptop computer for this course.

Material:

- Lecture Slides: Large PDF, Small PDF,
- Lab: Hands-on section worksheet
- Feedback: Muddy Point Assessment.
- Handout: Class Syllabus
- Computer Setup Instructions.



BIMM-143: INTRODUCTION TO BIOINFORMATICS (Lecture 1)

Bioinformatics Databases and Key Online Resources
https://bioboot.github.io/bimm143_W18/lectures/#1
Dr. Barry Grant
Jan 2018

Overview: The purpose of this lab session is to introduce a range of bioinformatics databases and associated services available on the Web whilst investigating the molecular basis of a common human disease.

Sections 1 and 2 deal with querying and searching GenBank, GENE and OMIM databases at NCBI. Sections 3 and 4 provide exposure to EBI resources for comparing proteins and visualizing protein structures. Finally, section 5 provides an opportunity to explore these and other databases further with additional examples.

Side-note: The Web is a dynamic environment, where information is constantly added and removed. Servers "go down", links change without warning, etc. This can lead to "broken" links and results not being returned from services. Don't give up - give it a second go and try a search engine using terms related to the page you are trying to access.

Section 1
The following transcript was found to be abundant in a human patient’s blood sample.

```
>example1
ATGGTGCATCTGACTCCTGTGGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAG
TTGGTGGTGAGGCCCTGGGCAGGCTGCTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTTGG
GGATCTGTCCACTCCTGATGCAGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAAGTGCTCGGT
GCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTCAAGGGCACCTTTGCCACACTGAGTGAGCTGCACT
GTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGCTCCTGGGCAACGTGCTGGTCTGTGTGCTGGCCCA
TCACTTTGGCAAAGAATTCACCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAAT
GCCCTGGCCCACAAGTATCACTAAGCTCGCTTTCTTGCTGTCCAATTT
```

The only information you are given is the above sequence so you must begin your investigation with a sequence search - for this example we will use NCBI’s **BLAST** service at: http://blast.ncbi.nlm.nih.gov/

Note that there are several different “basic BLAST” programs available at NCBI (including nucleotide BLAST, protein BLAST, and BLASTx).

YOUR TURN!

- There are five major hands-on sections including:

1. BLAST, GenBank and OMIM @ **NCBI** [~35 mins]
2. GENE database @ **NCBI** [~15 mins]

— BREAK —

3. UniProt & Muscle @ **EBI** [~25 mins]
4. PFAM, PDB & NGL [~30 mins]

— BREAK —

5. Extension exercises [~30 mins]

- Please do answer the last review question (**Q19**).
- We encourage discussion and exploration!

YOUR TURN!

- There are five major hands-on sections including:

		End times:
1.	BLAST, GenBank and OMIM @ **NCBI**	[11:05 am]
2.	GENE database @ **NCBI**	[11:25 am]
	— BREAK —	— 11:35 am —
3.	UniProt & Muscle @ **EBI**	[12:00 am]
4.	PFAM, PDB & NGL	[12:30 pm]
	— BREAK —	
5.	Extension exercises	

- Please do answer the last review question (**Q19**).
- We encourage discussion and exploration!

SUMMARY

- Bioinformatics is computer aided biology.
- Bioinformatics deals with the collection, archiving, organization, and interpretation of a wide range of biological data.
- The NCBI and EBI are major online bioinformatics service providers.
- Introduced Gene, UniProt, PDB databases as well as a number of 'boutique' databases including PFAM and OMIM.

HOMEWORK

https://bioboot.github.io/bimm143_S19/lectures/#1

☑ Complete the **initial course questionnaire**:

☑ Check out the "**Background Reading**" material online:

☑ Complete the **lecture 1 homework questions**: