BIMM 143

Introduction to Bioinformatics

Barry Grant

UC San Diego

http://thegrantlab.org/bimm143

Office Hours:
SignUp

Location:
TATA, #2501

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/

bioboot.github.io/bimm143_F18/

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.

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

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

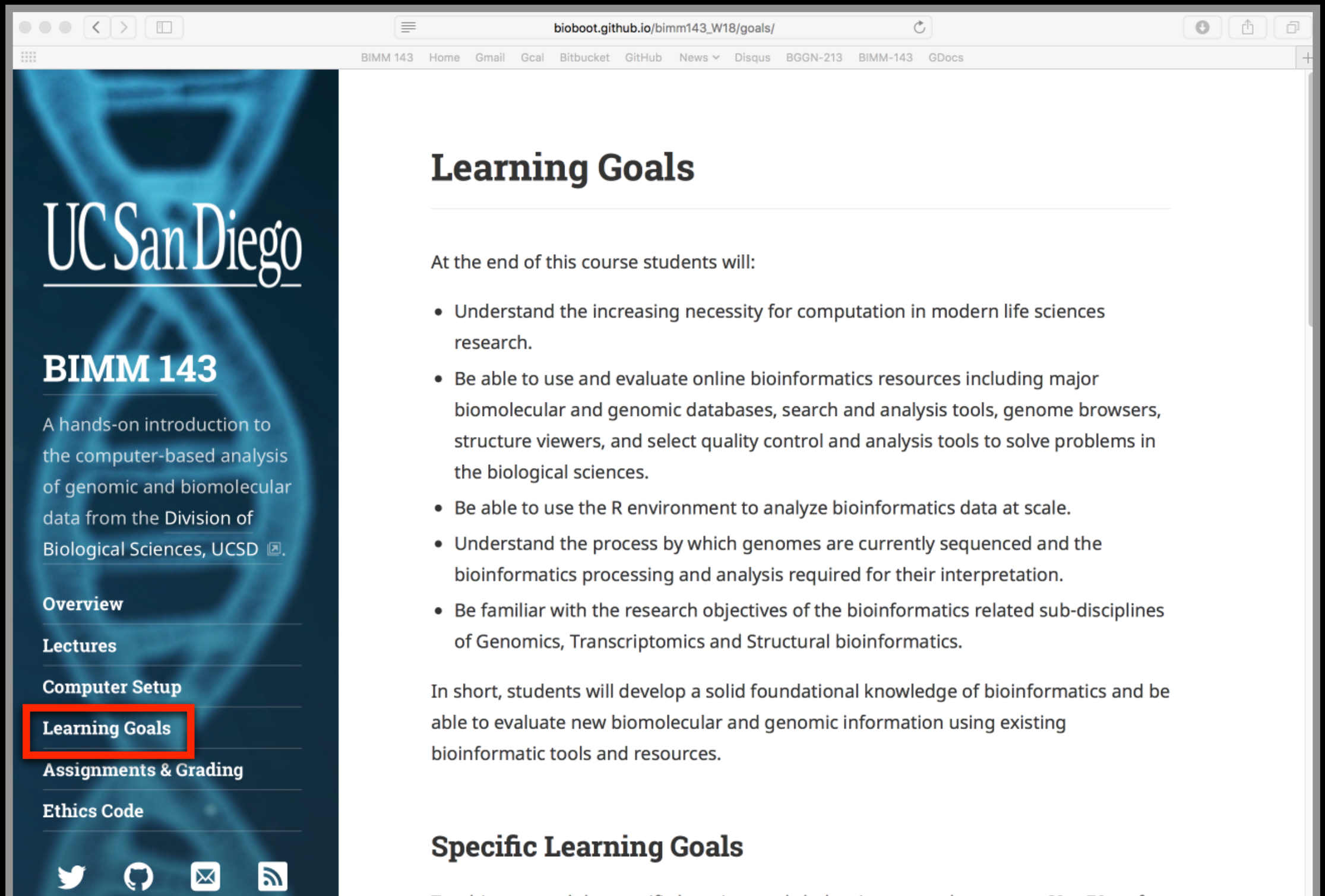
Fall 2018 (PDF)

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.

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



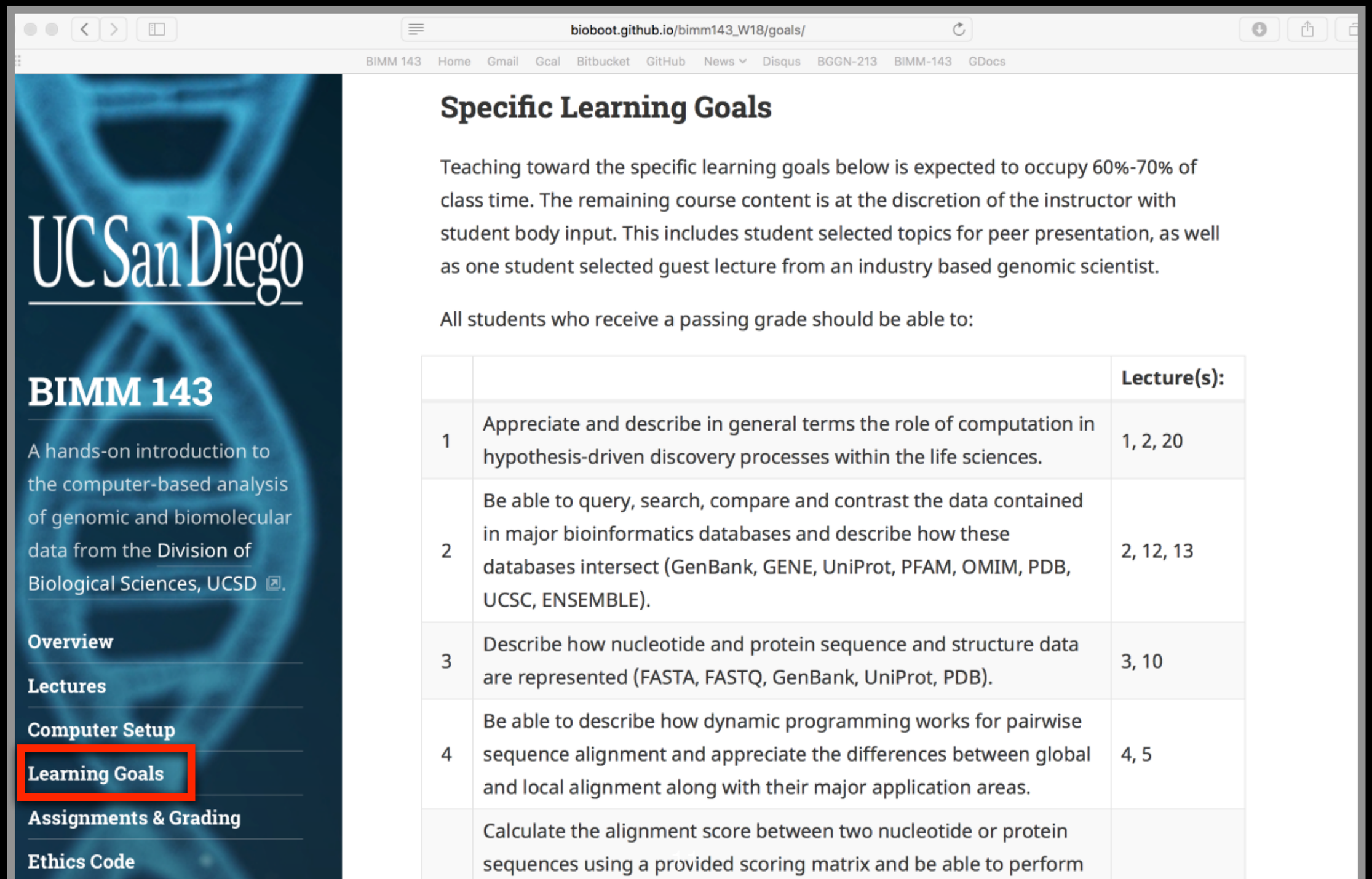
At the end of this course students will:

- 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....

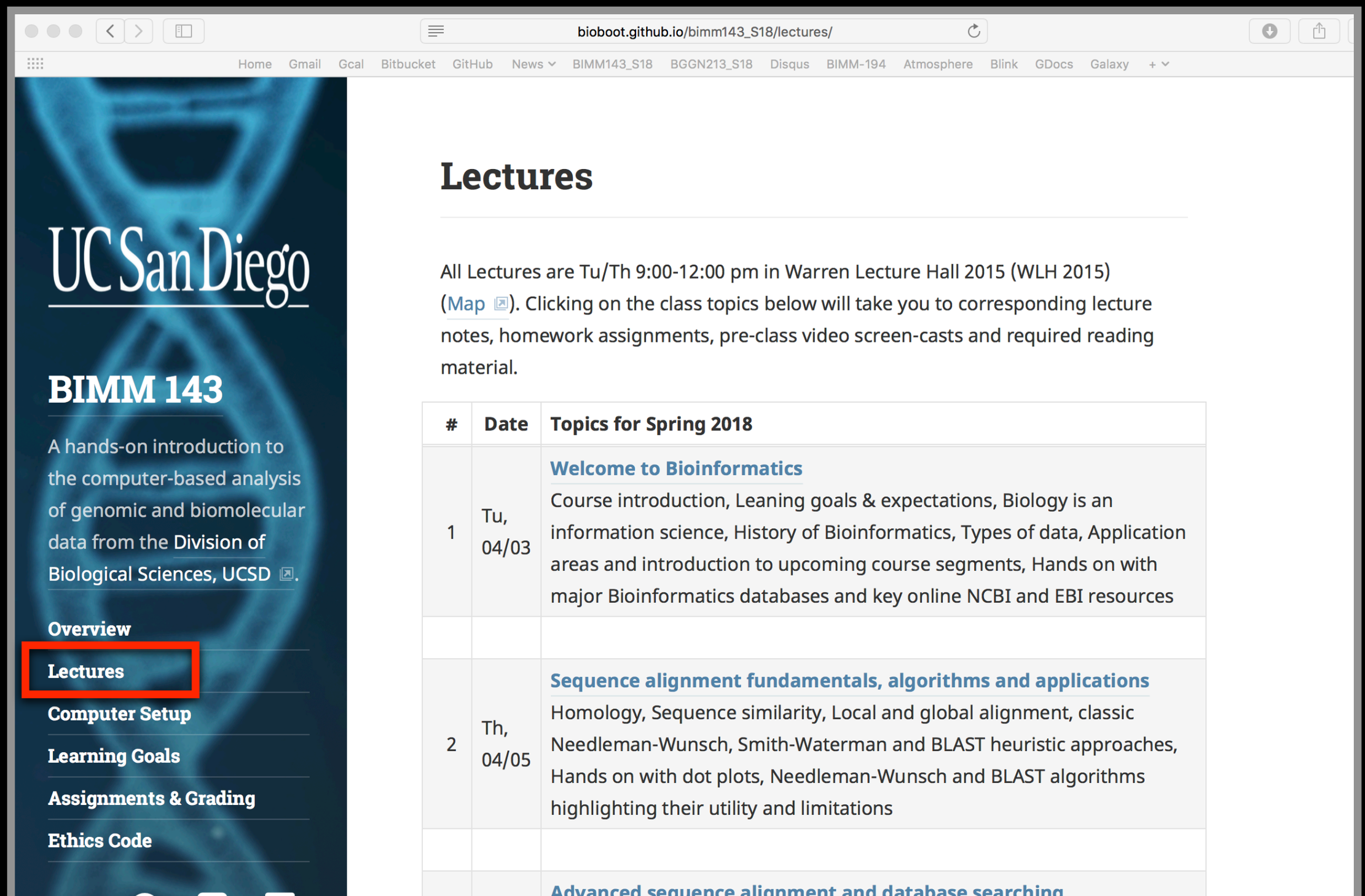
What I want you to know by course end!



		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	5, 10

Course Structure

Derived from specific learning goals



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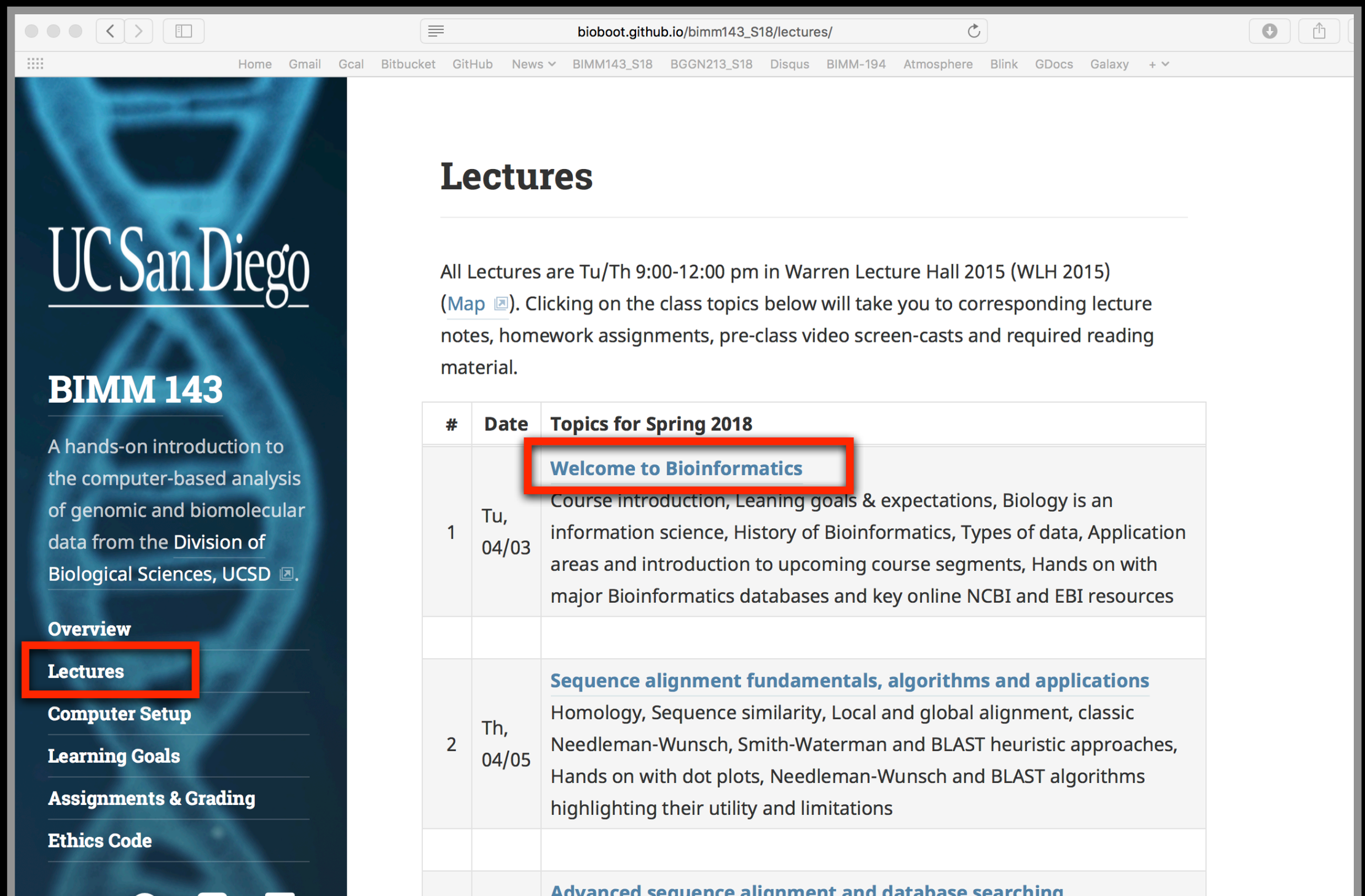
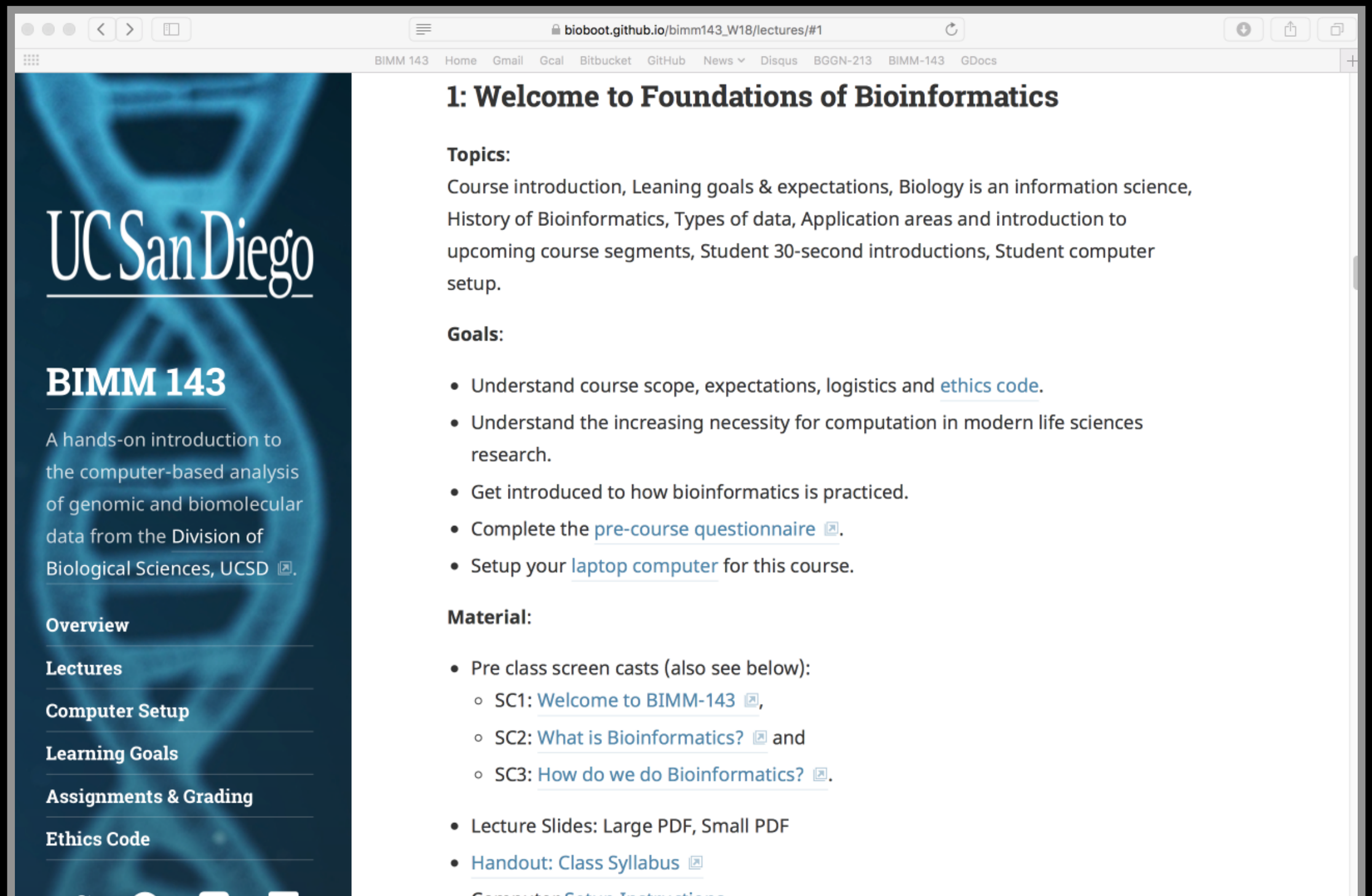


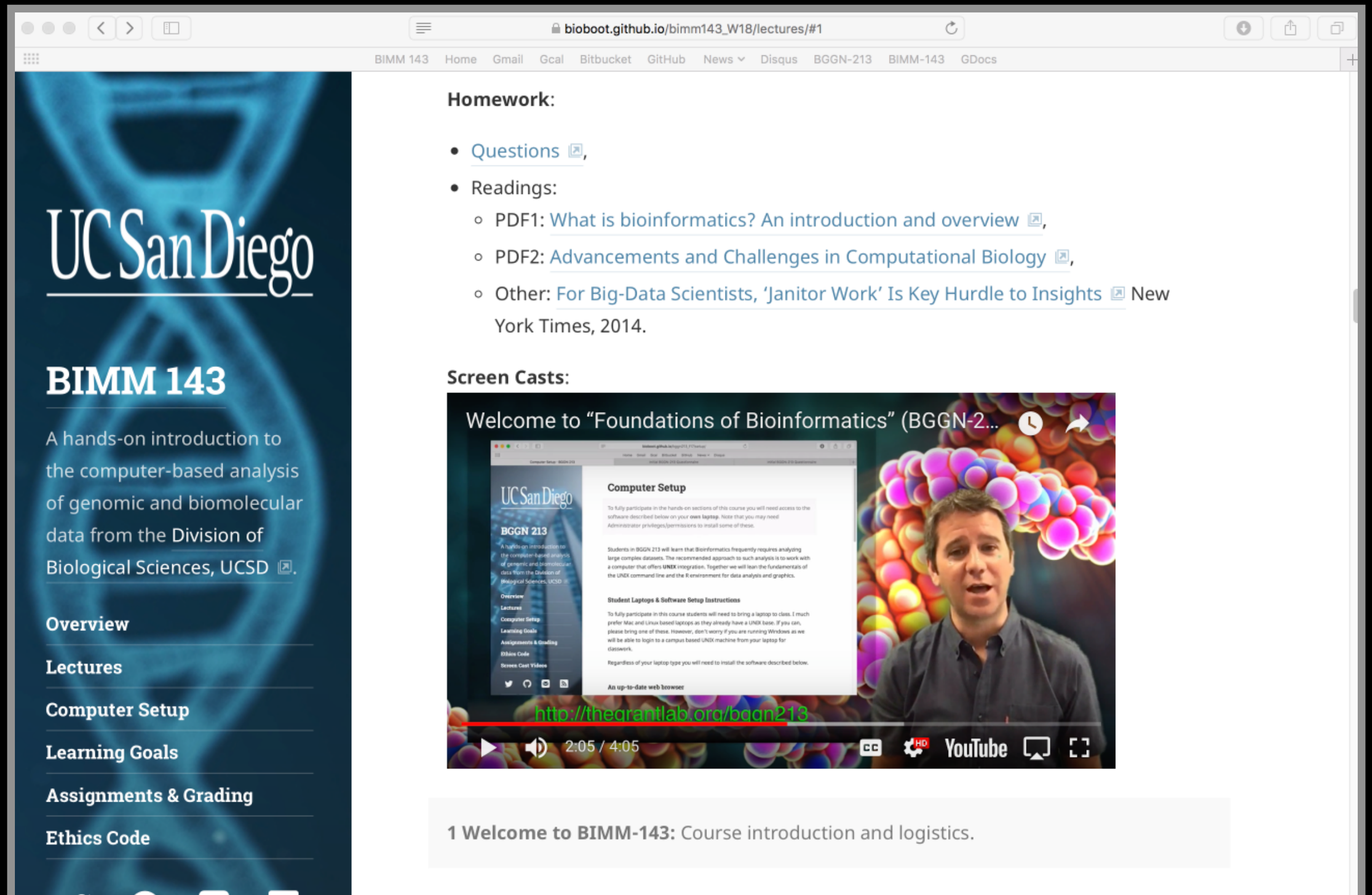
Class Details

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



Homework

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



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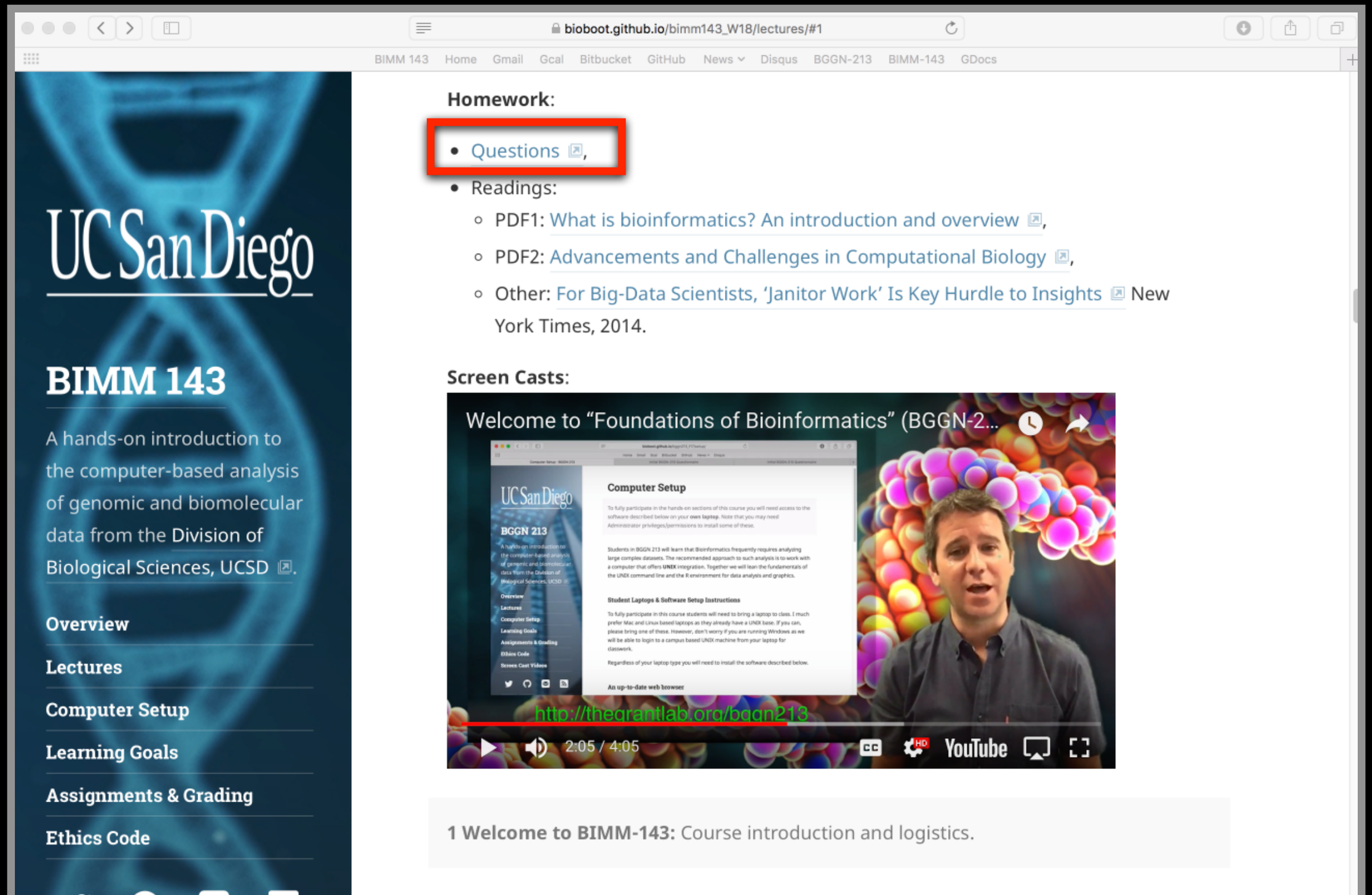


Homework

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

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)

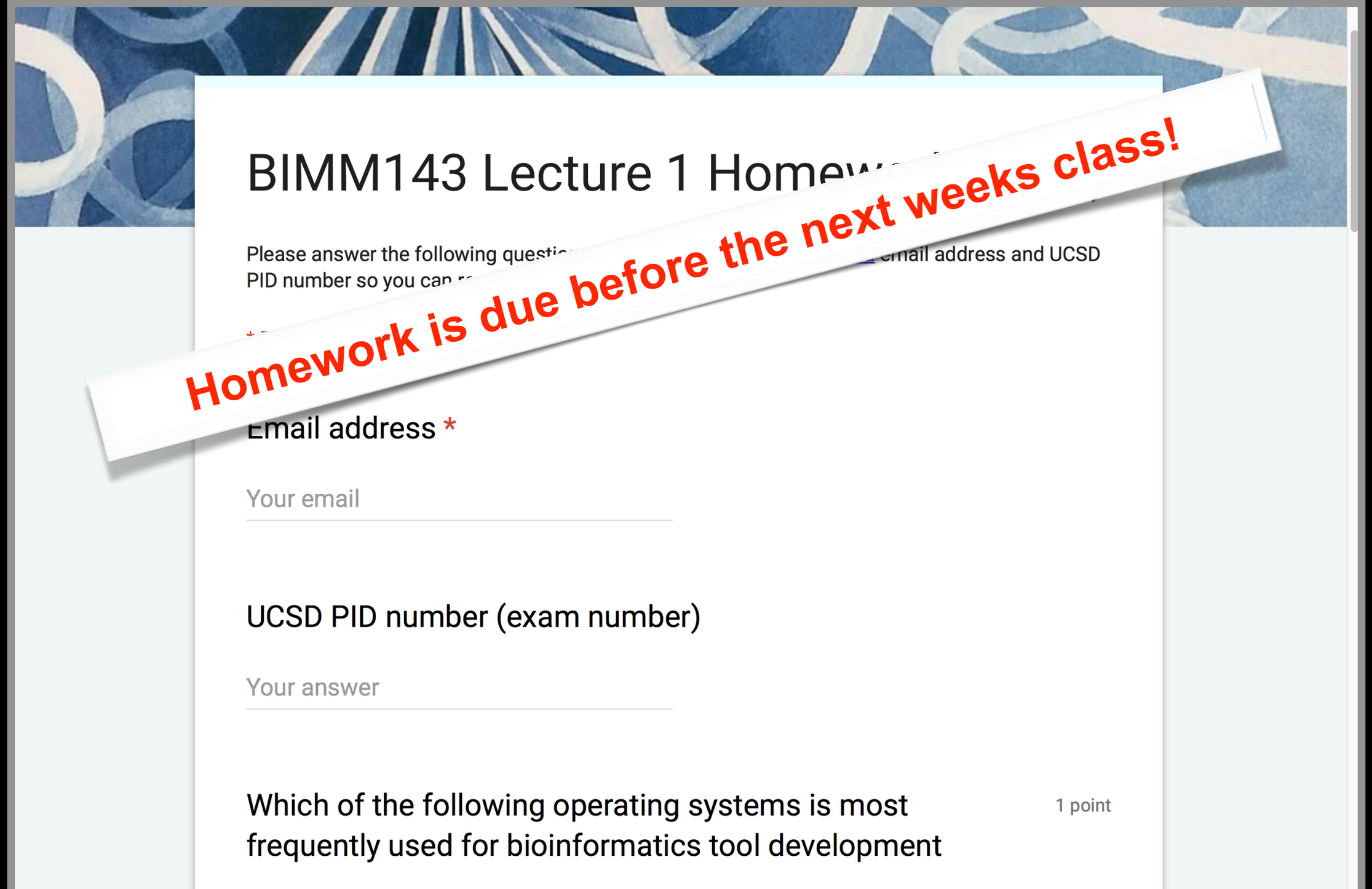
Your answer

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

1 point

Homework

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



Homework

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

DataCamp

Course Outline

Exercise

PCA analysis

To continue with the quality assessment of our samples, in the first part of this exercise, we will perform PCA to look how our samples cluster and whether our condition of interest corresponds with the principal components explaining the most variation in the data. In the second part, we will answer questions about the PCA plot.

To assess the similarity of the `smoc2` samples using PCA, we need to transform the normalized counts then perform the PCA analysis. Assume all libraries have been loaded, the DESeq2 object created, and the size factors have been stored in the DESeq2 object, `dds_smoc2` .

Instructions 1/2 50 XP

- Run the code to transform the normalized counts.
- Perform PCA by plotting PC1 vs PC2 using the DESeq2 `plotPCA()` function on the DESeq2 transformed counts object, `vsd_smoc2` and specify the `intgroup` argument as the factor to color the plot.

Take Hint (-15 XP)

script.R | RDocumentation

```
1 # Transform the normalized counts
2 vsd_smoc2 <- vst(dds_smoc2, blind = TRUE)
3
4 # Plot the PCA of PC1 and PC2
5 ___(___, intgroup=___)
```

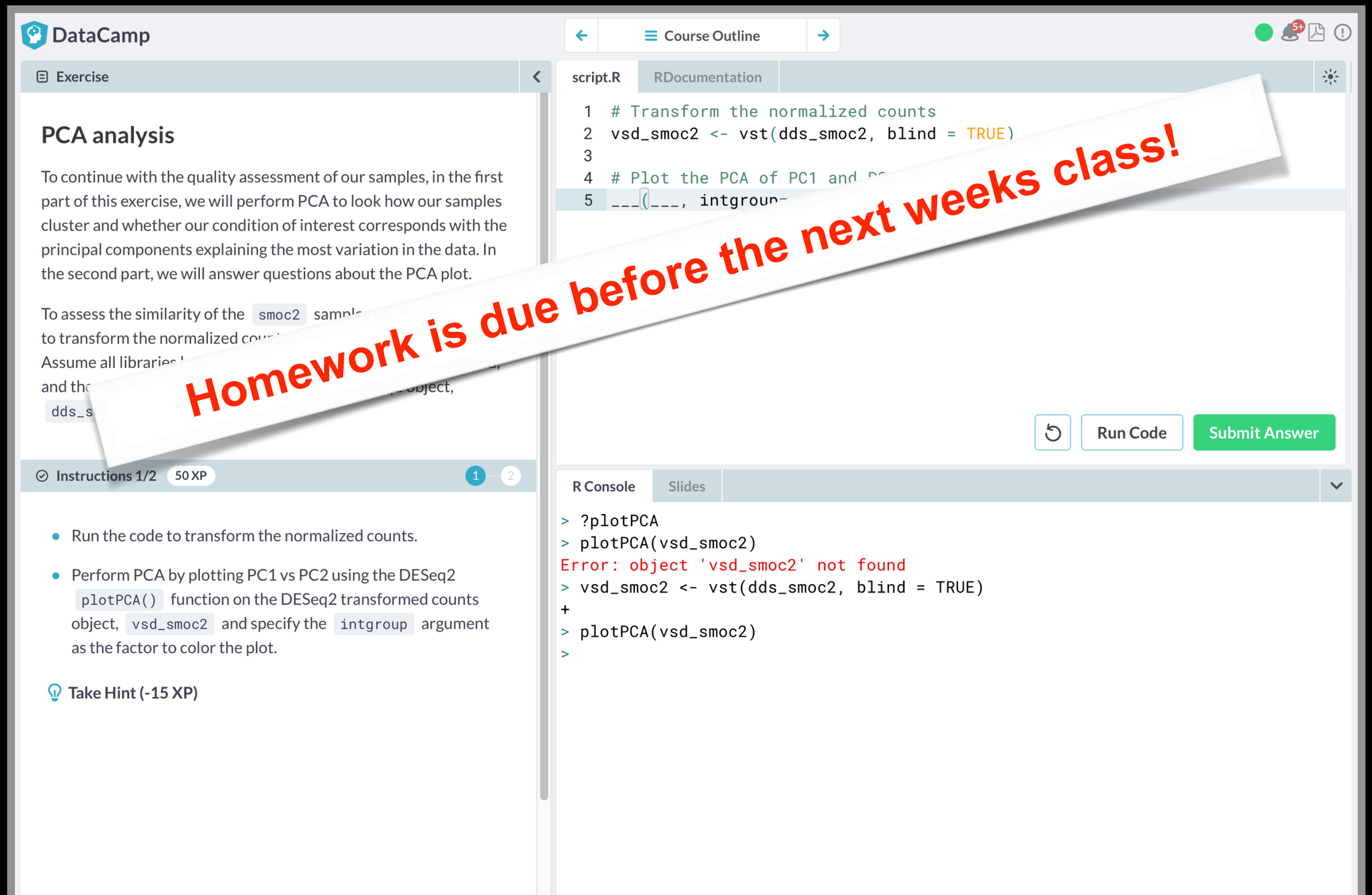
Run Code | Submit Answer

R Console | Slides

```
> ?plotPCA
> plotPCA(vsd_smoc2)
Error: object 'vsd_smoc2' not found
> vsd_smoc2 <- vst(dds_smoc2, blind = TRUE)
+
> plotPCA(vsd_smoc2)
>
```

Homework (35% of course grade)

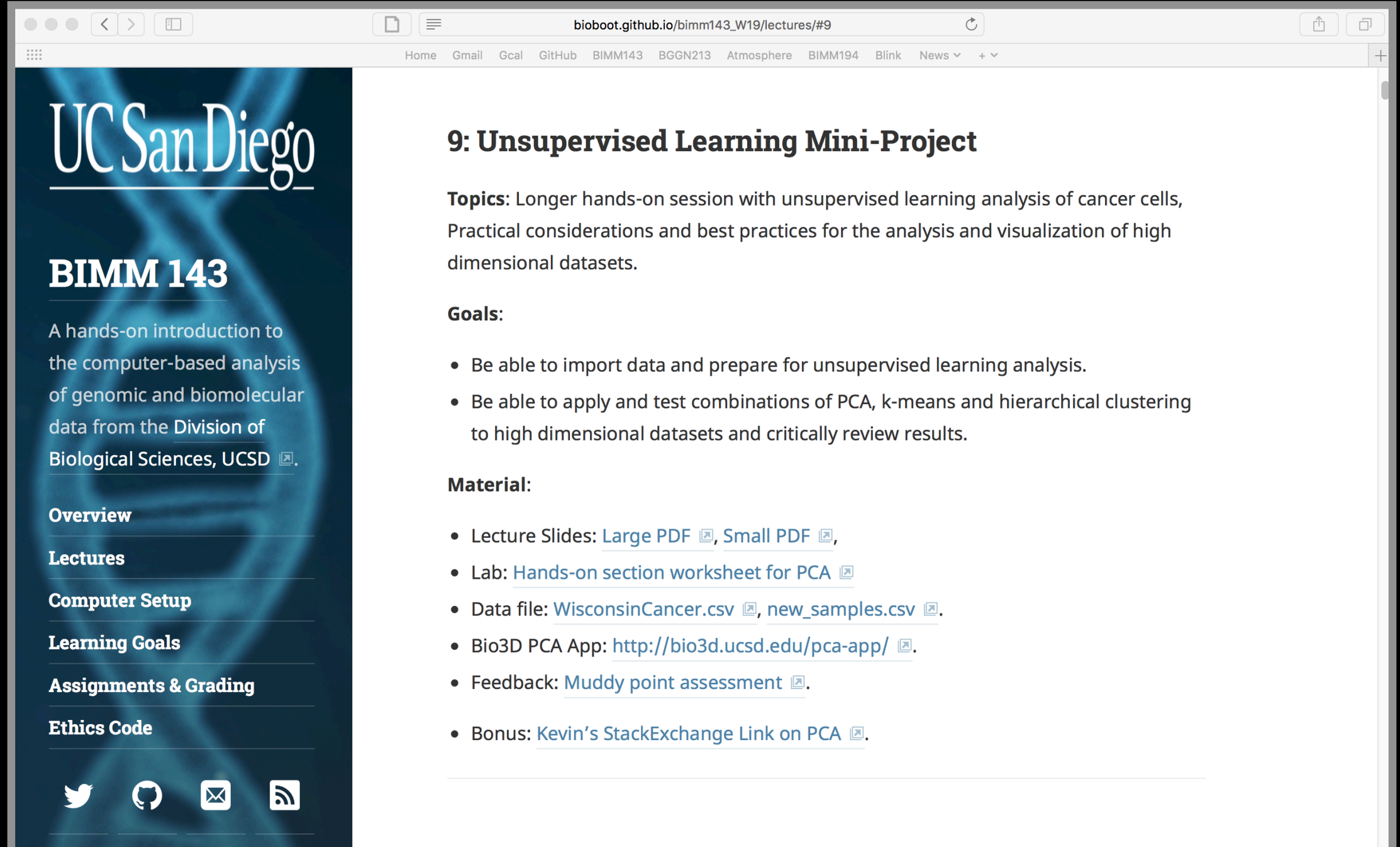
Goals, Class material, Screencasts & **Homework**



Homework is due before the next weeks class!

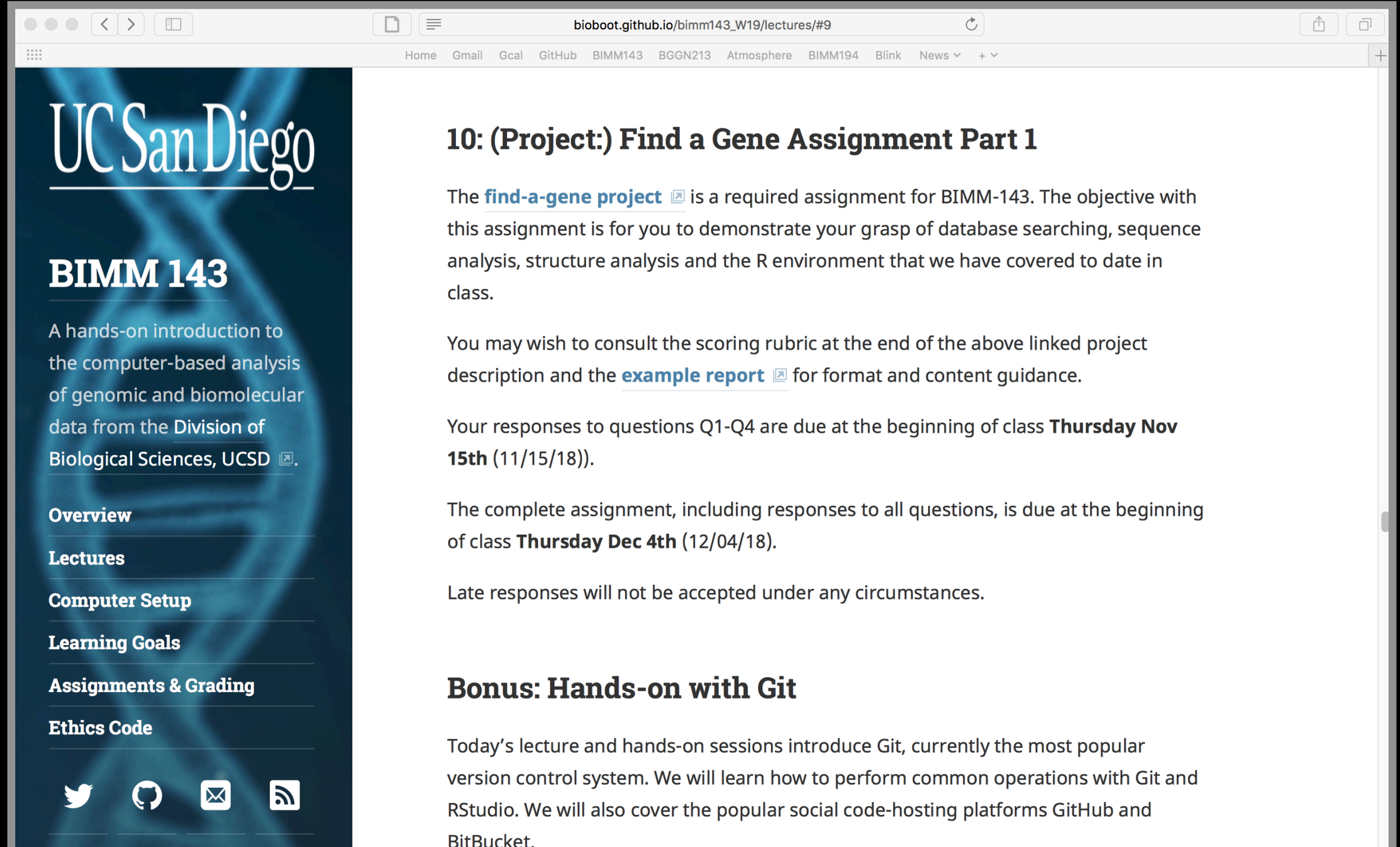
Projects

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



Projects (20% of course grade)

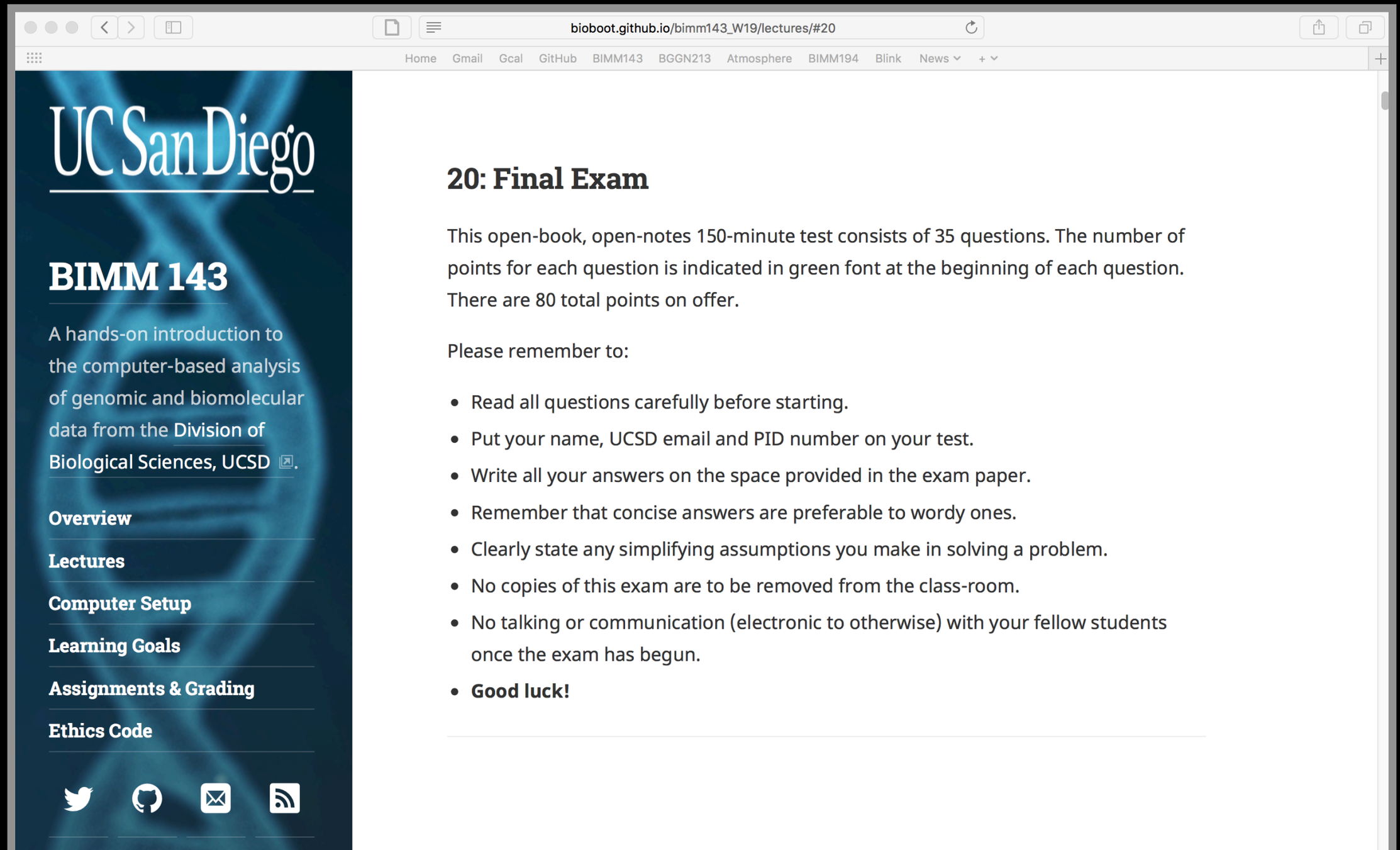
Week long mini-projects (x2),
and 1 five week **main project**



Final Exam

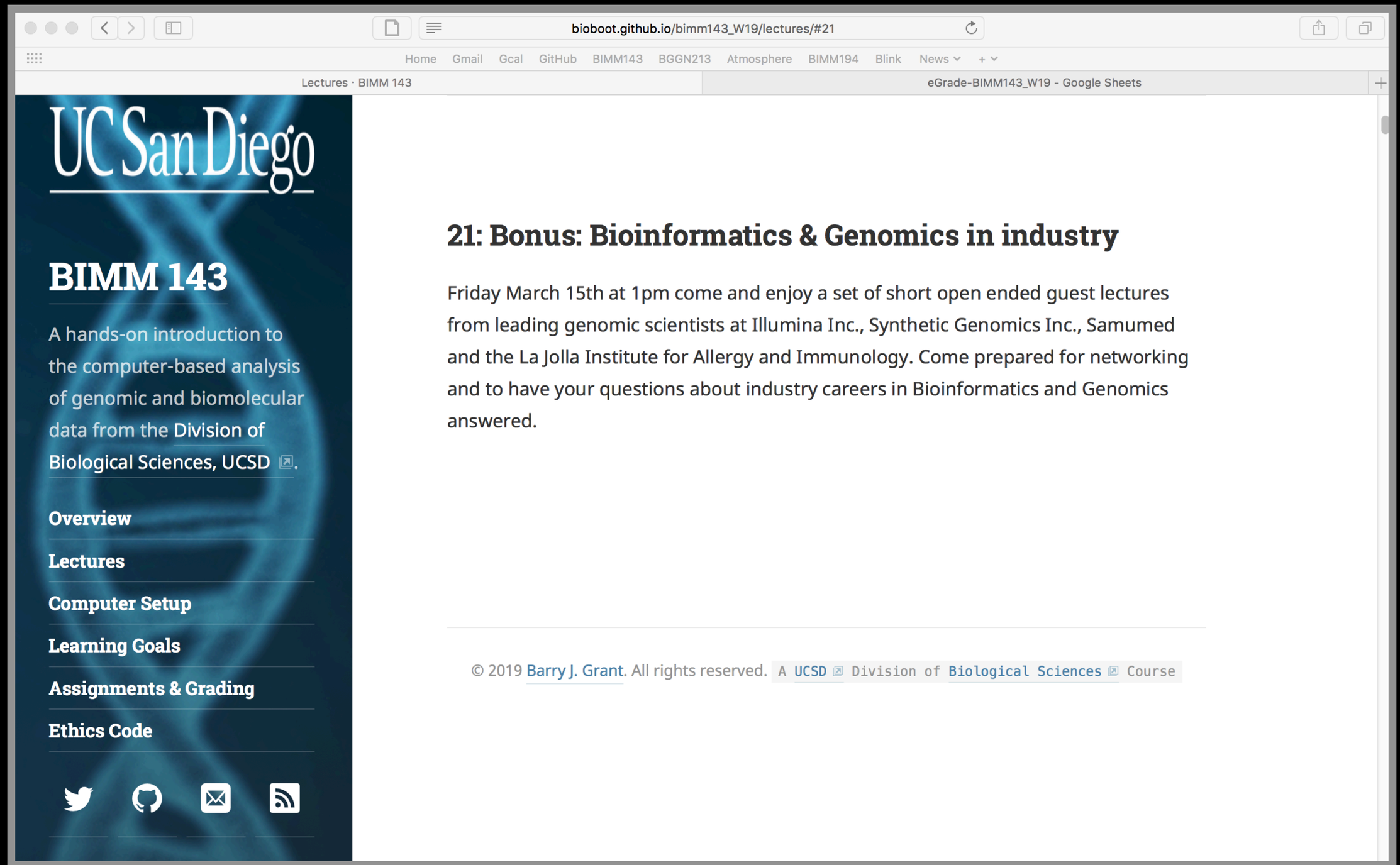
Open-book, open-notes 150-minute test

(45% of course grade)



Bonus:

Bioinformatics & Genomics in industry



Bonus:

Online portfolio of **your** bioinformatics work!

jasonpbennett.github.io/bimm143/

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

Bioinformatics Class BIMM-143

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

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!

jasonpbennett.github.io/bimm143/class13/NGS.html

class13 | Bioinformatics Class 5

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")
```

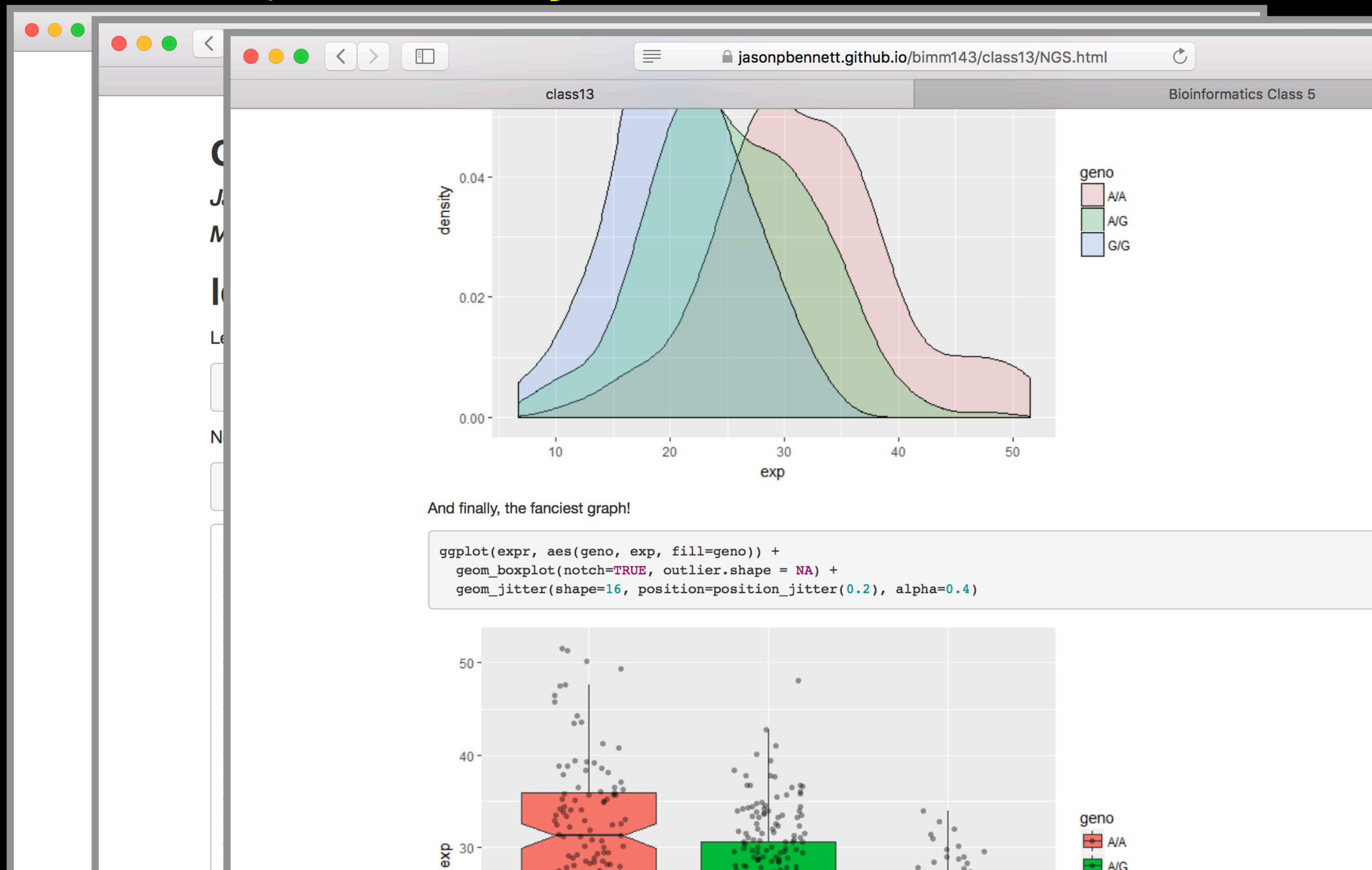
Now lets look at a table of the data:

```
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!



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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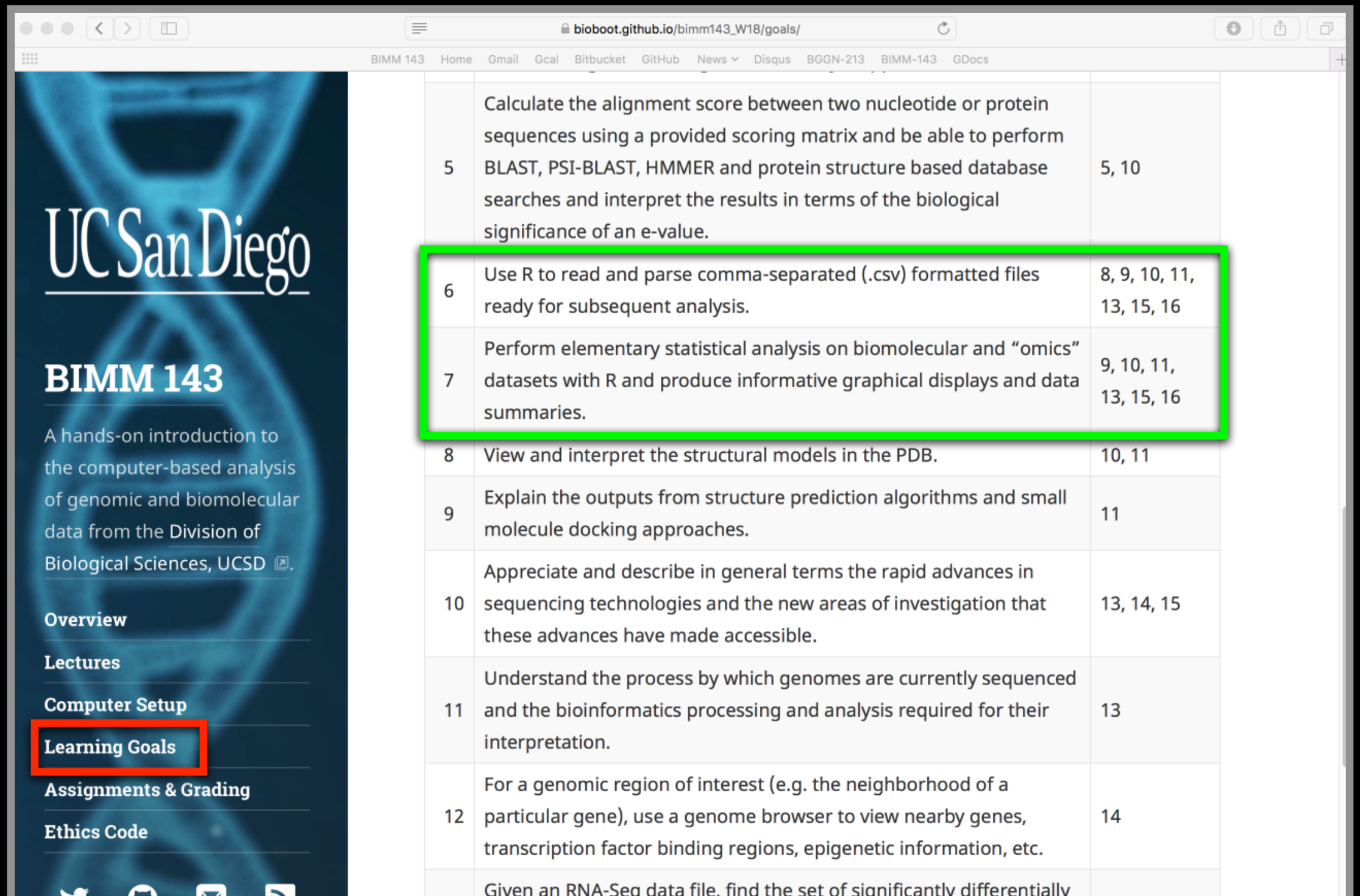
BIMM-143 Learning Goals....

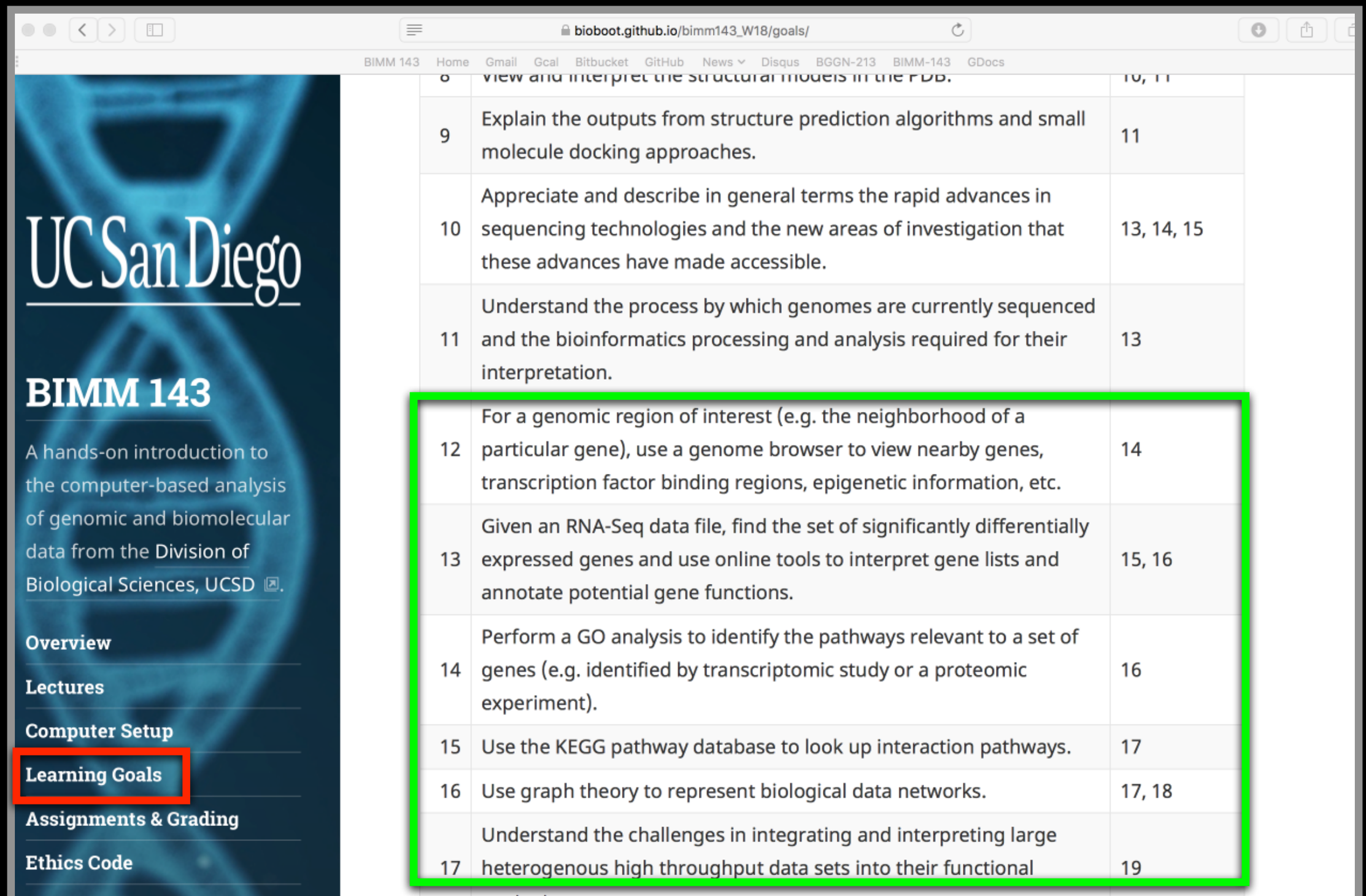
Data science R based learning goals



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



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

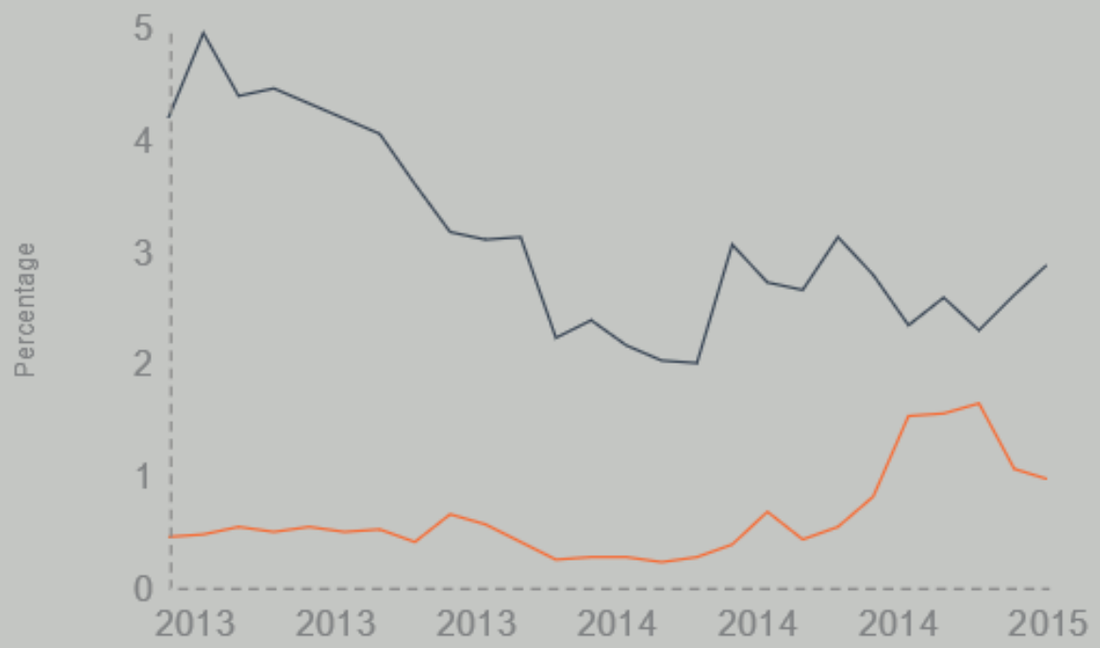
Language Rank	Types	Spectrum Ranking
1. C		100.0
2. Java		98.1
3. Python		98.0
4. C++		95.9
5. R		87.9
6. C#		86.7
7. PHP		82.8
8. JavaScript		82.2
9. Ruby		74.5
10. Go		71.9

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

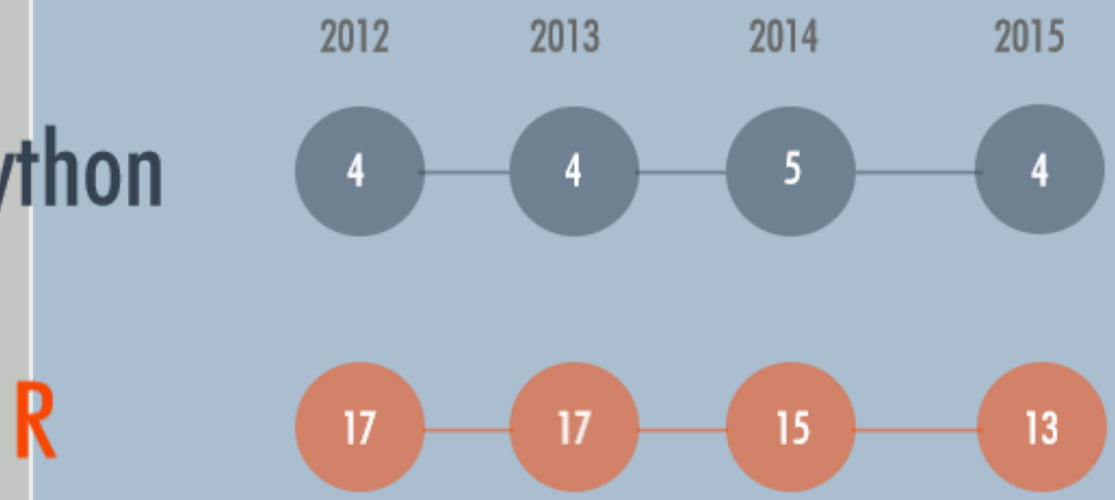
R and Python: The Numbers

Popularity Rankings

R and Pythons popularity between 2013 and February 2015 (Tiobe Index)



Redmonk ranking, comparing the relative performance of programming languages on GitHub and Stack Overflow (September 2012 and January 2013, 2014, 2015)



Jobs And Salary?

2014 Dice Tech Salary Survey:
Average Salary For High Paying Skills and Experience

$ 115,531

$94,139

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...

etherpad.net/p/bimm143_f18

Home Gmail Gcal GitHub BIMM143 BGGN213 Atmosphere BIMM194 Blink News +

bimm143 f18 | etherpad.net Pad | eGrade-BIMM143_W19 - Google Sheets

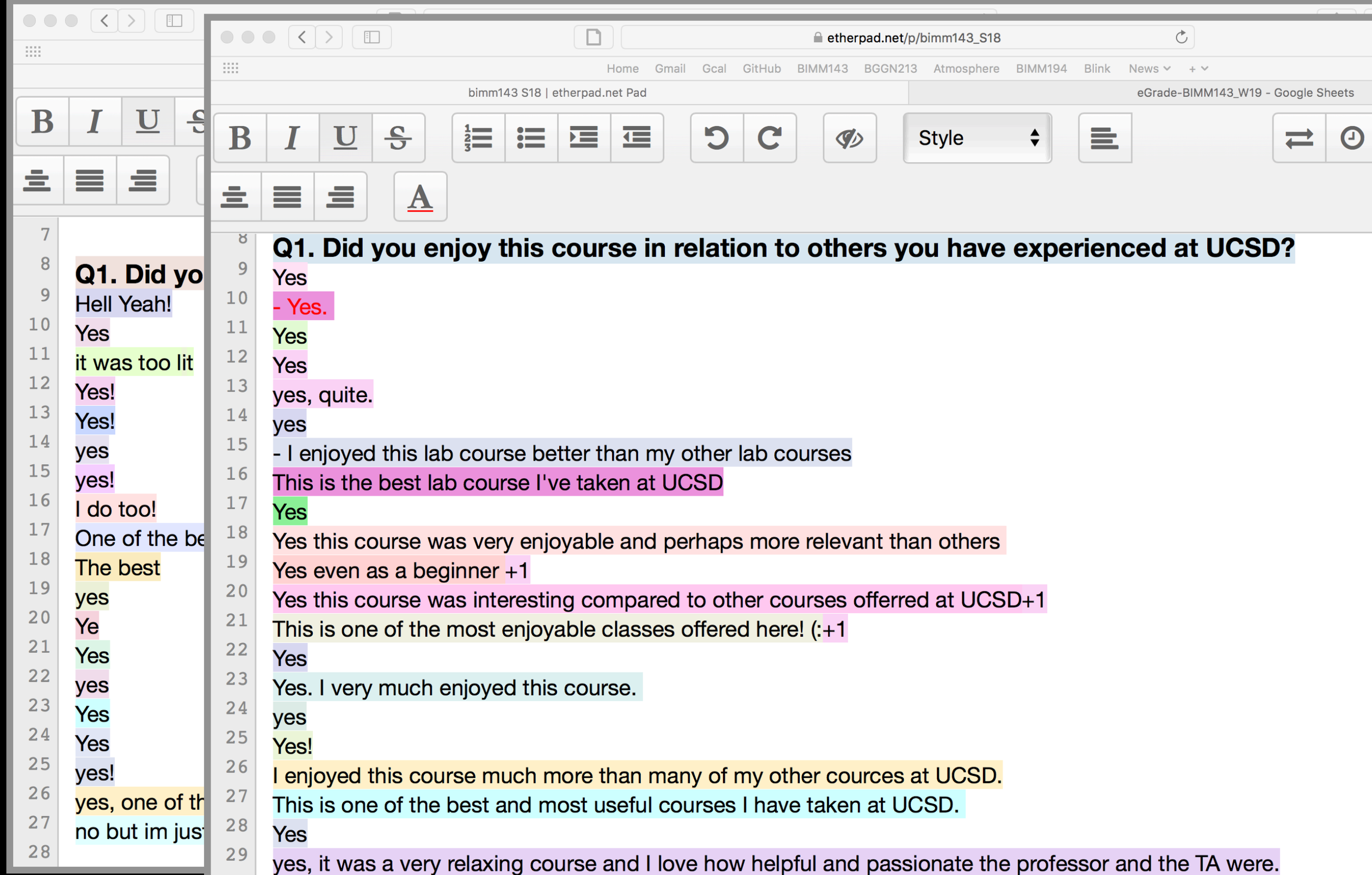
Style

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. :)

Chat 0

Past Student Opinions...



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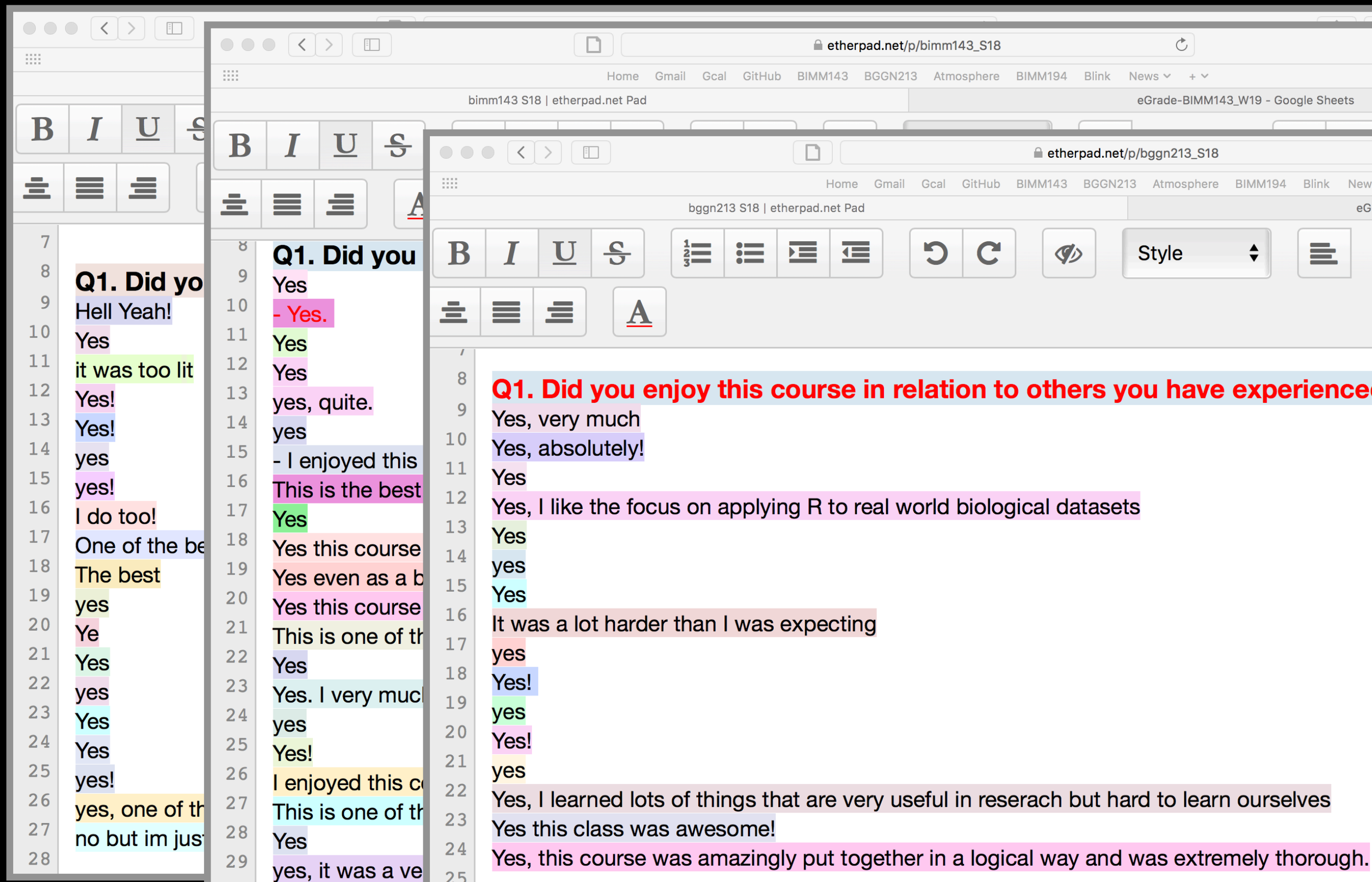

Instructor	Course	Term	Rcmnd Class	Rcmnd Instr	Study Hrs/wk	Avg Grade Expected	Avg Grade Received
Grant, Barry J	BIMM 143 - Bioinformatics Laboratory (A)	FA18	100.0 %	100.0 %	4.50	B+ (3.53)	N/A
Grant, Barry J	BIMM 143 - Bioinformatics Laboratory (A)	SP18	94.7 %	94.7 %	5.66	B+ (3.63)	B+ (3.35)
Grant, Barry J	BIMM 143 - Bioinformatics Laboratory (A)	WI18	100.0 %	100.0 %	5.64	B+ (3.64)	N/A
Grant, Barry J	BIMM 194 - Adv Topics-Molecular Bio (C)	WI18	92.9 %	100.0 %	1.30	A (4.00)	A (4.00)

Average for BIMM143: 98.2 % 98.2 % 5.27

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Bioinformatics Database	Hands-on exploration of several major databases and their associated tools.

Q. What is Bioinformatics?

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"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 the application of computers to the collection, archiving, organization, and analysis of biological data."

… 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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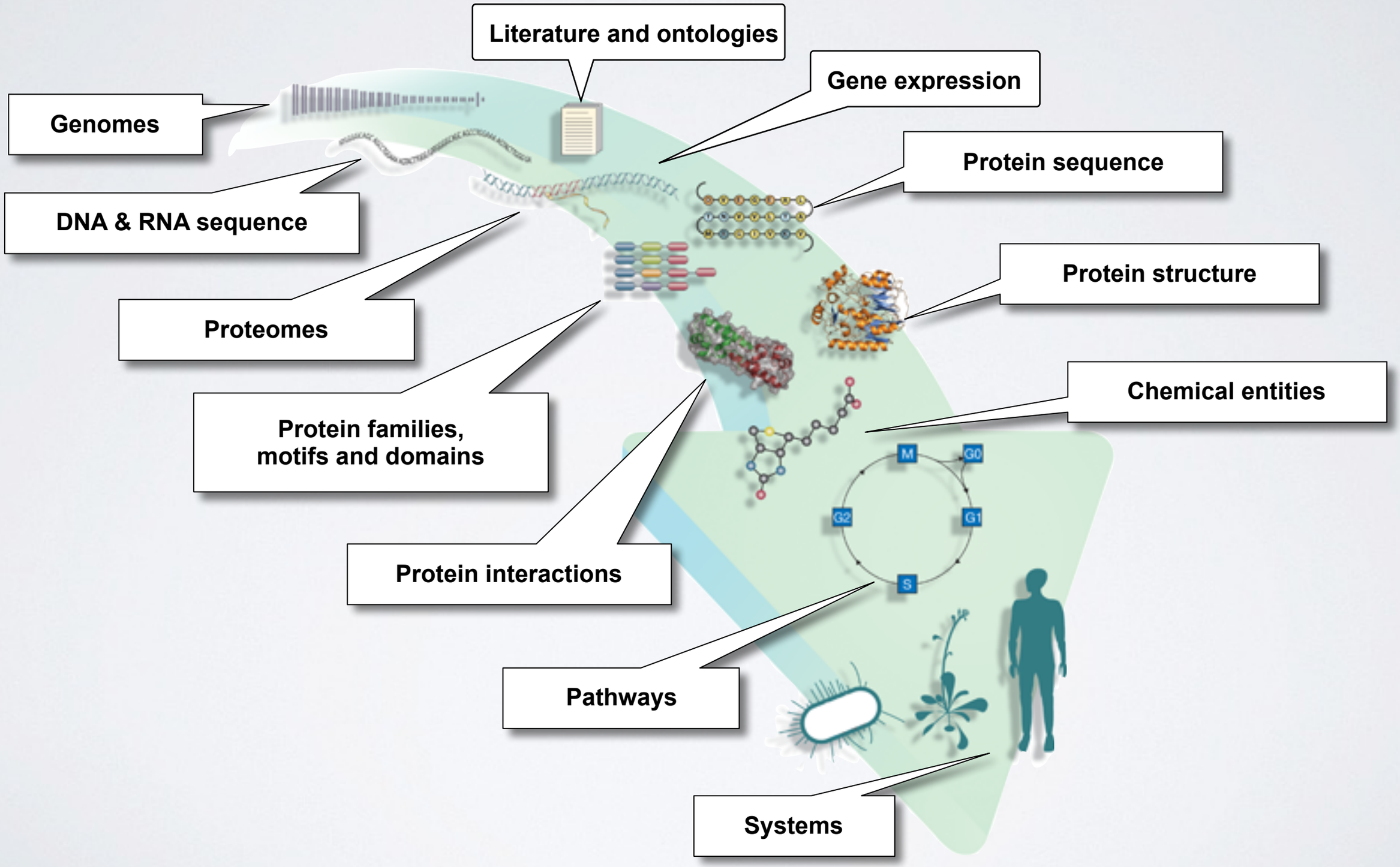
Key Point: Bioinformatics is Computer Aided Biology

Major types of Bioinformatics Data



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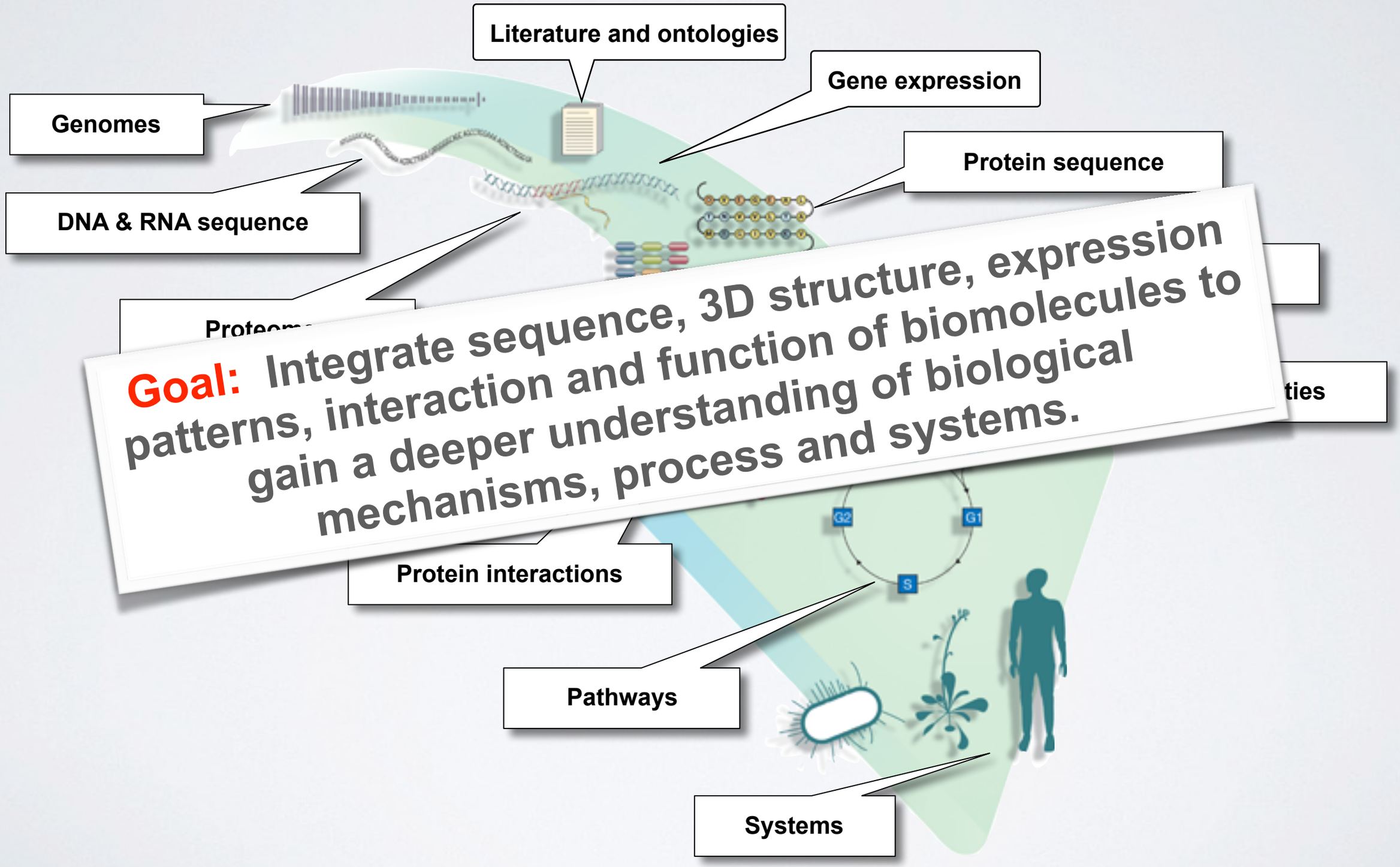
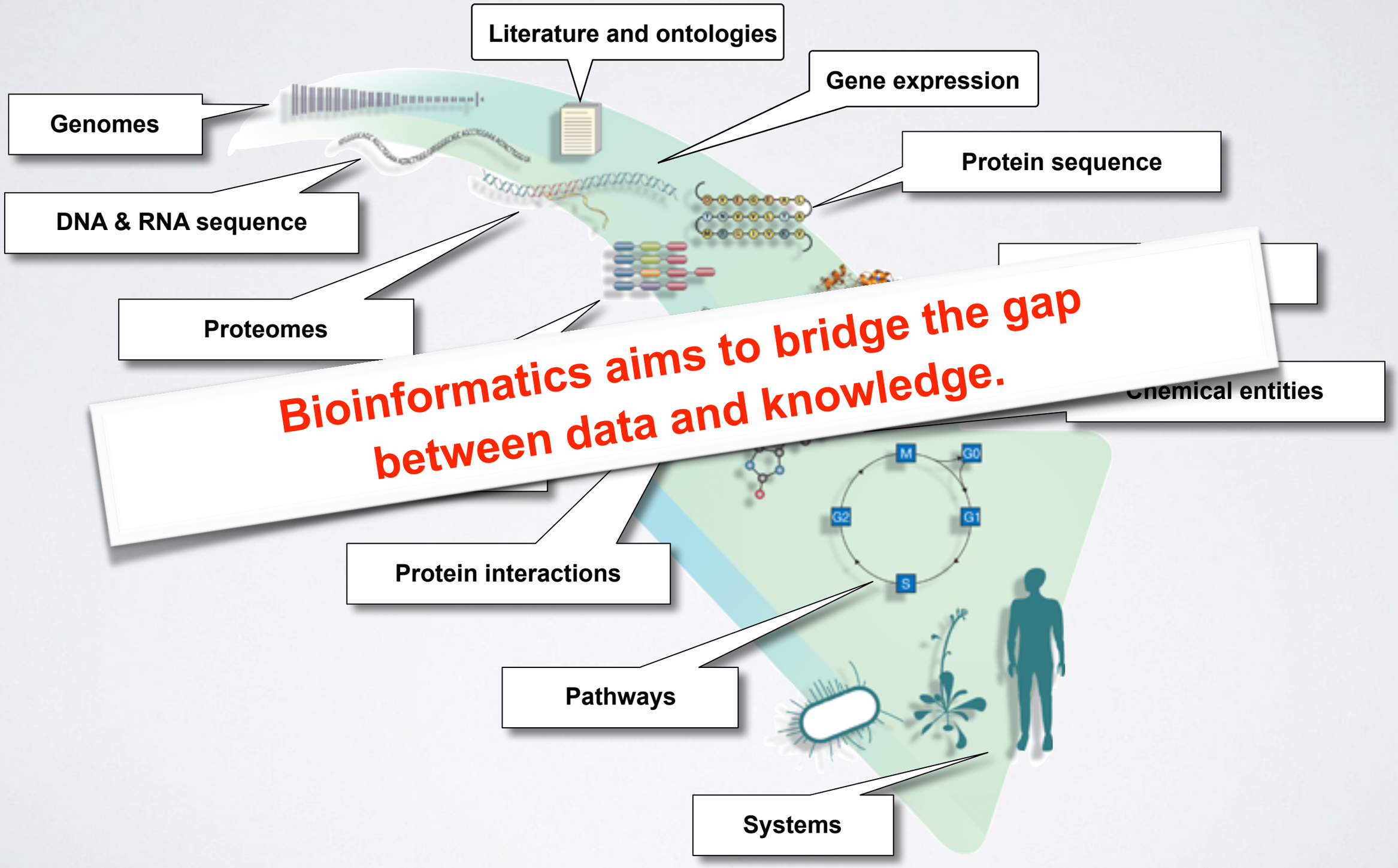


Major types of Bioinformatics Data



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

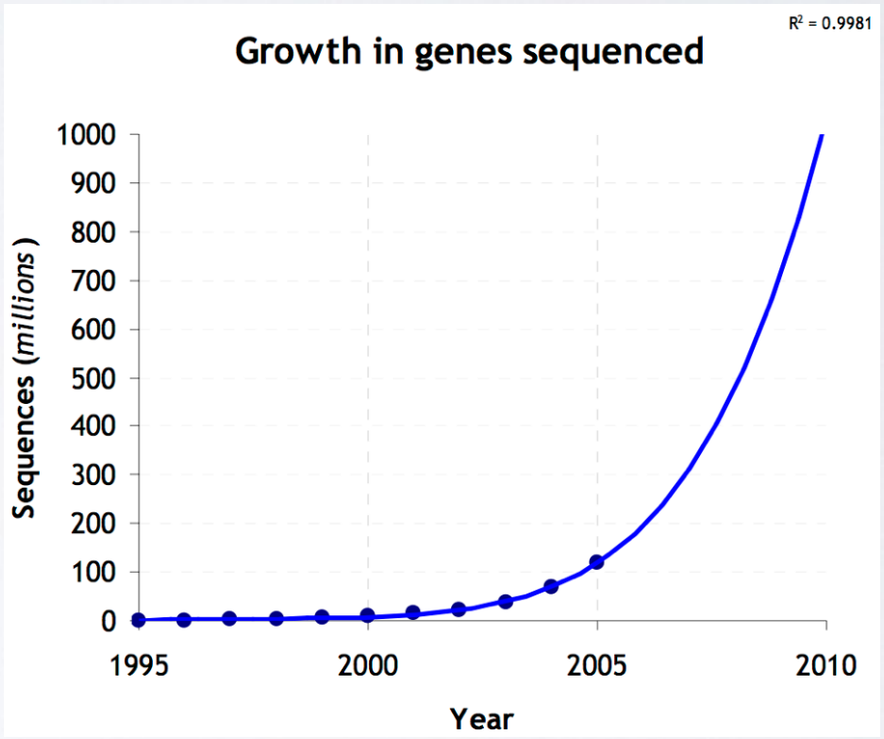
- *DNA sequence* determines *protein sequence*.
- *Protein sequence* determines *protein structure*.
- *Protein structure* determines *protein function*.
- *Regulatory mechanisms* (e.g. gene expression) determine the amount of a particular *function in space and time*.

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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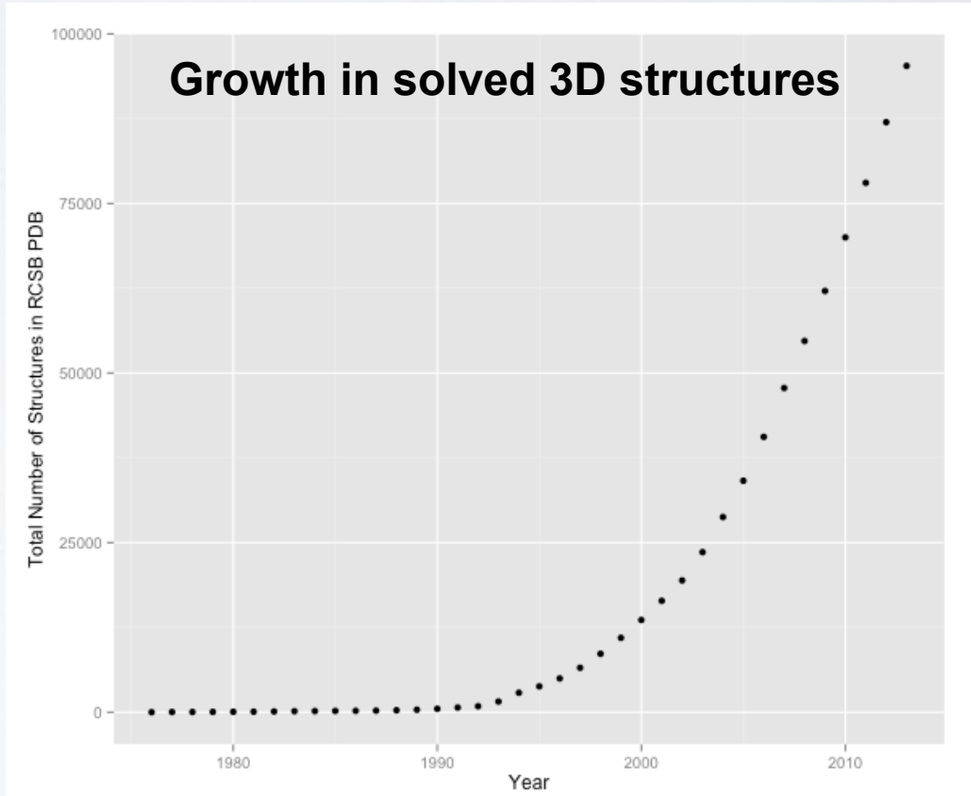

E.G. data from sequencing, structural genomics, proteomics, new high throughput assays, *etc…*

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.

DNA	→	RNA	→	Protein
Genome	→	**Transcriptome**	→	**Proteome**

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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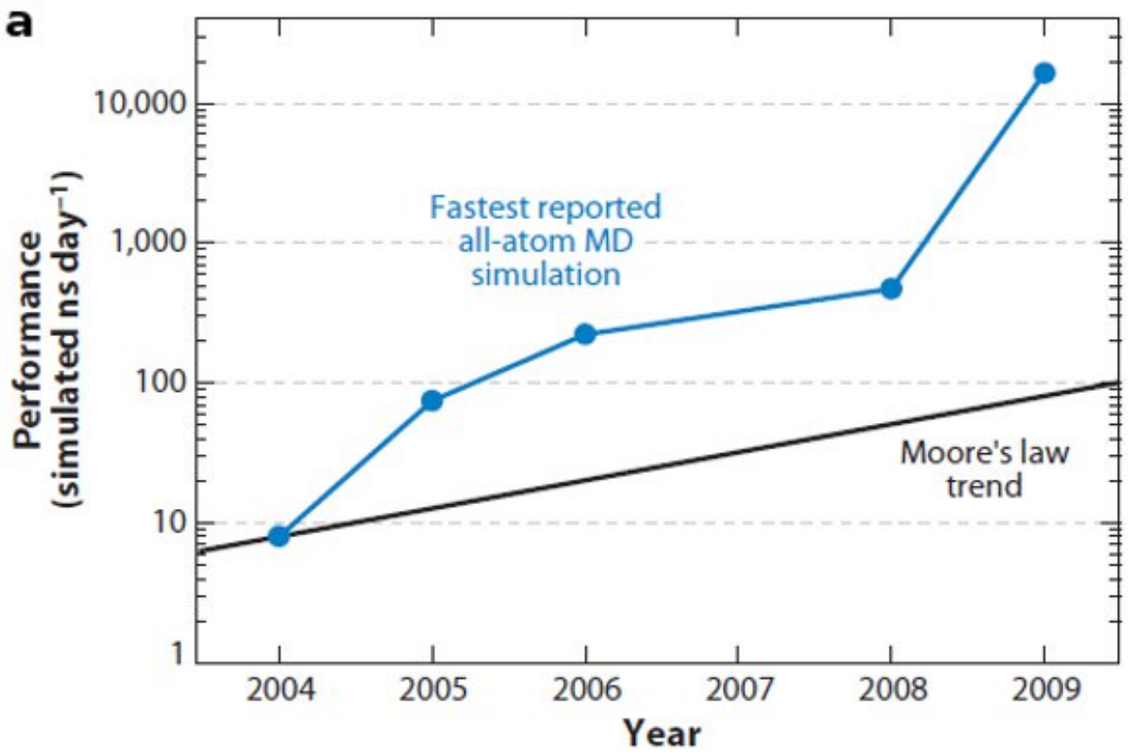
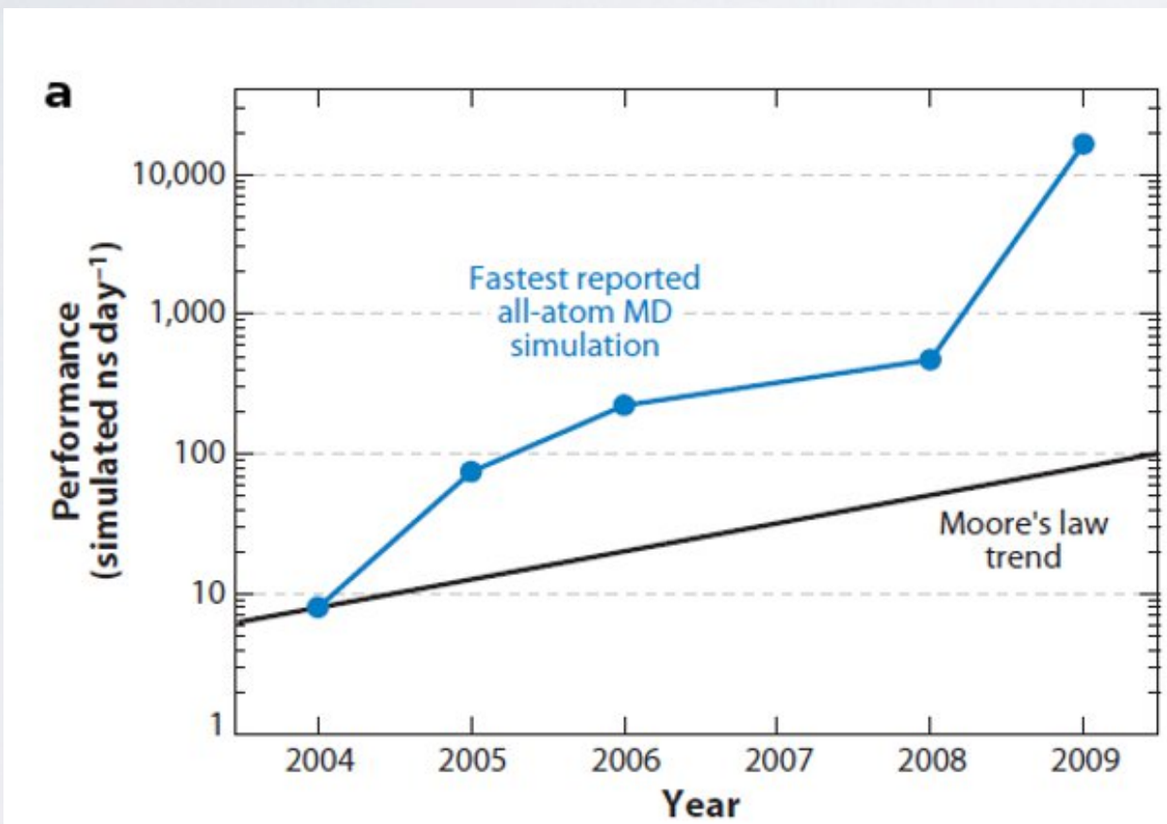
SIDE-NOTE: SUPERCOMPUTERS AND GPUS



SIDE-NOTE: SUPERCOMPUTERS AND GPUS



HOW COMPUTERS HAVE CHANGED

DATE	COST	SPEED	MEMORY	SIZE
1967	$4091	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

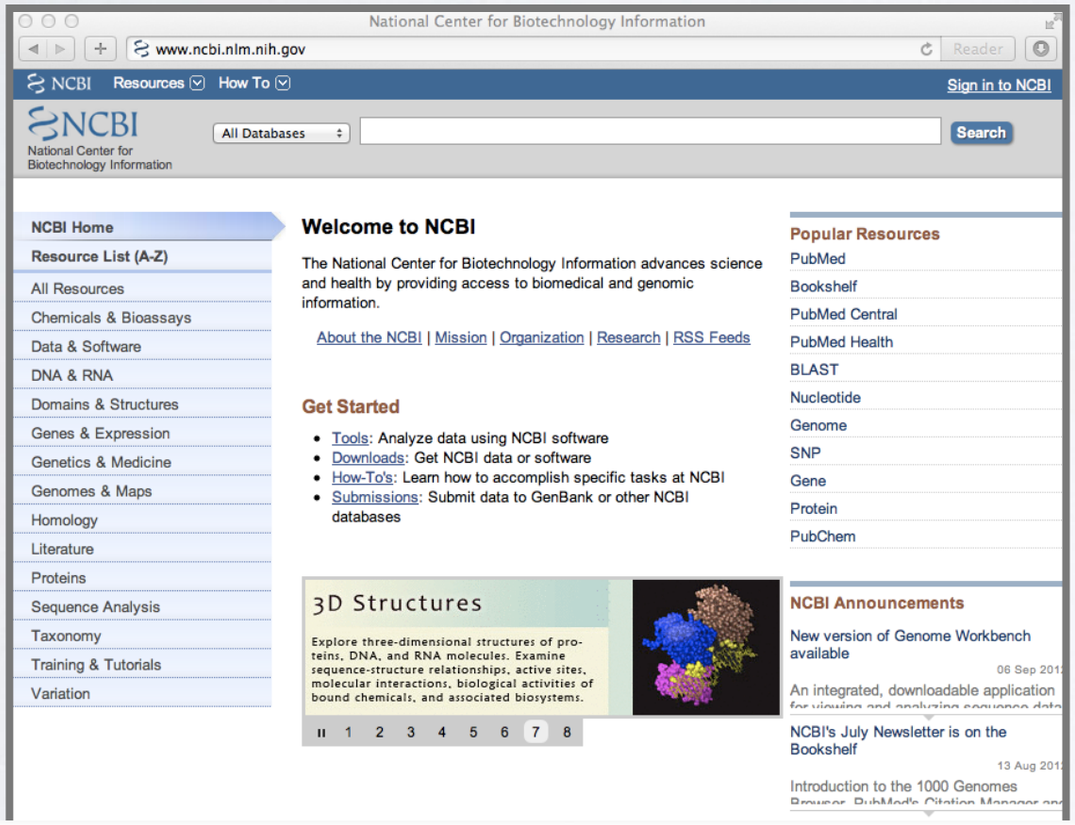
Related tools with different terminology

STEP 3 - Set you

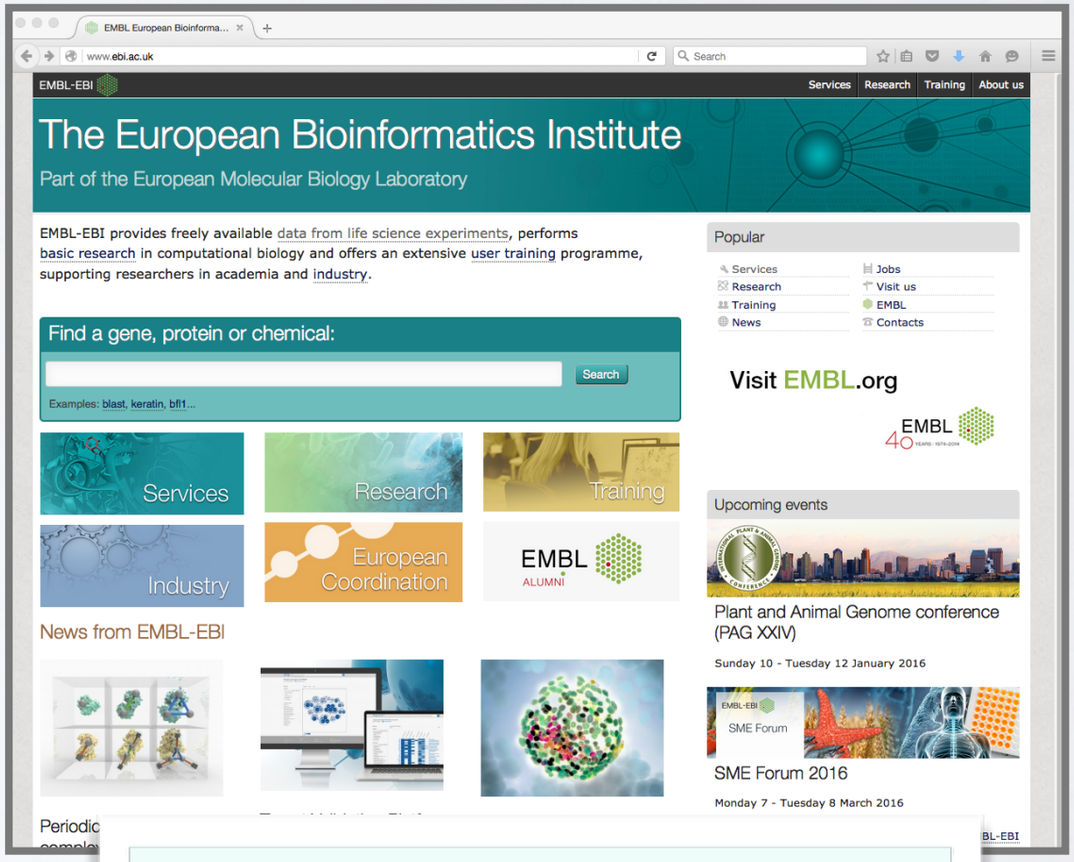
PROGRAM					
FASTA					
MATRIX	GAP OPEN	GAP EXTEND	KTUP	EXPECTATION UPPER VALUE	EXPECTATION LOWER VALUE
BLOSUM50	-10	-2	2	10	0 (default)
DNA STRAND	HISTOGRAM	FILTER		STATISTICAL ESTIMATES	
N/A	no	none		Regress	
SCORES	ALIGNMENTS	SEQUENCE RANGE	DATABASE RANGE	MULTI HSPs	
50	50	START-END	START-END	no	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



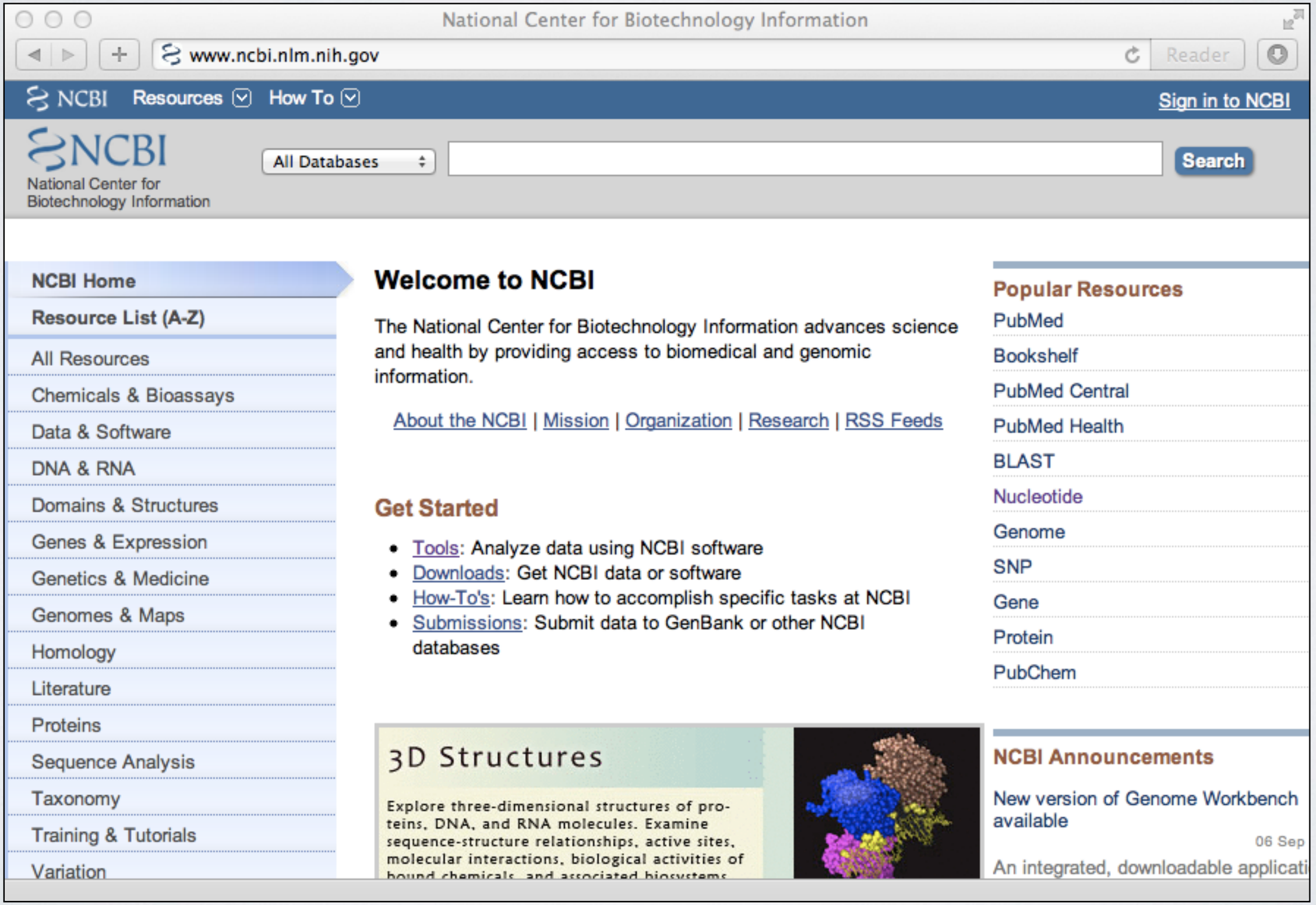
https://www.ebi.ac.uk

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

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

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



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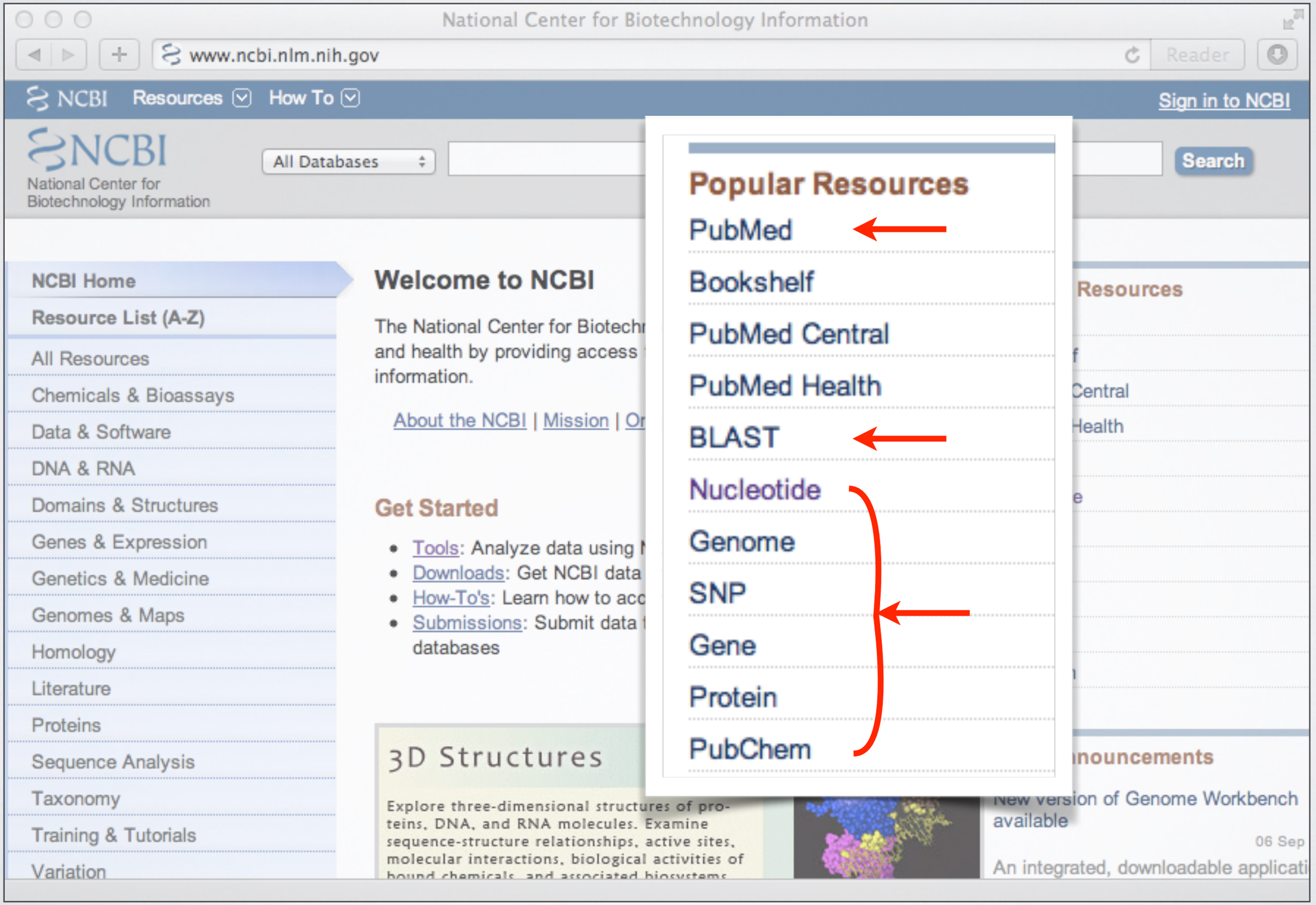

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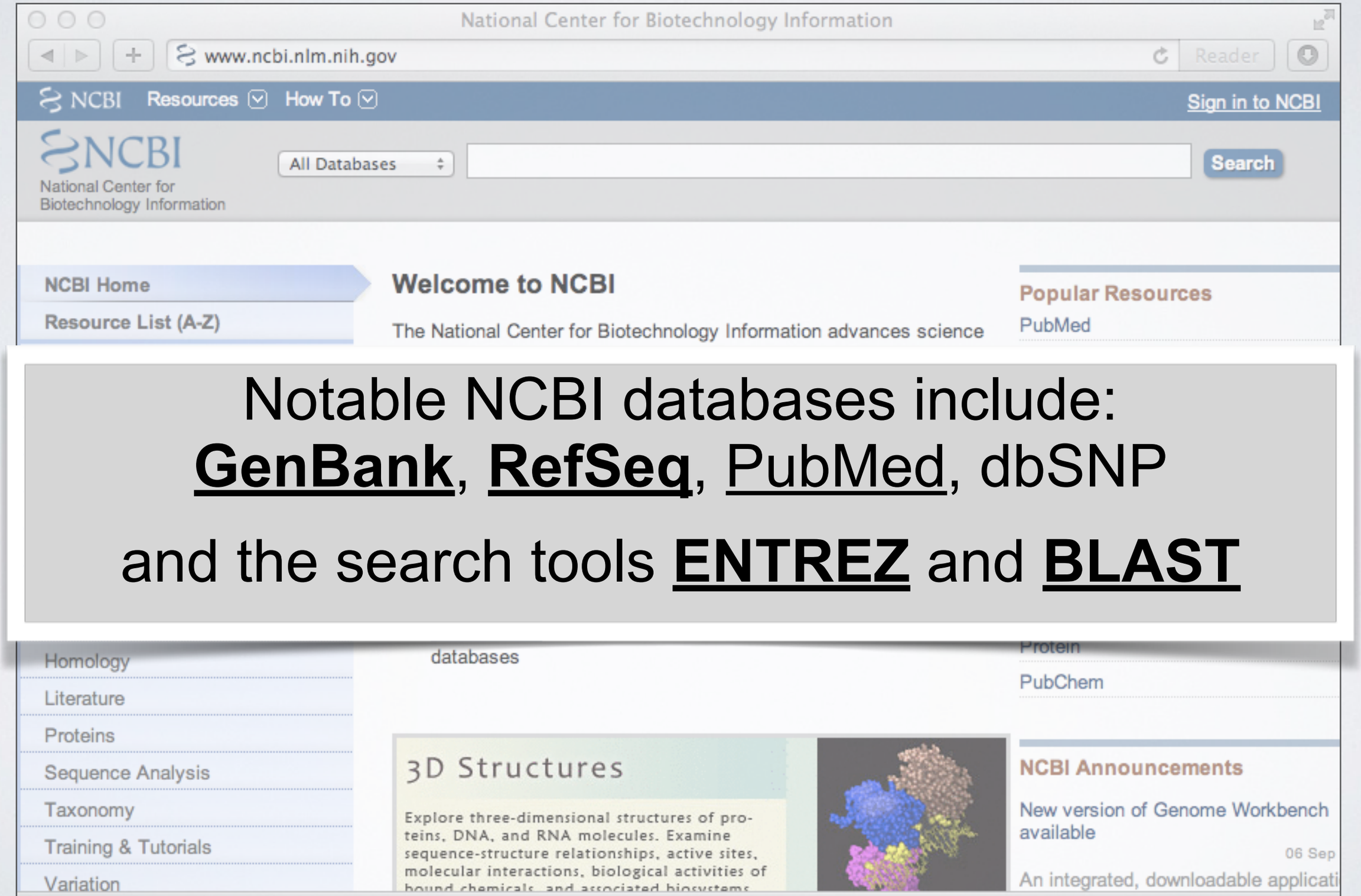
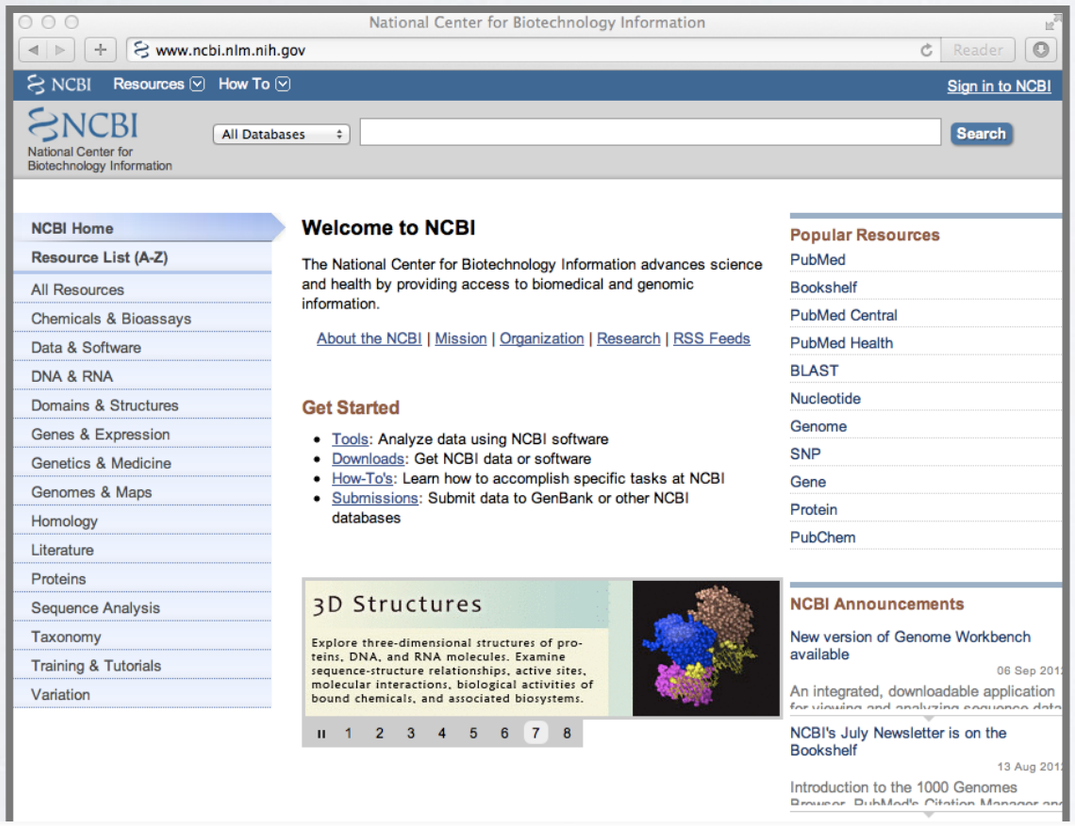


Notable NCBI databases include:
GenBank, **RefSeq**, PubMed, dbSNP

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



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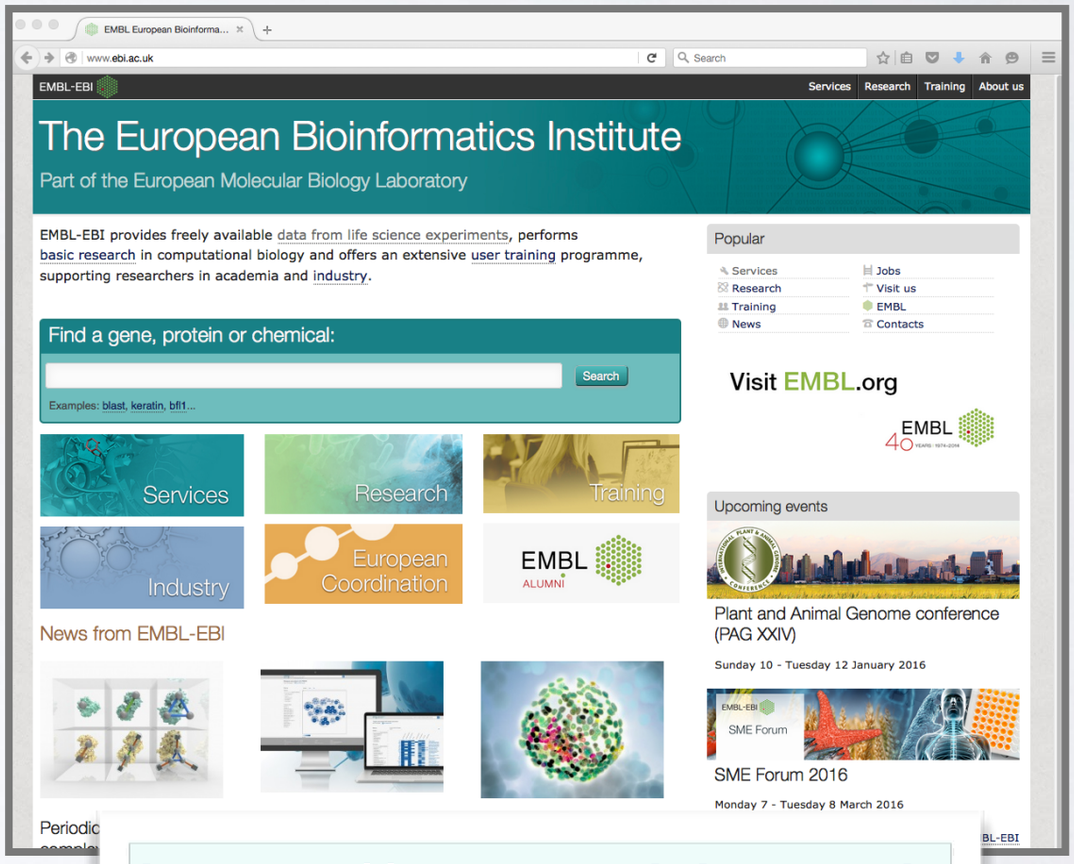


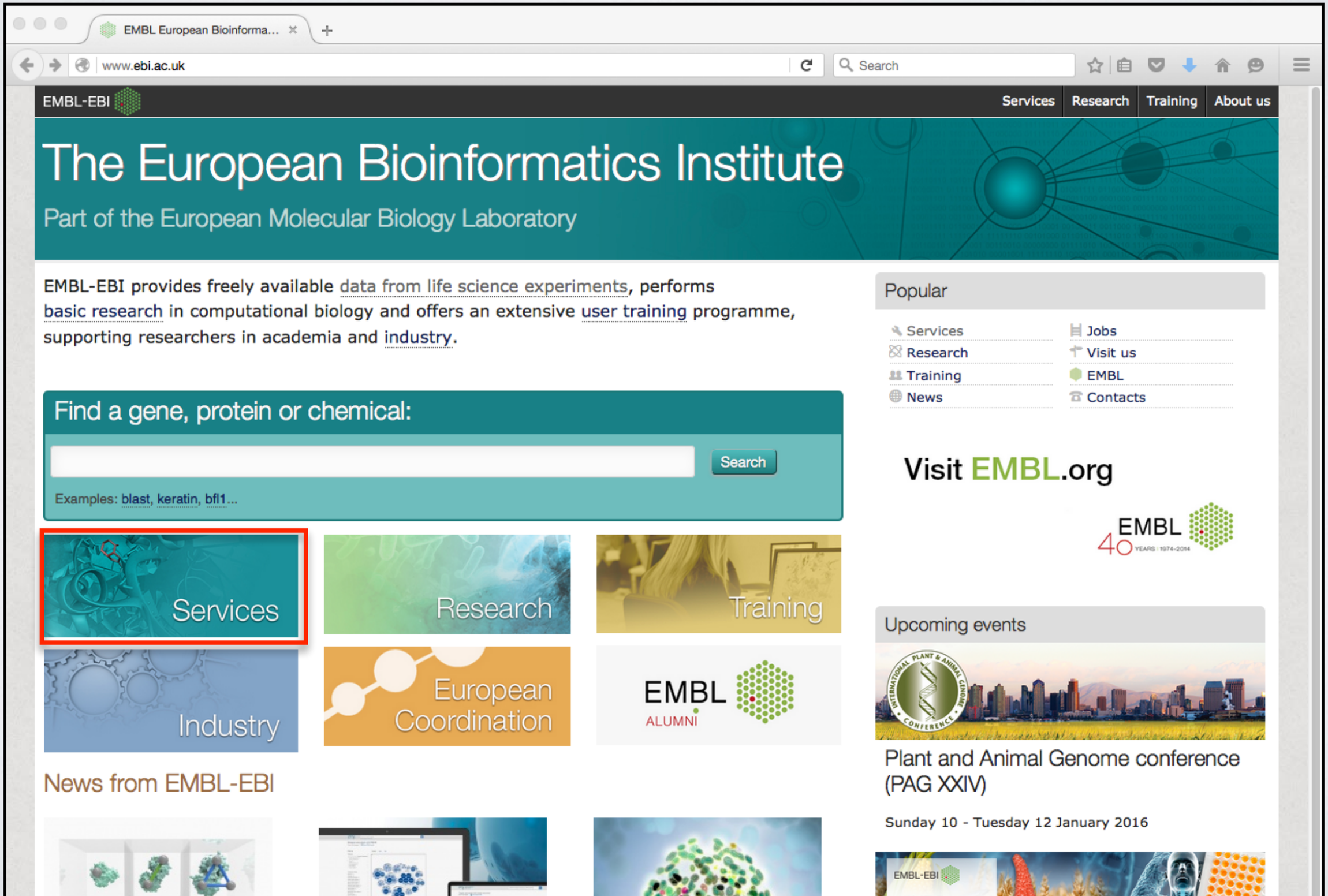
https://www.ebi.ac.uk

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



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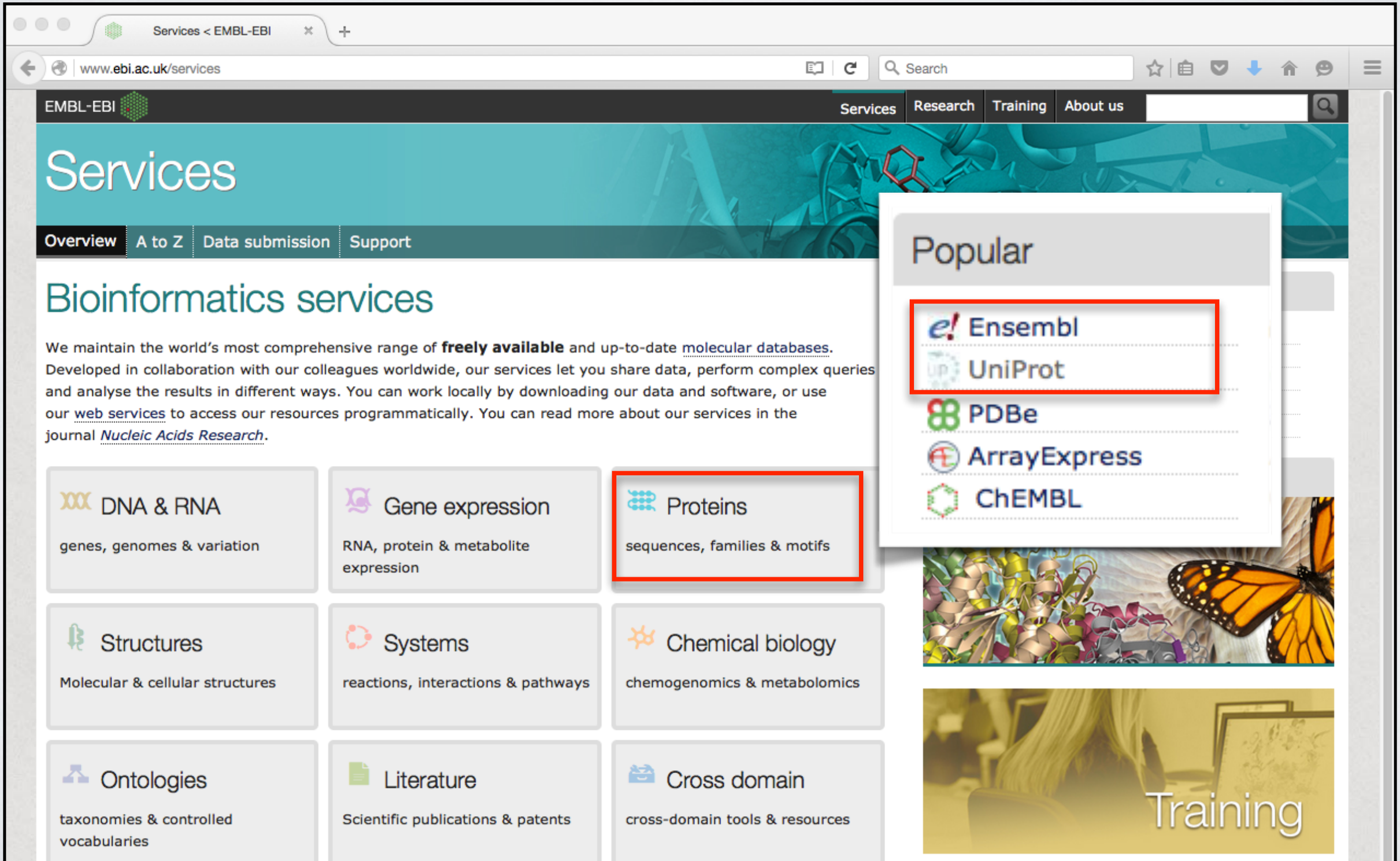
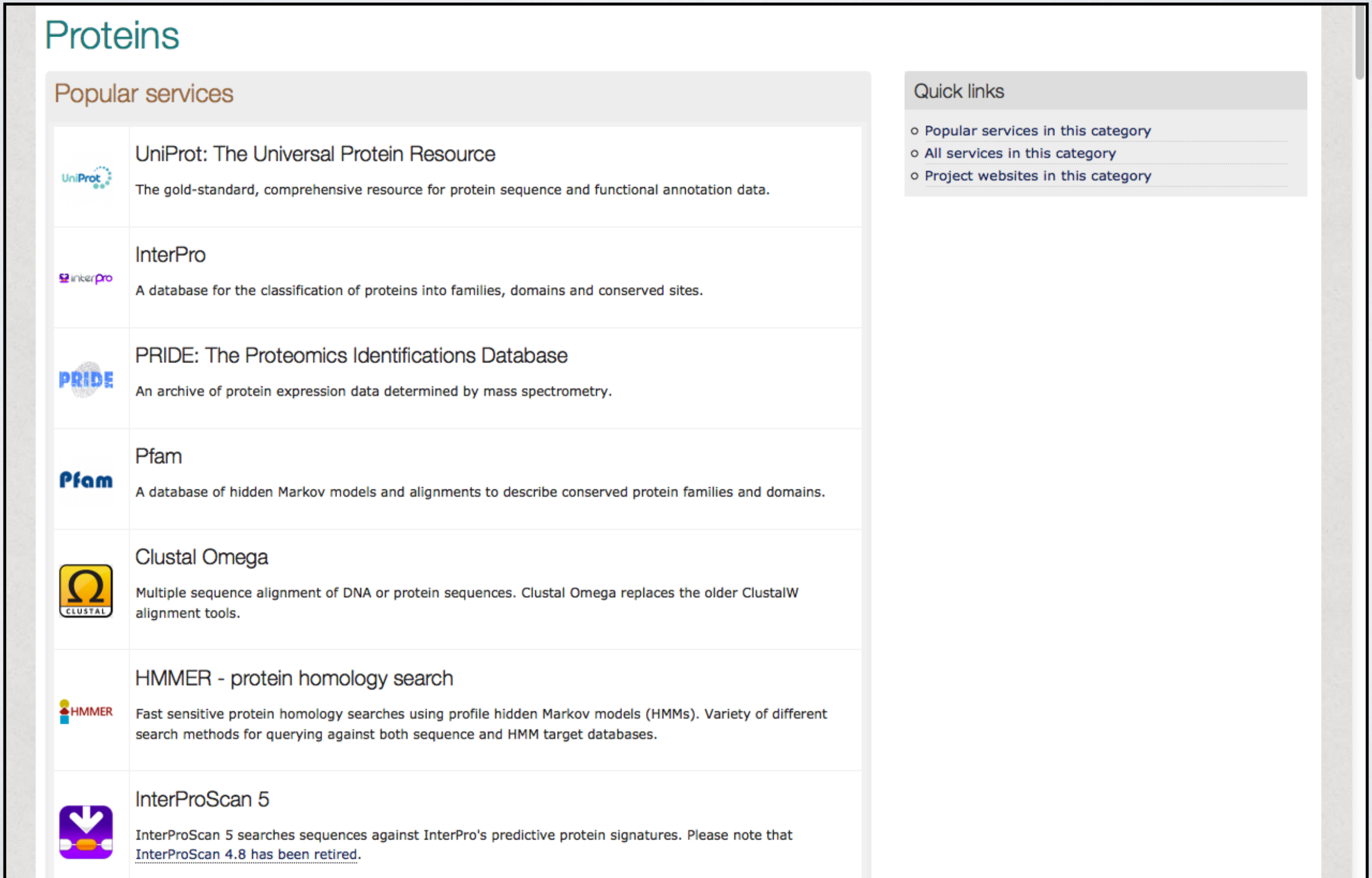
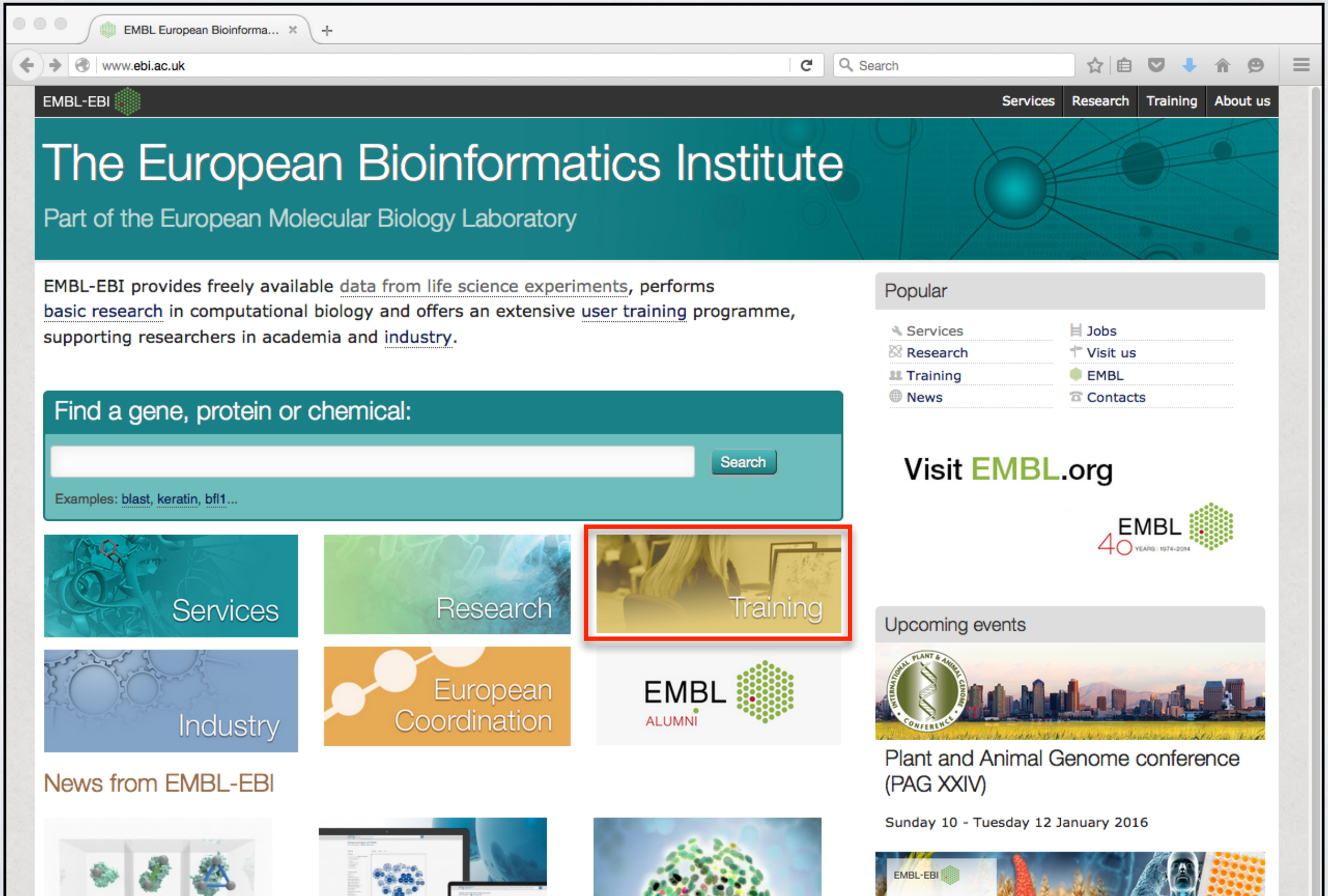


https://www.ebi.ac.uk

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



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



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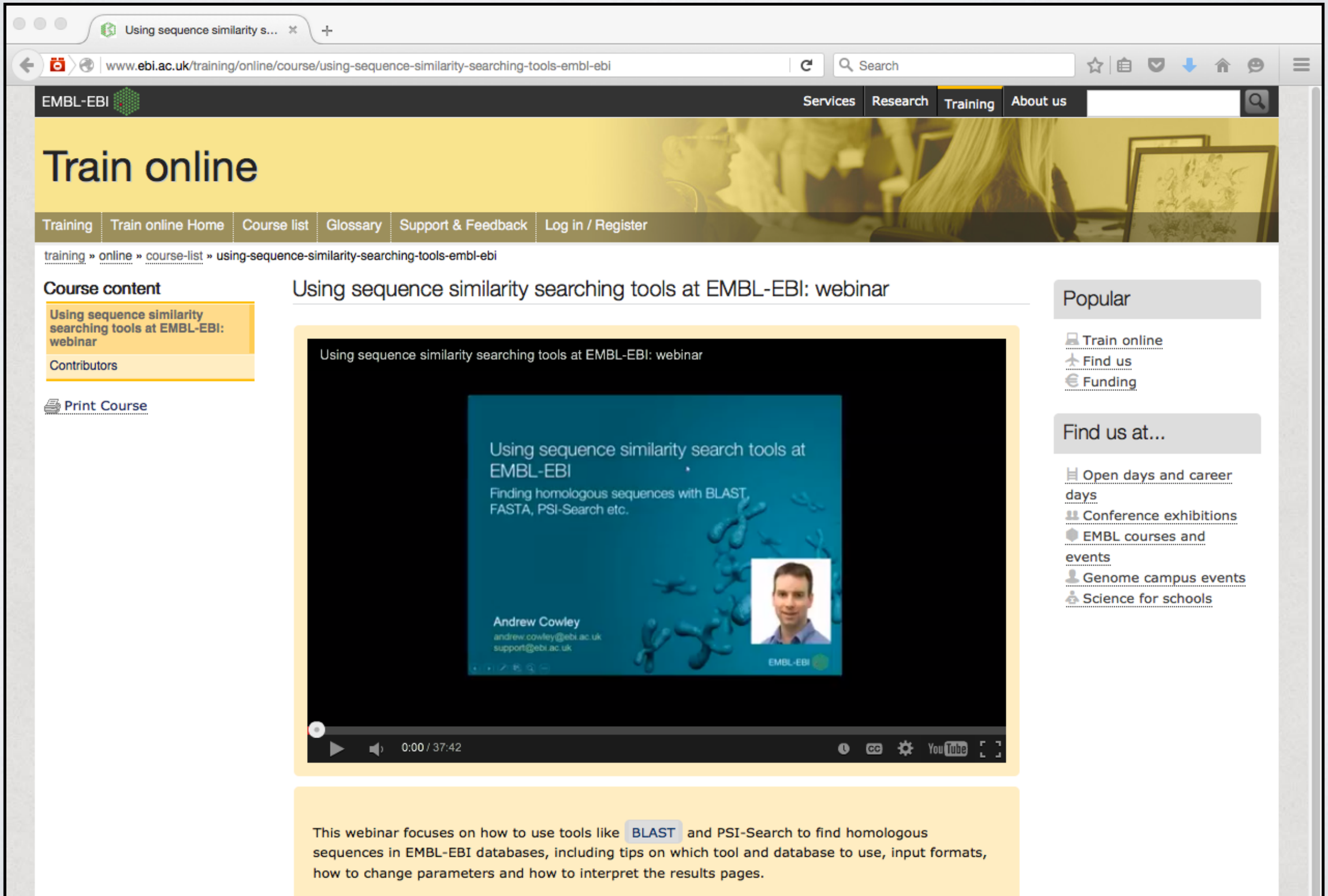

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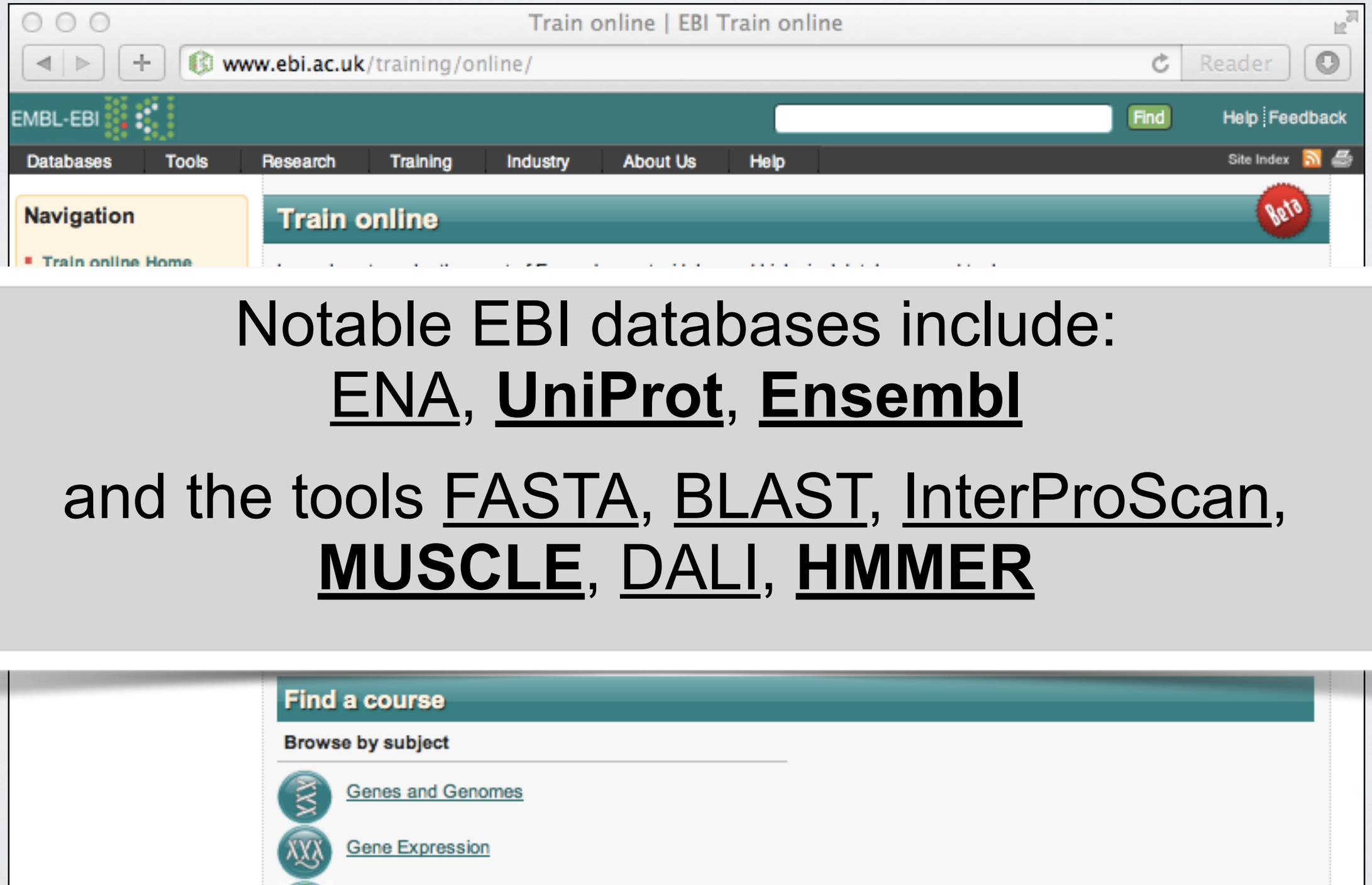


Notable EBI databases include:
ENA, **UniProt**, **Ensembl**

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, TeIDB, TGN, tmRDB, TOPS, TRANSFAC, TRR, UniGene, URNADB, V BASE, VDRR, VectorDB, WDCM, WIT, WormPep, etc ..... !!!!

Bioinformatics Databases

There are lots of Bioinformatics Databases

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

< Major_Databases.pdf >

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, … THER,
… Link,
… HAEMB,
… HotMolecBase,
… IMGT, Kabat, KDNA,
… Medline, Mendel, MEROPS, MGDB, MGI,
MHC … 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 .... !!!!

Side-note: Databases come in all shapes and sizes





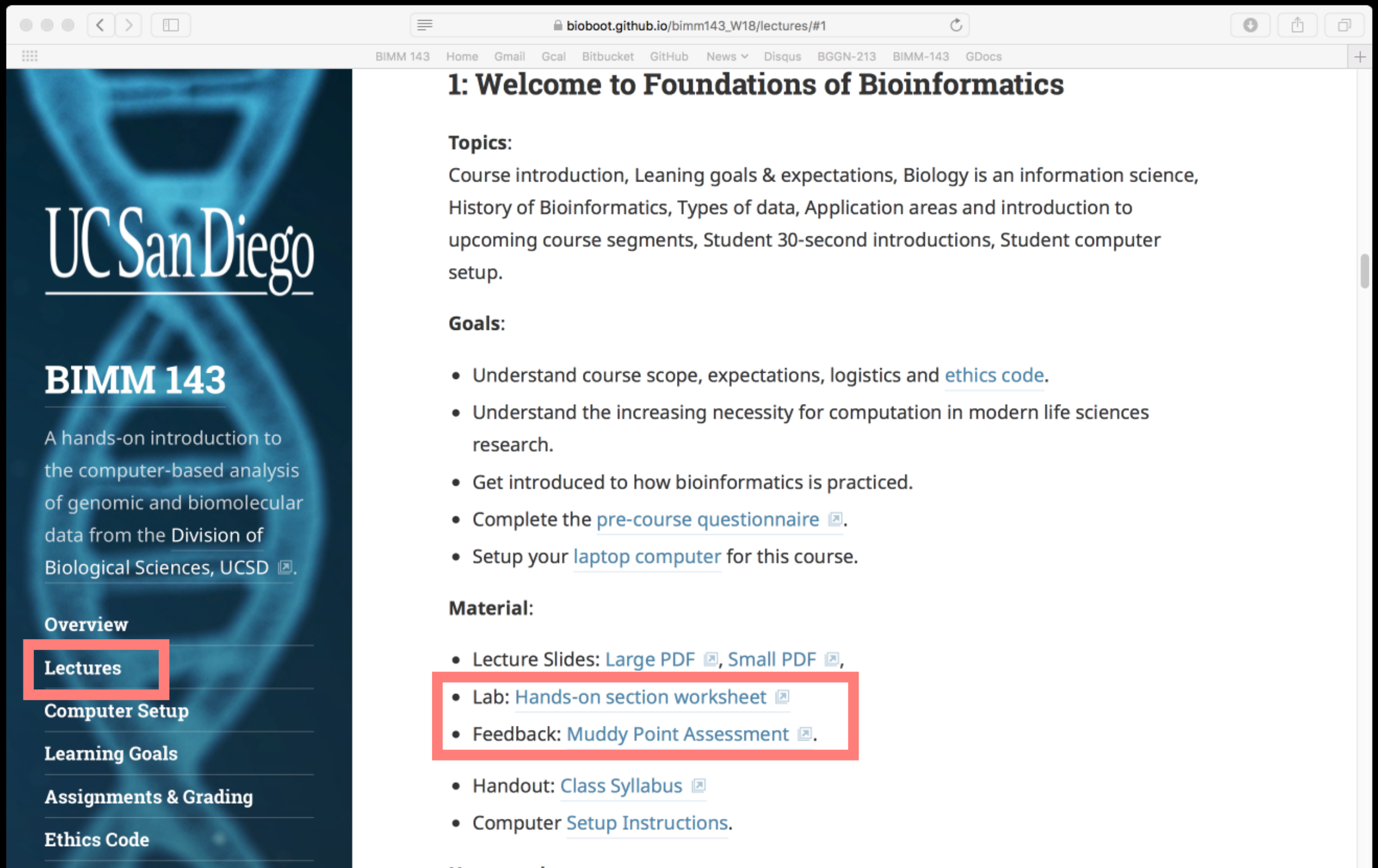
Databases can be of variable quality and often there are multiple databases with overlapping content.

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_W19/lectures/#1



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**	[10:35 am]
2. GENE database @ **NCBI**	[10:55 am]
— BREAK —	— 11:05 am —
3. UniProt & Muscle @ **EBI**	[11:30 am]
4. PFAM, PDB & NGL	[12:00 pm]
— BREAK —	— 12:10 am —
5. Extension exercises	[12:40 pm]

- 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_W19/lectures/#1

- ☑ Complete the **initial course questionnaire**:
- ☑ Check out the "**Background Reading**" material online:
- ☑ Complete the **lecture 1 homework questions**: