

BIMM 143
Introduction to Bioinformatics
 Barry Grant
 UC San Diego
<http://thegrantlab.org/bimm143>

HELLO
my name is
BARRY
bjgrant@ucsd.edu

HELLO
HIS name is
ALEX
arsharp@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 Bioinformatics	Introducing the <i>what, why</i> and <i>how</i> of bioinformatics?
Bioinformatics Database	Hands-on exploration of several major databases and their associated tools.

<http://thegrantlab.org/bimm143/>

Bioinformatics (BIMM 143, Winter 2018)

Course Director: Prof. Barry J. Grant (Email: bjgrant@ucsd.edu)
 Instructional Assistant: Alexander Sharp (Email: arsharp@ucsd.edu)
 Course Syllabus: Winter 2018 (PDF) [\[PDF\]](#)

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. An integrated lecture/lab structure with hands-on exercises and small-scale projects synthesizes modern developments in genomic and proteomic. A detailed listing of

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

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:

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- 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!

The screenshot shows the 'Specific Learning Goals' page. It includes an introduction stating that teaching toward these goals is expected to occupy 60%-70% of class time. Below this is a table with two columns: 'Lecture(s):' and 'Learning Goals'. The table lists four goals related to computation, database querying, sequence analysis, and alignment scoring.

	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, ENSEMBL).	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, BLASTX and multiple sequence based searches.	6, 10

Course Structure

Derived from specific learning goals

The screenshot shows the 'Lectures' page. It lists the lecture dates and topics for the winter 2018 semester. The 'Lectures' table is highlighted with a red box.

#	Date	Topics for Winter 2018
1	Tu, 01/09	Welcome to Bioinformatics Course introduction, Learning goals & expectations, Biology is an information science, History of Bioinformatics, Types of data, Application areas and introduction to upcoming course segments, Student computer setup
2	Tr, 01/11	Bioinformatics databases and key online resources NCBI & EBI resources for the molecular domain of bioinformatics, Focus on GenBank, UniProt, Entrez and Gene Ontology, Hands on with BLAST, GenBank, OMIM, GENE, UniProt, Muscle, PFAM and PDB bioinformatics tools and databases
	Tu,	Sequence alignment fundamentals, algorithms and applications

Course Structure

Derived from specific learning goals

This screenshot is identical to the one in the 'Course Structure' section, showing the 'Lectures' table with a red box around the first row.

Class Details

Goals, Class material, Screencasts & Homework

The screenshot shows the '1: Welcome to Foundations of Bioinformatics' page. It lists the topics, goals, and material for the first lecture. The 'Goals' and 'Material' sections are highlighted with red boxes.

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?
 - SC3: How do we do Bioinformatics?
- Lecture Slides: Large PDF, Small PDF
- Handout: Class Syllabus

Homework

Goals, Class material, Screencasts & Homework

UCSan Diego
BIMM 143
A hands-on introduction to the computer-based analysis of genomic and biomolecular data from the Division of Biological Sciences, UCSD. It.

Overview
Lectures
Computer Setup
Learning Goals
Assignments & Grading
Ethics Code

Homework:
• Questions 0/0
• Readings:
◦ PDF1: What is bioinformatics? An introduction and overview. It.
◦ PDF2: Advancements and Challenges in Computational Biology It.
◦ Other: For Bio-Data Scientists, 'Janitor Work' Is Key Hurdle to Insights It New York Times, 2014.

Screen Casts:
Welcome to "Foundations of Bioinformatics" (BIOIN-2)

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

Homework

Goals, Class material, Screencasts & Homework

BIMM143 Lecture 1 Homework (W18)

Please answer the following questions

* Required

Email address *

Your email

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

Windows
 IOS
 Unix
 Perl

Which of the following databases contains primarily protein sequences 1 point

Protein

Homework

Goals, Class material, Screencasts & Homework

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* Required

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Windows
 IOS
 Unix
 Perl

Which of the following databases contains primarily protein sequences 1 point

Protein

Homework is due before the next weeks class!

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 programming 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

UCSan Diego
BIMM 143
A hands-on introduction to the computer-based analysis of genomic and biomolecular data from the Division of Biological Sciences, UCSD. It.

Overview
Lectures
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5	Calculate the alignment scores 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 differentially

BIMM-143 Learning Goals...

Delve deeper into "real-world" bioinformatics

Goal Number	Description	Page Number
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
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 heterogeneous high throughput data sets into their functional	19

These support a major learning objective

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Why use R?

Productivity
Flexibility
Designed for data analysis

IEEE 2016 Top Programming Languages

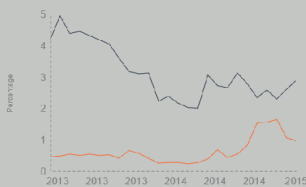
Language Rank	Types	Spectrum Ranking
1. C		100.0
2. Java		98.1
3. Python		98.0
4. C++		95.9
5. R		87.9
6. C#		86.7
7. PHP		82.8
8. JavaScript		82.2
9. Ruby		74.5
10. Go		71.9

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

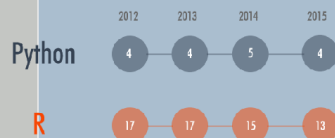
R and Python: The Numbers

Popularity Rankings

R and Python's popularity between 2013 and February 2015 (T.obe 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



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.
- Large user and developer community.
 - As of Jan 8th 2018 there are 12,039 add on **R packages** on **CRAN** and 1,473 on **Bioconductor** - more on these later!
- Virtually every statistical technique is either already built into R, or available as a free package.
- Unparalleled exploratory data analysis environment.

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Computer Setup	Ensuring your laptop is all set for future sections of this course.

OUTLINE

Overview of bioinformatics

- The *what*, *why* and *how* of bioinformatics?
- Major bioinformatics research areas.
- Skepticism and common problems with bioinformatics.

Online databases and associated tools

- Primary, secondary and composite databases.
 - Nucleotide sequence databases (GenBank & RefSeq).
 - Protein sequence database (UniProt).
 - Composite databases (PFAM & OMIM).

Database usage vignette

- How-to productively navigate major databases.

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 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

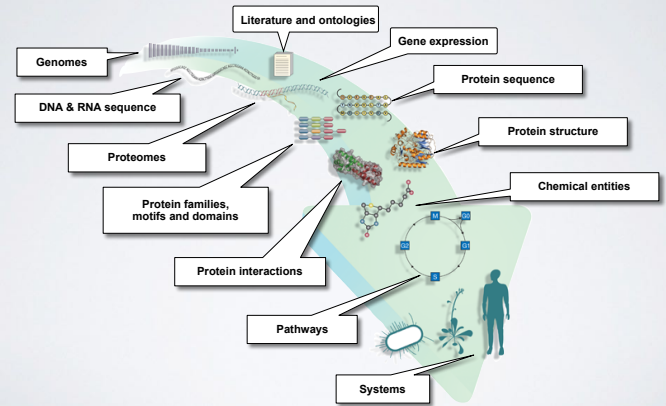
- ▶ "Bioinformatics is conceptualizing biology in terms of **macromolecules** and then applying "**informatics**" techniques (derived from disciplines such as applied maths, computer science, and statistics) to **understand** and **organize** the information associated with these molecules, on a **large-scale**.
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>)

MORE DEFINITIONS

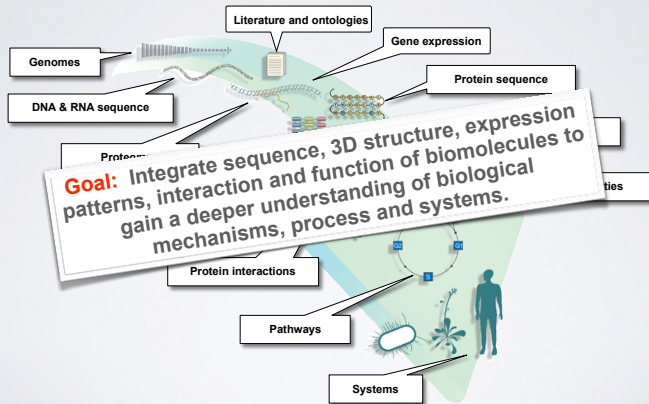
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Key Point: Bioinformatics is Computer Aided Biology

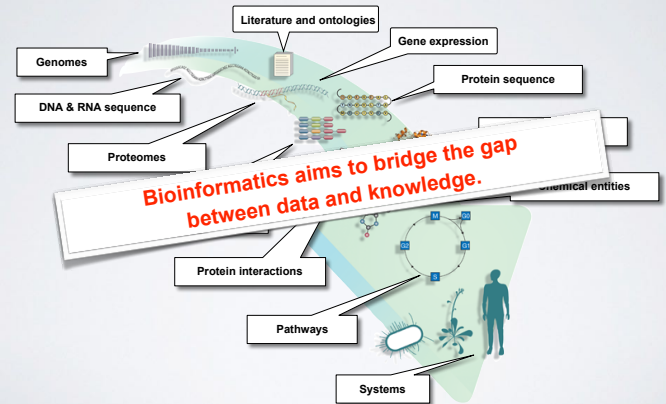
Major types of Bioinformatics Data



Major types of Bioinformatics Data



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

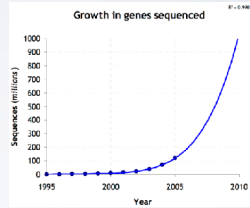
- DNA sequence determines protein sequence.
- Protein sequence determines protein structure.
- Protein structure determines protein function.
- Regulatory mechanisms (e.g. gene expression) determine the amount of a particular function in space and time.

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...

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.



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 programming languages frequently required (e.g. R, Python, Perl, C, Java, Fortran)
- May require specialized high performance computing...

How do we *actually* do Bioinformatics?

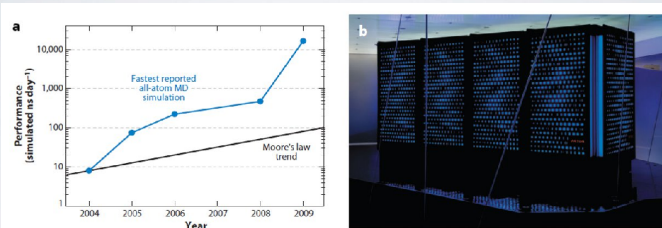
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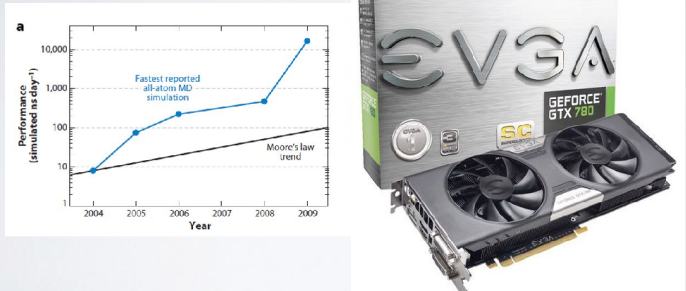
Advanced tool application & development

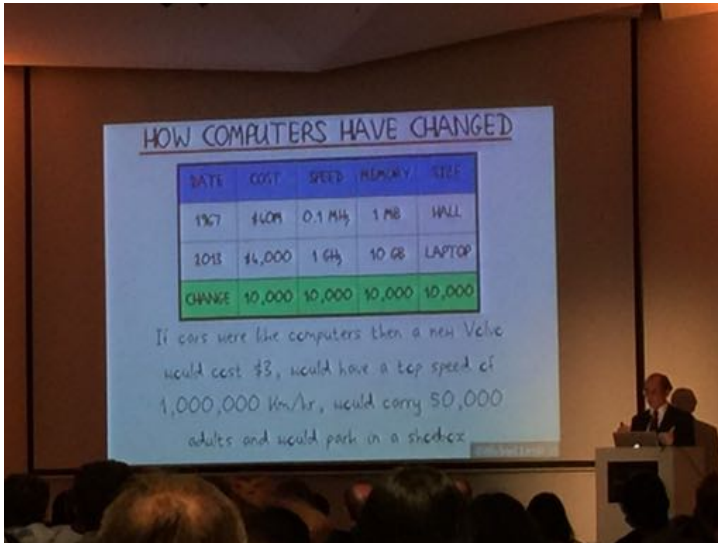
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- May require specialized high performance computing...

SIDE-NOTE: SUPERCOMPUTERS AND GPUS



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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 his old but quite readable treatise, *Sequence Analysis in Molecular Biology; Treasure Trove or Trivial Pursuit*, provides a very appropriate conclusion:

- “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!

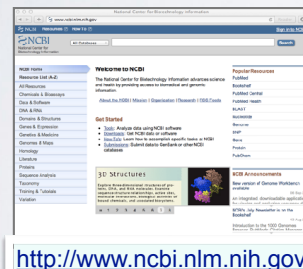
Most are developed independently

Notable exceptions are found at the:

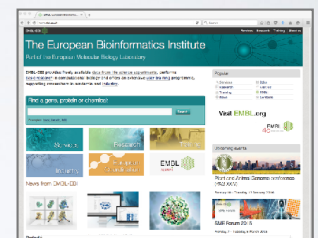
- EBI (European Bioinformatics Institute) and
- NCBI (National Center for Biotechnology Information)

Key Online Bioinformatics Resources: NCBI & EBI

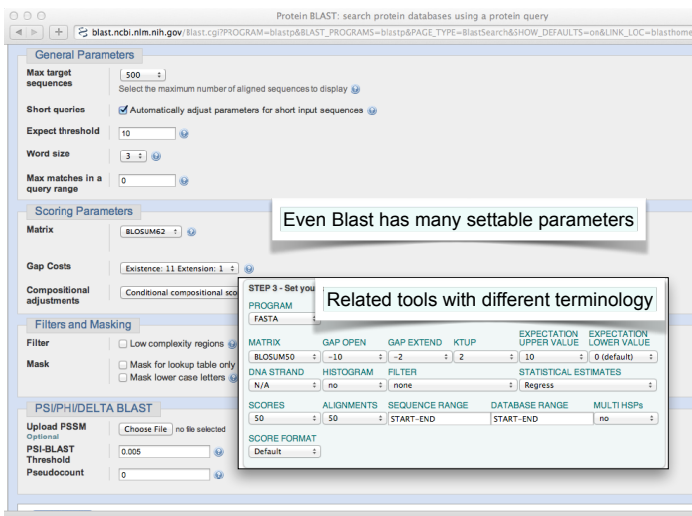
The NCBI and EBI are invaluable, publicly available resources for biomedical research



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



<https://www.ebi.ac.uk>



National Center for Biotechnology Information (NCBI)

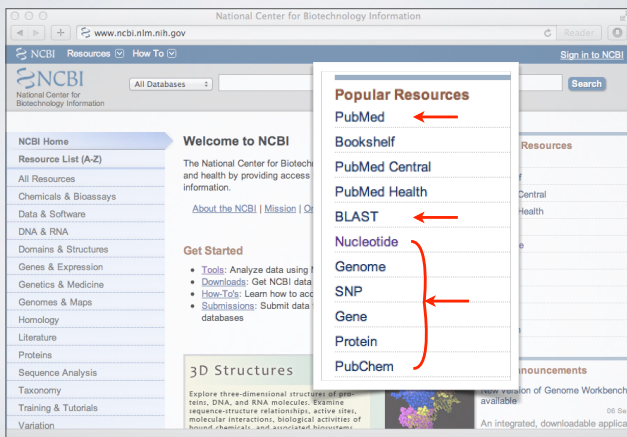
- Created in 1988 as a part of the National Library of Medicine (NLM) at the National Institutes of Health
- NCBI's mission includes:
 - ▶ Establish **public databases**
 - ▶ Develop **software tools**
 - ▶ **Education** on and dissemination of biomedical information
- We will cover a number of core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



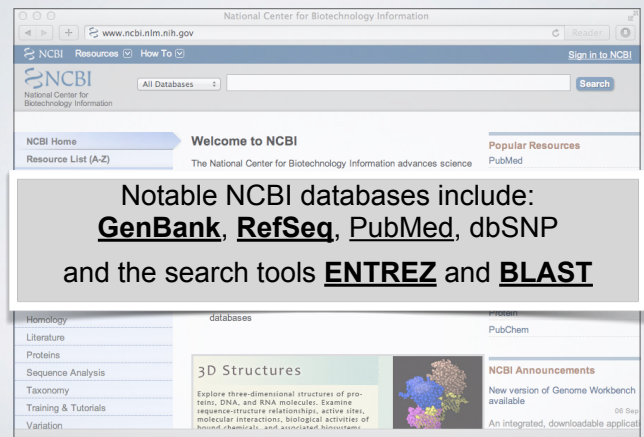
<http://www.ncbi.nlm.nih.gov>



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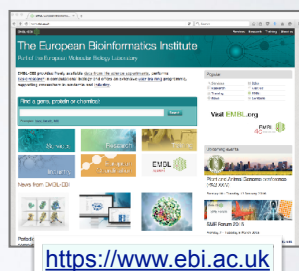


Key Online Bioinformatics Resources: NCBI & EBI

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



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



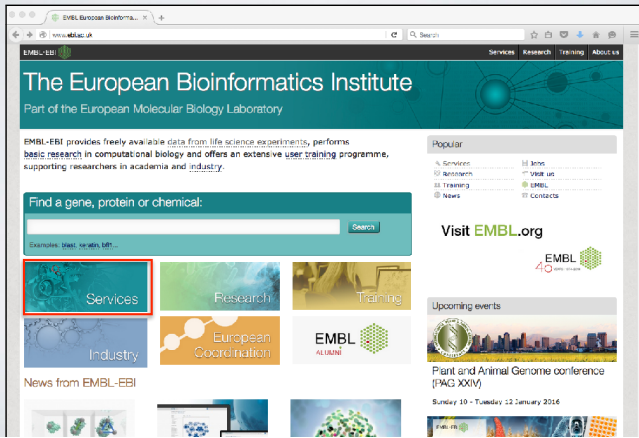
<https://www.ebi.ac.uk>

European Bioinformatics Institute (EBI)

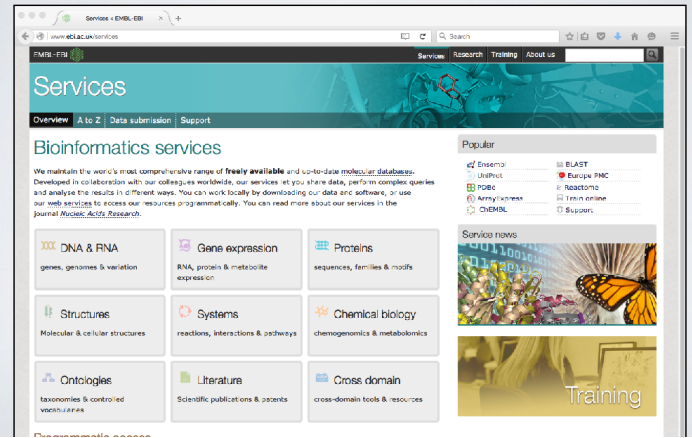
- Created in 1997 as a part of the European Molecular Biology Laboratory (EMBL)
- EBI's mission includes:
 - ▶ providing freely available **data and bioinformatics services**
 - ▶ and providing advanced **bioinformatics training**
- We will briefly cover several EBI databases and tools that have advantages over those offered at NCBI



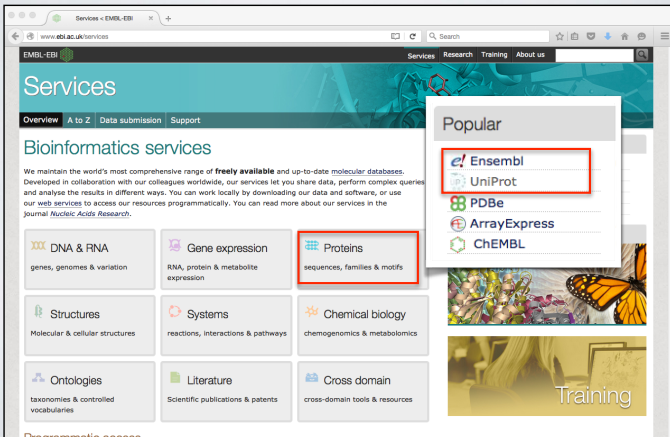
The EBI maintains a number of high quality curated **secondary databases** and associated tools



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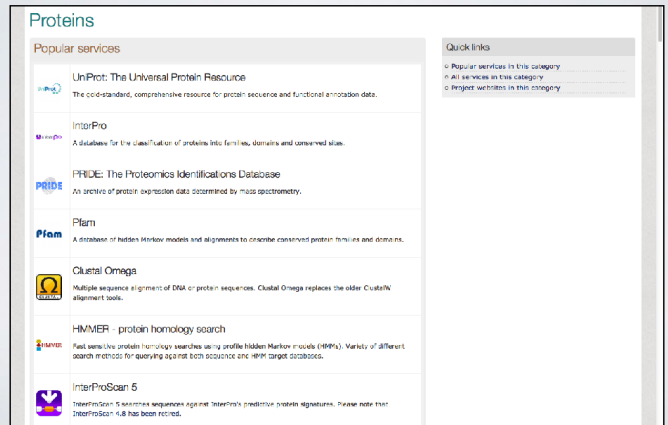


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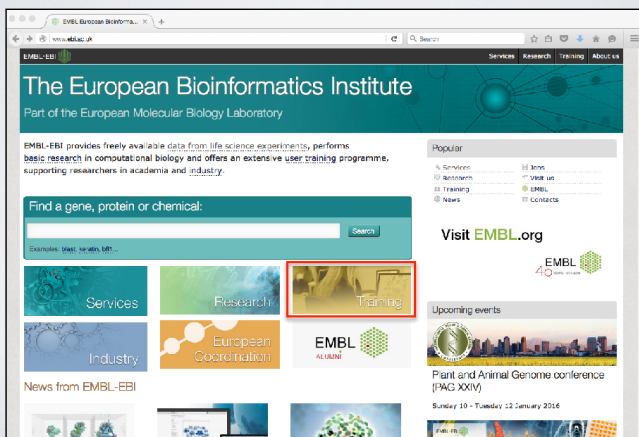


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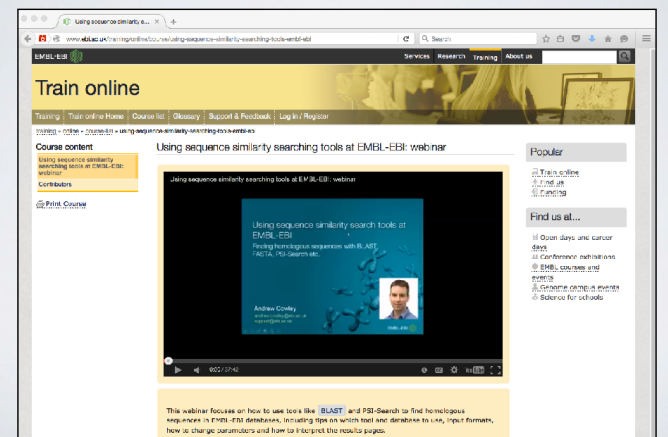
The EBI makes available a wider variety of **online tools** than NCBI



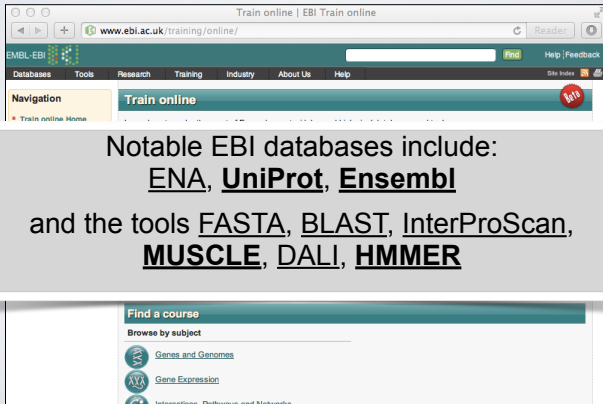
The EBI also provides a growing selection of **online tutorials** on EBI databases and tools



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Next Class...

MAJOR BIOINFORMATICS DATABASES AND ASSOCIATED ONLINE TOOLS

Bioinformatics Databases

AATDB, AceDb, ACUTS, ADB, AFDB, AGIS, AMSdb, ARR, AsDb, BBDB, BCGD, Beanref, BiImage, BioMagResBank, BIOMDB, BLOCKS, BovGBASE, BOVMAR, BSORF, BTkbase, CANSITE, Carbank, 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, Genillesne, 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, MHCPEPS, Micado, MitoDat, MITOMAR, MJDB, MmtDB, Mol-R-U, 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, PROTOMAR, RattMAP, RDR, REBASE, RGP, SBASE, SCOP, SeqAnalRef, SGD, SGP, SheepMap, Soybase, SPAD, SRNA db, SRPDB, STACK, StyGene, Sub2D, SubtilList, 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, BiImage, BioMagResBank, BIOMDB, BLOCKS, BovGBASE, BOVMAR, BSORF, BTkbase, CANSITE, Carbank, 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, Genillesne, 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, MHCPEPS, Micado, MitoDat, MITOMAR, MJDB, MmtDB, Mol-R-U, 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, PROTOMAR, RattMAP, RDR, REBASE, RGP, SBASE, SCOP, SeqAnalRef, SGD, SGP, SheepMap, Soybase, SPAD, SRNA db, SRPDB, STACK, StyGene, Sub2D, SubtilList, 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 an 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.

Primary, secondary & composite databases

Bioinformatics databases can be usefully classified into *primary*, *secondary* and *composite* according to their data source.

- **Primary databases** (or *archival databases*) consist of data derived experimentally.
 - ▶ **GenBank**: NCBI's primary nucleotide sequence database.
 - ▶ **PDB**: Protein X-ray crystal and NMR structures.
- **Secondary databases** (or *derived databases*) contain information derived from a primary database.
 - **RefSeq**: non redundant set of curated reference sequences primarily from GenBank
 - **PFAM**: protein sequence families primarily from UniProt and PDB
- **Composite databases** (or *metadatabases*) join a variety of different primary and secondary database sources.
 - **OMIM**: catalog of human genes, genetic disorders and related literature
 - **GENE**: molecular data and literature related to genes with extensive links to other databases.

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 Bioinformatics	Introducing the <i>what, why</i> and <i>how</i> of bioinformatics?
Bioinformatics Database	Hands-on exploration of several major databases and their associated tools.

Your Turn!

https://bioboot.github.io/bimm143_W18/lectures/#1

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

I: Welcome to Foundations of Bioinformatics

Topics:
Course Introduction, Learning 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.

```
>examp11
ATGTGGTCTGACCTGCTGTGGAGATCTCCCTTACCTCCCTCTGGGGGAGGTGAACTGGATGAG
TTTGTGTGTAGGCTCTGGCAGAGTGTGTGGTCTTACCTCTTGGACCCAGAGTGTCTTGGAGTCTTGG
GGATCTGTCCACTCTGATGCGTATGGGACCTTAGGTGAGGCTCATGGGAGAGTCTGCTGGT
GCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GTGACAGGCTCCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
TCACTTGGCAGAGATTCACCCACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GGCTGGCCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
```

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:

- BLAST, GenBank and OMIM @ **NCBI** [~35 mins]
- GENE database @ **NCBI** [~15 mins]
— BREAK —
- UniProt & Muscle @ **EBI** [~25 mins]
- PFAM, PDB & NGL [~30 mins]
— BREAK —
- 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:

- BLAST, GenBank and OMIM @ **NCBI** [10:45 am]
- GENE database @ **NCBI** [11:00 am]
— BREAK — 11:10 am —
- UniProt & Muscle @ **EBI** [11:35 am]
- PFAM, PDB & NGL [12:05 pm]
— BREAK — 12:15 am —
- Extension exercises [12:45 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.
- There are a large number of primary, secondary and tertiary bioinformatics databases.
- 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.