# Bioinformatics Prereqs and Topics For Crowdsourced Commenting At CSHL Biological Data Science 2016 (#BioData16)

# Please Edit & Comment on this Document ! (Further info. at document end.)

# Categories of Knowledge for Bioinformatics Education

U = Undergrad. level

G = Grad. level

C = CS

S = Stats/Math

B = Bio/Chem/Phys

I = Intro. Bioinformatics Topic (i.e., in a class like Yale CBB752)

A = Advanced Bioinformatics Topic (i.e., maybe beyond Yale CBB752)

Combining Abbreviations - viz:

UC, GC, US, GS, GI, GA, GB, UB

# Prerequisites for Bioinformatics: Stats & CS

These go beyond Basic Math (calculus), Biology, Chemistry & Physics taught in pre-medical education.

## Programming Topics [UC]

* Interpreted & compiled languages
* Recursion
* Data structures - lists (including data frames), arrays, hashes, stacks, trees, suffix arrays
* Computational complexity - related to operations as sorting
* Basics of computer architecture (caches, disks, bottlenecks)
* Practical Programming: modularization (OOP), version control, debugging, APIs & libraries, software carpentry, reproducible research/coding (Make or other build tools),, containers (Docker, bioboxes)
* Basics of web programming - stateless access, web protocols
* Databases
	+ Basics of SQL, with concept of indices & joining, schema
	+ non-relational architectures - NoSQL
* Regular expression & string processing
* Numeric computing issues: FP arithmetic & random numbers
* Encryption & compression

## Programming Topics [GC]

* VMs & cloud computing
* Computational optimization & integration of functions
* Relational database concepts
* DB interoperation
* Privacy & security
* Ontologies
* Distributed and high-performance computing (parallel computing)

## Statistical Topics [US]

* Knowledge of distributions, hypothesis testing & inference (includes mult. testing, t-test)
* Permutation Testing (bootstrapping, cross-validation)
* Regression
* Power analysis (Type 1 & 2 errors)
* Non-parametric vs. Parametric methods
* Bayesian inference
* Sampling

## Statistical Topics [GS]

* Regularization
* Unsupervised Methods (eg PCA, clustering, discriminants)
* Supervised Methods (SVM, Kernels)
* Bayesian Analysis
* Test of goodness of fit (eg, Kolmogorov-Smirnov test)
* Causal inference
* Missing data, imputation & EM algorithm
* Hierarchical Modelling
* Information theory - mut. information, complexity & entropy
* Graphical Models
* HMMs (Viterbi, Forward and Backward Algorithms)
* MCMC
* Feature Selection
* Assessing Predictions
	+ Training and testing data
	+ Cross validation
	+ ROC curves

# Specific Bioinformatics Topics

## Classical Sequence Analysis

* String Matching
	+ Pairwise Alignment via Dynamic Programming [GI]
	+ Local vs. Global Alignment & Suboptimal Alignment [GI]
	+ Hashing & Indexing to increase speed (BLAST, FASTA) [GI]
		- Suffix arrays & BWT
	+ Substitution scoring matrices (e.g., for amino acids) [GI]
	+ Scoring schemes & matching statistics
		- Score Distributions  (e.g., EVD)
	+ Time complexity of alignment algorithms
* Multiple Alignment and Consensus Patterns
	+ Identifying genomic regions such as genes & promoters with various statistical methods (e.g., HMMs) [GI]
	+ HMMs applied to biology, Profiles, Position dependent subst. matrices [GI]
	+ Motifs [GI]
	+ EM & Gibbs Sampling [GI]
* Whole-Genome analysis
	+ Genome Assembly [GA]
		- De Bruijn graphs
	+ Characterizing Repeats in Genomic DNA [GA]
	+ Identification Duplications in the Genome [GA]
	+ Whole-Genome Comparisons & large scale genomic alignments [GA]
		- Synteny
		- Orthologs & Function Classification
	+ Genome Annotation
		- Gene Prediction
		- Regulatory site and network prediction
		- miRNA prediction and targeting site prediction
		- Pseudogene prediction and functional prediction
		- Gene Evolution (eg gene conversion)

## Next-Gen Sequencing  Data Processing

* Variant Calling
	+ Germline
	+ Somatic
	+ Structural variation & rearrangements
* RNA-seq
	+ Recognizing and correcting batch effects
	+ Transcript assembly & splicing
	+ Quantification [GI]
	+ eQTLs & allelic transcription
	+ Normalization
	+ Expression Analysis
		- Time Course clustering/longitudinal clustering
		- Differential expression
* DNA methylation & epigenetic gene regulation
	+ ChIP-seq
	+ WGBS
	+ Peak calling
* Metagenomics (microbiome) [GA]
* Platform comparison (eg Illumina vs PacBio vs 10X vs nanopore)

## Statistical Genetics [GA]

* Population Genetics & Allele Freq.
* Prioritizing Pathogenic Variants
* Genotype-Phenotype Associations
	+ Case-control & GWAS (including rare-variant analysis methods, e.g., SKAT)
	+ Correlation vs. causality
	+ QTLs
* Survival Analysis
* Evolutionary Issues
	+ Rates of mutation and change
	+ Clustering & Trees [GI]
		- Distance vs. maximum likelihood tree methods

## Processing Other Big Data Sets

* Flow Cytometry & CyTOF data analysis
	+ Causal network
* Proteomics (Mass Spec)
* Metabolomics [GA]
* Phenomics (many many phenotypes)
* Literature & Text Mining
	+ Topic analysis
	+ Ontologies for terms
	+ Clinical Informatics (med. records, EHRs)
* Structural Genomics
* EM & fluorescent image analysis
* B/T cell repertoire sequencing

## Data Integration & Mining

* Information integration and fusion
	+ Dealing with heterogeneous data
* Ensemble Learning
	+ Random Forests
* Dimensionality Reduction (PCA etc.) in a biological setting
* Network Analysis
	+ Pathway analysis
	+ Topology Analysis (Hubs & Bottlenecks)
	+ Prediction of linkages
	+ Global structure vs. local network motifs
* Meta-analysis
	+ Fisher’s Method for combining p-values

## Sequence to Structure

* Secondary Structure Prediction
	+ via Propensities
	+ TM-helix finding
* Tertiary Structure Prediction
	+ Homology Modeling & Protein Threading (Fold Recognition)
	+ Ab initio
	+ Free energy changes due to individual amino acid changes
* Direct Function Prediction
	+ Active site identification

## 3D Structure Analysis

* Molecular Geometry
	+ Distances, Angles, Axes, Rotations
		- Calculating a helix axis
		- Molecular Graphics
	+ Calculation of Volumes & Surfaces
		- Hinge prediction
		- Packing Measurement
* Structural Comparison & Alignment
	+ Basic Protein Geometry and Least-Squares Fitting
	+ Aligning sequences on the basis of 3D structure
* Docking and Drug Design [GA]

## Simulation & Modelling

* Molecular Mechanics
	+ Basic interactions, potential energy functions
		- Geometry => Energy => Forces
		- Covalent Bonds
			* Bonds & Angles (as springs)
			* Dihedral
		- Noncovalent interactions
			* Electrostatics
			* VDW Forces
			* Hydrogen bonds
	+ Energy Minimization
		- Steepest Descent, Newton’s Method & Conjugate Gradient
	+ Molecular Dynamics & MC
* Simplifications
	+ Poisson-Boltzmann Equation
	+ Lattice Models
* Signaling & Pathway Modeling
	+ Population Dynamics w/ ODEs
	+ Regulatory network modeling via Boolean networks, ODEs
	+ Flux-balance calculations
	+ Agent based modeling
	+ Stochastic modeling: Extrinsic and intrinsic noise

# Prominent Stat/CS Topics NOT included

* Interrupts
* Advanced Parallel programming
* Machine language
* Compiler design
* Computer Graphics
* Advanced Crypto

Further information

# Associated Documents & Links

This document is

<http://goo.gl/303KXr>

The associated talk is <http://lectures.gersteinlab.org/summary/Education-in-Bio-DataScience--20161028-i0bds16/>

(See slide 21 for a lead in to this document.)

The Yale CBB program

<http://cbb.yale.edu>

CBB752 - Biomedical Data Science: Mining & Modeling

<http://www.gersteinlab.org/courses/452/>

Earlier versions of the crowd-source edit:

<http://cbb752b16.gersteinlab.org/assignments/homework0>

Also:

<http://blog.gerstein.info/2015/11/list-of-study-topics-prerequisites-for.html>

My list of US Bioinformatics Programs:

<http://blog.gerstein.info/2015/05/updated-again-listing-of-us-programs-in.html>

<https://twitter.com/markgerstein/status/600763647095341056>

# General Comments here

Seems like some of the topics e.g.

***Programming Topics [GC]***

* VMs & cloud computing
* Might be most amenable to teaching in short (say 1 day) “bootcamps” (mostly hands-on, rather than fitting into normal semester course)
* Ethics and privacy particular to biological data science?

Suggest adding some social engineering, writing, or how-to-work-in-science topics. Writing in science. How to work collaboratively. How to deal with different personalities in groups. How to network. How to present at conferences.

General comment: There is an effort to think about this problem on the undergraduate level in the context of competencies for bioinformatics [which is ~ but != to biological data science] (rather than a fine-grained list of topics): <https://qubeshub.org/groups/niblse> and <http://www.lifescied.org/content/14/4/le3.short>. An important part of the conversation will be how do we get this into the classroom. An analysis of a large survey of educators across the US is underway by this group and is relevant to discussion.