# More information is available at:

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

# 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 and in undergraduate majors such as Yale MB&B

## Programming Topics [UC]

* Interpretative & compiled languages.
* Recursion
* Data structures - lists, arrays, hashes, stacks
* 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
* 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
* Bayes Rule

## Statistical Topics [GS]

* Regularization
* Unsupervised Methods (PCA, clustering)
* Supervised Methods (SVM, Kernels)
* Bayesian Analysis
* Graphical Models
* Causal inference
* Missing data, imputation & EM algorithm
* Hierarchical Modelling
* Information theory - mut. information, complexity & entropy
* 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)
* 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

## 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
  + Peak calling
* Metagenomics (microbiome) [GA]

## Statistical Genetics [GA]

* Population Genetics & Allele Freq.
* Genotype-Phenotype Associations
  + Case-control & GWAS
  + 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]
* Literature & Text Mining
  + Topic analysis
  + Ontologies for terms
* Structural Genomics
* EM image analysis
* B/T cell repertoire sequencing

## Data Integration & Mining

* Information integration and fusion
  + Dealing with heterogeneous data
* Ensemble Learning
* 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
* 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
  + Energy Minimization
    - Steepest Descent & 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