Comp Sci 369: Computational Science 2013
Learning Outcomes

At the successful completion of CS369, a student should:

- Be familiar with basics of numerical analysis.
- Be familiar with methods for finding roots of equations and Taylor series.
- Understand methods for solving systems of linear equations.
- Understand standard matrix decompositions (SVD, QR, LU).
- Be familiar with eigen-vectors and principal component analysis (PCA).
- Understand the basic model of genetic sequence evolution.
- Be familiar with string matching algorithms.
- Understand dynamic programming
- Be familiar with the dynamic programming solution of the sequence alignment problem.
- Be familiar with basic probabilistic modelling techniques.
- Be familiar with common discrete and continuous distributions.
- Be familiar with Markov chains and simple stochastic processes.
- Understand methods for simulating stochastic models.
- Understand the maximum likelihood and the least squares framework.
- Be familiar with hidden Markov models (HMM) and standard HMM algorithms (Viterbi, Forward-Backward).
- Be familiar with phylogenetic models of sequence evolution.
- Know how to score and construct phylogenetic trees under neighbour joining, parsimony and Markov models.