

# Chapter 0

## Introduction

### 0.1 Outline

#### 0.1.1 Phylogenetics part

- Tree Notation
- Distance-Based and Maximum Parsimony Phylogeny Reconstruction
- Measures for how different two trees are
- Sequence Evolution Models (JC, F81, HKY, F84, GTR, PAM and  $\Gamma$ -distributed rates)
- Maximum-Likelihood (ML) in phylogeny estimation and Bootstrapping
- Bayesian phylogeny reconstruction and MCMC
- Common problems in phylogenetics and consequences for phylogenomics
- Modelling the substitution process on sequences
- Quantitative Characters and Independent Contrasts
- Model selection
- Statistical Alignment (TKF91, TKF92, pairHMMs, multiple HMMs)
- Tests for trees and branches

### **0.1.2 Population Genetics part**

- Wright-Fisher model and Estimators of  $\theta$
- population genealogy with Mutation and Immigration
- Important Sampling and Approximate Bayesian Computation (ABC)
- Recombination: ARG and approximations
- Selection: ASG and detection
- population cluster

### **0.1.3 Related mathematics**

- Basic concepts from probability theory
- Basic linear algebra
- Markov process and Markov chain
- ...

### **0.1.4 Aims**

- Understand principles and rationales underlying the methods
- Explore available software
- What is efficiently doable, what is difficult?
- What are the strengths and weaknesses of the methods?
- Which method is appropriate for which dataset?
- Learn what is necessary to read papers about new computational methods
- Future directions of phylogenetics

### **0.1.5 Recommended Books**

J. Felsenstein (2004) Inferring Phylogenies

Z. Yang (2006) Computational Molecular Evolution

R. Nielsen, [Ed.] (2005) Statistical Methods in Molecular Evolution

R. Durbin, S. Eddy, A. Krogh, G. Mitchison (1998) Biological Sequence Analysis

W. Ewens, G. Grant (2005) Statistical Methods in Bioinformatics