

## Day 0 (Sunday May 2<sup>nd</sup>, 2010)

15:30 For those who arrive early: computer trouble shooting session with Aidan Budd, Tim Massingham, and Sergio Vargas. We will meet at 15:30 at the hotel reception desk and decide ad hoc where to go.

## Day 1 (Monday May 3<sup>rd</sup>, 2010)

### **Giorgos Kotoulas & Alexandros Stamatakis**

09:00-10:15 Introduction and course overview, participants briefly introduce themselves

10:15-11:30 Free tour of the CreteAcquarium

11:30-12:00 Coffe break

### **Tim Massingham**

12:00-13:30 Unix/Windows command line basics and exercises

13:30 -15:00 Lunch at CreteAcquarium

### **Aidan Budd**

*topics: Introducing applications of phylogenies; Introduction to phylogenetic terminology, NEWICK/PHYLIP tree format; Rooted/unrooted phylogenies; Branch lengths Gene tree-species tree conflicts (gene duplication, horizontal transfer, lineage sorting); Phylogenetic networks*

15:00-18:30: Interpreting molecular phylogenetic trees (I) with coffee break

19:00-20:00: Evening lecture 1: **Ken Wolfe: “Using phylogenetics to study gene and gene family evolution”**

20:30 Dinner at hotel

## Day 2 (Tuesday May 4<sup>th</sup>, 2010)

09:00 - 10:00 Free Computing & Analysis practice with TAs

### **Aidan Budd**

10:00 - 13:30: Interpreting molecular phylogenetic trees (II) with coffee break

13:30 - 15:00 Lunch at CreteAcquarium

### **Bill Pearson & Javier Herrero**

*topics: Sequence databases (EMBL nucleotides; UniProt; others) and genome databases (Ensembl; UCSC genome browser; plants;*

*bacteria; others); Databases of (or at least containing) alignments and/or trees (TreeBASE, Pfam, Pandit, TreeFam; others); Searching sequence databases (by keywords; by accession numbers; search software e.g. Blast; others); Pairwise alignment; Multiple sequence alignment (concepts, heuristics, softwares, “improvement by eye”); GBLOCKS (and others) to extract conserved blocks of alignments; Obtaining nucleotide alignments given protein alignment and associated nucleotide sequences – RevTrans (others); Struggling with formats — problems with getting your software of choice to accept your alignment of interest*

15:00-18:30: Genomics resources and sequence alignment (I) with coffee break

19:00-20:00: Evening lecture 2: **Martin Embley: “The Tree of Life”**

20:30 Dinner at hotel

### **Day 3 (Wednesday May 5<sup>th</sup>, 2010)**

09:00-10:00 Free Computing & Analysis practice with TAs

#### **Bill Pearson & Javier Herrero**

10:00-13:30: Genomics resources and sequence alignment (II) with coffee break

13:30 -15:00: Lunch at CreteAcquarium

15:00-16:30: Genomics resources and sequences alignment (II)

16:30-17:00: Coffee break

17:00-18:30 Participants can (no obligation) present research posters and talk about the posters with the lecturers/instructors

20:30 Dinner at hotel

### **Day 4 (Thursday May 6<sup>th</sup>, 2010)**

09:00 -10:00 Free Computing & Analysis practice with TAs

#### **Olivier Gascuel & John Huelsenbeck**

*topics: Probabilistic models of character change/substitutions; Distance (minimum evolution, NJ, Fitch-Margoliash, etc.) and Parsimony methods; Likelihood and Bayesian methods; Tree search; Sources of error, both systematic and non-systematic, and approaches to address them: Stochastic variation, Model mis-specification (base composition; substitution matrices; others), Long-branch attraction, Taxon-sampling; others*

10:00-13:30: Phylogeny-reconstruction methods (I) with coffee break

13:30 -15:00 Lunch at CreteAcquarium

15:00-18:30: Phylogeny-reconstruction methods (II) with coffee break

19:00-20:00: Evening lecture 3: **Aoife McLysaght: “Origins of New Genes”**

20:30 Dinner at hotel

#### **Day 5 (Friday May 7<sup>th</sup>, 2010)**

09:00-10:00 Free Computing & Analysis practice with TAs

**Olivier Gascuel & John Huelsenbeck**

10:00-13:30: Phylogeny-reconstruction methods (III) with coffee break

13:30 -15:00 Lunch at CreteAcquarium

15:00-18:30: Phylogeny-reconstruction methods (IV) with coffee break

19:00-20:00: Evening lecture 4: **Jeff Thorne: “Using phylogenetics to estimate species divergence times”**

20:30 Dinner at hotel

#### **Day 6 (Saturday May 8<sup>th</sup>, 2010)**

09:00-10:00 Free Computing & Analysis practice with TAs

**Mikkel Schierup & Rasmus Nielsen**

*topics: Fisher-Wright model and neutral coalescent; Population demography and subdivision; Ancestral polymorphism and lineage sorting*

10:00-13:30: Coalescent model and inference from population data (I) with coffee break

13:30-15:00 Lunch at CreteAcquarium

15:00-18:30: Coalescent model and inference from population data (II) with coffee break

19:00-20:00: Evening lecture 5: **Michail Averof: “Evolution of development”**

20:30 Dinner at hotel

**Day 7 (Sunday May 9<sup>th</sup>, 2010)**

08:00-14:00 Excursion & hike through Rouvas gorge, bus will pick us up at 08:00 at the hotel. After the hike, lunch at Zaros

20:30 Dinner at hotel

**Day 8 (Monday May 10<sup>th</sup>, 2010)**

09:00-10:00 Free Computing & Analysis practice with Tas

**Mikkel Schierup & Rasmus Nielsen**

10:00-13:30: Coalescent model and inference from population data (III) with coffee break

**Nick Goldman & Ziheng Yang**

*topics: Approaches (Likelihood/Bayesian); Tests of Substitution Models (Simple models [e.g. JC vs. HKY; PAM vs. WAG], Rate heterogeneity, Clocks, Selection/adaptation, others); Test of topologies (Bootstrapping [parametric and non-parametric], Comparisons of topologies [KH-test; SOWH-test]); Confidence sets/congruency of topologies (SH-test, Bayesian methods)*

13:30-15:00: Lunch at CreteAcquarium

15:00-18:30: Hypothesis testing in phylogenetics (I)with coffee break

19:00-20:00: Evening lecture 6: **Antonis Rokas: “Experimental Molecular Evolution”**

20:30 Dinner at hotel

**Day 9 (Tuesday May 11<sup>th</sup>, 2010)**

09:00-10:00 Free Computing & Analysis practice with TAs

**Nick Goldman & Ziheng Yang**

10:00-13:30: Hypothesis testing in phylogenetics (II) with coffee break

13:30-15:00: Lunch at CreteAcquarium

15:00-18:30: Hypothesis testing in phylogenetics (III) with coffee break

19:00-20:00: Evening lecture 7: **Carolyn Kosiol: “Advances in codon models”**

20:30 Dinner at hotel

**Day 10 (Wednesday May 12th 2010)**

09:00-10:00 Free Computing & Analysis practice with TAs

**Nick Goldman & Ziheng Yang**

10:00-13:30: Hypothesis testing in phylogenetics (IV)with coffee break

13:30-15:00: Lunch at CreteAcquarium

15:00-18:30: Q&A session, students can give oral presentations if they want to, with coffee break

20:30 Dinner at hotel

**Teaching Assistants**

Maria Anisimova

Detecting positive selection using codon models

Computational Biochemistry Research Group, ETH Zurich, Switzerland

Clemens Lakner

Bayesian inference of phylogeny

School of Computational Science, Florida State University, USA

Tim Massingham

Likelihood methods in phylogenetic analysis

EMBL-European Bioinformatics Institute, Hinxton, UK

Natalie Cusimano

Systematic Botany

University of Munich, Germany