

# Minutes of the 5<sup>th</sup> EDEN meeting

## Faro, February 12-13, 2009

This was the fifth meeting of the EDEN project, which is by itself part of a deliverable (D.6.2). It was used also as a meeting for the Project Steering Committee. It has been used to update the participants on the latest scientific developments within the project, and to plan the last EDEN year.

### **Participants**

#### IFISC/IMEDEA-UIB

Emilio Hernández-García  
Alejandro Herrada  
Tomas Sintes  
Murat Tugrul  
Alex Rozenfeld

#### BioInf Leipzig

Markus Riester  
Konstantin Klemm  
Stephanie Keller-Schmidt

#### TKK/LCE

Jari Saramaki  
Mikko Kivelä  
Jenni Hulkkonen

#### CCMAR

Ester Serrão  
Sophie Arnaud-Haond  
Filipe Alberto  
Mirjam Vliet  
Onno Dieckman  
Yann Moalic (Ifremer)  
Gareth A. Pearson

## Agenda

### Thursday 12:

9h Welcome and coffee

9h30 Talks

#### POPULATION GENETICS

**9h30-9h50: Ester Serrão** (and João Neiva; CCMar)

**9h50-10h10: Mirjam Vliet** (CCMar): Metapopulation genetics of endangered amphibians in Algarve

**10h10-10h30: Filipe Alberto** (and Pablo; CCMar):

**10h30-10h50: Filipe Alberto** Population genetics and evolution of *Macrocystis sp.*

10h50: coffee break

**10h50-11h10: Onno Dieckman** (CCmar): Phylogeography of the Seagrass *Zostera noltii*

**11h10-11h30: Fernando Canovas** (CCMar): Developing and using Single Nucleotide Polymorphism (SNP's) to address gene expression and polymorphism in different environmental stress in the algae *Fucus sp.*

**11h30-11h50: Yann Moalic** (Ifremer, CCMar): Networks in the deep: addressing the biogeography of deep sea hydrothermal vents using network analysis

11h50-13h: Discussion on datasets and analysis

13h-14h30: Lunch

14h30: TALKS

#### PHYLOGENY:

**14h30-15h00: Alejandro Herrada** (IMEDEA) 'Allometric scaling of branch length in phylogenies'

**15h-15h30: Markus Riester** (Leipzig) 'A differentiation-based phylogeny of cancer'

#### DATA ANALYSIS:

**15h30-16h00: Markus Riester** (Leipzig) 'Pedigree: a new software for parentage analysis'

16h: Coffee break

**16h30-17h: Mikko Kivelä** (Helsinki) distance measures in genetics

**17h-17h30: Jenni Hulkkonen** (Helsinki) hierarchical community detection

**17h30-18h: Alex Rozenfeld** (IMEDEA) simulations of gene source-sink systems

**18h-18h30: Emilio Hernández-García and Konstantin Klemm:** models for constructing trees with properties somehow similar to real phylogenies

19h30: Dinner at the beach

### **Friday 13:**

9h30 -10h30: administrative issues/sequence and milestones for the EDEN commitments

Discussions:

Software: 'state of the art' (i.e. current facilities programmed, comments, suggestion for more data analysis and improvement).

Modelling clonal growth, and simulation clonality

Distribution of size in clonal organisms

The issue of genetic distances among individuals

Choosing genes for phylogenies

- The consortium has checked that all deliverables are being completed on time. After the problems originated by the delay in the genomic sequencing, tasks are now back in schedule.
- A listing of the data sets available in Faro has been distributed to the participants (available in the resources (private) section of EDEN web site:  
<http://ifisc.uib-csic.es/EDEN/fichaResource.php?idResource=42> )
- The next EDEN meeting will be held in Mallorca next summer.