Project no. 043251

EDEN

ECOLOGICAL DIVERSITY AND EVOLUTIONARY NETWORKS

Instrument: Specific Targeted Project (STREP)

Thematic Priority:	Integrating and strengthening the European Research Area NEST Pathfinder initiative Tackling Complexity in Science

D6.2 (D1). **Project meetings**

(version 2: full project duration)

Due date of deliverable: Months 1, 6, 12, 18, 24, 30, 36
Actual submission date: Months 1, 6, 13, 19, 26, 33, 36

Start date of project: 1 January 2007 Duration: 36 months

Organisation name of lead contractor for this deliverable: IMEDEA-UIB
Other contributors: CCMAR, Bioinf Leipzig, TKK/LCE

Project co-funded by the European Commission within the Sixth Framework Programme (2002-2006)		
Dissemination Level		
PU	Public	
PP	Restricted to other programme participants (including the Commission Services)	PP
RE	Restricted to a group specified by the consortium (including the Commission Services)	
CO	Confidential, only for members of the consortium (including the Commission Services)	

NOTE: This is a short summary of the project meetings, which were by themselves the deliverables. Additional information including files with most of the meeting talks can be found at
`http://ifisc.uib-csic.es/EDEN/fichaOutput.php?idOutput=4`

MINUTES FROM THE EDEN START-UP MEETING

Ca's Jai, Campus Universitat de les Illes Balears, Palma de Mallorca, Spain
29-30 January 2007

This was the first meeting of all participants in the EDEN project. It is by itself the first deliverable (D.6.2.1) and signals the first milestone (M1) in project development. It was used also as the first meeting of the Project Steering Committee.

The objectives were to provide an overview of the activities of the four participating teams, to present scientific results providing background for EDEN objectives, to have a global view of the project as a whole, and to plan the project activities, specially those to be carried during the first months.

List of attendants to the meeting:

IMEDEA-UIB:	Emilio Hernández-García	(emilio@imedea.uib.es)
	E. Alejandro Herrada	(alejandro@imedea.uib.es)
	Alejandro Rozenfeld	(alex@imedea.uib.es)
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	Carlos M. Duarte	(carlosduarte@imedea.uib.es)
	Tomàs Sintes	(tomas@imedea.uib.es)
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	Sophie Arnaud-Haond	(sarnaud@ualg.pt)
BioInf Leipzig:	Konstantin Klemm	(klemm@bioinf.uni-leipzig.de)
	Peter F. Stadler	(studla@bioinf.uni-leipzig.de)
	Markus Riester	(markus@bioinf.uni-leipzig.de)
TKK/LCE:	Kimmo Kaski	(kimmo.kaski@hut.fi)
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AGENDA

Monday, January 29, 2007

The morning of the first day was devoted to presentations of activities of the participant groups, as a way to improve mutual knowledge of the different interests and expertises:

Welcome and introductory remarks
09:30 - 10:15 - Overview of activities of the IMEDEA groups (Mallorca), Cross-Disciplinary Physics and Natural Resources.
10:15 - 11:00 - Overview of activities of the CCMAR MAREE group (Faro).
Coffee break
11:30 - 12:15 - Overview of activities of the BioInf group (Leipzig).
12:15 - 13:00 - Overview of activities of the LCE group (Helsinki).
Lunch

The afternoon of the first day was devoted to presentations of recent scientific results related to the objectives of EDEN:

15:00 - 15:55 - Neutral population genetic structure and adaptive evolution in marine plants and algae. Gareth Pearson & Sophie Arnaud-Haond (Faro).
15:55 - 16:25 - Identification of Homoplastic Characters in Multiple Sequence Alignments. Peter F. Stadler (Leipzig).
15:25 - 16:50 - Networks and cycle spaces. Konstantin Klemm (Leipzig).
Coffee break
17:10 - 18:05 - Structural analysis of weighted complex networks, Jari Saramäki (Helsinki).
18:05 - 18:30 - Scaling properties in the Tree of Life. Alejandro Herrada (Mallorca).
18:30 - 19:00 - Networks of genetic similarity in populations of clonal plants. Alex Rozenfeld (Mallorca).

Tuesday, January 30, 2007

During the morning of the second day, the structure, tasks, deliverables, etc. associated to the different workpackages were discussed.

09:00 – 13:00 – Detailed Workpackage discussions:
WP1: Data collection.
Discussion leader: CCMAR (Faro).
WP2: Network theory toolbox.
Discussion leader: LCE (Helsinki).
WP3: Dynamical and spatio-temporal modelling.
Discussion leader: BioInf (Leipzig).
WP4: Population ecology networks.
Discussion leader: CCMAR (Faro).
WP5: Phylogenies and the tree of life.
Discussion leader: IMEDEA (Mallorca).
WP6: Management and assessment.
Discussion leader: IMEDEA (Mallorca).

Lunch

15:00 - ...
The afternoon of the second day was the time for discussions on the different formats in which data and results should be stored and interchanged.

Most of the meeting discussions confirmed and made more concrete the tasks specified in the *Description of the Work* document.

For future reference, and because they are among the first deliverables to be due, we summarize here some basic requirements established for the Project webserver (D6.1) and the internal version of the Project Software Toolbox (D2.1):

The Project webserver should be organized in a public and a private areas.
- The public area should contain a Project description, partner listing, and dissemination material.
- The private area should allow the use of mailing lists, and to provide tools to share and deposit software, data, bibliography, and completed deliverables.

TKK/LCE is beginning to collect the software specifications for the 'Software Toolbox' of Workpackage 2. Some of the initial requirements already established are:
- The Toolbox should work both with a graphic interface and without it (by using command line instructions).
- All the results and output should be done, at least, as flatfiles.
- Interoperability (Win, Unix, Mac) is important. Python may be a good language for that.
- The Toolbox should be able to perform standard calculations on unweighted and weighted networks, as well as to use correlation and distance data and to introduce different kinds of thresholding.

MINUTES FROM THE 2nd MEETING OF THE EDEN PROJECT

Campus de Gambelas, Universidade do Algarve, Faro, Portugal
20-22 June 2007

This was the second meeting of participants in the EDEN project. It is part of one of the deliverables (D.6.2.1) and was also used as a meeting of the Project Steering Committee.

The objectives were to share information of the advances during the first months of the project, and to plan for the next steps in project development.

List of attendants to the meeting:

IMEDEA-UIB:	• Emilio Hernández-García	(emilio(_at_)imedea.uib.es)
	• E. Alejandro Herrada	(alejandro(_at_)imedea.uib.es)
	• Alejandro Rozenfeld	(alex(_at_)imedea.uib.es)
CCMAR:	• Ester Serrão	(eserrao(_at_)ualg.pt)
	• Gareth Pearson	(gpearson(_at_)ualg.pt)
	• Sophie Arnaud-Haond	(sarnaud(_at_)ualg.pt)
BioInf Leipzig:	• Konstantin Klemm	(klemm(_at_)bioinf.uni-leipzig.de)
	• Markus Riester	(markus(_at_)bioinf.uni-leipzig.de)
	• Camille Stephan-Otto Attolini	(camille(_at_)bioinf.uni-leipzig.de)
TKK/LCE:	• Kimmo Kaski	(kimmo.kaski(_at_)hut.fi)
	• Jari Saramäki	(jsaramak(_at_)cc.hut.fi)
	• Tapio Heimo	(taheimo(_at_)lce.hut.fi)

June 20, 2007

During the morning, Faro and Helsinki teams discussed on the questions relevant to network analysis which the proposed software toolbox should address. It was agreed that the software will analyze fragment/proteins data (allele frequency/genotyping) instead of sequences. Faro team will send to Helsinki (and also deposit on the web site) datasets of the most used molecular markers as examples of the types of data and formats which should be analyzed, as well as a selection of distances measures used in the literature.

During the afternoon session, all the teams discussed on the topics described below. References and data on these topics will be uploaded to the EDEN web.

GENOTYPE DATASETS: microsatellite data for 15 locus of *Fucus* (a nonclonal alga) and 10 locus of *Zimodocea* (a seagrass, both from Mediterranean as from Atlantic meadows) are nearly ready and will be uploaded to the web by the Faro team as soon as possible. Different mating systems are represented. The main interest of analyzing these new data sets with network methods is to elucidate the impact of habitat differences, and of mating systems on the genetic network structure. Can network methodologies help to distinguish a situation of recent hybridization between two species from the alternative scenario of an incipient speciation event? Correlations with geography will be different in the two scenarios.

SOFTWARE TOOLBOX: It is becoming increasingly clear that the project should not only address network *analysis*, but more importantly, network *building*. Developing methodologies for scanning different threshold values instead of a single one, and extracting information from the sequences of outcome, would be important.

COMMUNITY DETECTION: Participants reviewed different methodologies to detect community structure.

From classical genetics, F_{st} and methods based on it are the most important: one performs a statistical test to check the hypothesis that there is panmixia among two different groups. The groups are given a priori. With AMOVA one compares the variance of some genetic property inside groups and between groups, and checking statistically the hypothesis that they are really different groups. Here again the groups should be given a priory and there is a single level of hierarchy. With Bayesian methods, one sets up a model for evolution, and fits the parameters to data, which allow to estimate if there have been population differentiation on the data set analyzed or not.

From recent network theory, there is a bunch of methods based on the modularity approach of Girman and Newman, including Potts-model type. Nevertheless, the most consistent methods seem to be the ones based on Clique Percolation. New approaches by Arenas et al. seem to improve the modularity approach but not strongly enough (only communities of particular size are detected). One should try also to understand recent information theoretic methods.

RESULTS FROM ANALYSIS OF POSIDONIA NETWORKS: Sophie Arnaud-Haond and Alex Rozenfeld described recent results on the analysis of interpopulation and intrapopulation networks built from microsatellite data from *Posidonia*.

June 21, 2007

On Thursday morning. all groups discussed on the following topics:

NETWORK PHYLOGENIES: Markus Riester exposed that the convenient method to build Network Phylogenies is Neighbor-Net. It searches for conflicts in tree-reconstruction methods (violation of triangular identities, e.g.) and solves them by introducing cycles.

SEQUENCE DATA: After discussing several candidates (picoplankton, pathogens from TreeBase, transposable elements …) it was agreed that the sequence data set that would be used as benchmark for Network Phylogenies construction (deliverable D1.1, due in September) would be data from *Fucus*, and from *Cyanobacteria*. The Faro team will collect that and upload to the web as soon as possible.

MODELLING: The need to have some models of population dynamics running to really understand the *networks of genetic similarity* constructed so far (deliverable D3.1) was stressed. It seems that, at the interpopulation level, migration is an important process to consider, being mutations more important only at the largest distances. Development of other models of biological interactions and evolution is also a subject of EDEN. In this context, Camille Stephan-Otto Attolini described her recent work on a model of interacting cells including genes which interact with the environment and express factors leading to cell mobility and metabolism.

On Thursday afternoon:

PHYLOGENETIC TREE TOPOLOGY: Alejandro Herrada exposed results from Palma analyzing a large set of interspecific and intraspecific phylogenies. The topological analysis reveals correlations either in the extinction or in the branching frequency inside related lineages. In fact one would expect that neighbours of misfit taxa (i.e. the closely related taxa) will have a high probability of being misfit and getting extinct as well that the other taxa, and the same may apply to positively selected taxa having suddenly an evolutionary advantage they share. But this feature is missing in the macroevolutionary models usually used to model phylogenetic topology. Competition among lineages may be another factor to be taken into account.

GENETIC FLOW: Konstantin Klemm came out with an idea on how to quantify the amount of gene flow between populations. It was based in a formula describing how well is the set of alleles in one population contained in the set of alleles from another one. The *most contained* set should have exported genes to the *container* one. The proposal seems very interesting and the teams will develop it.

June 22, 2007

During the morning the different teams discussed informally in small groups on different topics including:

- Bayesian coalescence methods (Pritchard software Structure) applied to *Posidonia* populations evolution.
- Circadian rhythms in gene expression in algae, and the impacts of the tide.
- Genetic and spatial data for Cimodocea in the Ebro delta.
- Folding of RNA of Fucus.
- Networks of genetic similarity for *Trypanosoma* cruzi.
- Sampling problems for genetic data arising from clones which may have a power law size distribution.

It was agreed that the next EDEN meeting will take place in Finland next winter.

MINUTES FROM THE 3rd EDEN MEETING

LCE / Helsinki University of Technology
22-23 January 2008

This was the third 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.

In addition of providing an overview of the present status of the scientific issues related to the project, a revision was made of the first year project development, and the next steps were planned.

List of attendants to the meeting:

IFISC/IMEDEA-UIB:
- Emilio Hernández-García (emilio(_at_)ifisc.uib.es)
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- Alejandro Rozenfeld (alex(_at_)ifisc.uib.es)
- Víctor M. Eguíluz (victor(_at_)ifisc.uib.es)
- Tomàs Sintes (tomas(_at_)ifisc.uib.es)

CCMAR:
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BioInf Leipzig:
- Konstantin Klemm (klemm(_at_)bioinf.uni-leipzig.de)
- Peter F. Stadler (studla(_at_)bioinf.uni-leipzig.de)
- Markus Riester (markus(_at_)bioinf.uni-leipzig.de)
- Camille Stephan-Otto Attolini (camille(_at_)bioinf.uni-leipzig.de)

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AGENDA

Tuesday, January 22, 2008

- 09:30-12:00
  - Welcome, practical matters, etc.
  - Alejandro Herrada: Statistical analysis of protein family trees
  - Tomas Sintes: Space occupation and growth of clonal plants
    - LUNCH
- 13:00-17:00
  - Markus Riester: Reconstructing pedigrees
  - Sophie Arnaud-Haond: Analysis of T. Cruzi data
  - Alex Rozenfeld: Analysis of C. Nodosa genetic data
  - Gareth Pearson: Cyanobacterial genome data
    - 20:00 Diner at restaurant Lasipalatsi

Wednesday, January 23, 2008

- 09:30-12:00
  - Jari Saramäki: Community detection for the P. Oceanica data
  - Software Demo (the Helsinki Team)
  - Konstantin Klemm: Models and invariants of growing trees
    - LUNCH
- 13:00-17:00 Additional discussions, workpackage revision and planning.

- In addition to the EDEN website and the different EDEN meetings (deliverables D6.1 and D6.2), the data set of sequence alignments (from cyanobacteria, deliverable D1.1) was already posted into the web site and the first version of the Software Toolbox (deliverable D2.1) is about to be uploaded. Thus, project output is being produced at the expected rhythm. During the meeting it was reminded, and adequate actions were planned, that we are expected to produce three new deliverables (Reports on correlation methods, on population network structure, and on allometric phylogenetic scaling, D2.1, D2.2 and D3.1) by month 18 (next June), in coincidence with the Mid-Term report to the Commission.
- It is important to keep track of the research and dissemination activities performed by the EDEN team. Thus, members are requested to mention into the

‘outputs’ section of the EDEN web the publications, conferences, or workshop presentations given on the project subjects, uploading also, if appropriate, the relevant files (they can be marked as public or as private to EDEN partners).

- As a result from the scientific discussions, several proposals for additional calculations/studies arose, such as comparing the scaling of real phylogenies with the one from phylogenies constructed from random distance matrices, constructing network phylogenies from the cyanobacteria data set (by using SplitTree), performing metapopulation genetic simulations, or evaluating a new similarity matrix which counts the possible common ancestors of two individuals.
- It was decided that the next EDEN meeting will be held in Leipzig at the beginning of next summer.

Minutes of the 4th EDEN meeting

Leipzig, 7-8 July, 2008

This was the fourth 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. In addition of providing an overview of the present status of the scientific issues related to the project, the first 18 months of the project's development were reviewed. The contents of the midterm report were discussed and the next steps were planned.

Participants

IFISC/IMEDEA-UIB

- Alejandro Herrada, alejandro(_at_)ifisc.uib.es
- Emilio Hernández-García, emilio(_at_)ifisc.uib.es
- Tomas Sintes, tomas(_at_)ifisc.uib.es
- Murat Tugrul, mtugrul(_at_)ifisc.uib.es

CCMAR

- Sophie Arnaud-Haond, sarnaud(_at_)ualg.pt
- Cymon Cox, cy(_at_)cymon.org
- Ester Serrão, eserrao(_at_)ualg.pt

BioInf Leipzig

- Stephanie Keller-Schmidt, stephanie(_at_)bioinf.uni-leipzig.de
- Konstantin Klemm, klemm(_at_)bioinf.uni-leipzig.de
- Markus Riester, markus(_at_)bioinf.uni-leipzig.de
- Peter Stadler, peter.stadler(_at_)bioinf.uni-leipzig.de

TKK/LCE

- Mikko Kivelä, mtkivela(_at_)lce.hut.fi
- Jari Saramäki, jari.saramaki(_at_)tkk.fi

Agenda

Monday, 7 July

10:00	Welcome, practical matters
10:05	*Microsatellite data used to understand Atlantic-Mediterranean connectivity in the seagrass Cymodocea nodosa*, Ester Serrão
10:35	*Detecting communities in the P. Oceanica data*, Jari Saramäki
11:10	*Mutual information and genetic distance for the P. Oceanica data*, Konstantin Klemm
11:30	Coffee / Tea
12:00	*Integrating plant growth modeling with genetics*, Tomas Sintes
12:45	*FRANz: Fast reconstruction of pedigrees*, Markus Riester
13:15	Lunch
14:45	*Informed Generation: functional self-organization in biological evolution*, Peter Wills (Auckland)
15:30	*A discussion on the use of network approaches for the analysis of patterns of lateral gene transfer in the Tree of Life*, Cymon Cox
16:00	*Phylogenetic Trees and the AB-model*, Stephanie Keller-Schmidt
16:30	Coffee / Tea
17:00	Management and reporting, WP6
18:45	end of session

Tuesday, 8 July

10:00	*Using networks to distinguish ancestral polymorphism versus hybridization using msat data for species of the alga Fucus*, Sophie Arnoud-Haond and Ester Serrão
10:30	*Networks applied to the understanding of the evolution of pathogen lineages, with an example of T. cruzii*, Sophie Arnoud-Haond
10:50	Discussion WP1
11:30	Coffee / Tea
12:00	Discussion WP2
12:40	Discussion WP3
13:20	Lunch
14:55	*Structure and dynamics of yeast gene regulation*, Murat Tugrul
15:25	session interval
15:30	*Modeling the emergence and collapse of autocatalytic structure in evolving networks*, Sanjay Jain (Delhi)
16:15	Coffee / Tea
16:40	Discussion WP4
17:20	Discussion WP5
18:00	Final remarks, end of meeting

- The consortium made sure that all deliverables due by project month 18 (midterm) are actually finished or that the material constituting them is finished. All deliverables will be uploaded on the project webpage by the time the midterm report is due (14 August, 2008).
- Planned visits: Murat Tugrul (IFISC/IMEDEA-UIB) stays at Bioinf Leipzig during July 9-12,2008. Konstantin Klemm (Bioinf Leipzig) visits IFISC/IMEDEA-UIB from 01 September to 30 November, 2008.
- The next EDEN meeting is planned to take place at CCMAR in Faro, January 8-9, 2009.

Minutes of the 5th 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.

6th EDEN Meeting

Hotel Sentido Cala Viñas, Mallorca

17-18 September 2009

This was the sixth 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.

This was the last meeting before the final one. Thus, in addition to the usual update of scientific achievements and task completion, time was devoted to planning the last part of the project.

Participants:

IFISC/IMEDEA-UIB:

Víctor M. Eguíluz
Emilio Hernández-García
Alejandro Herrada
Paolo Masucci
Tomàs Sintes.

CCMAR:

Ester Serrão
Sophie Arnaud-Haond
Fernando Cánovas-García.

BioInf Leipzig:

Stephanie Keller-Schmidt
Konstantin Klemm
Markus Riester
Peter Stadler.

TKK/LCE:

Mikko Kivela
Jari Saramäki

AGENDA

Thursday, September 17

9:30 - Welcome, etc.

09:30->10:15 - Sophie Arnaud-Haond (Faro/Brest): Genetic Diversity Spectrum and simulations.

10:15->11:00 - Tomàs Sintes (Mallorca): Genetic diversity indices in seagrasses.

Coffee

11:30->12:15 - Markus Riester (Leipzig): News on pedigree reconstruction and clonal reproduction rates.

12:15->13:00 – A. Paolo Masucci (Mallorca): Information theoretic approach to genetic networks.

Lunch

15:00 -> 15:45 - Ester Serrão (Faro): A summary of the data sets available at CCMAR

15:45 -> 16:30 – Jari Saramäki (Helsinki): The EDEN Software Toolbox. An update.

Coffee

17:00->19:00 - Coordination, deliverables. Planning for the remaining part of the project.

Friday, September 18

9:30->10:15 - Konstantin Klemm (Leipzig): Depth scaling and models of growing trees

10:15->11:00 - Stephanie Keller-Schmidt (Leipzig): Likelihood estimation for binary tree shapes

Coffee

11:30 -> 12:15 – Fernando Cánovas-García (Faro). Data on Single-Nucleotide Polymorphisms (SNPs)

12:15 –> … - Additional discussions.

- During the meeting provisions were made to insure that all tasks and deliverables will be completed on due time.
- Attention should be given to the software SIMUPOP, for population genetics simulations, and to igraph, a R package to analyze networks.
- From the scientific perspectives opened by the tasks in EDEN, it is now clear that opportunities for network approaches to analyze evolutionary and ecological process will continue to be available after project completion. EDEN partners will continue to be involved in such developments, for which the present collaboration has been instrumental.
- Last June the question was posed to the EC officer on extending EDEN duration a couple of months in 2010. This would allow postponing the final EDEN meeting to the beginning of 2010, and integrate into the project possible insights gained at the Darwing09 conference to be held in Palma at the end of November. The answer was that he current policy line of DG RTD is to strongly limit FP6 contract extensions.
- In consequence, last EDEN meeting will be held next December. Lapland was chosen as venue.

7th EDEN Meeting

Levi, Lapland, Finland

17-18 December 2009

This was the seventh and final meeting of the EDEN project. It is by itself part of deliverable D.6.2.
As usual, the meeting was used also as a meeting for the Project Steering Committee. Because of its final character, the Steering Committee meeting was more formal and longer.

Participants:

IFISC/IMEDEA-UIB:

Emilio Hernández-García
Paolo Masucci
Tomàs Sintes
Alejandro Rozenfeld

CCMAR:

Ester Serrão
Sophie Arnaud-Haond
Gareth Pearson

BioInf Leipzig:

Stephanie Keller-Schmidt
Peter Stadler.

TKK/LCE:

Mikko Kivela
Jari Saramäki

AGENDA

Thursday, December 17

9:00 - Welcome

09:15 - Stephanie Keller-Schmidt (Leipzig): Efficient calculation of likelihood for growth models.

09:45 – Emilio Hernández-García (Mallorca): Age and activity-like models for macroevolution

Coffee

10:30 – Alejandro Rozenfeld (Mallorca). Sources and sinks in gene flow

11:30 – Discussion

Lunch

13:30 – A. Paolo Masucci (Mallorca): Genetic information flow between populations defined by a set of symbolic vectors.

14:30 – Ester Serrao (Faro): Macrocystis and amphibians networks

Coffee

16:00 – Discussion on network extraction from data and its directionality

17:00 – Project management

Friday, September 18

9:30 – Project steering committee meeting

Lunch

13:30 – Peter Stadler (Leipzig): Update from Leipzig

14:30 - Sophie Arnaud-Haond (Faro/Brest): Zostera marina from Brittany

Coffee

16:00 – Final Discussion

1 During the meeting it was checked that deliverables are all completed. Provisions were made to make them properly posted in the web site before the end of the year.

2 There is an issue with the public availability of different datasets: The policy of some journals forbids them to be made public before formal publication. It was agreed that the different datasets (and associated reports) will be marked as ‘public’ and freely accessible from the web site just after the corresponding papers have been published.

3 On the economic side, all partners have adequately used their budged. Planning of the final scientific and financial reporting was made.

4 On the scientific side, the growing interest in network methods in ecology and evolution is patent. It was very useful to run the EDEN project in the right time, so that contributions from EDEN groups will permeate the community. Join collaborations will continue and special effort should be made to let the community know about the different software tools developed by EDEN, which will be good instruments for performing serious research.