

EDEN

Ecological Diversity and Evolutionary Networks

<http://ifisc.uib.es/EDEN>

NEST Pathfinder initiative
Tackling Complexity in Science



EDEN (Ecological Diversity and Evolutionary Networks) is a research project supported by the New and Emerging Science and Technology programme (**NEST**) of the 6th Framework Programme of the European Commission, under the **NEST-Pathfinder Complexity** initiative.

It started on 1st January 2007 and will run for three years.

The EDEN objectives

Biological systems and their highly organized constituents are paradigms of **Complexity**. The study of **Complex Networks**, representing interactions among components, has become central in the science of Complex Systems.

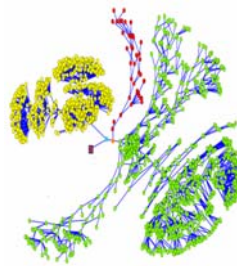
The EDEN proposal aims at considering in depth the representation of **ecological and evolutionary relationships** among biological entities -organisms, populations, taxa- in terms of networks by developing methods to construct them from **genetic data** and by expanding the toolbox for their analysis.

Evolutionary relationships between species are usually represented in **phylogenies**, i.e. evolutionary **trees**. Intraspecific gene genealogies and population structure are also conventionally represented as tree-like objects. However, processes such as sexual reproduction or lateral gene transfer introduce cycles and need richer structures -**networks**- to be properly represented. EDEN will develop tools to build networks of ecological and of evolutionary relationships from genetic data, and study them with the modern methods of network theory. More specifically, EDEN will focus on:

Networks of genetic diversity, constructed from genetic data of a large sample of marine plants in coastal ecosystems. Innovative network methods will be developed to address questions on population structure, gene flow, evolution, biogeography and conservation of these threatened ecosystems.

The tools of **reticulate evolution**, and novel approaches based on network theory will be used to build and analyze phylogenies with rich structure beyond trees. The aim is to gain biological insight on the evolution of life, from specific lineages to the entire spectrum of life forms, by evolving from the present concept of a **'Tree of Life'** to a more flexible concept of **'Network of Life'**.

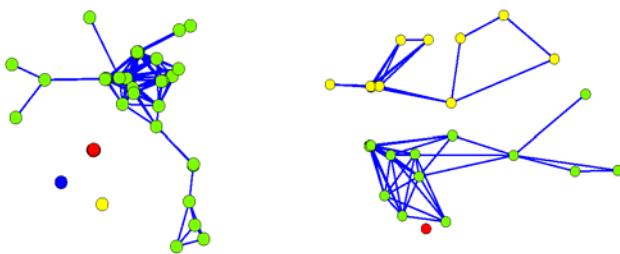
The synergy between **extensive data collection and analysis** together with **individual-based modeling** (including genetic, ecological, and spatial factors) will be pursued in all these focus cases.



Rendering of the first branching levels of a conventional reconstruction of the Tree of Life (data from tolweb.org)



Posidonia oceanica in the Mediterranean, and two genet networks: from Es Pujols (Formentera, Balearic Islands), left, and Campomanes (Mediterranean Spanish coast), right



Workpackage structure

WP1: Data collection

To produce and/or compile the intraspecific and interspecific genetic databases for the organisms used in the project:

Microsatellite data for populations of the seagrasses *Posidonia oceanica*, *Cymodocea nodosa*, *Zostera noltii*, and the macroalgae *Fucus* spp. and *Caulerpa* spp. Trait-associated gene (TAG) marker data derived from EST (Expressed Sequence Tag) databases and consisting of EST-microsatellites and/or single nucleotide polymorphisms (SNPs) for *Fucus* spp. and *Zostera noltii*. Sequence data compiled from public databases for different domains of the Tree of Life.

WP2: Network theory Toolbox

Provide tools for network analysis to be used by the rest of the Project. Develop novel conceptual frameworks: weighted networks, networks embedded in physical space, thresholded correlation networks and their community structure and percolation properties. Analyze the potential of classical and modern phylogeny construction methods to understand community structure in more general complex networks.

WP3: Dynamical and spatiotemporal modelling

Understanding the genetic structure of clonal plant meadows in terms of the biological and spatial processes occurring in them. To obtain evolution models allowing the interpretation of reticulate phylogenies.

WP4: Population ecology networks

Obtaining relevant information on the ecological processes influencing the extent of clonality, and on the evolutionary processes (mating system, migration) shaping the genetic structure of meadows of clonal plants with the tools developed in the project. Extending the above to the whole biogeographical range of the studied plants, and to the general analysis of metapopulations dynamics.

WP5: Phylogenies and the Tree of Life

Get insight into the way evolution shapes phylogenetic trees. Advance in the consideration of the whole Tree of Life and its different parts as complex objects arising from interactions that can give them a topology richer than the one of a simple tree.

WP6: Management and assessment

To provide the Scientific Coordination, Administrative Coordination, and the efficient communication that would give coherence and excellence in the results to the project as a whole.

The EDEN partners

IMEDEA/IFISC-UIB



The University of the Balearic Islands (UIB), at Palma de Mallorca, Spain, is the coordinating institution. It participates through its research institutes **IFISC** (Institute for Cross-Disciplinary Physics and Complex Systems) and **IMEDEA** (Mediterranean Institute for Advanced Studies), join research institutes with the Spanish Higher Research Council (CSIC)

CCMAR



The Center of Marine Sciences (CCMAR), a leading center in Marine Genomics at Faro, Portugal, participates through its Ecology and Evolution of Marine Plants and Algae (**MAREE**) team.

BioInf Leipzig



Leipzig University, Institute for Computer Science, The **Bioinformatics Group**, from the Institute for Computer Science of Leipzig University, Germany (**BioInf Leipzig**), is part of the Bioinformatics initiative of the German research council (DFG).

TKK/LCE



The Laboratory of Computational Engineering (**LCE**), at the Helsinki University of Technology, Finland, is a Finnish national Center of Excellence in Computational Complex Systems Research.

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