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EcoGenetics:

Simulate species with complex life cycles

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I. Purposes

- Simulating Population Dynamics or Population Genetics within a spatially-explicit metapopulation, by means of an Individual-Based Model
- Offering an user-friendly interface to define the species' life-cycle, the spatial settings and sensitivity-analysis parameters.

II. Input and Output

Landscape (Patch size and location)

Species life history

Genome (# of loci and alleles, mutation rate)

EcoGenetics

Demography (local abundances, patch occupancy, sex ratio)

Genetic data (Coancestries, allele frequencies)

III. Spatial Structure

The spatial interface allows defining the habitat patches' coordinates, carrying capacity, growth rate, and extinction risk, along with the resistance to dispersal of the surrounding environment.

Landscape-dependent survival probability during dispersal (green=high survival)

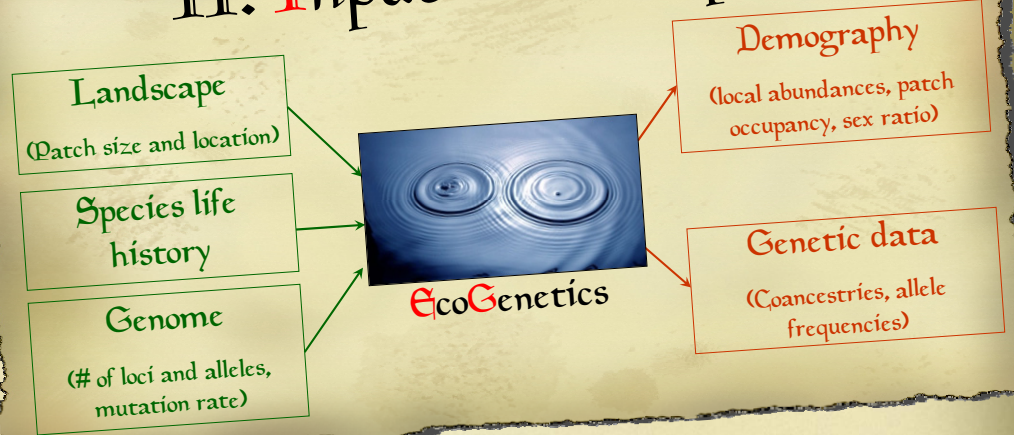habitat patch. Size proportional to carrying capacity

Connectivity: Prob. to disperse (line width) and prob. to survive (line shade)

Patch's parameters table

Many patch geometries

IV. Life-Cycle

The life cycle is defined as a sequence of Events:

Simple Events

- Birth
- Survival
- Dispersal
- Aging (goes to the next life stage)
- Reproduction (density-dependent or not)
- Death

Branching Events

- Sex-dependence
- Density-dependence (Regulation)
- Gene-dependence (for mendelian selection)
- Random branching

Special Events

- Synchronisation (wait for other individuals to reach the same stage)
- Tag (to compute tag-dependent statistics)

Life-cycle interface, showing the common Shrew life cycle (sex-dependent philopatry and dispersal distance, annual species)

Firebug life cycle (genetically controlled philopatry and dispersal distance (2 morphs), annual species)

Tree Frog (tentative) life cycle (sex-dependent philopatry and dispersal distance, lives up to 7 years, reproduces since age 2)

V. Genetics

- Clonal, hermaphrodite or sexuate mating system
- Neutral genetics (e.g. microsatellites)
- Up to 8 loci, with up to 256 alleles
- KAM and stepwise mutations
- Nuclear, mitochondrial, X- and Y-chromosome genomes
- Separate sampling of juveniles and adults
- Outputs readable by FStat and GenePop

VI. Sensitivity Analysis

The Batch Generator allows one to vary factorially any combination of parameters.

VII. Outputs

- Graphic output: Abundances, occupancy, sex ratio, coancestries (F, theta and alpha).
- Batch (or sensitivity analysis) produces tabulated text files for statistical analyses.

Time variation of population abundances.
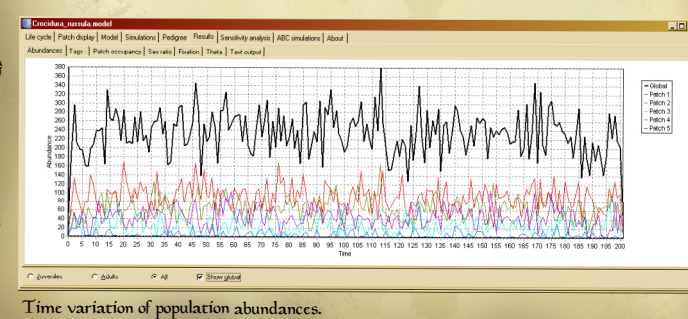
VIII. Potential Uses

- Population Viability Analyses
- Customised "null models" to compare real data to.
- "What-if" scenarios (patch removal, reduced of enhanced connectivity, bottlenecks, management strategies, etc.)
- Simulate data to test analytical tools
- Testing hypotheses of evolutionary genomics
- Teaching in population dynamics and genetics

For collaborations, please contact A. Hirzel, at Alexandre.Hirzel@unil.ch