

EcoGenetics:

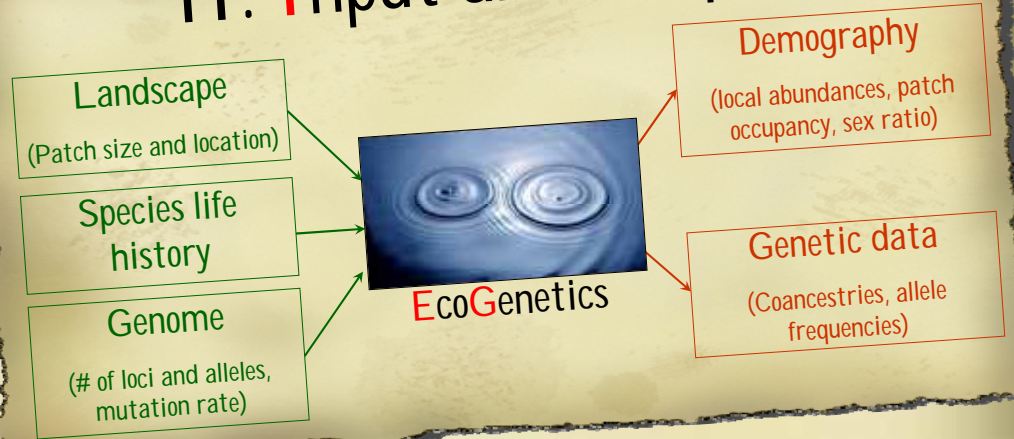
Simulate species with complex life cycles

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I. Purposes

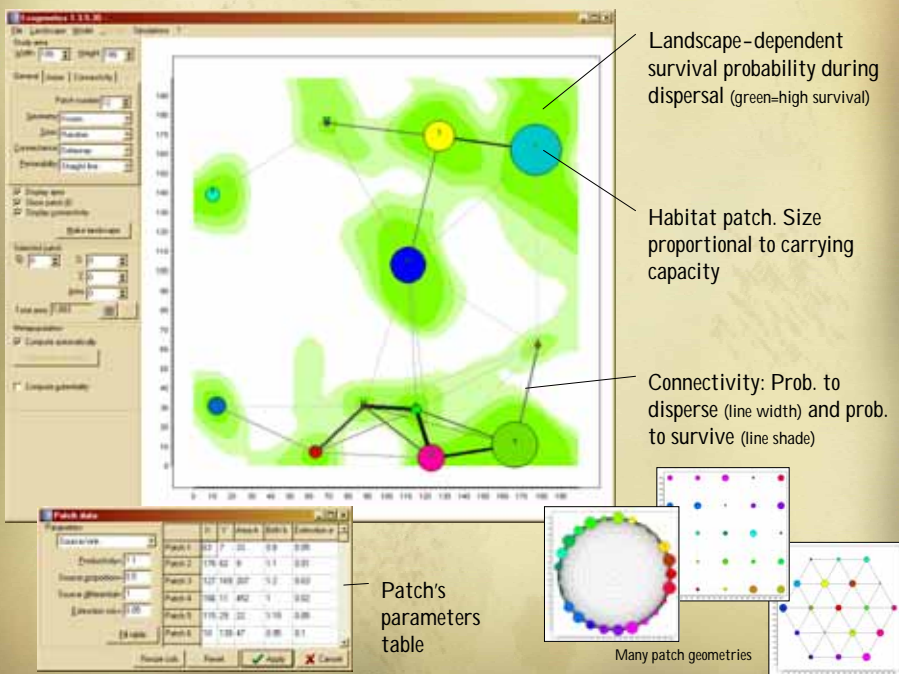
- Simulating **Population Dynamics** or **Population Genetics** within a **spatially-explicit** metapopulation, by means of an **Individual-Based Model**
- Offering an **user-friendly interface** to define the species' life-cycle, the spatial settings and **sensitivity-analysis** parameters.

II. Input and Output



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.



IV. Life-Cycle

The life cycle is defined as a sequence of **Events**:

Simple Events

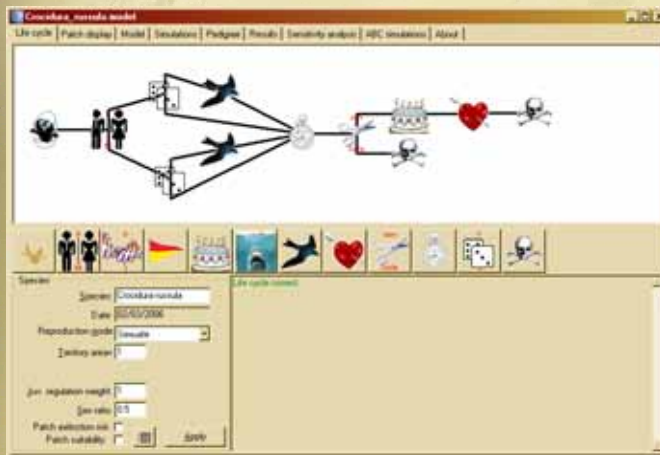
- Birth
- Survival
- Dispersal
- Aging (goes to the next life stage)
- Reproduction (density-dependent or not)
- Death

Branching Events

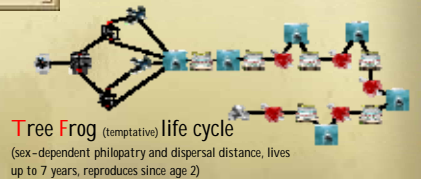
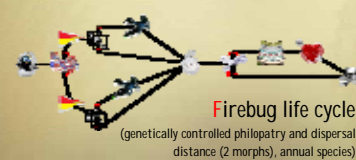
- Sex-dependence
- Density-dependence (Regulation)
- Gene-dependence (for mendelian selection)
- Random branching

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)

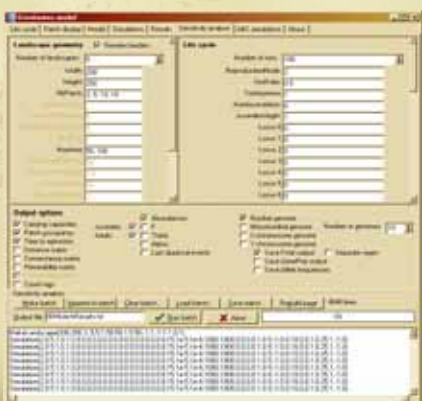


V. Genetics

- 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

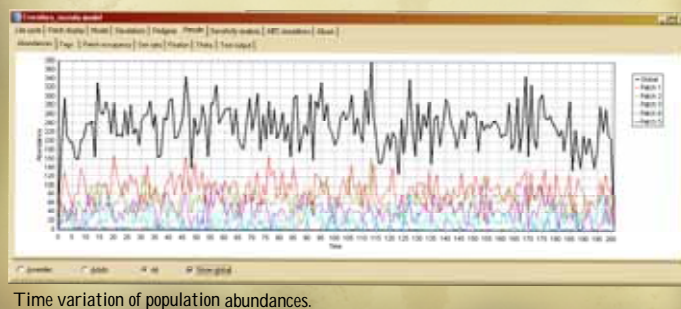
VI. Sensitivity Analysis

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



VII. Outputs

- Graphic output: Abundances, occupancy, sex ratio, coancestries (F , θ and α).
- 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 or enhanced connectivity, bottlenecks, management strategies, etc.)
- **Simulate data** to test analytical tools
- Testing hypotheses of **evolutionary genomics**
- **Teaching** in population dynamics and genetics

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