Course Summary: Biology 301, Spring 2001

I. Ecological models

I.1. Ecological models in discrete time

- I.1.1. Linear (density-independent) single species models: exponential growth
- I.1.2. Linear (density-independent) age-structured models: Leslie matrices, eigenvalues, eigenvectors, long-term growth rate, stable age distribution
- I.1.3 Non-linear (density-dependent) single species models: Equilibrium population size (carrying capacity), cobwebbing, stability analysis (tangent line approximation), periodic dynamics, chaos, computer simulations of iterated next generation maps
- I.1.4. Non-linear predator-prey models:

Equilibrium population sizes, phase plane, stability analysis, Jacobian matrix, partial derivatives, predator-prey oscillations, stabilizing influences on predator-prey dynamics (density-dependence in the prey, spatial structure, interference among predators), computer simulations

I.2. Ecological models in continuous time

- I.2.1 Linear (density-independent) single species models: Differential equations, exponential growth and decay, exact solution, separation of variables
- I.2.2. Logistic (density-dependent) growth: Equilibrium population size (carrying capacity), local stability, four methods of analysis (graphical (flow diagram), analytical (separation of variables), computer algebra system, computer simulations)
- I.2.3. Competition between two species: Lotka-Voterra equations, 0-isoclines, graphical analysis in phase plane, three qualitatively different outcomes, conditions for coexistence, various extensions (competition for space, harvesting, Allee effect)

II. Evolutionary models:

Evolution = 'variation in reproductive success' + 'heritable variation in a trait' (no correlation: neutral evolution, strong correlation: adaptive evolution)

II.1. Simple population genetic models in discrete time:

Basic setup (gamete pool at beginning of a generation, zygote pool at birth, adult zygote pool before reproduction, gamete pool at the beginning of the next generation)

- II.1.1. One locus, two alleles, no selection: Hardy-Weinberg equilibrium (example: blood groups), assumptions for Hardy-Weinberg equilibrium (no selection, random mating, no mutation, Mendelian segregation)
- II.1.2. One locus, two alleles models with selection:

Basic equation for the gene frequency dynamics, three qualitatively different outcomes, polymorphic equilibrium points, stability analysis, maintenance of polymorphism through heterozygote advantage (example: sickle cell anemia), invasion dynamics of dominants and recessives (example: industrial melanism), extinction dynamics of recessive lethals, mutation-selection balance, optimization of mean fitness