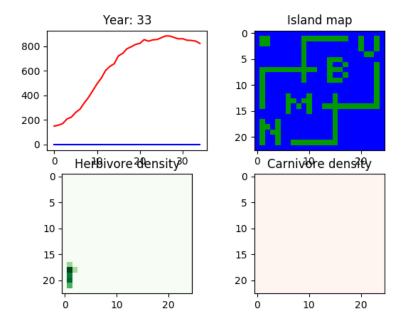
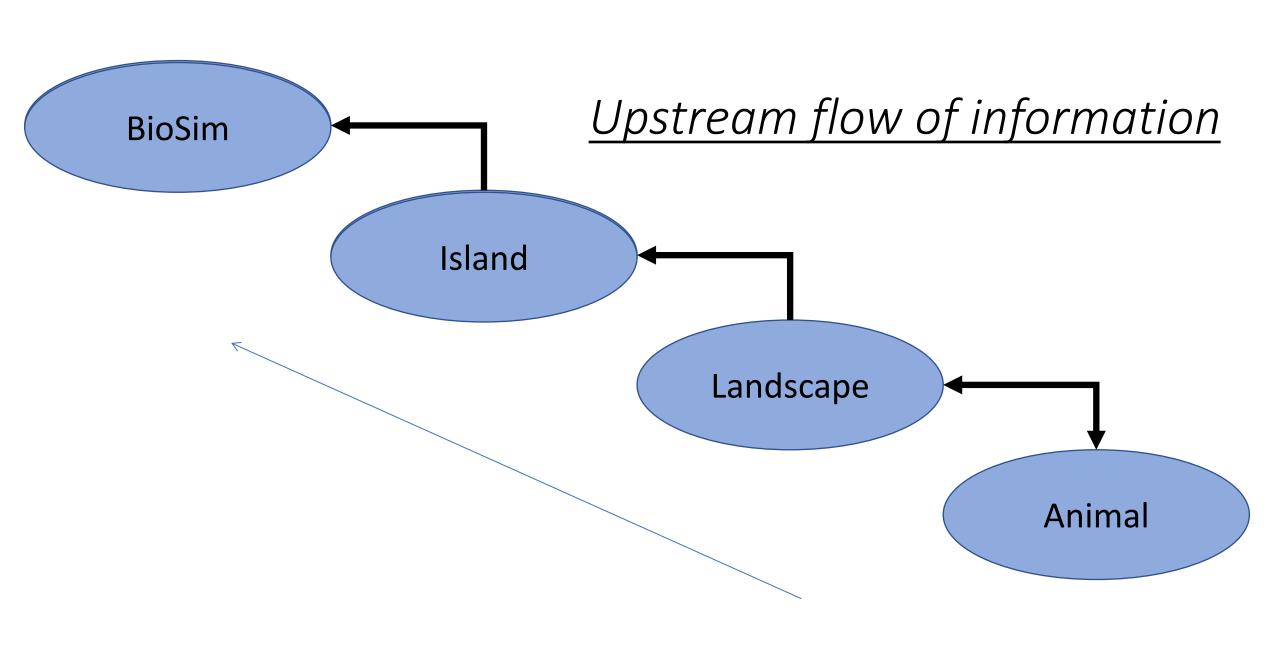
Population dynamics simulation

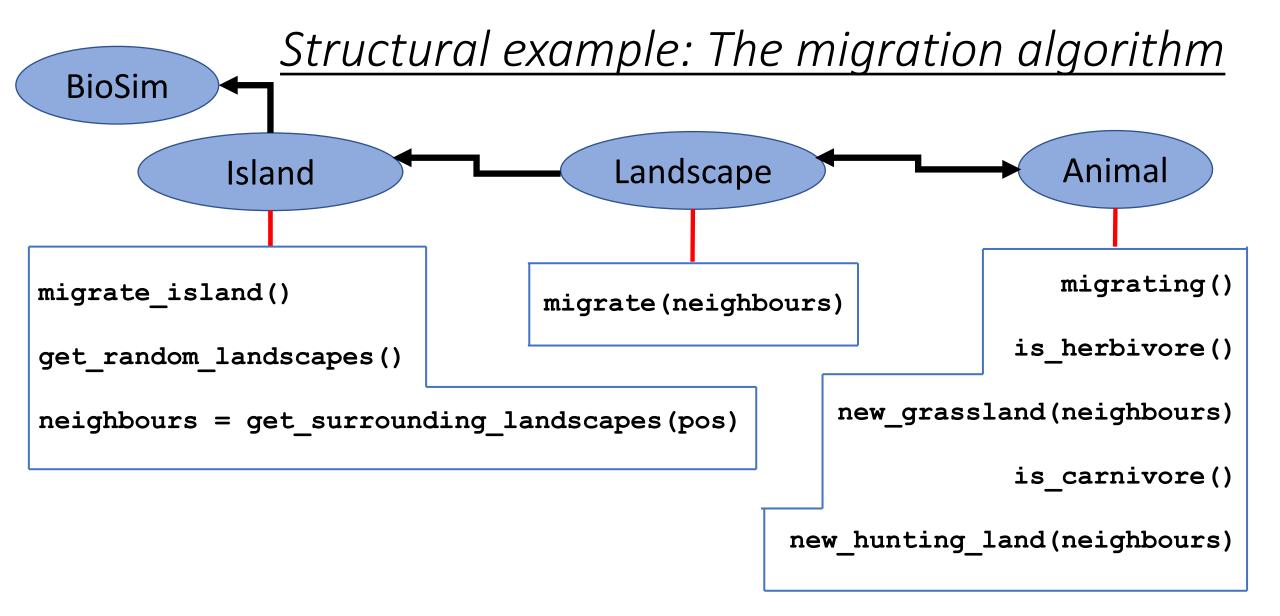
Modelling the Ecosystem of Rossumøya

Filip Rotnes & Sigve Sørensen

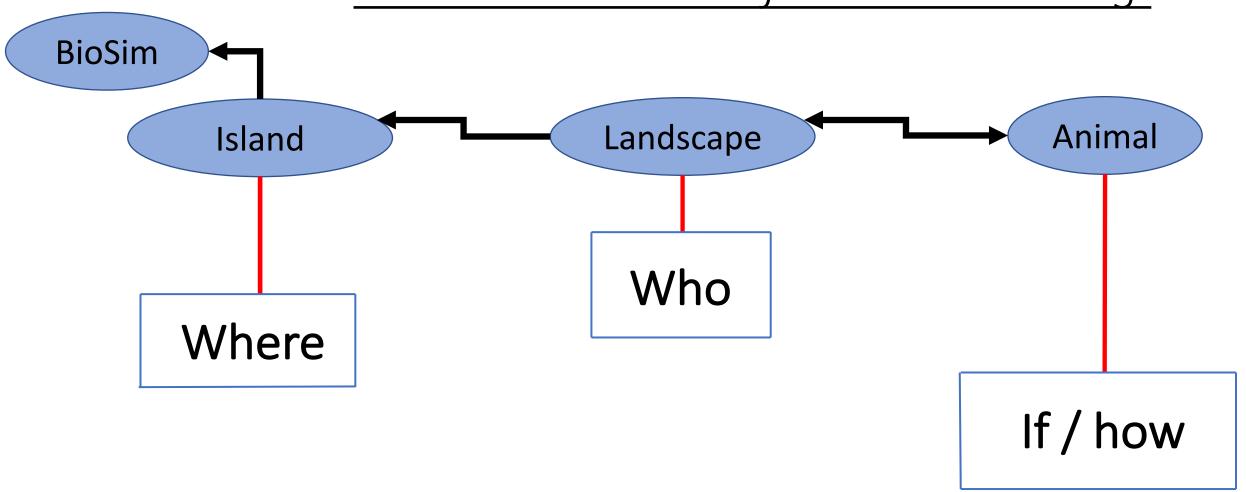


Norges miljø- og biovitenskapelige universitet





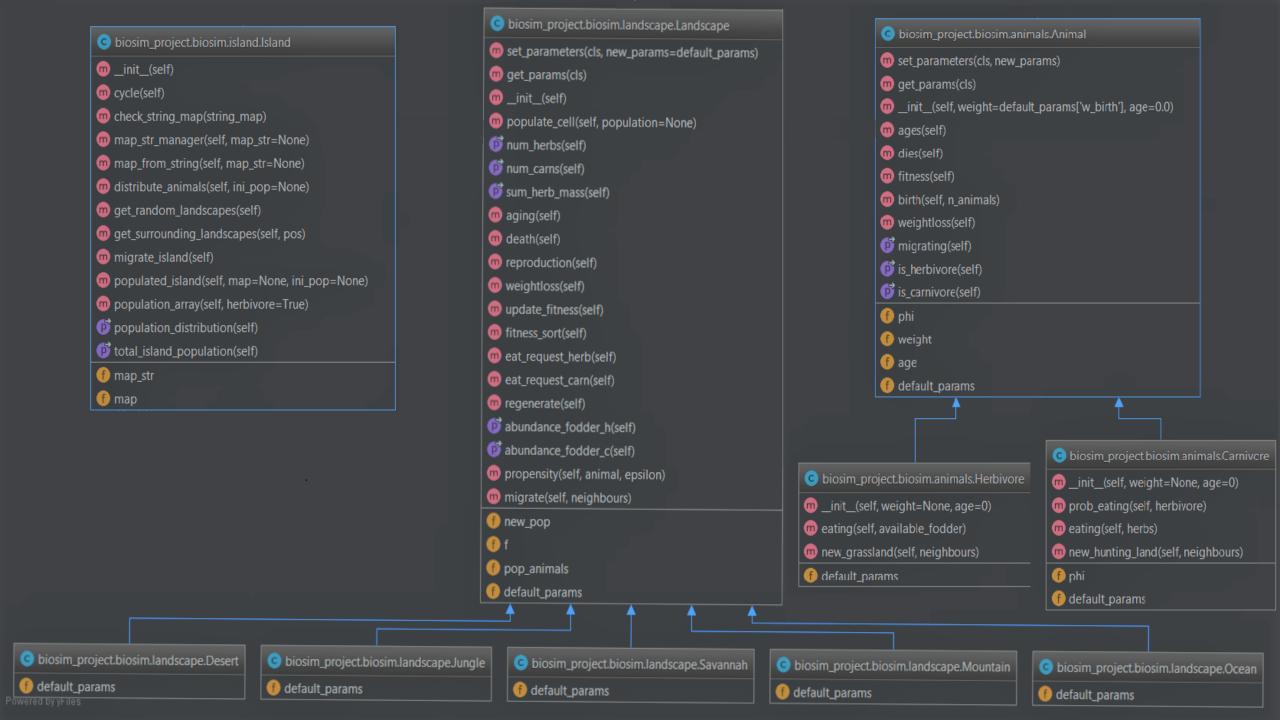
General structure of decision-making

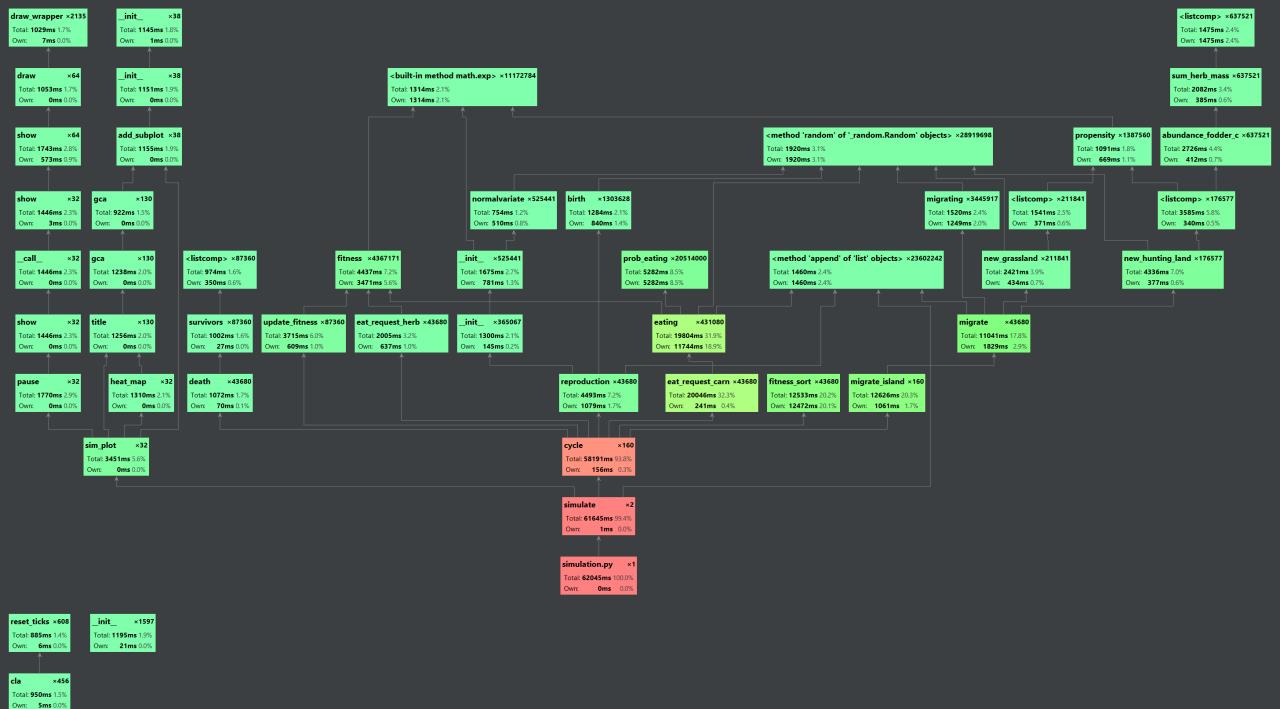


UML-diagrams

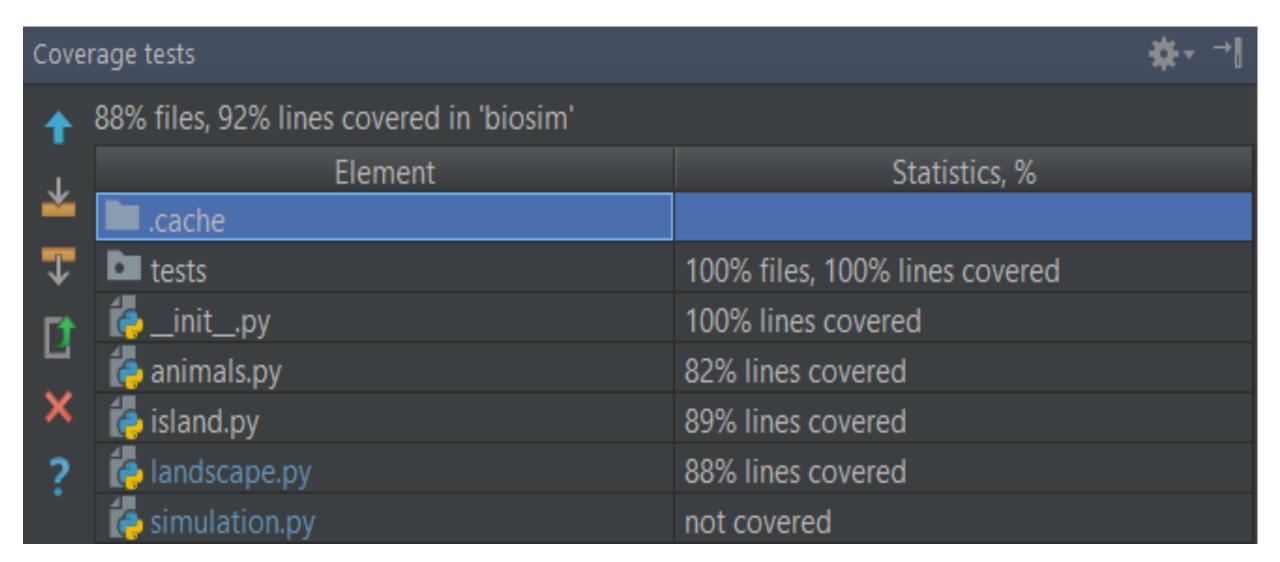
- c biosim_project.biosim.simulation.BioSim
- m __init__(self, island_map, ini_pop, seed)
- population_by_cell(self)
- population_by_species(self)
- years_passed(self)
- total_animals(self)
- m simulate(self, num_steps, vis_steps=1, img_steps=None)
- m add_population(self, population=None)
- m sim_plot(self)
- m heat_map(self)
- m plot_pop_density(self)
- m plot_map(self)
- f pop_by_cell
- f ini_pop
- f herb_list
- f carn_list
- 🕧 year
- 🅧 island
- new_sim
- f ax_herb
- f ax_carn
- f ax_map
- f ax_graph
- f version

Powered by yrile





Test coverage



The code:

- Tidy, categorical
- Expandable
- Focus on readability
- Task specific functions
- Benefits of the Numpy array

If we had better time:

- Package completeness
 - Examples -> Model potential
 - User friendliness -> UI
 - Terminal -> GUI
- Further statistical analysis
- Optimization
- Task specific functions
- Diversify output data