

Trajectory Simulations for Sympatric Speciation by Symmetry-breaking: The Three-Clade Case

Simulations performed February 2026

authors: Thomas Fuhrmann-Lieker, Gokul Nair, Werner Seiler, University of Kassel

This data set contains Python programs and Maple worksheets together with output files for numerical integration of the trajectories, and for bifurcation analysis of the following coupled nonlinear differential equations ($i = 1, \dots, N$):

$$\frac{dx_i}{dt} = -(o_1 x_i^2 + p_1 x_i + q_1 - \mu)(o_2 x_i^2 + p_2 x_i + q_2 - \mu)(x_i - r\mu) + \beta \sum_{j=1}^N x_j \quad (\beta \text{ coupling})$$

or

$$\frac{dx_i}{dt} = -(o_1 x_i^2 + p_1 x_i + q_1 - \mu)(o_2 x_i^2 + p_2 x_i + q_2 - \mu)(x_i - r\mu) + \gamma x_i \sum_{j=1}^N x_j \quad (\gamma \text{ coupling})$$

with $o_1 = o_2 = 1, p_1 = -1, q_1 = 0, p_2 = -2, q_2 = 3, r = 0$ as specific values.

Such systems of ordinary differential equations arise in models for biological speciation (M. Golubitsky & I. Stewart “The Symmetry Perspective”, Birkhäuser, Basel 2003). The specific systems without coupling allows for $-0.25 < \mu < 2.0$ two and for $\mu > 2.0$ three stable states. The simulations look for possible three-level states of the coupled system and the distributions of N entities („populations“) on x levels in these states. Results are contained for $N=3, 4, 5$.

There are three types of simulations:

a) Files within archive file *Attractor.tar*

Program source code file: *ThreeSpecies_Speciation3.3_attractor.py*

The program follows trajectories starting from all possible combinations of the uncoupled system which are given by the roots of the equations above without the coupling term. In order to avoid starting on metastable trajectories, a statistic fluctuation (uniform distribution with maximal amplitude of ± 0.0025) is included. By this algorithm, attracting stable states depending on μ and β or γ are found.

As first output, μ - β and μ - γ graphs are given as *.png files in which the occurrence of three-level-states is indicated as follows:

$$N=3: \bullet (1,1,1) \quad N=4: \begin{matrix} \bullet (2,1,1) \\ \bullet (1,2,1) \\ \bullet (1,1,2) \end{matrix} \quad N=5: \begin{matrix} \bullet (3,1,1) \\ \bullet (1,3,1) \\ \bullet (1,1,3) \end{matrix} \begin{matrix} \bullet (2,2,1) \\ \bullet (2,1,2) \\ \bullet (1,2,2) \end{matrix}$$

Given are the occupation of the levels x_i in ascending order. E.g. (2,1,2) means that of $N=5$ populations two population share the same lowest x value, one has a medium value and two the highest value.

As second output, the endpoints of underlying trajectories are recorded in *.txt files.

Simulation parameters are given in the header lines. The six data columns, separated with TAB, are for each set of runs as follows: μ, β, γ , number of detected states in a set of runs with different initial conditions, x values of these states, occupations of these states as explained above.

File naming: *3splitmap_N4_beta_attractor_daks* means $N=4$, beta coupling, simulated with *ThreeSpecies_Speciation3.3_attractor.py*, quality-checked for DaKS. Files were renamed manually after the simulation.

b) Files within archive file *Jump.tar*

Program source code file: *ThreeSpecies_Speciation5.1_jump.py*

In this program variant, as initial conditions only fluctuations around the origin are considered, with the same statistical distribution as above.

Outputs and file names follow the same rules as in the archive *Attractor.tar*.

Remark: Due to technical reasons, in some output files the format specifier *np.float64* is attached to numerical values. This specifier was deleted in the quality check.

c) Files within archive file **Ramp.tar**

Program source code file: *ThreeSpecies_Speciation4.2_ramp.py*

In this program variant, μ is ramped from zero to a certain end value (10). For every single trajectory (1000 for a specific value of the coupling parameter), the state is monitored for the specified μ values. The time for reaching the final μ value and thus the ramping rate is varied.

First output: *.png file as before (for $N=3$, points are black here)

Second output: *.txt file including four header lines with parameter values

For each trajectory, three columns are given: current μ value, x values of state, occupation (distribution). β and γ values are repeated for each run.

File naming: *3splitmap_N4_beta_ramp100_daks* means $N=4$, beta coupling, simulated with *ThreeSpecies_Speciation4.2_ramp.py*, end time 100 time units, quality-checked for DaKS.

d) Files within archive file **Trajectory.tar**

Program source code file: *ThreeSpecies_Speciation2.1_trajectory.py*

This program displays the bifurcation program of the uncoupled system as well as single time plots, either with a ramp or a jump. In the latter, set $\mu_{end}=\mu_{start}$.

e) Files within archive file **BasinAttraction.tar**

Jupyter notebooks: *boa_mollweide_projn v1.1.ipynb*, *traj from origin v1.1.ipynb*

The Python code in the first notebook computes trajectories for initial points chosen as the Fibonacci points on a small sphere ($N=3$) and determines in which steady state they terminate. This is recorded by a colour code and the points are then plotted using the Mollweide projection to preserve areas. In the second notebook, the trajectories are plotted for some random initial points. There are no separate output files; the output is stored in the notebooks.

f) Files within archive file **CouplingBifurcation.tar**

Maple worksheets: *BetaBifDiagramN3M3.mw*, *GammaBifDiagramN3M3.mw*

These worksheets determine bifurcation diagrams with the coupling parameters β (for first-order coupling) and γ (for second-order coupling) as bifurcation parameters for $N=3$. The value of the environmental parameter μ can be chosen by the user. For readers with no access to Maple, pdf files of the worksheets are included.

First output: *.png files with statistics about the number of steady states

Second output: *.txt files with the coordinates of all found bifurcation points

File naming: *BetaBifN3M3Mu15.png* and *BetaBifPointsN3M3Mu1.50.txt* means bifurcation parameter β , $N=M=3$, $\mu=1.5$.

g) Files within archive file **EnvironmentalBifurcation.tar**

Maple worksheets: *BifDia2DN3M3B1-Grid.mw*, *BifDia2DN3M3G1-Grid.mw*

These worksheets determine bifurcation diagrams with the environmental parameter μ as bifurcation parameter for $N=3$. The value of the coupling parameters β and γ can be chosen by the user. As output bifurcation diagrams are plotted with either the distance R from the origin or the coordinate sum σ as ordinate. For readers with no access to Maple, pdf files of the worksheets are included.

First output: *.png files bifurcation diagrams

Second output: *.txt files with the coordinates of all found bifurcation points

File naming: *BifDia2DN3M3B1-r.png* and *BifPointsN3M3B1.00.txt* means coupling parameter $\beta=1.0$, $N=M=3$, R used as ordinate.

h) Files within archive file SteadyStates.tar

Maple worksheet: *SteadyStatesSecondOrder.mw*

This worksheet determines all steady states up to a prescribed dimension N_{max} . The values of the environmental parameter μ and the coupling parameters β and γ can be chosen by the user. For readers with no access to Maple, a pdf file of the worksheet is included.

Output: *.txt files with coordinates of the steady state (one for each dimension) and one with statistics about the found steady states

Interpretation of the data set is done in the publication *Sympatric speciation by symmetry-breaking: The three-clade case* by G.-I. Chlomoudis, T. Fuhrmann-Lieker, M.A. Mebratie, G. Nair, W.M. Seiler (deposited at arXiv.org).

Disclaimer: The data files are created with the attached programs. However, parameters have to be entered by the user manually, and random number generators are involved. So there is no guarantee that other users will obtain exactly the same output. But of course that is the reason why the actual trajectory data behind the figures are stored in this repository.