

D-NOVL v1.3 USER MANUAL

D-NOVL is a Monte Carlo program designed to generate a null expectation of overlap between two niche-based distribution models.

INSTALLATION

1. Download and install LabVIEW Run-time Engine v.7.1, freely available:

For Windows:

<http://digital.ni.com/softlib.nsf/websearch/71b1d78c8dfba33786256e7d00724692>

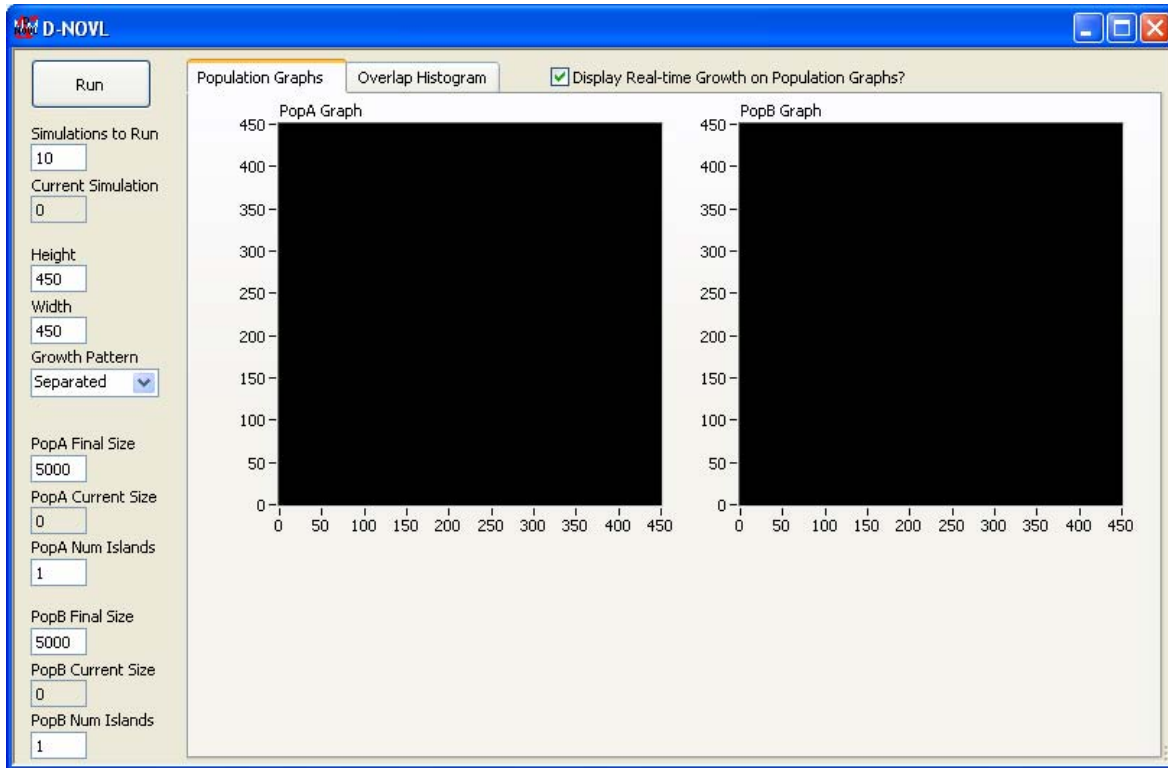
For Macs:

<http://digital.ni.com/softlib.nsf/websearch/B19A9B5C43C8BB2286256E86006C9606>

2. Download platform-specific D-NOVL software from <http://www.mygalomorphae.org/mygalwebsite/Pages/data.html>. This is a .zip file which contains both the executable and an .ini file. After extraction, these two files need to be located in the same directory.

IMPLEMENTATION

1. Open D-NOVL:

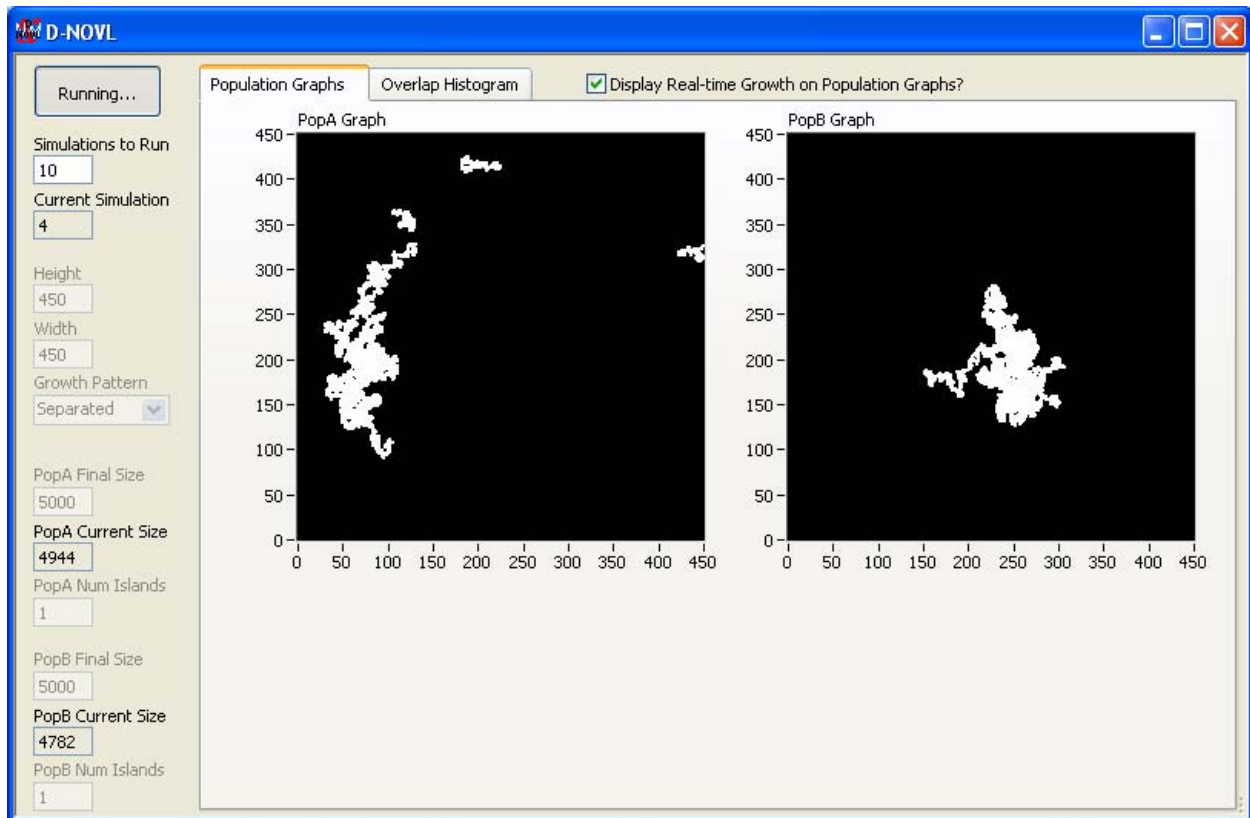


The GUI window may be resized.

The program opens displaying the POPULATION GRAPHS window and the following default settings:

SIMULATIONS TO RUN = 10
HEIGHT = 450
WEIGHT = 450
GROWTH PATTERN = Separated
POPA FINAL SIZE = 5000
POPB FINAL SIZE = 5000
DISPLAY REAL-TIME GROWTH ON POPULATION GRAPHS = checked

2. Click RUN. You will see the real-time growth simulation of the two populations:

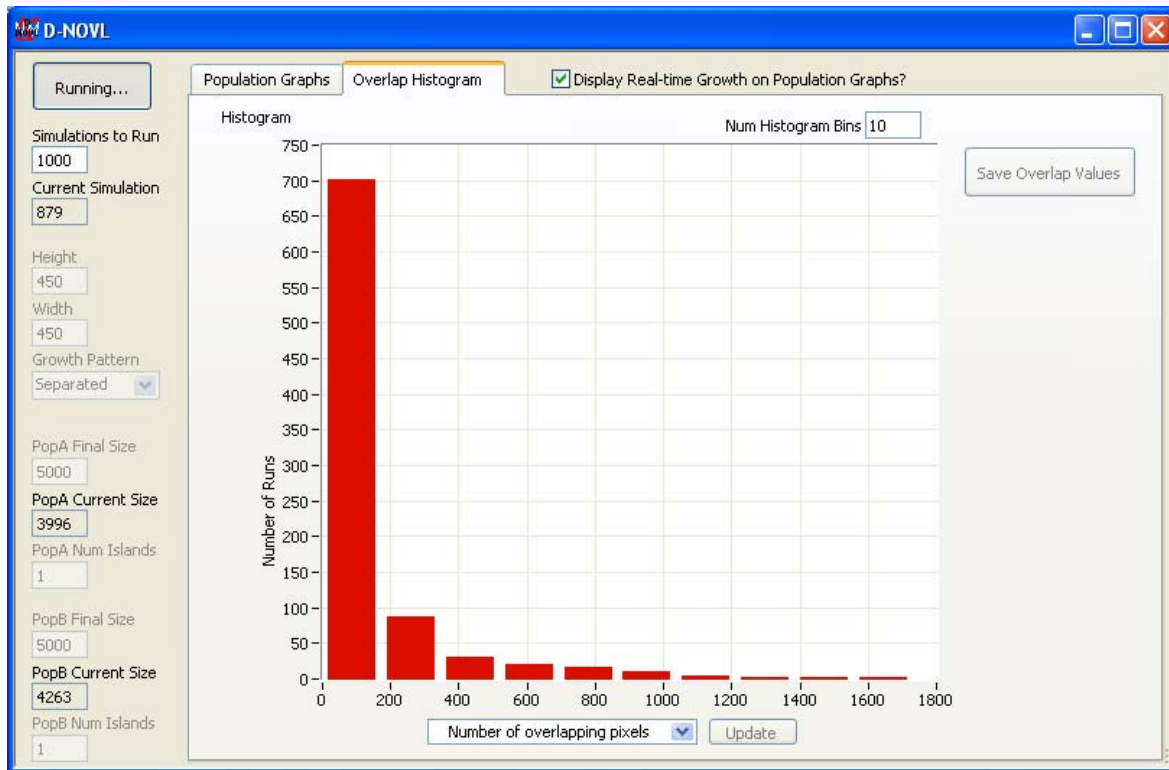


The number of the current simulation is displayed in the CURRENT SIMULATION box, and the current size of the populations are shown in the POPA CURRENT SIZE and POPB CURRENT SIZE boxes.

Note: The program runs slower when real-time growth is displayed. To decrease simulation time, either uncheck DISPLAY REAL-TIME GROWTH ON POP GRAPHS, click on the OVERLAP HISTOGRAM tab, or minimize the window.

To stop the program before all simulations are completed, click on RUNNING.

3. After the simulations are completed, select the OVERLAP HISTOGRAM tab.



The default display is NUMBER OF OVERLAPPING PIXELS. Select the drop-down menu for more choices:

- NUMBER OF OVERLAPPING PIXELS
- % OVERLAP
- % POP_A CONTAINED WITHIN POP_B
- % POP_B CONTAINED WITHIN POP_C

Select histogram display and click UPDATE.

The histograms can also be displayed while the program is running. If different output is selected, the histogram will change when the program updates during the next simulation.

NUM HISTOGRAM BINS defaults to 10. This may be changed by entered a desired number of histogram bins and clicking UPDATE.

4. Select SAVE OVERLAP VALUES to save the output as a text file. For easiest viewing and further statistical analyses, open the .txt file with spreadsheet or statistical software.

	A	B	C	D
1	Number of Simulations	1000		
2	Height	450		
3	Width	450		
4	POP1 Final Size	5000		
5	POP2 Final Size	5000		
6				
7	Num overlapping pixels	% Overlap	% PopA in PopB	% PopB in PopA
8	0	0	0	0
9	0	0	0	0
10	0	0	0	0
11	0	0	0	0
12	1159	13.1	23.2	23.2
13	0	0	0	0
14	9	0.1	0.2	0.2
15	56	0.6	1.1	1.1
16	0	0	0	0
17	209	2.1	4.2	4.2
18	242	2.5	4.8	4.8

SETTINGS

SIMULATIONS TO RUN

The number of simulations or iterations of the growth process. The default is 10; the program would grow two populations and calculate their overlap ten times. The results of each simulation or iteration will be displayed in the output .txt file.

Most user will probably want to greatly increase the number of simulations (e.g. 500 or 1000) for better null model probabilities.

HEIGHT and WIDTH

The growth area must be rectangular. Size of the growth area may be approximate to that used to create the original niche-based distribution models, and can be determined using a GIS.

GROWTH PATTERN

The user may choose between two growing algorithms: SEPARATED and NUM ISLANDS. SEPARATED will grow a random number of separate islands, or patches, for each populations. With NUM ISLANDS algorithm selected, the user can choose the desired number of islands for each population. This algorithm should be chosen and

POP A/B NUM ISLANDS set to 1 if the user wants a single contiguous patch for each population.

Further details of the algorithms can be found in Stockman AK, Danell RM, Bond JE (2007) D-NOVL: a program to simulate overlap between two niche-based distribution models. *Molecular Ecology Notes* **in review**.

POP A/B FINAL SIZE

The size of each original niche-based distribution model, in pixels, can be found using a GIS (e.g., ArcView). Note that this does require a threshold to be chosen so that each pixel will be marked as either predicted present or absent (or habitat suitable/unsuitable).

LITERATURE

Stockman AK, Danell RM, Bond JE (2007) D-NOVL: a program to simulate overlap between two niche-based distribution models. *Molecular Ecology Notes* **in press**.

Stockman AK, Bond JE (2007) Delimiting cohesion species: extreme population structuring and the role of ecological interchangeability. *Molecular Ecology* **in press**.