

## How to use the Netlogo polyploidization model

1. Install NetLogo: <http://ccl.northwestern.edu/netlogo/download.shtml>
2. Store the following files together in a folder:

- Polyploidization (Model)
- Script\_to\_process\_the\_results.R
- Bioclimatic variable V1, February solar radiation: V1\_Rad2.asc
- Bioclimatic variable V2, Isothermality: V2\_Bio3.asc
- Bioclimatic variable V3, Annual Precipitation: V3\_Bio12.asc
- Soil variable V4, Available soil water capacity: V4\_SWC.asc
- Soil variable V5, Soil organic carbon content: V5\_SOCC.asc

Alternatively, you can use other environmental variables.

All variables used in the model must have the same resolution between them. Although the resolution of the raster and the modeled world ( $100 \times 100$  patches) may differ, when this happens the variable values contained in the raster cells will be repeated or averaged to obtain the patch values. The variables must be in ASCII format and have the same height  $\times$  width ratio as the modeled world ( $1 \times 1 = \text{square}$ ). If the name of the variables is different from the current variables, you must go to the “code” tab in the model, and change the name in the “Setup\_characteristics” section to match the new variables names.

If you need a different world size, you must modify the necessary parameters from the model “configuration” section, however, it is not recommended to increase the world excessively, since the model will slow down and may stop depending on the processor used.

It should be noted that, due to the small scale with which the work was done, the variables used were “disaggregated” before being introduced into the model, in order to achieve greater variability in the modeled area.

3. Open the “Polyploidization” model.
4. Once opened, you will find the interface:
5. Modify the different variables according to your needs.
6. Press the “Setup\_characteristics” button to create the “world”. The file (.txt) where the modeling information will be collected is created at this point in the same folder as the model.
7. Press the “Setup” button to create the initial 30 plants.
8. Press the “go” button to run the model. By default, each run will last 1000 generations (or until the tetraploid cytotype is fixed), and will be repeated 1000 times.
9. Once the modeling is finished, the output file created must be processed in the R environment with the “Script\_to\_process\_the\_results.R”.

If you have any questions regarding the model, or need help making modifications to the code, please send an email to [schneider.s.juan@gmail.com](mailto:schneider.s.juan@gmail.com).