

In order to calculate the nestedness temperature of binary matrices with BINMATNEST (Rodríguez-Gironés & Santamaría 2006. “A new algorithm to calculate the nestedness temperature of presence-absence matrices.” *Journal of Biogeography* 33, 924-935), please follow these instructions:

1. Download the program to your computer.
2. Prepare your data according to the instructions provided below.
3. Double-click on the icon for BINMATNEST and provide the information requested. You will be asked to provide the names of the input and output files (the file where your matrix is stored and the file where the results will be saved), and a number of parameters. When giving the file names, remember to provide the full path if the input file and your copy of BINMATNEST are in different directories. The results are saved as plain text, so unless you have a good reason to do otherwise, the name for the output file should end with the “.txt” extension.
4. When you have entered all the required information, BINMATNEST will perform all the relevant calculations, save the results in a file with the name you have provided and exit without further ado. You can now open the output file with any text processor in order to see the temperature of your matrix, the probability of obtaining this temperature by chance (according to the null model of your choice) and the optimal packing of your matrix.

*Your data file:*

The data you want to analyse must be in a text file (extension txt: you can prepare it with any text processor).

Your input file may (but needs not) start with some text describing the nature of the data.

Whether or not you add an initial text, you **MUST** include the word “endnotes” just before your data. The input data starts on the following line.

The input data must be included as a series of zeroes and ones organised in rows and columns. All rows must have the same number of elements. Within one row, all

elements must be typed consecutively, without blanks, commas or any other characters separating them. Rows must be separated by line returns.

### *Examples of input files*

Example 1: this would be a properly formatted file.

NOTE: these data are anything but real

endnotes

100101

011010

110010

Example 2: this file is not properly formatted, because the word endnotes does not appear before the matrix:

NOTE: these data are anything but real. They were invented on 2006

100101

011010

110010

Example 3: this file is not properly formatted, because there is an empty line between endnotes and the matrix:

NOTE: these data are anything but real. They were invented on 2006

endnotes

100101

011010

110010

Example 4: this file is not properly formatted, because the matrix elements include numbers other than 0 or 1.

NOTE: these data are anything but real. They were invented on 2006

100501

012010

110010

Example 5: this file is not properly formatted, because some rows are longer than others.

NOTE: these data are anything but real. They were invented on 2006

```
1001
0110110
110010
```

Example 6: this file is not properly formatted, because the matrix elements are separated by commas.

NOTE: these data are anything but real.

```
1,0,0,1,0,1
0,1,1,0,1,0
1,1,0,0,1,0
```

#### *Parameter values:*

The parameters that you must provide are:

- a) The number of null matrices that you want to use to calculate p values.  
BINMATNEST will use three different null models to assess the probability that a random matrix has the same level of nestedness (equal or lower temperature) than your data. For each null model, a certain number of random matrices are chosen, their temperature is calculated, and the proportion of random matrices having the same or lower temperature than your matrix is returned as the p value. The estimated p value will be meaningless if the number of random matrices is much less than 50. The larger the number of matrices, the higher the accuracy of your estimated p value. (And the longer the program will take to run!)
- b) The “population size”: BINMATNEST uses a genetic algorithm (GA) to calculate the nestedness temperature of your matrix. The GA starts with a certain number of “individuals” (matrices obtained from the input data permuting rows and columns), selects low-temperature individuals and searches for more efficient permutations by creating random mutations. The “population size” is the number of “individuals” that BINMATNEST works with. It should be at least 15, and the results improve with larger population sizes. Computing time also increases, and we recommend that you work with a population size of 30.
- c) In each generation, a subset of individuals from your population are chosen at random. From within this subset, the individuals with lowest temperature are

selected to produce “mutant offspring”. You must choose the number of individuals entering this subset. It must be greater than 4, and smaller than the total population size. We recommend 7.

- d) Finally, you must select the number of “generations” through which the GA is iterated. We suggest that you use 2000.

The time that BINMATNEST requires to analyse your data will depend on the size of your data matrix, the speed of your computer and the settings that you have selected. BINMATNEST will store all the results in a single file, containing the following information: the row and column permutation of your data matrix that is closest to perfect nestedness (this permutation is obtained after removing empty rows and columns, and duplicated all-black rows and columns), the nestedness temperature of your matrix, and the probability that a “random” matrix has the same level of nestedness as your data. Three such probabilities are actually provided, corresponding to different null models. Null models 1 and 2 are given for completeness: to allow comparisons with previous work. Unless you have a very good reason to do otherwise, you should use null model 3. (See the main article for a full discussion of this point.)

Thank you very much for using BINMATNEST to analyse your data. Should you encounter any difficulty, please do not hesitate to contact us ([rgirones@eeza.csic.es](mailto:rgirones@eeza.csic.es)). We will do our best to help you.