BioVeL – Biodiversity Virtual e-Laboratory

Workflow Documentation

Generation Time (*T*) Workflow for local execution

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Generation Time (*T*) Workflow for local execution

1 Description

The Generation Time (*T*) Workflow provides an environment to calculate the generation time. The generation time is the time *T* required for the population to increase by a factor of *Ro* (net reproductive rate). In other words, *T* calculates how much time takes to a plant/animal to replace itself by a factor of *Ro.*

2 General

2.1 Name of the workflow in myExperiment.

Name: Generation Time (*T*) Workflow for local execution

Download: The pack can be downloaded at myExperiment under the following address: http://www.myexperiment.org/packs/637.html or the workflow: www.myexperiment.org/workflows/3289.html

2.2 Date, version and licensing

Last updated: 24th July 2012

Version: 2

Licensing: CC-BY-SA

2.3 How to cite this workflow

To report work that has made use of this workflow, please add the following credit acknowledgement to your research publication:

The input data and results reported in this publication (tutorial) come from data (Dr. Gerard Oostermeijer unpublished results and publication: Oostermeijer, J.G.B. M.L. Brugman, E.R. de Boer; H.C.M. Den Nijs. 1996. Temporal and Spatial Variation in the Demography of *Gentiana pneumonanthe*, a Rare Perennial Herb. *The Journal of Ecology*, 84: 153-166.) using BioVeL workflows and services (www.biovel.eu). the Generation time (*T*) workflow was run on *<date of the workflow run>*. BioVeL is funded by the EU's Seventh Framework Program, grant no. 283359.

3. Scientific specifications

3.1 Keywords

Matrix Population Models, stage matrix with not density dependence, BioVeL, demography, Generation time (*T*), *Gentiana pneumonanthe*, matrix, package 'popbio' in r, population

3.2 Scientific workflow description

The aim of the Generation time (*T*) Workflow is to provide a connected environment for the analysis of the Generation time (*T*). The workflow accepts input data (matrix) in a .txt format. The output is provided as an R result.
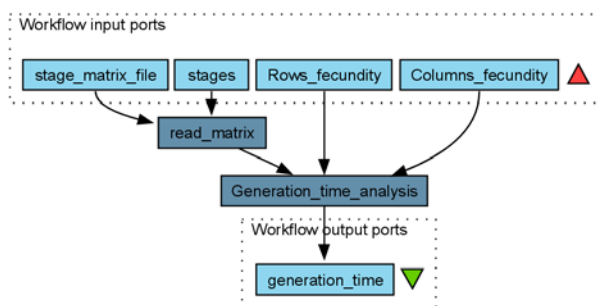

Figure 1. Generation Time (*T*) workflow in Taverna workbench.

For more detailed description of the functions, please visit the Tutorial section.

4 Technical specifications

4.1 Execution environment and installation requirements

The Workflow requires a Taverna Engine. The simplest way to install a Taverna Engine is to install Taverna Workbench. The workflow also requires an Rserve installation with popbio package installed. It is possible to setup the workflow to use a remote Rserve. However, instructions for installing a local Rserve are provided below.

4.2 Taverna installation, including updates and plugins

4.2.1 Taverna installations

- Taverna Workbench: Version 2.4 or 2.5. For installation files and instructions, please go to http://www.taverna.org.uk/download/workbench

4.2.2 Taverna Dependencies

- Install R software in your computer. See: http://www.r-project.org/
- Start R, and install package Rserve:
    - o install.packages("Rserve")
- Install package popbio
    - o install.packages("popbio")
- Local R Server: (Rserve) running at port 6311. See https://wiki.biovel.eu/x/3ICD for additional information.

4.2.3 How it works

- First, open R;, once R is opened, type library(Rserve) and press enter; then type Rserve() and press enter again. You will see then the following message: Starting Rserve...

    "C:\PROGRA~1\R\R-30~1.1\library\Rserve\libs\x64\Rserve.exe"

After this operation you can open Taverna and run the workflow.

5 Tutorial

5.1 Introduction

In this tutorial, you will use an input file MTers87_88.txt, called in myexperiment.org: Stage Matrix of Gentiana pneumonanthe 1987-88. This file will be used to perform the Generation time (*T*) analyses on it. Finally you will be able to export your results to different formats.

5.2 Input data.

5.2.1 Data preparation/format

The workflow accepts input data (matrices) in a .txt format, all decimal numbers in the matrix must be indicated by dots e.g.: 0.578. The example matrix for the tutorial is available in: http://www.myexperiment.org/packs/637.html or here below.

5.2.2 Input data

The input files are in a .txt format: to download click here in each file:
   Terschelling
   - MTers87_88.txt

Example from:
J. Gerard B. Oostermeijer; M.L. Brugman; E.R. de Boer; H.C.M. Den Nijs. 1996. Temporal and Spatial Variation in the Demography of *Gentiana pneumonanthe*, a Rare Perennial Herb. *Journal of Ecology*, Vol. 84(2): 153-166.

Please note that the workflow as well as the tutorial is a beta version, and may contain errors. We hope you will still find it interesting to work with this workflow, and look forward to your feedback.

5.3 Select input data dialogue boxes.

The first step is to fill out the input ports:

5.3.1 INPUTPORTS

1) ***columns_fecundity*:** the column(s) in which the fecundity values are found, should be selected.

In the example of the *Gentiana* species (Oostermeijer et al. 1996. *Journal of Ecology*): The selected column is G

	S	J	V	G	D
S	0	0	0	7,666	0
J	0,0579	0,01	0	8,5238	0
V	0,4637	0,83	0,9009	0,2857	0,8604
G	0	0,04	0,009	0,619	0,1162
D	0	0,03	0,018	0	0,0232

(reproductive individuals), the number 4 will be used to identify the fecundity column (G) (see matrix next to text).

The numbers of the reproductive columns must be added one by one (in the case that there is more than one reproductive column. In this example there is only one). First press add value, fill the number of the column and press enter, then press add value and fill once again the next reproductive column, repeat the action until you have fill all the numbers of all reproductive columns (Fig 2).
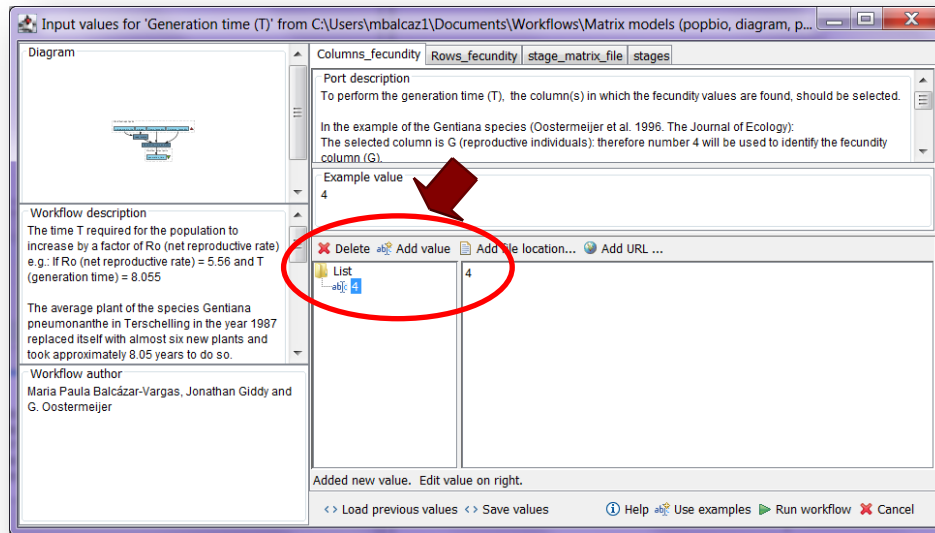
e.g.: 4

Figure 2. The number(s) of the column(s) to be filled in.

2) ***rows_fecundity:*** the row(s) in which the recruitment values are found, should be selected.

In the example of the *Gentiana* species (Oostermeijer et al. 1996. *Journal of Ecology*): Selected rows are S and J (seedlings and juveniles; these stages receive recruits each year from the stage G): therefore, the numbers 1 and 2 are used to identify these rows (see matrix next to the text).

	S	J	V	G	D
S	0	0	0	7,666	0
J	0,0579	0,01	0	8,5238	0
V	0,4637	0,83	0,9009	0,2857	0,8604
G	0	0,04	0,009	0,619	0,1162
D	0	0,03	0,018	0	0,0232

The numbers of the stages that receive recruits each year from the stage G must be added one by one (in the case that there are more than one recruit stage row). First press add value, fill the number of the row and press enter, then press add value and fill once again the next recruit stage row, repeat the action until you have fill all the numbers of all recruits rows (Fig. 3).
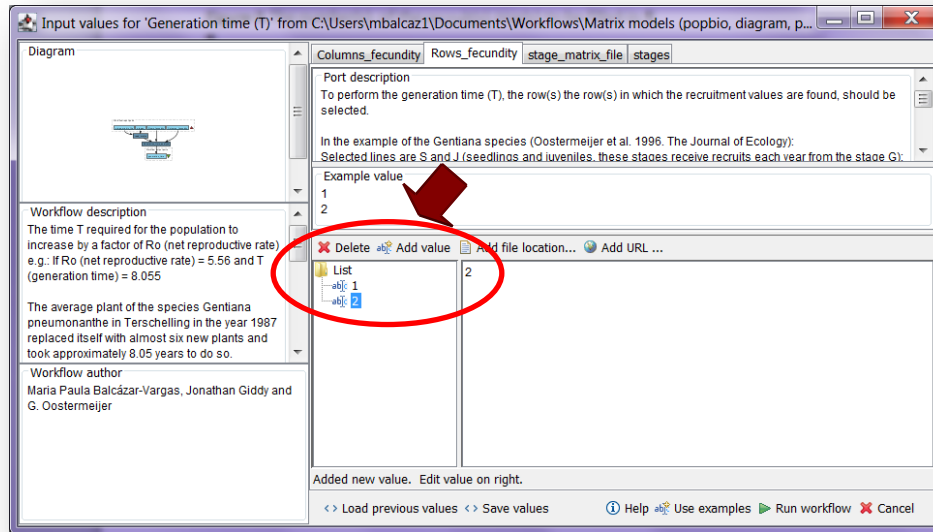
e.g.: 1 and 2

Figure 3. The number(s) of the recruit(s) row(s) to be filled in.

3) ***stage_matrix_file:*** Matrix in a .txt file format. Click in Set file location (red arrow in Fig 4), a window dialog appears and the user selects the file (e.g. MTers87_88.txt, Fig 5) and then clicks the Open button. Then the link to the file will appear on the Taverna window.
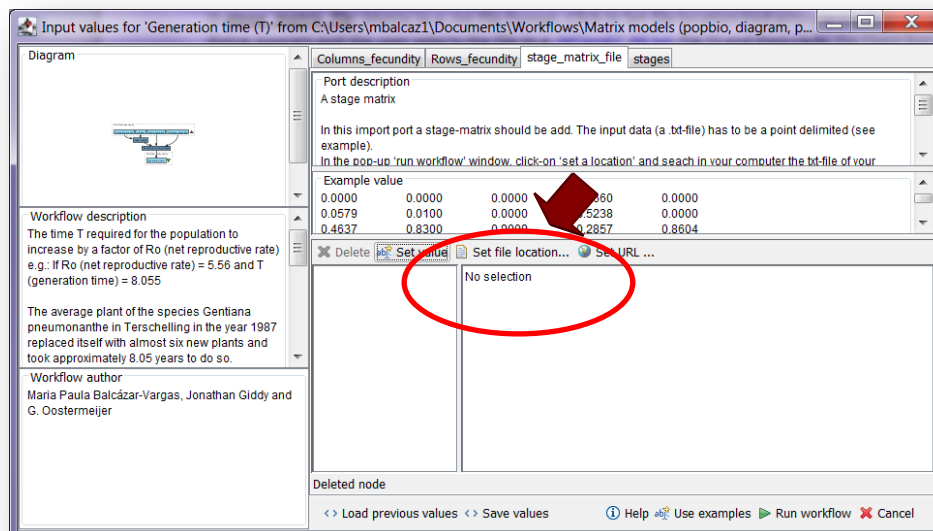

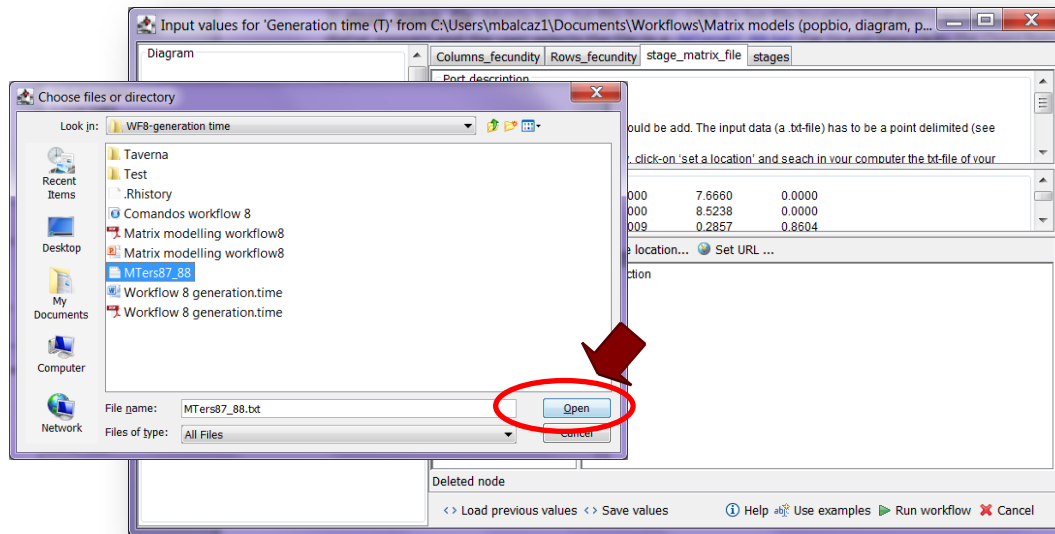**Figure 4.** Set the Location of the matrix file.

Figure 5. Choose the matrix file and click in Open.

4) ***stages***: the names of the stages or categories of the input matrix. In the following example, the matrix has 5 stages or categories.

e.g. the stages of this matrix are called:

1) Seedlings	S
2) Juveniles	J
3) Vegetative	V
4) Reproductive individuals	G
5) Dormant plants	D

The name of stages or categories must be added one by one. First press add value, fill the name of the stage no longer than 8 characters and press enter; then press add value and fill once again the next name of the stage; repeat the action until you have fill all the names of all stages (Fig 6).
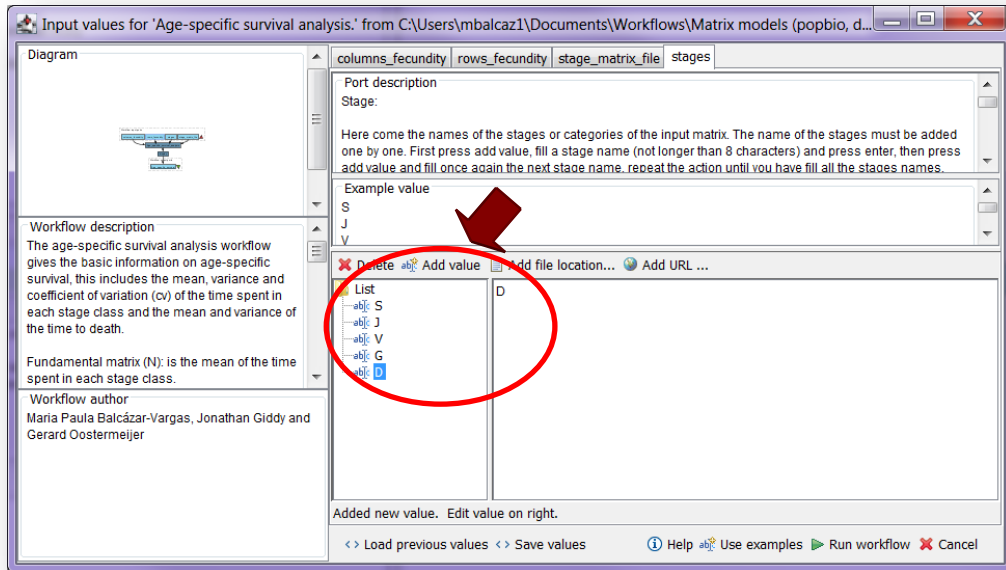
Figure 6. The name of the stages to be filled in.

After the user has filled out the input ports and has clicked the ***Run Workflow button***, the workflow performs the analysis. To complete all the analysis may take few seconds.

When the analyses are completed, they appear on a different window under results in Taverna, the user have to save each output separately.

5.4 Save data/results

5.4.1 OUTPUTS

First, click in the selected result window e.g. **generation_time** (Fig 7). Second, click in the left window on value 1 (red oval), Third, on the right window click on the save value (blue oval). Fourth, name the file and determinate the extension file. For a text file: e.g. .csv or .txt. For images: .jpg or png (Fig 8), Finale, save the file in the chosen map.
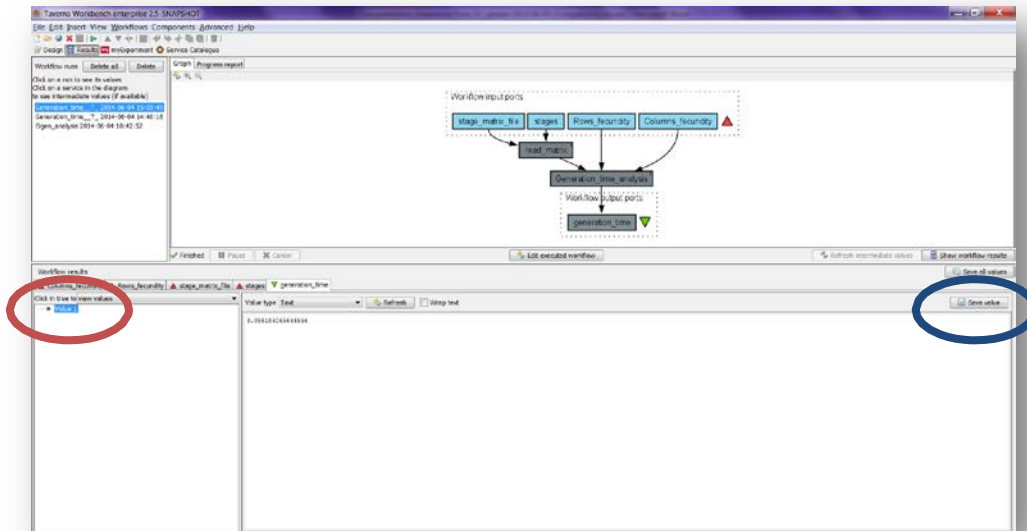
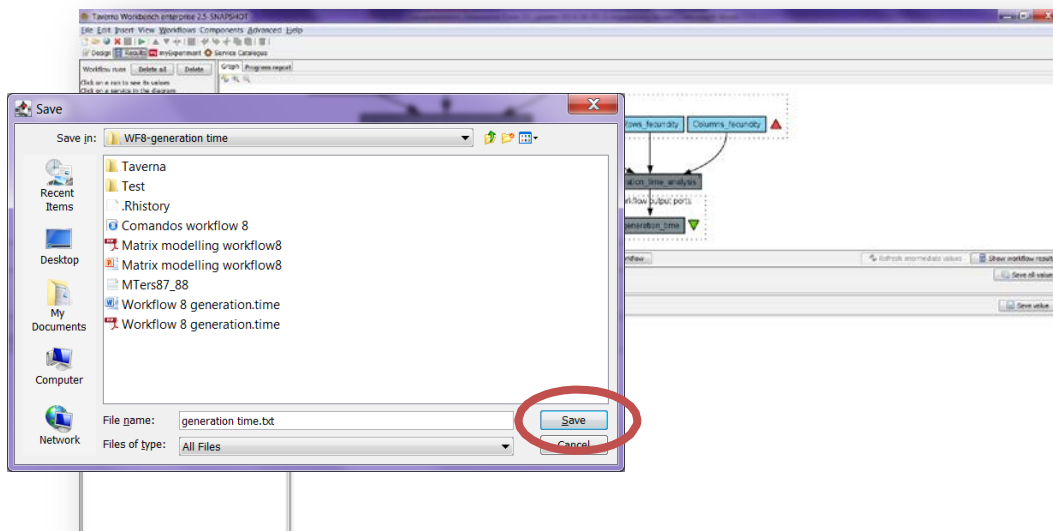

Figure 7. Generation time output window.

Figure 8. Name the file and determinate the extension file. For a text file: e.g. .csv or .txt.

Generation time (T)

Generation time: Generation time is the time *T* required for the population to increase by a factor of *Ro* (net reproductive rate).

[1] 8.055186

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6 Support

For questions with using the workflow, please write *support @biovel.eu*

For definitions of technical and biological terms, please visit the BioVeL glossary page:
https://wiki.biovel.eu/display/BioVeL/Glossary

7 References

This workflow was created using and based on Packages 'popbio' in R. (Stubben & Milligan 2007; Stubben, Milligan & Nantel 2011).

Caswell, H. 2001. Matrix population models: Construction, analysis and interpretation, 2nd Edition. Sinauer Associates, Sunderland, Massachusetts.

Jongejans E. & H. de Kroon. 2012. Matrix models. Chapter in Encyclopaedia of Theoretical Ecology (eds. Hastings A & Gross L) University of California, p415-423

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Stubben, C & B. Milligan. 2007. Estimating and Analysing Demographic Models Using the popbio Package in R. Journal of Statistical Software 22 (11): 1-23

Stubben, C., B. Milligan, P. Nantel. 2011. Package 'popbio'. Construction and analysis of matrix population models. Version 2.3.1

7.1 Acknowledgements

7.1.1 Authors

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7.2 Publications