BioVeL – Biodiversity Virtual e-Laboratory

Workflow Documentation

Transient dynamics Workflow for local execution

July 2014

Capacities Programme of Framework 7: EC e-Infrastructure Programme –
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Project Co-ordinator:	Mr Alex Hardisty
Project Homepage:	http://www.biovel.eu
Duration of Project:	36 months

SEVENTH FRAMEWORK PROGRAMME

e-infrastructure

Transient dynamics Workflow for local execution

1 Description

The Transient dynamics or Calculate population growth rates by projection Workflow provides an environment to calculates the population growth rate and stable stage distribution by repeated projections of the equation n(t+1)=An(t) and to produce plots of the short-term dynamics and convergence to stable stage distribution using stage vector projections.

Transient dynamic analysis

1) ***Population projection***

- Lambda or dominant eigenvalue
- The stable stage distribution (stable.stage)
- Stage vector (stage.vectors)
- Population sizes (pop.sizes)
- Population change (pop.changes)

2) ***Damping Ratio***

2 General

2.1 Name of the workflow in myExperiment.

Name: Transient dynamics Workflow for local execution

Download: The pack can be downloaded at myExperiment under the following address: http://www.myexperiment.org/packs/636.html or the workflow: http://www.myexperiment.org/workflows/3288.html

2.2 Date, version and licensing

Last updated: 25th 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 Gerard Oostermeijer unpublished results and publication: Oostermeijer, J.G.B. M.L. Brugman, E.R. de Boer; H.C.M. Den Nijs. 1996.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). Transient dynamics 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

BioVeL, damping ratio, demography, *Gentiana pneumonanthe*, lambda or dominant eigenvalue, matrix, matrix population models, package 'popbio' in r, population, population change, population projection, population sizes, projection, stable stage distribution (w), stage matrix, stage vectors, transient dynamics.

3.2 Scientific workflow description

The Transient dynamics Workflow provides an environment to produce plots of the short-term dynamics and convergence to stable stage distribution using stage vector projections. The workflow accepts input data in a .txt format. The outputs are provided as a set of R results and graphic plots.

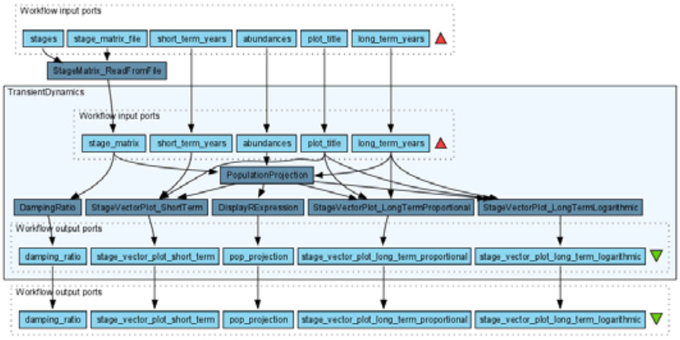


Figure 1. Transient dynamics workflow in Taverna workbench.

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:
    - install.packages(“Rserve”)
- Install package popbio
    - 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 Transient dynamics 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/636.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:

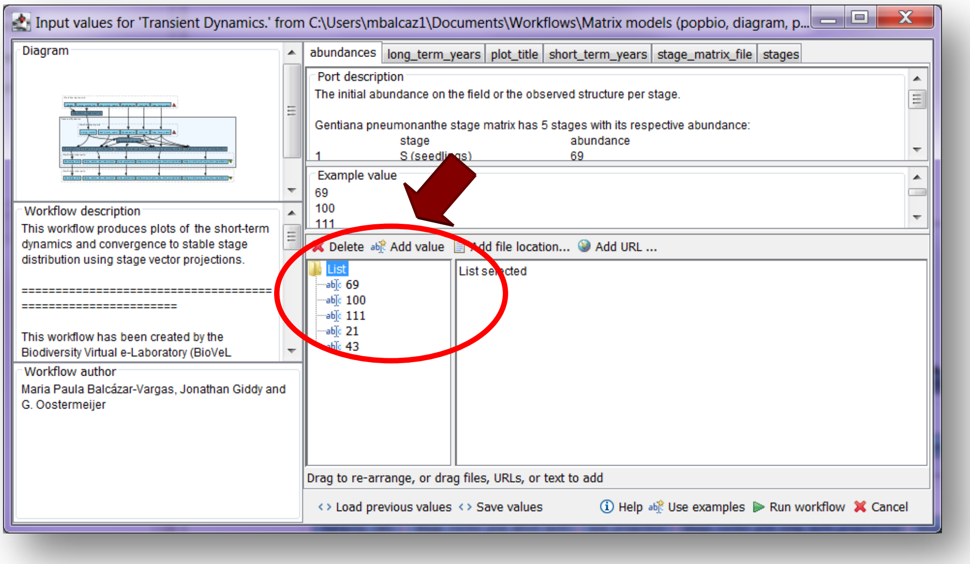
5.3.1 INPUTPORTS

1) ***abundances:*** In this dialogue must be filled the abundance per stage observed in the field (Fig 2). As an example *Gentiana pneumonanthe* has 5 stages with its respective abundance.

Stage abundances of the year 1987:

S (Seedlings)	69
J (Juveniles)	100
V (Vegetative)	111
G (Reproductive individuals)	21
D (Dormant plants)	43

The abundances must be added one by one. First press Add value, fill the number of the first stage (e.g. S) and press enter, then press Add value and fill once again the next recruit stage row (e.g. J), repeat the action until you have fill all the abundances of all stages (Fig. 2).



The initial abundance on the field or the observed structure per stage.

Gentiana pneumonanthe stage matrix has 5 stages with its respective abundance:

```
            stage                   abundance
1           S (seedlings)           69
```

69
100
111

List
- 69
- 100
- 111
- 21
- 43

Drag to re-arrange, or drag files, URLs, or text to add

This workflow produces plots of the short-term dynamics and convergence to stable stage distribution using stage vector projections.

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This workflow has been created by the Biodiversity Virtual e-Laboratory (BioVeL

Maria Paula Balcázar-Vargas, Jonathan Giddy and G. Oostermeijer

Figure 2. The abundance to be filled in.

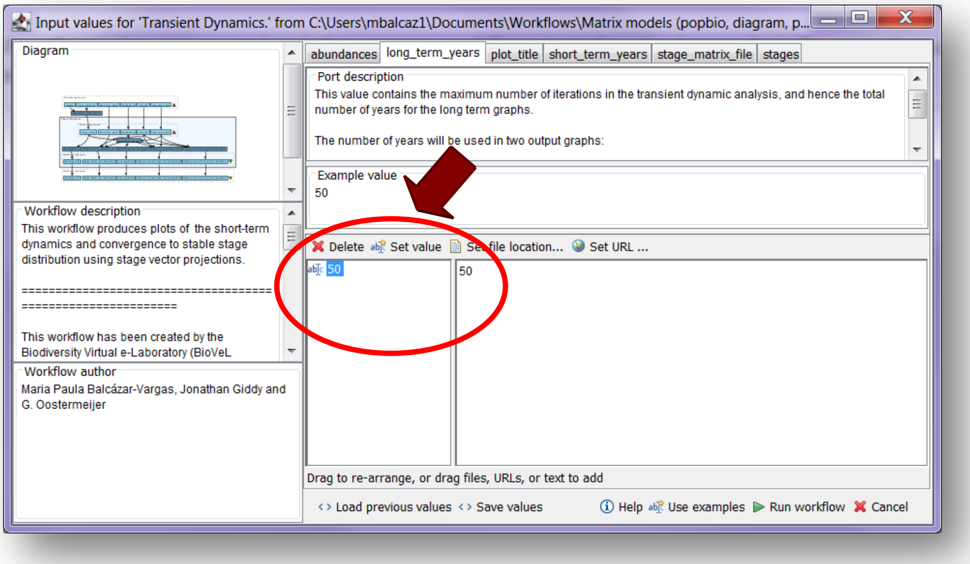
1) ***long term years*:** It is the maximal number of iteration or repetitions in the transient dynamic analysis, and hence the total number of years for the long term graphs.

The number of years will be used in two output graphs:

a. *StageVectorPlotLongTermProportional*: the proportion of individuals per stage in the long term.
b. *StageVectorPlotLongTermLogarithmic*: the number of individuals per stage in the long term.

e.g. 50

To fill the long term years, first press Add value, fill the number and press enter (Fig. 3).


Input values for 'Transient Dynamics.' from C:\Users\mbalcaz1\Documents\Workflows\Matrix models (popbio, diagram, p...

Port description
This value contains the maximum number of iterations in the transient dynamic analysis, and hence the total number of years for the long term graphs.

The number of years will be used in two output graphs:

Example value
50

50

50

Workflow description
This workflow produces plots of the short-term dynamics and convergence to stable stage distribution using stage vector projections.

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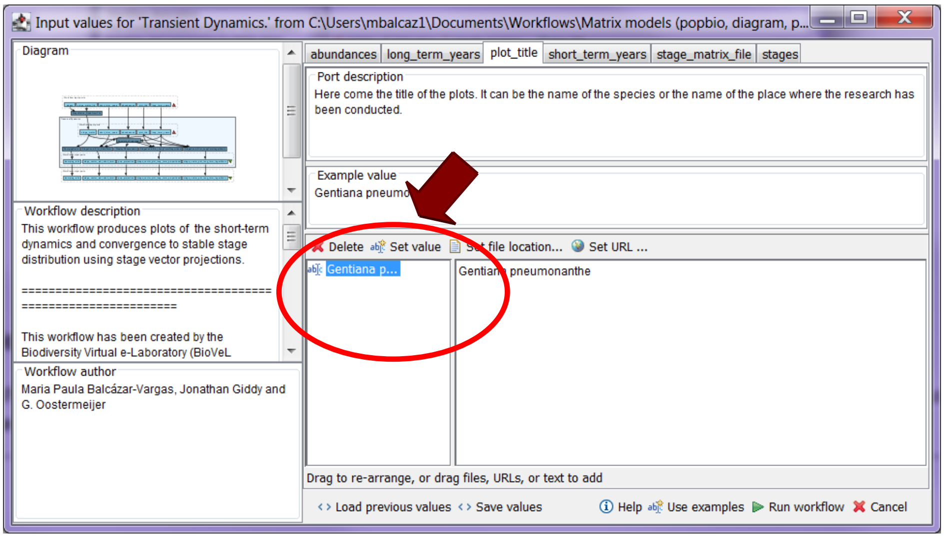
Figure 3. The long term years to be filled in.

3) ***plot_title*****:** the title of the plots. As an example, it can be the name of the species or the name of the place where the research has been conducted.

e.g. *Gentiana pneumonanthe*

To fill the plot title, first press Add value, fill the title and press enter (Fig. 4).


Input values for 'Transient Dynamics.' from C:\Users\mbalcaz1\Documents\Workflows\Matrix models (popbio, diagram, p...

Port description
Here come the title of the plots. It can be the name of the species or the name of the place where the research has been conducted.

Example value
Gentiana pneumo

Gentiana p...

Gentiana pneumonanthe

Workflow description
This workflow produces plots of the short-term dynamics and convergence to stable stage distribution using stage vector projections.

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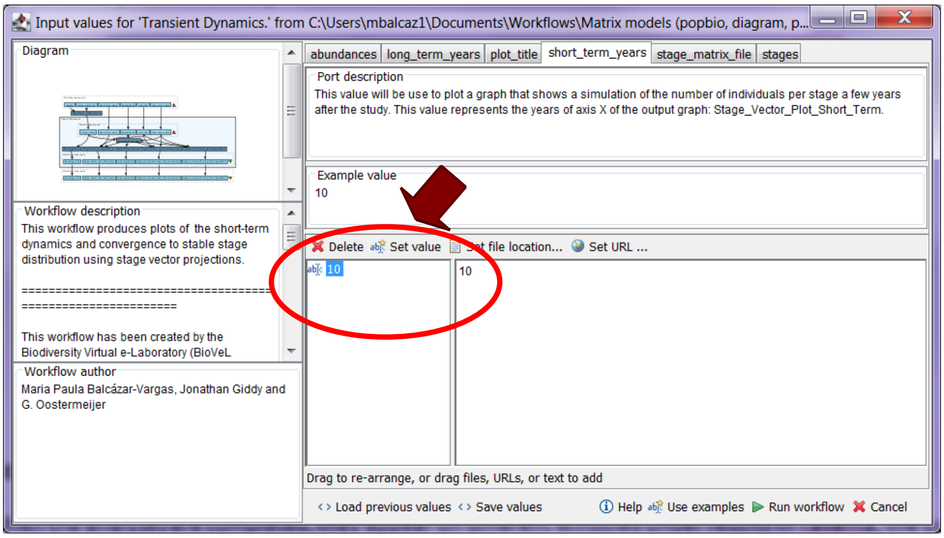
Figure 4. The title of the output graphs to be filled in.

5) ***short_term_years:*** This value will be used to plot a graph that shows a simulation of the number of individuals per stage in a few years after the study. This value represents the years of axis X of the output graph: *StageVectorPlotShortTerm* (see output port):

a. *StageVectorPlotShortTerm:* the number of individuals per stage vs years in the short-term e.g. 10.

To fill the short term years, first press Add value, fill the number and press enter (Fig. 5).



Input values for 'Transient Dynamics.' from C:\Users\mbalcaz1\Documents\Workflows\Matrix models (popbio, diagram, p...

Workflow description
This workflow produces plots of the short-term dynamics and convergence to stable stage distribution using stage vector projections.

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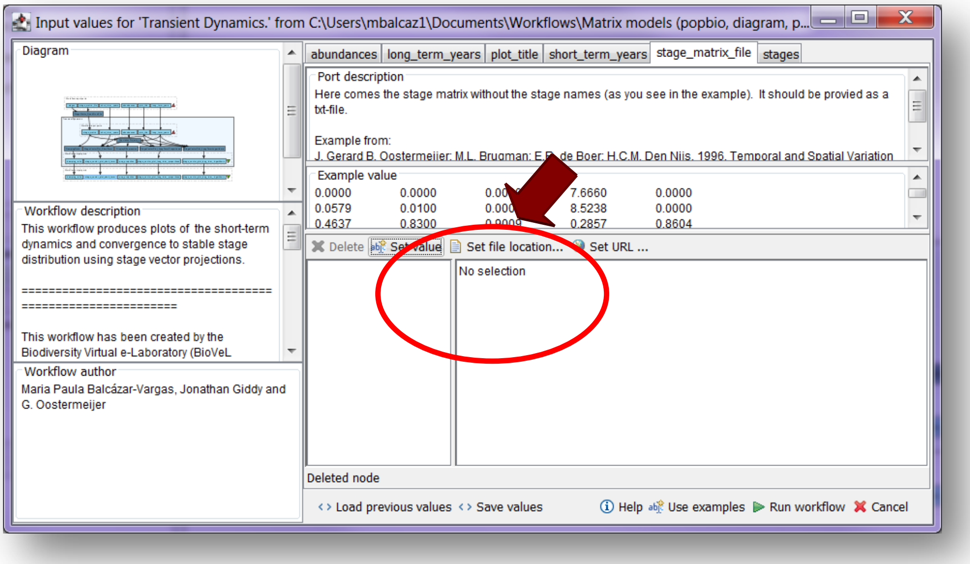
Port description
This value will be use to plot a graph that shows a simulation of the number of individuals per stage a few years after the study. This value represents the years of axis X of the output graph: Stage_Vector_Plot_Short_Term.

Example value
10

Drag to re-arrange, or drag files, URLs, or text to add

Figure 5. The short term years to be filled in.

3) ***stage_matrix_file:*** Matrix in a .txt file format. Click in Set file location (red arrow in Fig 6), a window dialog appears and the user selects the file (e.g. MTers87_88.txt, Fig 7) and then clicks the Open button. Then the link to the file will appear on the Taverna window.



Input values for 'Transient Dynamics.' from C:\Users\mbalcaz1\Documents\Workflows\Matrix models (popbio, diagram, p...

Workflow description
This workflow produces plots of the short-term dynamics and convergence to stable stage distribution using stage vector projections.

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Port description
Here comes the stage matrix without the stage names (as you see in the example). It should be provied as a txt-file.

Example from:
J. Gerard B. Oostermeijer; M.L. Brugman; E.R. de Boer; H.C.M. Den Nijs. 1996. Temporal and Spatial Variation

Example value
0.0000 0.0000 0.00 7.6660 0.0000
0.0579 0.0100 0.000 8.5238 0.0000
0.4637 0.8300 0.0009 0.2857 0.8604

No selection

Deleted node

Figure 6. Set the Location of the matrix file.

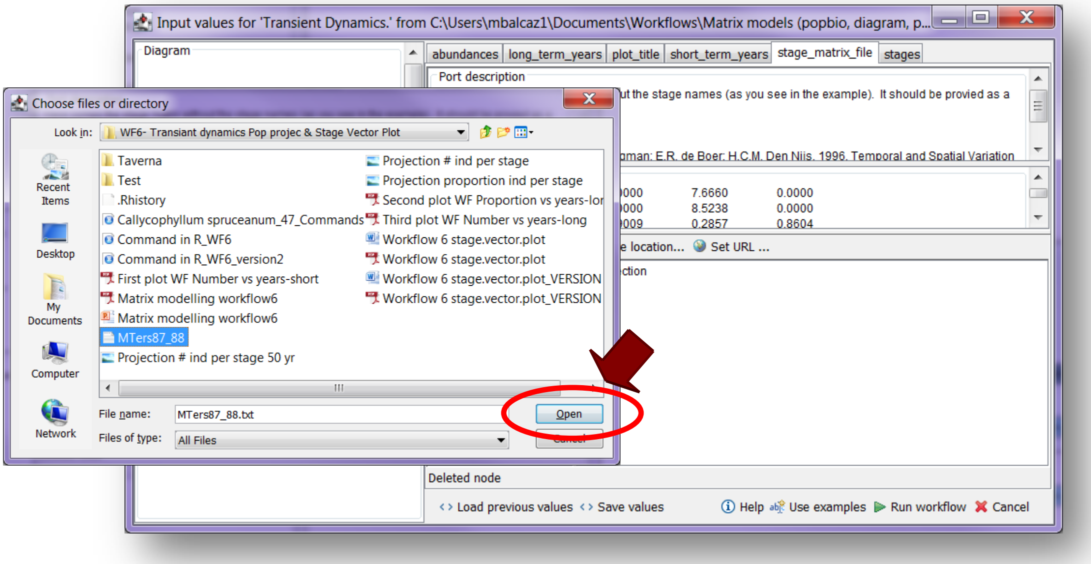


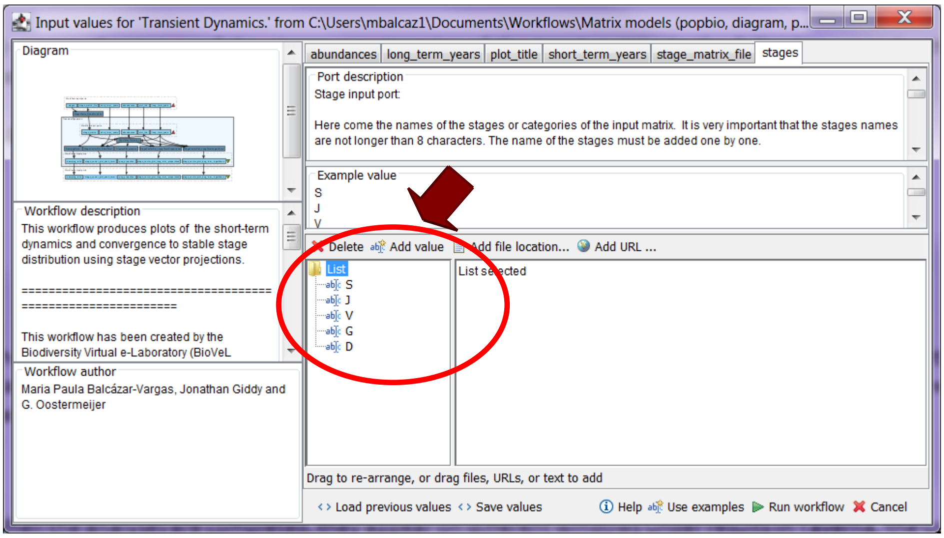
Figure 7. Choose the matrix file and click in Open.

6) ***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 8).



Input values for 'Transient Dynamics.' from C:\Users\mbalcaz1\Documents\Workflows\Matrix models (popbio, diagram, p...

Workflow description

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Port description

Stage input port:

Here come the names of the stages or categories of the input matrix. It is very important that the stages names are not longer than 8 characters. The name of the stages must be added one by one.

Example value

S
J
V

List
- S
- J
- V
- G
- D

List selected

Drag to re-arrange, or drag files, URLs, or text to add

Figure 8. 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. **damping_ratio** (Fig 9). Second, click in the left window on value 1 (red oval), Third, on the right window click on the save value (green 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 10), Finale, save the file in the chosen map.

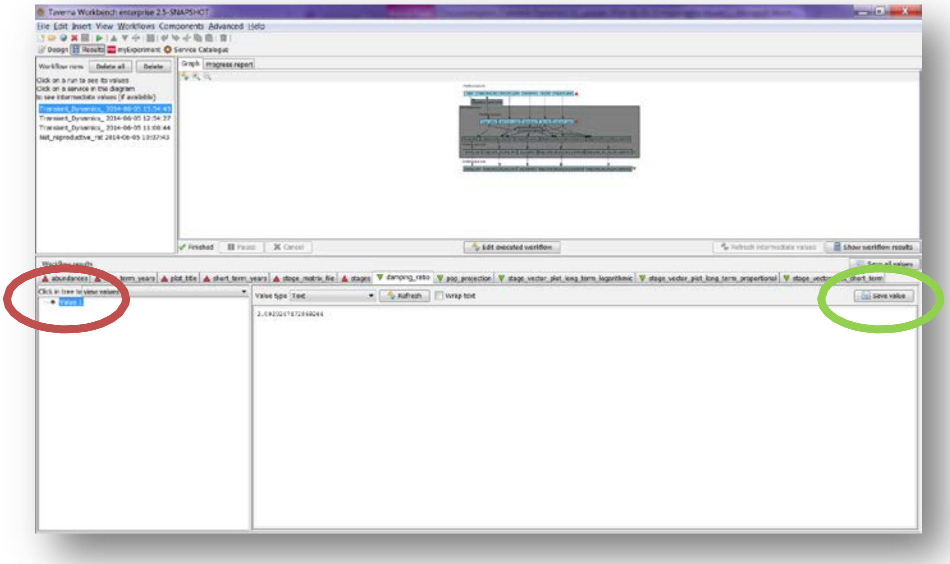
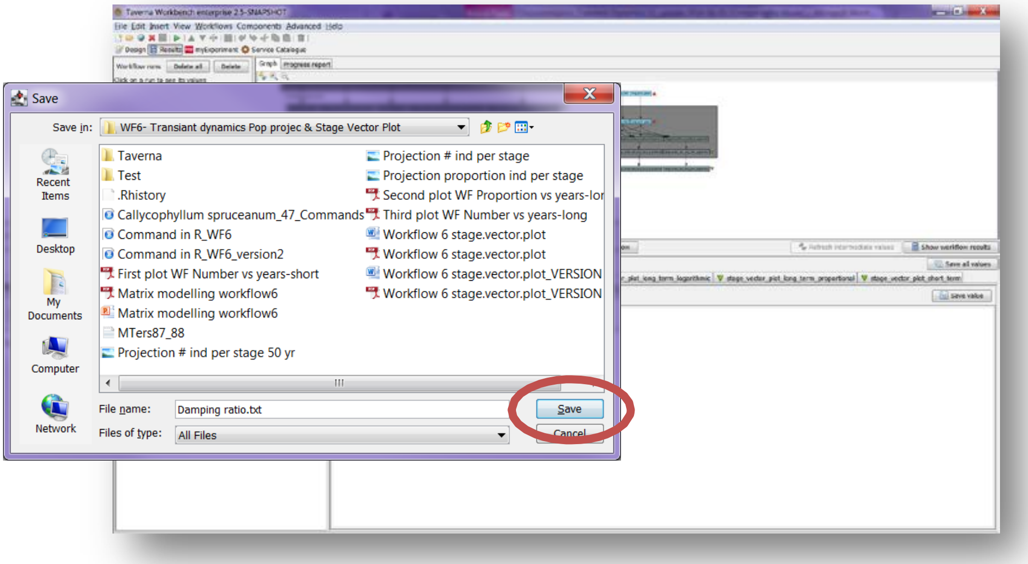


Figure 9. Damping_ratio output window.



Save in: WF6- Transiant dynamics Pop projec & Stage Vector Plot

File name: Damping ratio.txt

Files of type: All Files

Figure 10. Name the file and determinate the extention file. For a text file: e.g. .csv or .txt. For images: e.g.: .jpg or png.

Transient dynamic analysis

1) ***Population projection*** (Fig 11).

   a) ***Lambda or dominant eigenvalue***: The population will be stable, grow or decrease at a rate given by lambda: e.g.: $\lambda = 1$ (population is stable), $\lambda > 1$ (population is growing) and finally $\lambda < 1$ (population is decreasing). e.g. The projected population growth rate (λ) is 1.237, meaning that the population is projected to increase with 23% per year if these model parameters remain unchanged.

   b) ***The stable stage distribution*** (stable.stage): It is the proportion of the number of individuals per stage and it is given by (w).

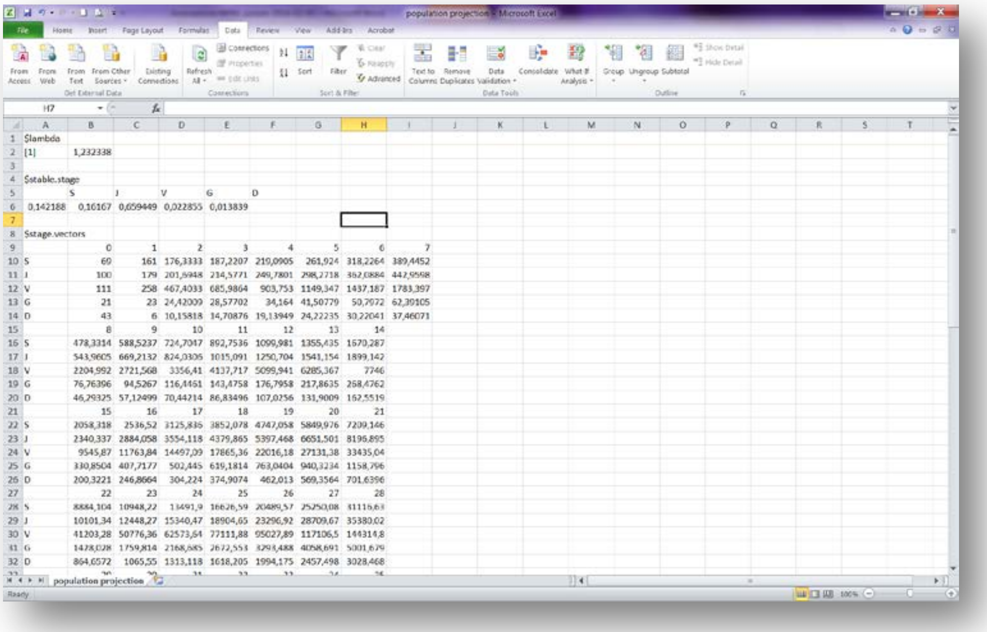
   c) ***Stage vector*** (stage.vectors): it is the projection of the number of individuals per category per year in the long term, the long term was stipulated in the input port (long term years) (e.g. 50 years).

   d) ***Population sizes*** (pop.sizes): it is the total population size per year in the long- term (e.g. 50 years).

   e) ***Population change*** (pop.changes): are the lambda values per year in the long-term
   (e.g. 50 years).

2) ***Damping Ratio:*** The ratio between the dominant eigenvalue and the second highest eigenvalue of a transition matrix is called the damping ratio, and it can be considered as a measure of the intrinsic resilience of the population, describing how quickly transient dynamics decay following disturbance or perturbation regardless of population structure, (the larger the damping ratio, the quicker the population converges). High damping ratios tell you that the dominant stable stage distribution is reached fairly soon.

e.g. damping ratio= 2.0901.



	A	B	C	D	E	F	G	H	I
1	$lambda								
2	[1]	1,232338							
3									
4	$stable.stage								
5		S	J	V	G	D			
6	0,142188	0,16167	0,659449	0,022855	0,013839				
7									
8	$stage.vectors								
9		0	1	2	3	4	5	6	7
10	S	69	161	176,3333	187,2207	219,0905	261,924	318,2264	389,4452
11	J	100	179	201,6948	214,5771	249,7801	298,2718	362,0884	442,9598
12	V	111	258	467,4033	685,9864	903,753	1149,347	1437,187	1783,397
13	G	21	23	24,42009	28,57702	34,164	41,50779	50,7972	62,30105
14	D	43	6	10,15818	14,70876	19,13949	24,22235	30,22041	37,46071
15		8	9	10	11	12	13	14	
16	S	478,3314	588,5237	724,7047	892,7536	1099,981	1355,435	1670,287	
17	J	543,9605	669,2132	824,0306	1015,091	1250,704	1541,154	1899,142	
18	V	2204,992	2721,568	3356,41	4137,717	5099,941	6285,367	7746	
19	G	76,76396	94,5267	116,4461	143,4758	176,7958	217,8635	268,4762	
20	D	46,29325	57,12499	70,44214	86,83496	107,0256	131,9009	162,5519	
21		15	16	17	18	19	20	21	
22	S	2058,318	2536,52	3125,836	3852,078	4747,058	5849,976	7209,146	
23	J	2340,337	2884,058	3554,118	4379,865	5397,468	6651,501	8196,895	
24	V	9545,87	11763,84	14497,09	17865,36	22016,18	27131,38	33435,04	
25	G	330,8504	407,7177	502,445	619,1814	763,0404	940,3234	1158,796	
26	D	200,3221	246,8664	304,224	374,9074	462,013	569,3564	701,6396	
27		22	23	24	25	26	27	28	
28	S	8884,104	10948,22	13491,9	16626,59	20489,57	25250,08	31116,63	
29	J	10101,34	12448,27	15340,47	18904,65	23296,92	28709,67	35380,02	
30	V	41203,28	50776,36	62573,64	77111,88	95027,89	117106,5	144314,8	
31	G	1478,028	1759,814	2168,685	2672,553	3293,488	4058,691	5001,679	
32	D	864,6572	1065,55	1313,118	1618,205	1994,175	2457,498	3028,468	

Figure 11. ***Population projection*** opens in excel.

3) ***stageVectorPlotLongTermProportional***: Is the proportion of individuals per stage in the long term (e.g.: 50 years) (Fig 12)

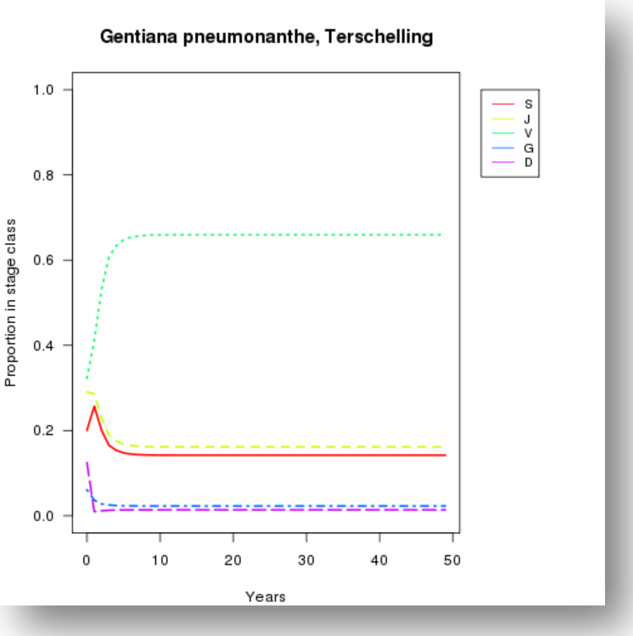


Figure 12. ***Stage vector plot long term proportional*** opens as a graph.

4) ***stageVectorPlotLongTermLogarithmic***: Is the number of individuals per stage in the long term (e.g.: 50 years) (Fig 13).

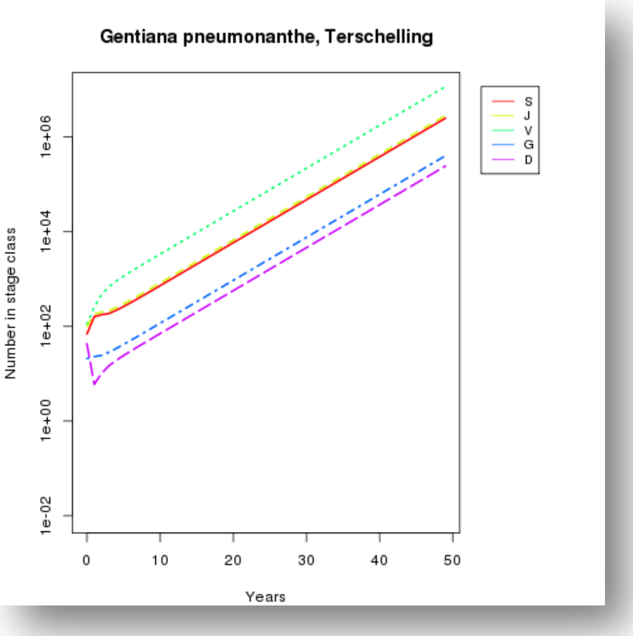


Figure 13. ***Stage vector plot long term logarithmic*** opens as a graph.

5) ***stageVectorPlotShortTerm***: It is a plot that charts the number of individuals per stage vs. years in the short-term (e.g. 10 years). This value (10 years) is related to the short-term years input value. (Fig 14).

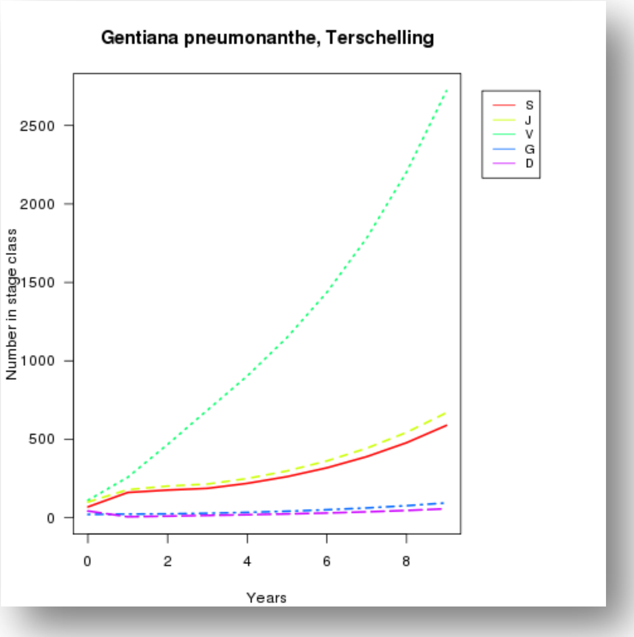


Figure 14. ***Stage vector plot short term*** opens as a graph.

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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

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, Vol. 84(2): 153-166.

Stott, I., S. Townley and D.J. Hodgson 2011. A framework for studying transient dynamics of population projection matrix models. Ecology Letters 14: 959–970

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

van Groenendael, J., H. de Kroon, S. Kalisz, and S. Tuljapurkar. 1994. Loop analysis: Evaluating life history pathways in population projection matrices. Ecology 75: 2410-2415.

7.1 Acknowledgements

7.1.1 Authors

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7.1.2 Project funding

The workflow described in this documentation has been designed and implemented as part of the BioVeL project.

BioVeL is funded by the European Commission 7th Framework Programme (FP7) as part of its e-Infrastructures activity. Under FP7, the e-Infrastructures activity is part of the Research Infrastructures programme, funded under the FP7 'Capacities' Specific Programme. It focuses on the further development and evolution of the high-capacity and high-performance communication network (GÉANT), distributed computing infrastructures (grids and clouds), supercomputer infrastructures, simulation software, scientific data infrastructures, e-Science services as well as on the adoption of e-Infrastructures by user communities.

7.2 Publications