

BioVeL – Biodiversity Virtual e-Laboratory

Workflow Documentation

Stage vectors, Survival and Growth rate curves Workflow for local execution

July 2014

Capacities Programme of Framework 7: EC e-Infrastructure Programme –
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Project Homepage:
Duration of Project:

283359
Mr Alex Hardisty
<http://www.biovel.eu>
36 months

Matrix Population: Stage vectors, Survival and Growth rate curve Workflow

1 Description

The Stages vectors plots, Survival and Growth rate curves Workflow provides an environment to perform several analyses on a series of stage-matrices:

- Population projection
- Survival values calculations per stage per year and its respective plot;
- Growth rates (λ) calculations per year and its respective plot;
- Stage Vectors calculations and their respective plots.

2 General

2.1 Name of the workflow in myExperiment.

Name: Stage vectors, Survival and Growth rate curves workflow

Download: The workflow pack can be downloaded at myExperiment under the following address:
<http://www.myexperiment.org/packs/613.html> or only the workflow:
<http://www.myexperiment.org/workflows/4319.html>

2.2 Date, version and licensing

Last updated: 25th July 2014

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:

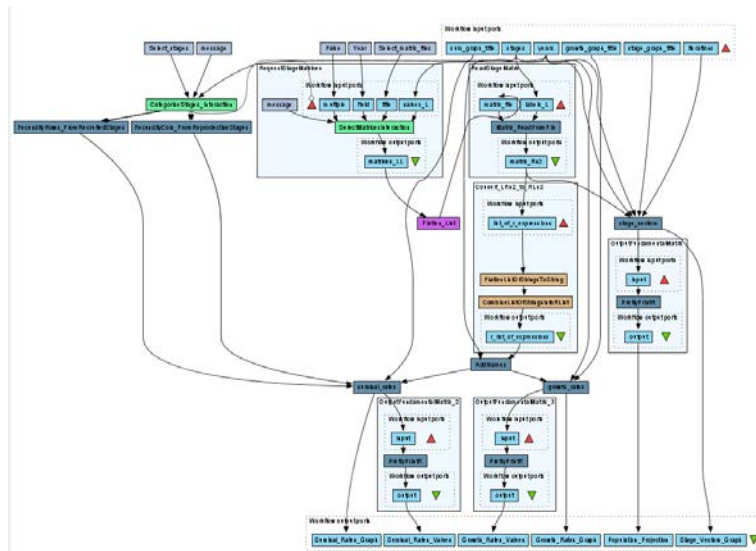
The input data and results reported in this publication (tutorial) come from data (Dr. Gerard Oostermeijer unpublished results and publication: Oostermeijer, J.G.B. M.L. Brugman, E.R. de Boer; H.C.M. Den Nijs. 1996. Temporal and Spatial Variation in the Demography of *Gentiana pneumonanthe*, a Rare Perennial Herb. *The Journal of Ecology*, 84: 153-166.) using BioVeL workflows and services (www.biovel.eu). Stage vectors, Survival and Growth rate curves 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, demography, *Gentiana pneumonanthe*, population growth rates (lambda), population growth rates curves, matrix, matrix population models, package 'popbio' in r, population, stage matrix, stage vectors, survival curve

3.2 Scientific workflow description



The aim of the Stage vectors, Survival and Growth rate curves Workflow is to provide a connected environment to calculate and plot from two or more matrices the following results: Population projection, population growth rate λ over the years, survival of all stages over the years and stage vectors: proportions of individuals per stage per year. The workflow accepts input data (matrices) in a .txt format (decimal numbers indicated by dots e.g.: 0.578). The output is provided as a set of R results and graphic plots.

Figure 1. A) Graph of the Stage vectors, Survival and Growth rate curves 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 including the Interaction Service plugin. The simplest way to install a Taverna Engine is to install Taverna Workbench, and then install the Interaction Service plugin.

The workflow also requires an Rserve installation with the *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 Plug-ins

- Please install the [Interaction](#) plugin: version 1.0.2+

4.2.3 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.biodel.eu/x/3ICD> for additional information.

4.2.4 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

This tutorial requires 6 input files or matrices of 6 consecutive years (from 87-88 to 92-93) of the same place (Terschelling, The Netherlands).

5.2 Input data.

5.2.1 Data preparation/format

The workflow accepts input data (matrices) in a .txt format, all decimal numbers in each matrix must be indicated by dots e.g.: 0.578. All examples matrices for the tutorial are available in the PACK: <http://www.myexperiment.org/packs/613.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 matrices

- [MTers87_88.txt](#)
- [MTers88_89.txt](#)
- [MTers89_90.txt](#)
- [MTers90_91.txt](#)
- [MTers91_92.txt](#)
- [MTers92_93.txt](#)

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) **Growth graph title:** Is the main title to be display in the Growth rate graph. Click in set value and write the text in the right space.

e.g.: *Gentiana pneumonanthe* growth rates (*Gentiana pneumonanthe*: species name, Fig 2).

Matrix Population: Stage vectors, Survival and Growth rate curve Workflow

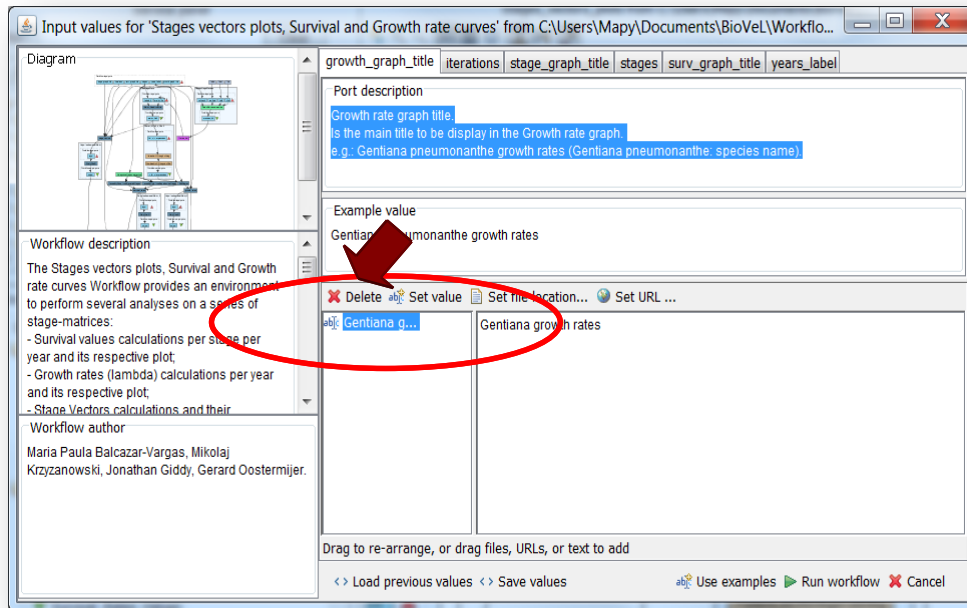


Figure 2. Growth graph title to be filled in (example).

2) **Iterations:** This value will be used to plot an output graph that shows a simulation of the number of individuals per stage a few years after the study (e.g. 10). This value represents the years of axis X of the output graph: **Stage_Vector_Graph** (Fig 3). Click in set value and write the number in the right space.

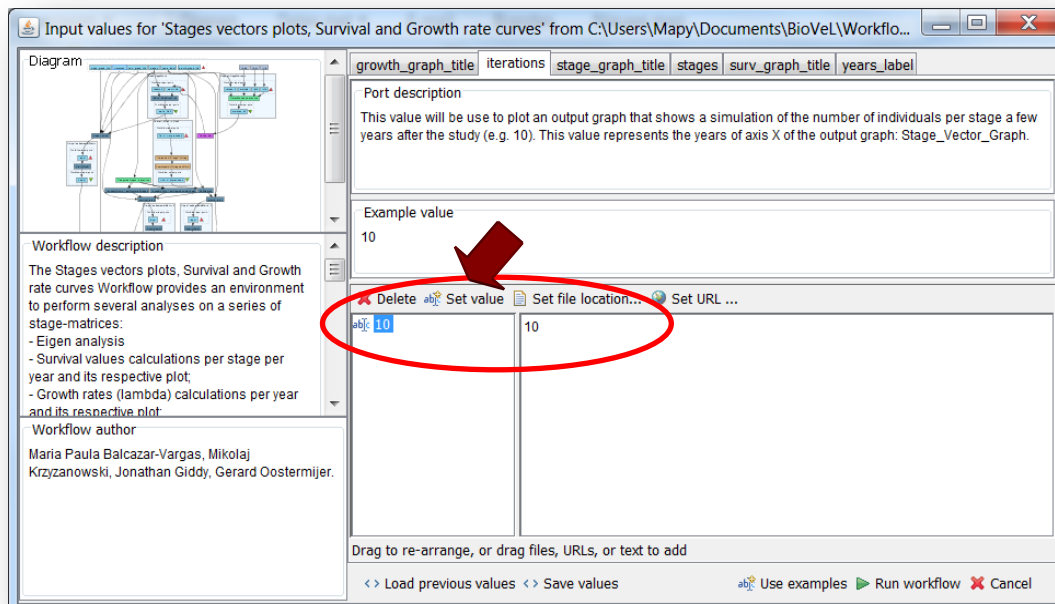


Figure 3. The number of iterations to be filled in.

Matrix Population: Stage vectors, Survival and Growth rate curve Workflow

3) **Stage Graph title:** Is the main title to be display in the Stage Vectors Graphs. (Note: it will appear as Title - Year). The year will automatically be incorporate base on the year of each matrix. Click in set value and write the text in the right space.

e.g.: *Gentiana pneumonanthe* stage vectors.

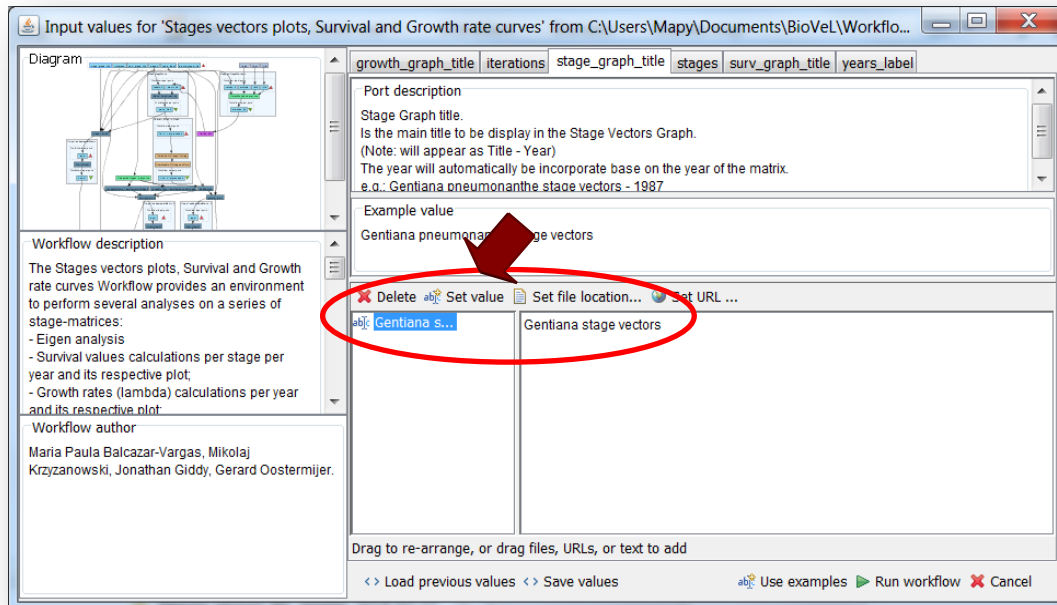


Figure 4. Stage graph title to be filled in.

4) **Stages:** the names of the stages or categories of the input matrix. In the following example, the matrix has 5 stages or categories. The respective name stages must be filled one by one. First press add value (see arrow in Fig 5), fill a stage name (not longer than 8 characters) and press enter; then press add value and fill once again the next stage name, repeat the action until you have fill all the stages names.

In the following example, the matrix has 5 stages or categories:

The stages of this matrix are called:

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

Matrix Population: Stage vectors, Survival and Growth rate curve Workflow

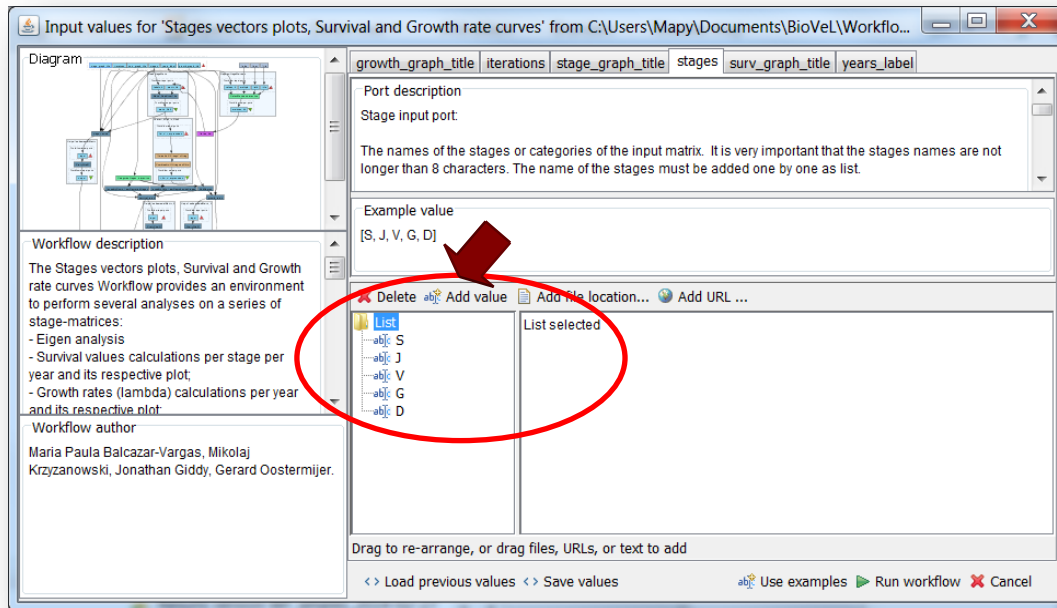


Figure 5. Inputs stages names to be filled in (example).

5) **Surv graph title:** Is the main title to be display in the Survival Rates Graph. Click in set value and write the text in the right space.

e.g.: *Gentiana pneumonanthe* survival curves (*Gentiana pneumonanthe*: species name).

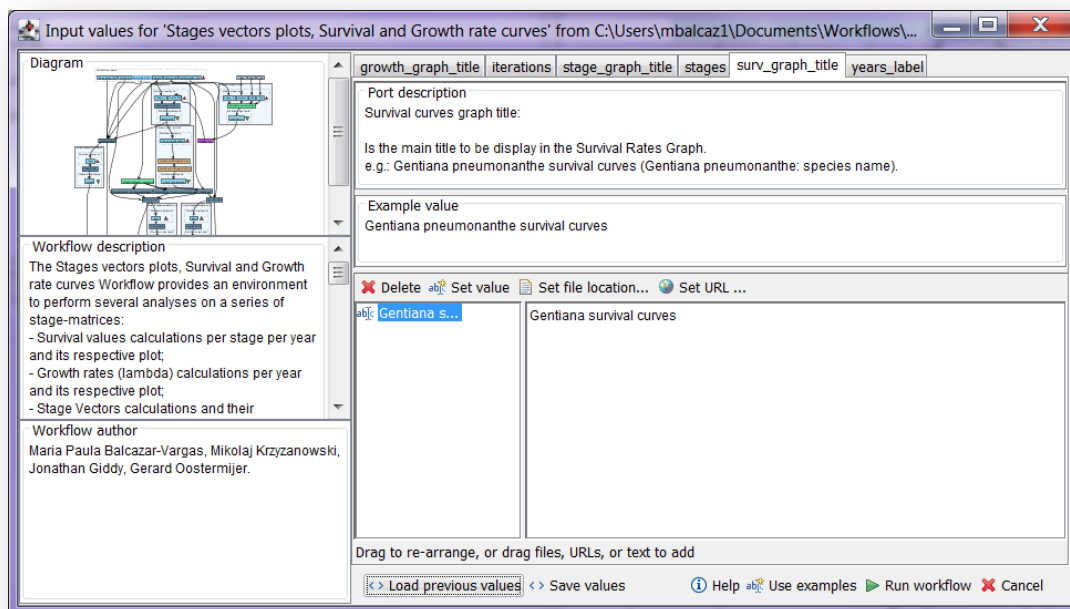


Figure 6. Survival graph title to be filled in.

6) **Years:** Years in which the data of the matrices were collected. The years must be added one by one

Matrix Population: Stage vectors, Survival and Growth rate curve Workflow

as list. First press add value, fill the first year and press enter, then press add value and fill once again the next year, repeat the action until you have fill all the years.

The years can be display as follow:

e.g.

- 1987
- or
- 1987-1988

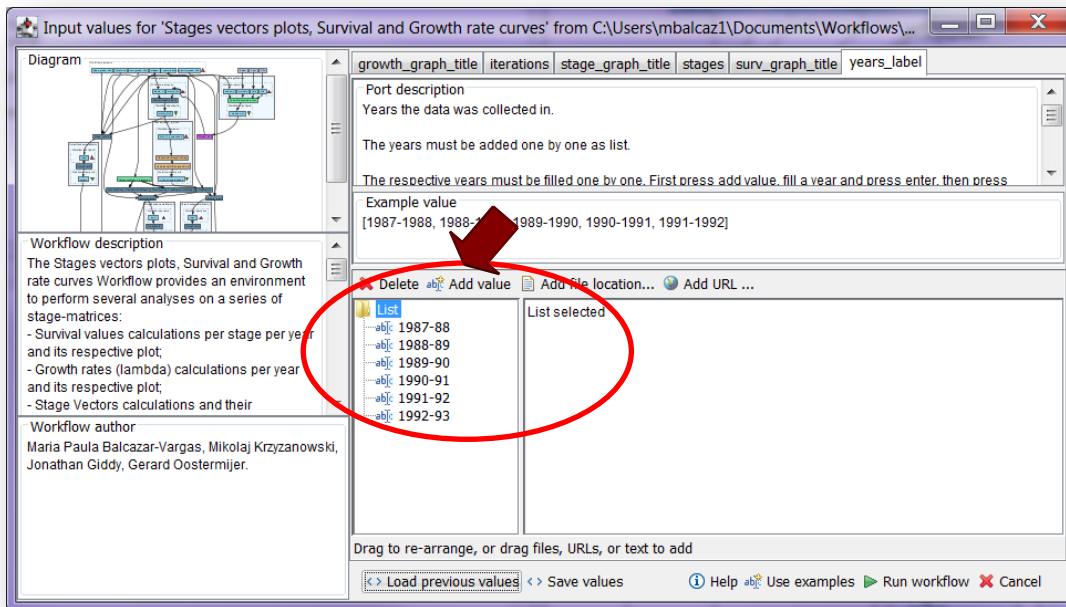


Figure 7. Inputs years to be filled in (example).

After the user has filled out the input ports and has clicked the **Run Workflow button**, a dialogue pages appear in the user's internet browser. See the next section:

5.3.2 INTERACTION

1) **Stages:** With this dialogue automatically appear the names of the stages or categories of the input matrices. When the dialogue appears, the author chooses if the stage belongs to the recruited or reproductive category (Fig 8 and 9). Recruited means that new individuals can be recruited to this (these) stage(s). Reproductive stages are those that reproduce (produce offspring) (in this example the stage G). Then the user clicks in confirm and you will read stages submitted (Fig 10).

In the following example, the life cycle of *Gentiana pneumonanthe* has 5 stages or categories:

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

Matrix Population: Stage vectors, Survival and Growth rate curve Workflow

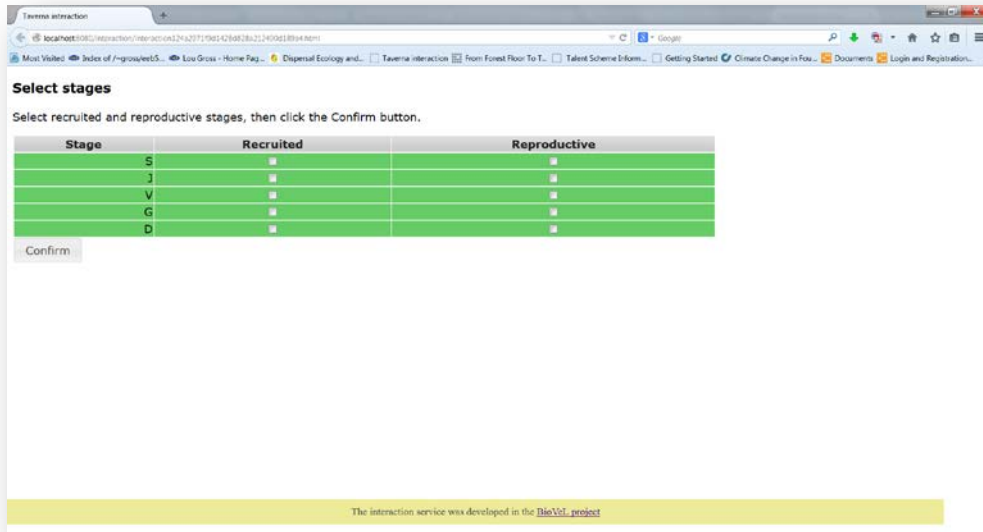


Figure 8. Stages dialogue. When the dialogue appears.

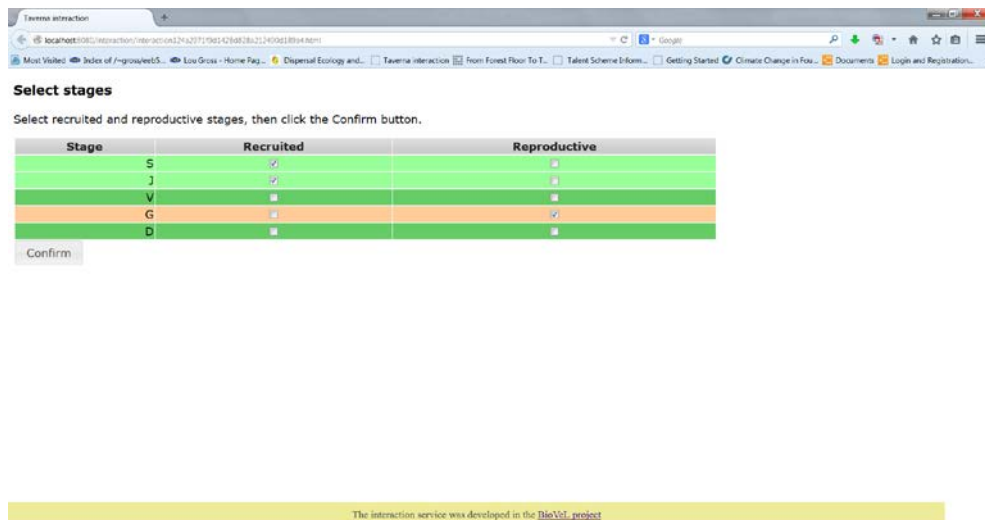


Figure 9. Stages dialogue. Choose if the stage belongs to the recruited or reproductive category.

Matrix Population: Stage vectors, Survival and Growth rate curve Workflow

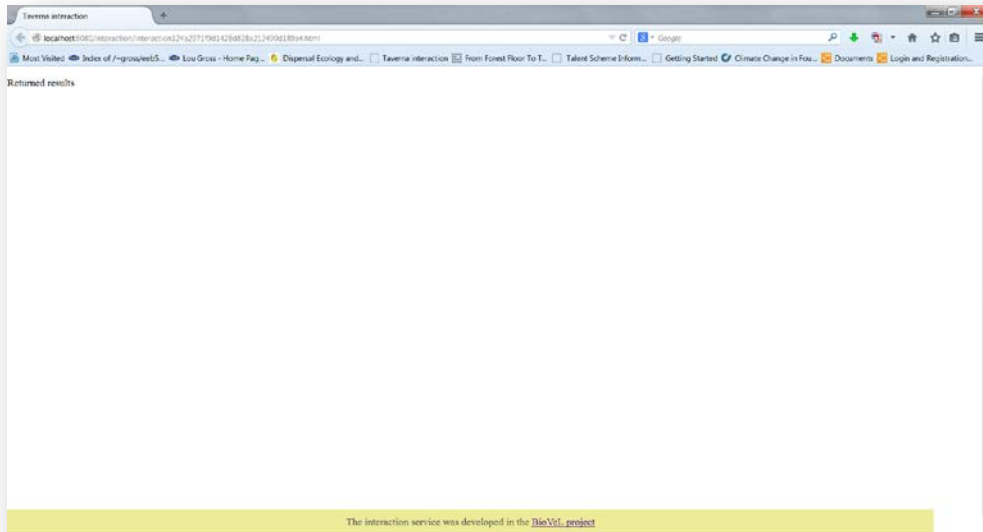


Figure 10. Stages dialogue. Then the user clicks in confirm and you will read Returned results.

2) **Years:** the interaction page will show the submitted years. When the dialogue appears (Fig 11), click Browse for the first year (1987-1988). A file dialog appears. Select the file (one matrix that belong to that year) and clicks Open (Fig 12). Then the selected matrix appears in the browser. Repeat the procedure for each year (Fig 13). Once all the matrices are submitted, click the Confirm button (Fig 14). After clicking Confirm, the confirmation "Returned Results" appears (Fig 15). When the analyses are completed, they appear on different windows under results in Taverna workbench, the user can save each output separately (Fig 16).

In the following example, there are 6 years:

- 1) 1987-88
- 2) 1988-89
- 3) 1989-90
- 4) 1990-91
- 5) 1991-92
- 6) 1992-93

Matrix Population: Stage vectors, Survival and Growth rate curve Workflow

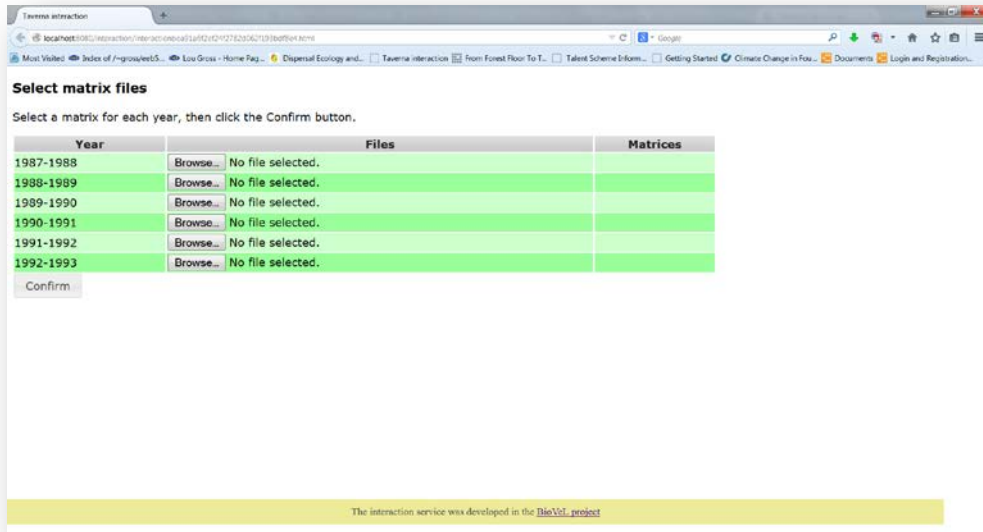


Figure 11. Year's dialogue appears.

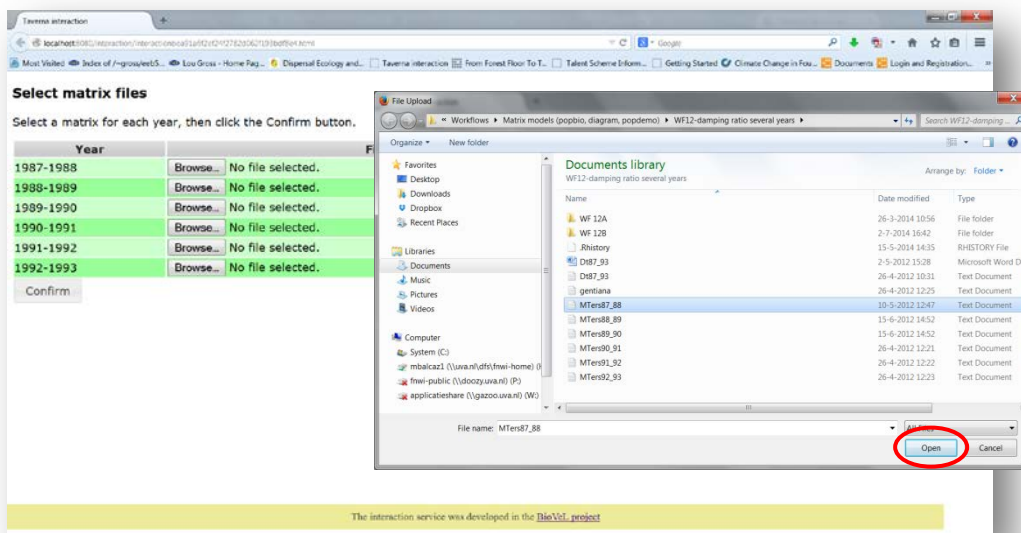


Figure 12. Years dialogue browse. Click in browse (1987-1988), and select the file (one file) and then click in Open button.

Matrix Population: Stage vectors, Survival and Growth rate curve Workflow

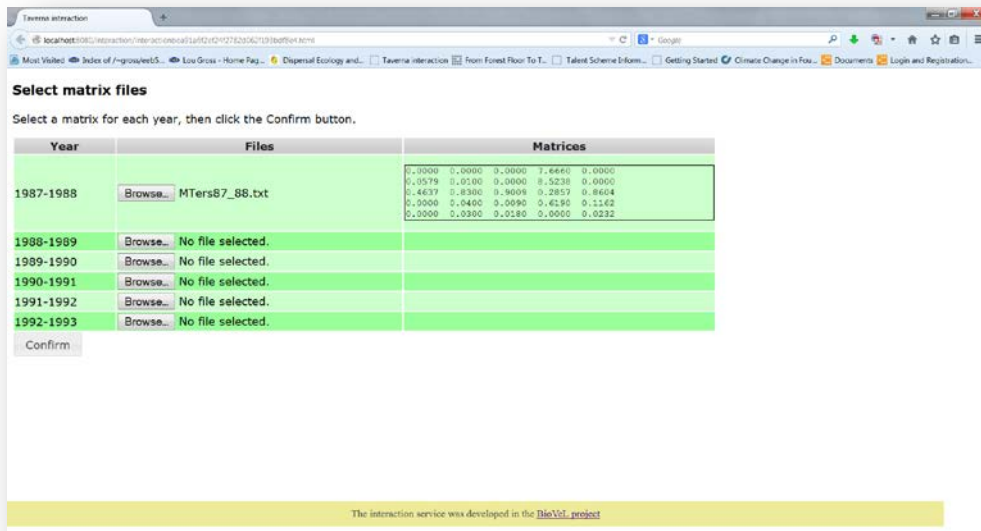


Figure 13 Years dialogue. The selected matrices appear. Repeat the procedure for each year.

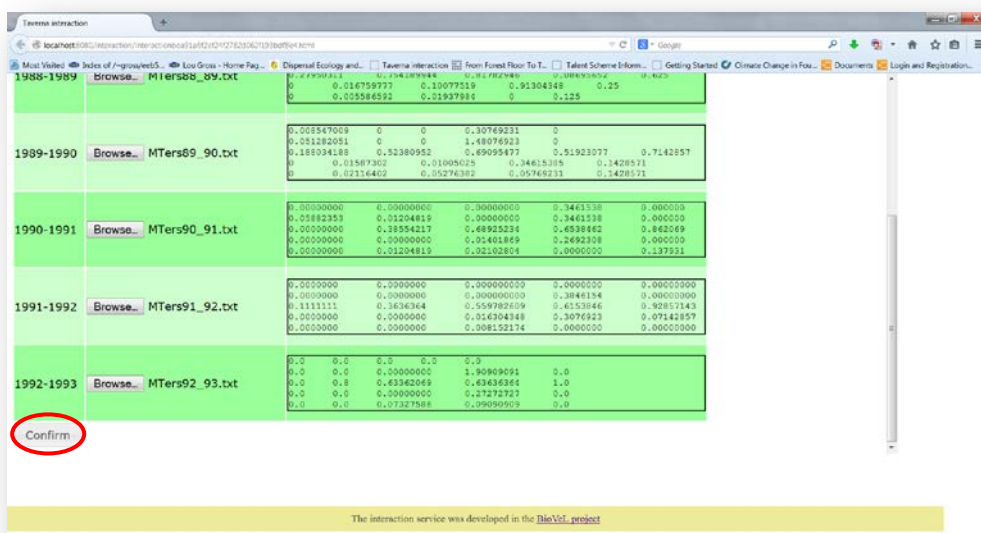


Figure 14. Year's dialogue. Once all the matrices are submitted, click in Confirm.

Matrix Population: Stage vectors, Survival and Growth rate curve Workflow

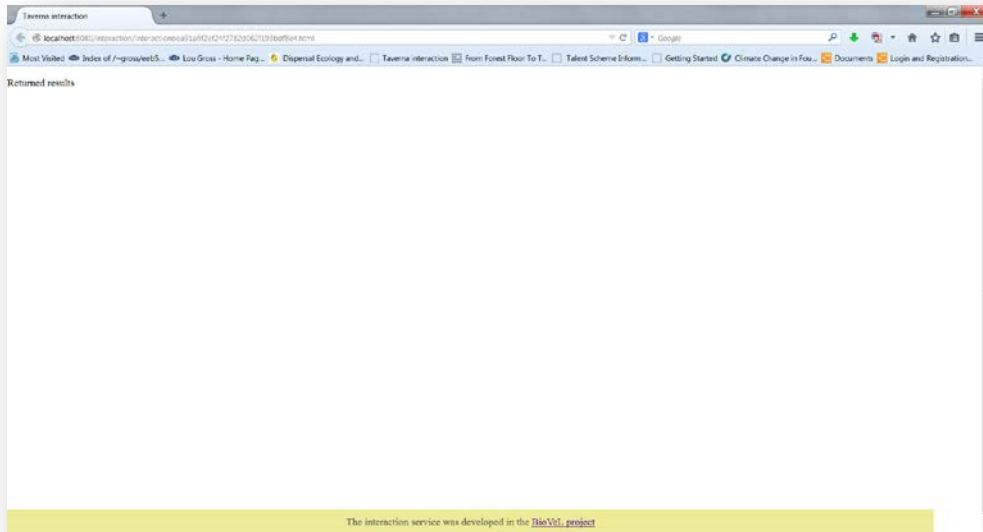


Figure 15. Year's dialogue. After the user clicks Confirm, the confirmation "Returned Results" appears. Refer back to Taverna workbench.

5.4 Save data/results

5.4.1 OUTPUTS

When the analyses are completed, they appear on different windows under results in Taverna. First, click in the selected result window e.g. **Population projection** (Fig 16, red oval). Second, click in the left window on value 1 (Fig 16, blue oval) and you will see the **Population projection** results of the first submitted matrix (1987-1988) in the right window; then click on value 2 and you will see the results of the second submitted matrix (1988-1989), etc. Third, on the right window click on save value (Fig 16). Fourth, name the file and determinate the extension file. For a text file: e.g. .csv or .txt. For images: .jpg or .png (Fig 17). Finally, save the file in the chosen map (Fig 17).

Matrix Population: Stage vectors, Survival and Growth rate Workflow

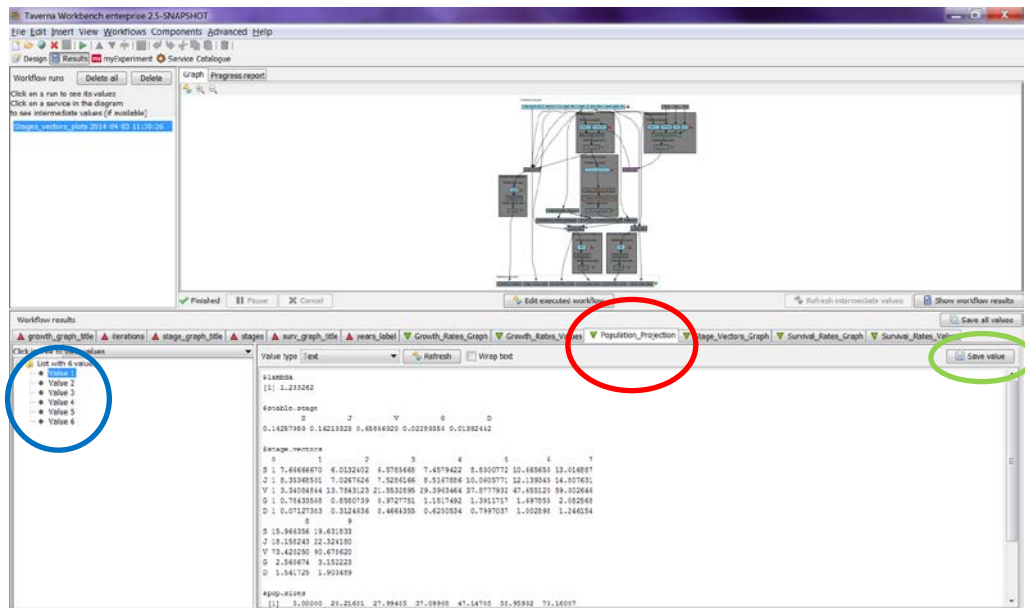


Figure 16. Taverna workbench results. When the analyses are completed, they appear on different windows under results in Taverna. Click on **Population projection** window (red oval). **Population projection** will have in this case from Value 1 to 6 (6 matrices were submitted). Do click on Value 1 on the left window of the **Population projection** output results (blue oval). Save value on the right window of the **Population projection** output results (green oval).

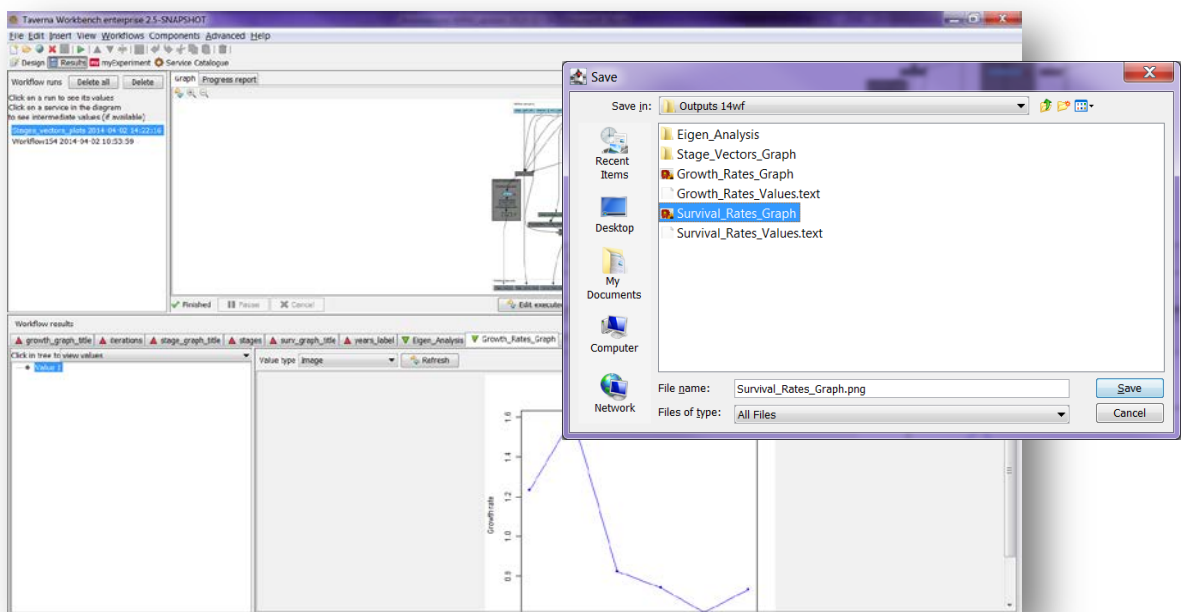


Figure 17. Name the file and add the extension, for a text file: e.g. .csv or .txt. For images: e.g.: .jpg or png. Click on Save.

Matrix Population: Stage vectors, Survival and Growth rate curve Workflow

- 1) **Growth_Rates_Graph:** Plots the population growth rate or lambda values of each submitted matrix (Fig 18).

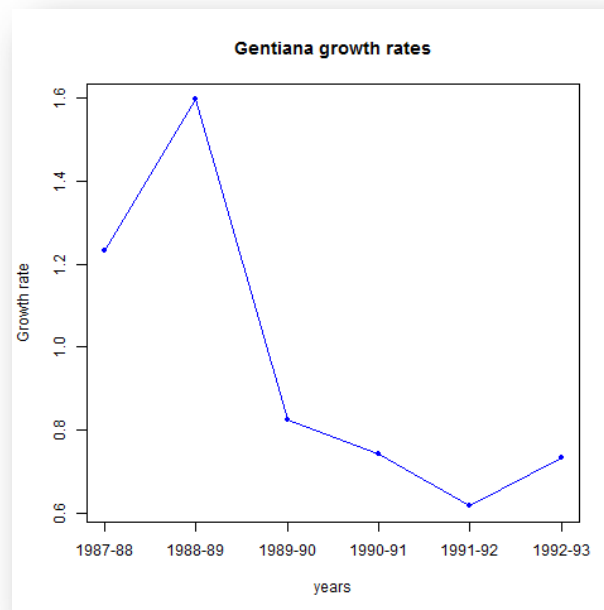


Figure 18. Growth rate graph (.png or .jpg).

- 2) **Growth_Rates_Values:** It is a table showing the population growth rate or lambda values of each submitted matrix (Fig 19).

The screenshot shows a Microsoft Excel spreadsheet with the following data:

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
1	1987-88	1988-89	1989-90	1990-91	1991-92	1992-93										
2	1,232338	1,59471	0,826321	0,744482	0,61868	0,733517										
3																
4																
5																
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Figure 19. Growth rate Values (.csv or text files).

Matrix Population: Stage vectors, Survival and Growth rate curve Workflow

3) Population projection

Calculates the population growth rate and stable stage distribution by repeated projections of the equation $n(t+1)=An(t)$ (Fig 20).

a) **Lambda or dominant eigenvalue:** This value describes the population growth rate of a stage matrix. 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).

b) **The stable stage distribution (w):** It is the proportion of the number of individuals per stage. It is given analytically by the right eigenvector (another property of the transition matrix) that corresponds to the dominant eigenvalue

c) **Stage.vector:** A matrix with the number of projected individuals in each stage class.

d) **Pop.sizes:** Total number of projected individuals.

e) **Pop.changes:** Proportional change in population size.

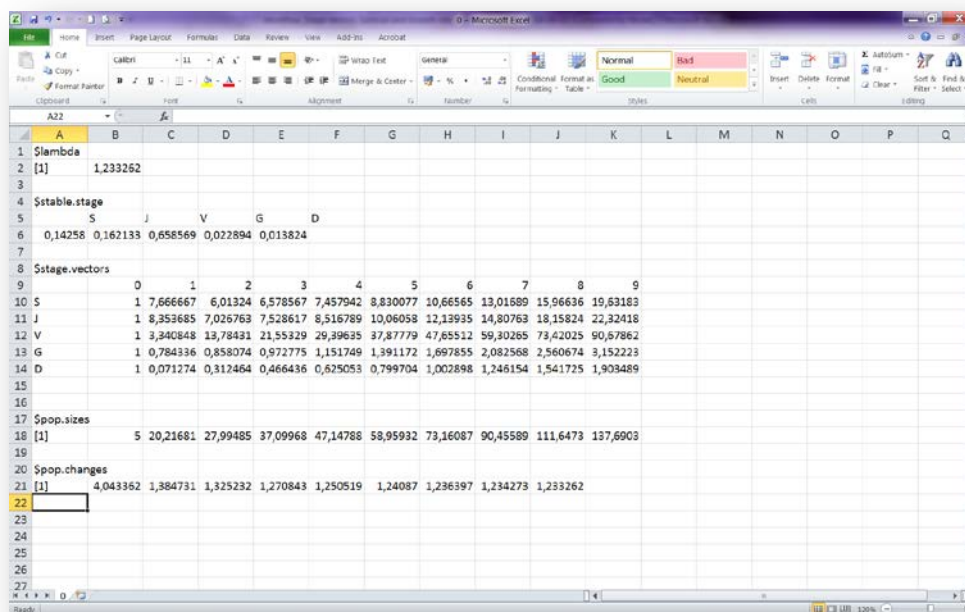


Figure 20. Population projection results of one matrix (.csv or text files).

4) **Stage Vector Plot:** Plots short-term dynamics and convergence to stage distribution. It is a plot that charts the number of individuals per stage vs. years in the short-term (e.g. 5, 10 years) per matrix (Fig 21).

Matrix Population: Stage vectors, Survival and Growth rate curve Workflow

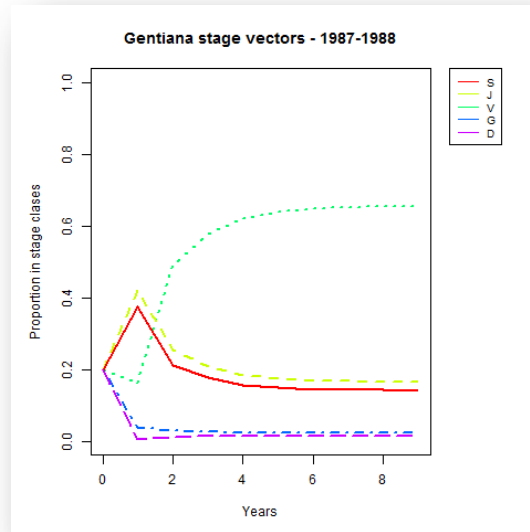


Figure 21. Stage Vector Plot (.png or .jpg).

5) **Survival Rates Graph:** The graph shows the changes of the survival values per stages across the years (Fig 22).

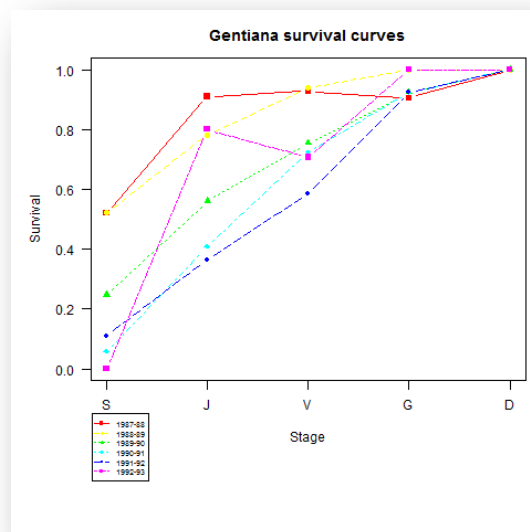
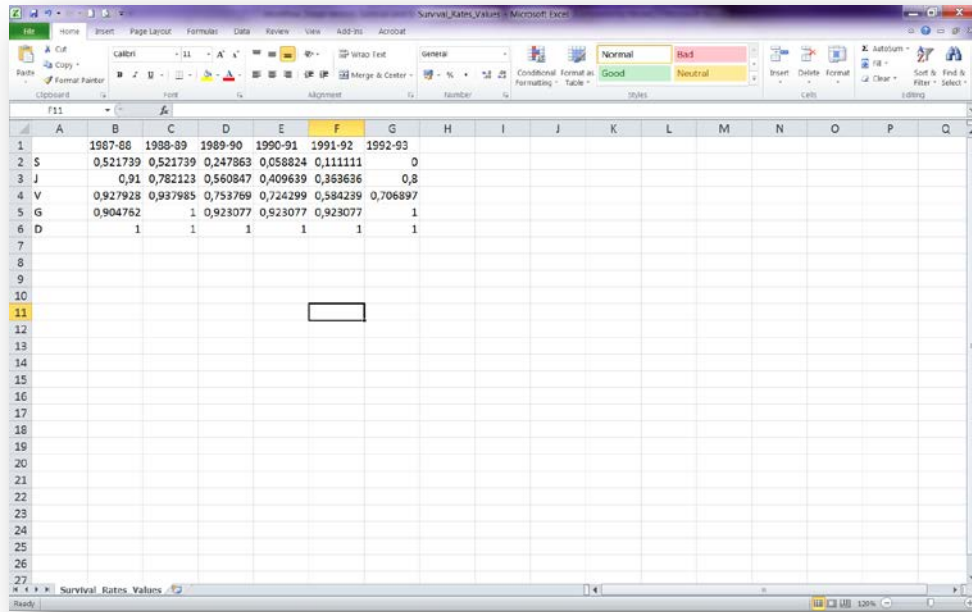


Figure 22. Survival Rates Graph (.png or .jpg).

6) **Survival Rates Values:** It is a table showing the survival rates values per stage per year, these values are plotted in the Survival Rates Graph (Fig 23).

Matrix Population: Stage vectors, Survival and Growth rate curve Workflow



The screenshot shows a Microsoft Excel spreadsheet with the following data:

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1		1987-88	1988-89	1989-90	1990-91	1991-92	1992-93										
2	S	0,521739	0,521739	0,247863	0,058824	0,111111	0										
3	J	0,91	0,782123	0,560847	0,409639	0,363636	0,8										
4	V	0,927928	0,937985	0,753769	0,724299	0,584239	0,706897										
5	G	0,904762	1	0,923077	0,923077	0,923077	1										
6	D	1	1	1	1	1	1										
7																	
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Figure 23. Survival Rates Values (.csv or text files).

6 Support

For questions with using the workflow, please write [support @biovel.eu](mailto:support@biovel.eu)

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

7 Bibliography

This workflow was created using and based on Package '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.

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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3. **J. Gerard B. Oostermeijer** Instituut voor Biodiversiteit en Ecosysteem Dynamica (IBED), Universiteit van Amsterdam.

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

Matrix Population: Stage vectors, Survival and Growth rate curve Workflow

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