

BioVeL – Biodiversity Virtual e-Laboratory

Workflow Documentation

Matrix Population Models analyses (Integrated) Workflow for local execution

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283359
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36 months



Matrix Population Models analyses (Integrated) Workflow for local execution

1 Description

The Matrix Population Models Workflow provides an environment to perform several analyses on a stage-matrix with no density dependence.

Analyses:

- Eigen analysis.
- Age specific survival.
- Generation time (T).
- Net reproductive rate (R_0).
- Transient Dynamics.
- Resample a projection matrix (Confidence intervals of λ).
- Survival curve
- Keyfitz's Δ
- Cohen's cumulative distance

2 General

2.1 Name of the workflow in myExperiment.

Name: Matrix Population Models analyses (Integrated) Workflow for local execution

Download: The workflow pack can be downloaded at myExperiment under the following address:
<http://www.myexperiment.org/packs/484.html> or only the workflow:
<http://www.myexperiment.org/workflows/3686.html>

2.2 Date, version and licensing

Last updated: 9th July 2013

Version: 12

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 Gerard Oostermeijer unpublished results and publication: Oostermeijer, J.G.B. M.L. Brugman, E.R. de Boer; H.C.M. Den Nijs. 1996.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). Matrix Population Models analyses (Integrated) 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, Lambda (λ), Sensitivity analysis, Elasticity analysis, Age specific survival, Generation time (T), Net reproductive rate (R_0), Transient Dynamic, Damping ratio, Resample a projection matrix (Confidence intervals of λ), Survival curve, Keyfitz delta, Cohen's cumulative distance.

3.2 Scientific workflow description

The aim of the Matrix Population Models Workflow is to provide a connected environment to perform several analyses on a stage-matrix with no density dependence. The workflow accepts input data in a .txt format. The output is provided as a set of R results and graphic plots. Currently, the workflow is composed of six distinct analyses (Fig 1a and B):

1. Eigen analysis of a stage matrix model. This component of the workflow performs the Eigen analysis. This analysis results are a set of demographic statistics:

- a) Lambda or dominant eigenvalue (λ).
- b) The stable stage distribution.
- c) The sensitivity matrix
- d) The Elasticity matrix.
- e) Reproductive value.
- f) The damping ratio.

2. Age specific survival. This component of the workflow calculates the age-specific survival: that includes the mean, variance and coefficient of variation (cv) of the time spent in each stage class and

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the mean and variance of the time to death.

- a) Fundamental matrix (N): is the mean of the time spent in each stage class.
- b) Variance (var): is the variance in the amount of time spent in each stage class.
- c) Coefficient of variation (cv): is the coefficient of variation of the time spent in each class ($sd/mean$ - the ratio of the standard deviation to the mean).
- d) Meaneta: is the mean of time to death, of life expectancy of each stage.
- e) Vareta: is the variance of time to death.

3. Generation time (T): This component of the workflow calculates the generation time. The time T required for the population to increase by a factor of R_0 (net reproductive rate). In other words, T calculates how much time takes to a plant/animal to replace itself by a factor of R_0 .

4. Net reproductive rate (R_0): This section of the workflow calculates the net reproductive rate (R_0). R_0 is the mean number of offspring by which a new-born individual will be replaced by the end of its life, and thus the rate by which the population increases from one generation to the next.

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

6. Resample a projection matrix or parametric Bootstrap: Resample a projection matrix using a multinomial distribution for transitions and a log normal distribution for fertilities. The resample is based on number of plants surveyed.

The projection matrix A is first split into separate transition and fertility matrices. Dead fates are added to the transition matrix and the columns are then sampled from a Multinomial distribution based on the size in each corresponding stage class in n . The fertility rates are sample from a Log Normal distribution using the `lnorms` function. The variance can be a single value which is applied to all rates, or vector of different values to apply to each rate. In this case, the values are recycled to match the number of non-zero fertilities (Stubben, Milligan and Nantel 2013, Caswell 2001 see section 12.1.5.2).

7. Survival curve: Plots the survival curve.

8. Keyfitz's Δ : This workflow produces the Keyfitz's delta and the Cohen's cumulative distance, which are measurements of the distance to the stable stage distribution (SSD). Keyfitz's delta is a measure of the distance between any two probability vectors (Keyfitz 1968). In this case is a measure of the distance between n (Observed Stage Distribution) and w (Stable Stage Distribution). The maximum value is 1 and the minimum value is 0 (when the vectors are identical).

9. Cohen's cumulative distance: The Cohen's cumulative distance measures the difference between observed and expected vectors along the matrix path that the population would take to reach the expected population vector. It is a function of both the observed stage distribution (n_0) and the structure of the matrix (A) (Williams et al 2011). Cohen's cumulative distance will not work for reducible matrices or imprimitive matrices with nonzero imaginary components in the dominant eigenpair, and returns a warning for other imprimitive matrices (Caswell 2001).

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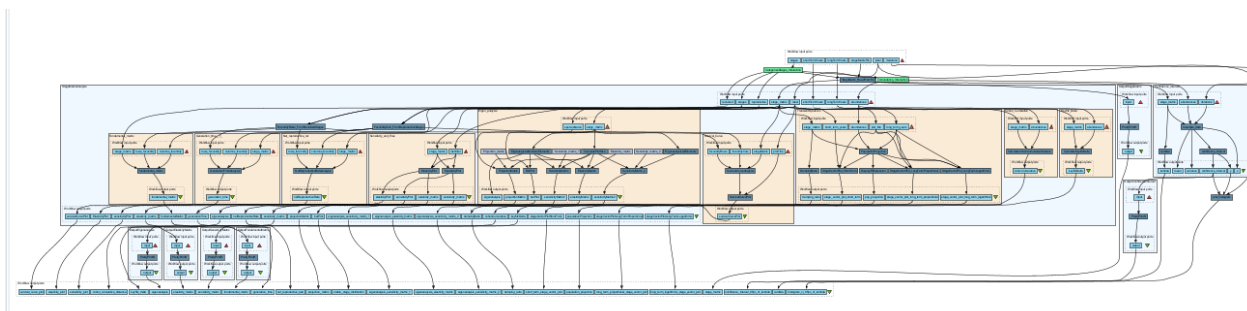


Figure 1. Stage matrix analysis workflow in Taverna workbench

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 and popdemo packages 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")`

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- Install package popbio
 - `install.packages("popbio")`
- For package popdemo, as it is archived in CRAN, use the package devtools to install it
 - `install.packages("devtools")`
 - `require(devtools)`
 - `install_url("http://cran.r-project.org/src/contrib/Archive/popdemo/popdemo_0.1-3.tar.gz")`
- Local R Server: (Rserve) running at port 6311. See <https://wiki.biovel.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:\PROGRAMS~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 File. You will use this file to perform several 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 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/484.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](#)

5.3 Select input data dialogue boxes.

The first step is to fill out the input ports:

5.3.1 INPUTPORTS

1)) ***Iterations***: Number of iterations for calculation of the resample analysis of the projection matrix or parametric Bootstrap. Click in Set Value (red arrow in Fig 2), tip the number in the right window.

e.g.: 1000

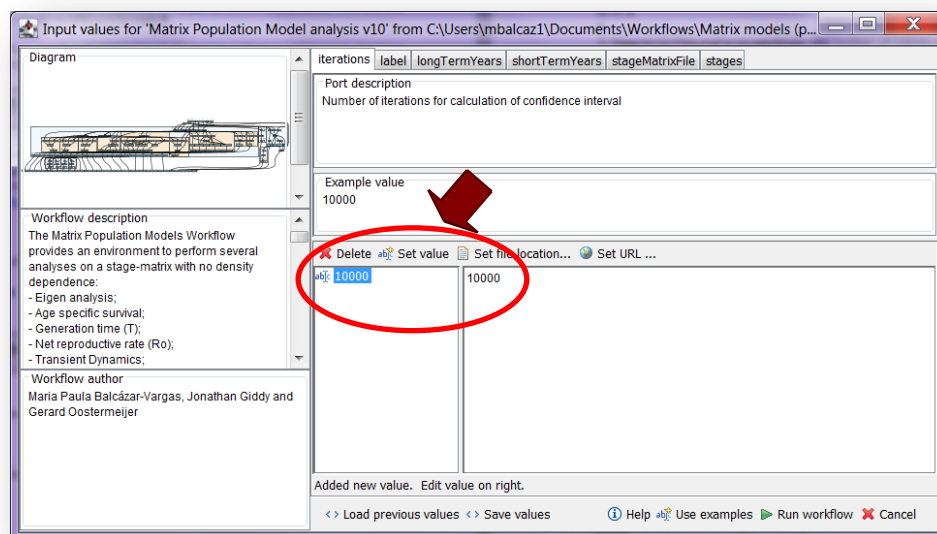


Figure 2. A number of iteration's to be filled in.

2) ***Label***: Descriptive title for labelling generated outputs (graphs). Click in Set Value (red arrow in Fig 3), tip the text in the right window.

e.g.: *Gentiana pneumonanthe*, **Terschelling** (*species taxonomic name*, **place where the research was conducted**)

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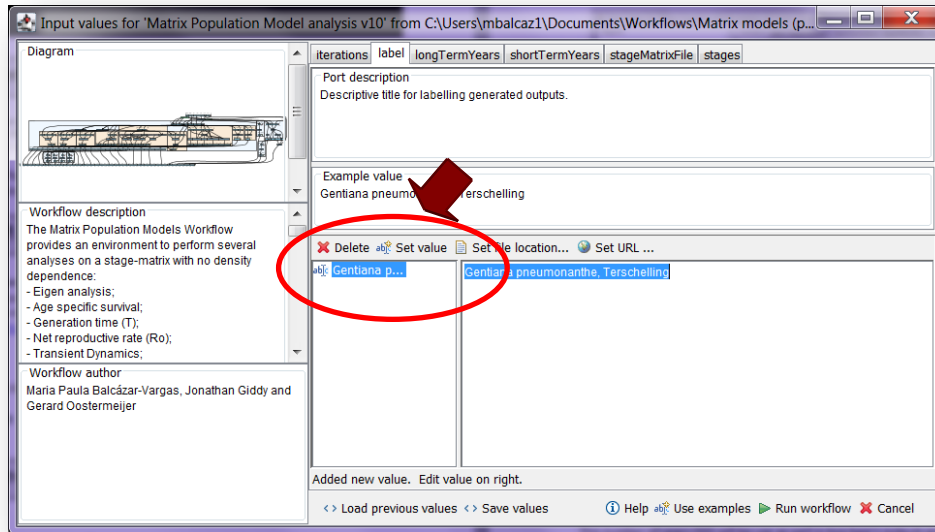


Figure 3. Text to be filled in.

3) **LongTermYears**: It is the maximal number of iteration or repetitions in the transient dynamic analysis. . Click in Set Value (red arrow in Fig 4), tip the number in the right window.

e.g.: 50

This number of years (50) will be use as well in two type's outputs graphs (see output ports):

- 1) StageVectorPlotLongTermProportional: the proportion of individuals per stage in the long term..
- 2) StageVectorPlotLongTermLogarithmic: the number of individuals per stage in the long term.

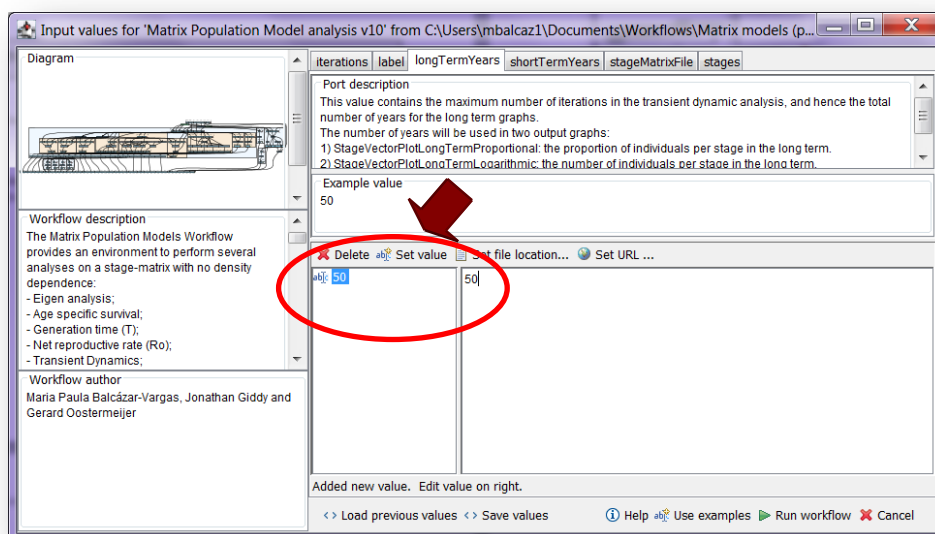


Figure 4. Number to be filled in.

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4) **ShortTermYears:** This value will be used to plot a graph that shows a simulation of the number of individuals per stage in a few years period after the study. This value represents the years of axis X of the output graph: StageVectorPlotShortTerm (see output port). Click in Set Value (red arrow in Fig 5), tip the number in the right window.:

Example of Input page:

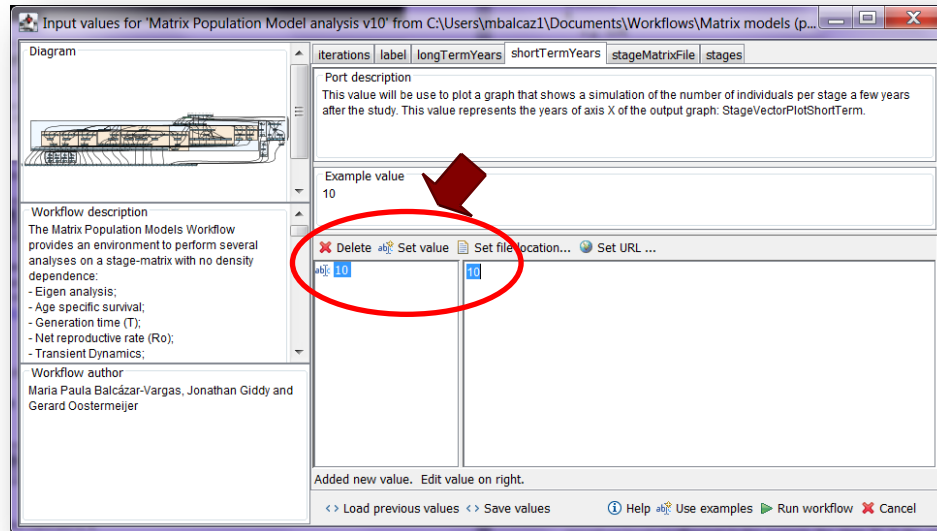


Figure 5. Inputs file to be filled in.

5) **StageMatrixFile:** 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.

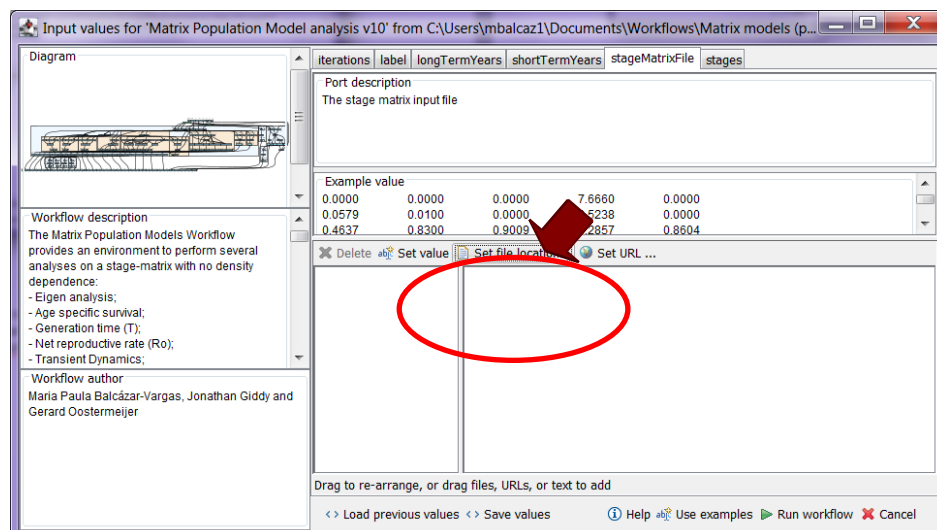


Figure 6. Set the Location of the matrix file.

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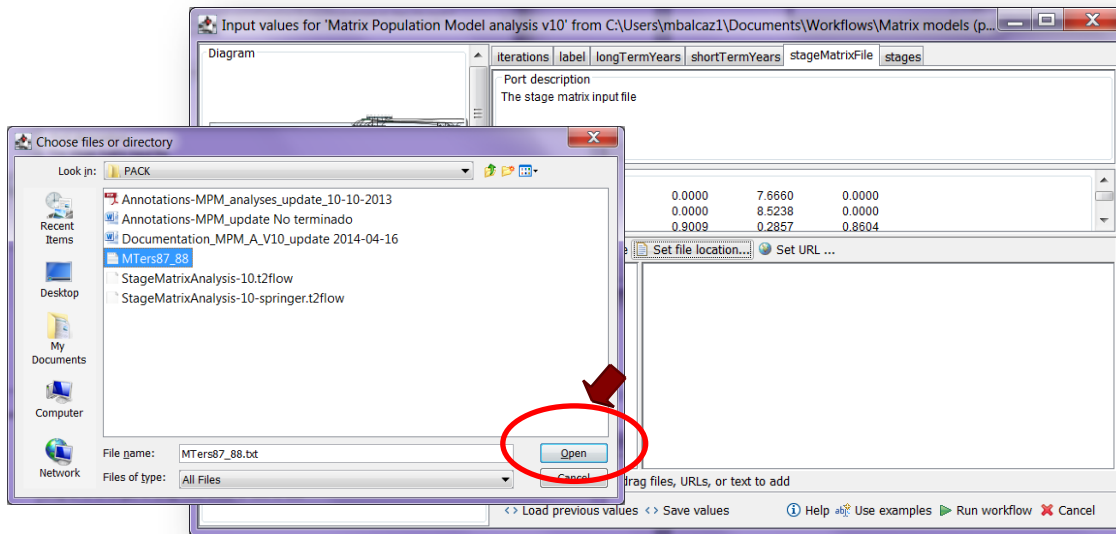


Figure 7. Choose the matrix file and click in Open.

6) **Stages:** the names of the stages or categories of the input matrix. In the following example, the matrix has 5 stages or categories. The respective name stages must be filled one by one. First press add value (see arrow in Fig 8), 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 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 |

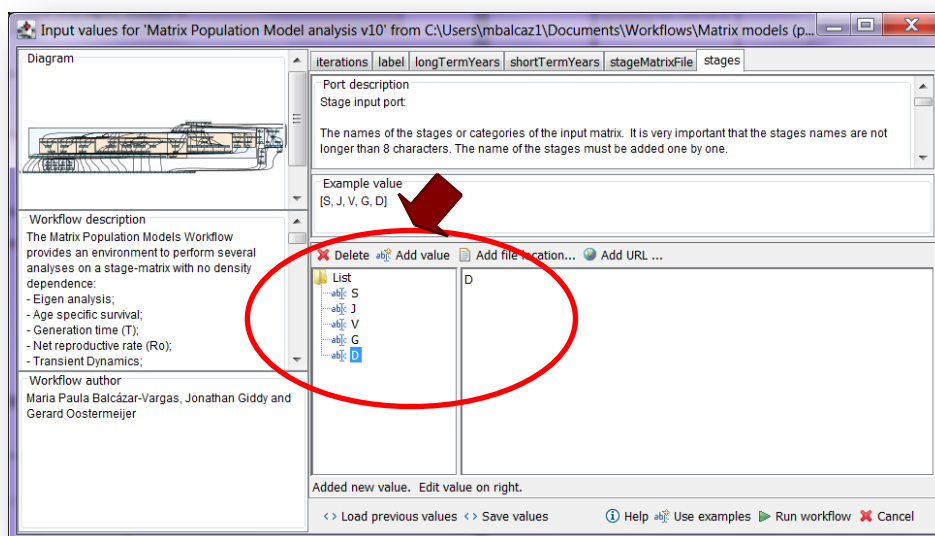


Figure 8. Stages to be filled in.

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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 that were submitted in the stages input port. When the dialogue appears, the author chooses if the stage belongs to the recruited and reproductive category (Fig 9 and 10). 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 and 11). This workflow supports rectangular or square fecundity shape matrix values.

Stage	Recruited	Reproductive	Exclude
S	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
J	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
V	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
G	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
D	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Confirm

Drag stages to sort, then click Confirm

The interaction service was developed in the BioVid project

Figure 9. Stages dialogue. Appears (e.g. S, J, V, G, D).

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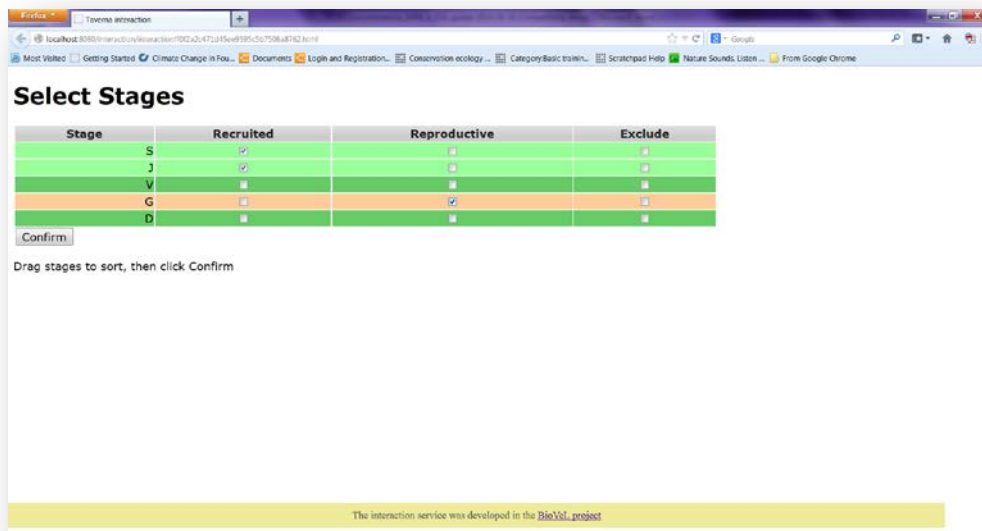


Figure 10. Stages dialogue. Choose if the stage belongs to the recruited or reproductive category.

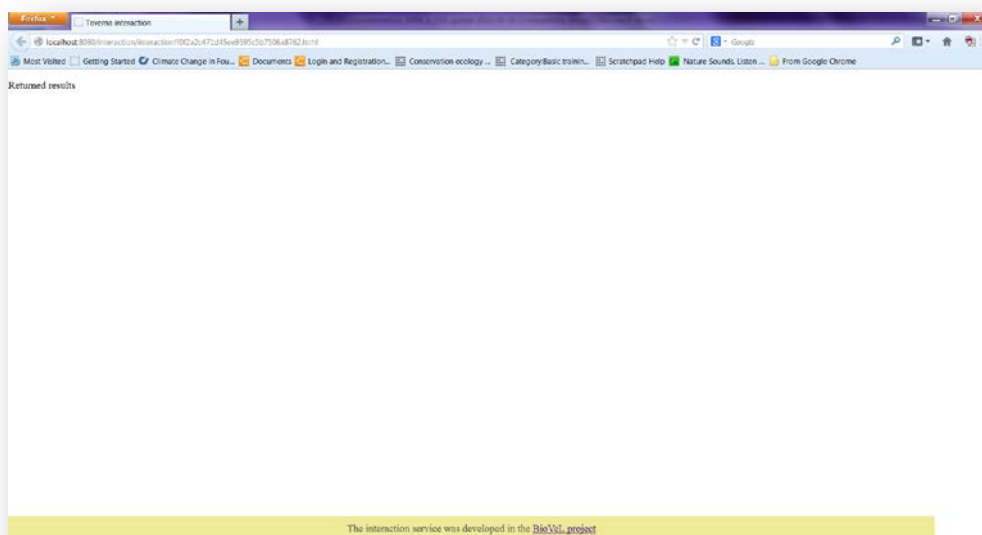
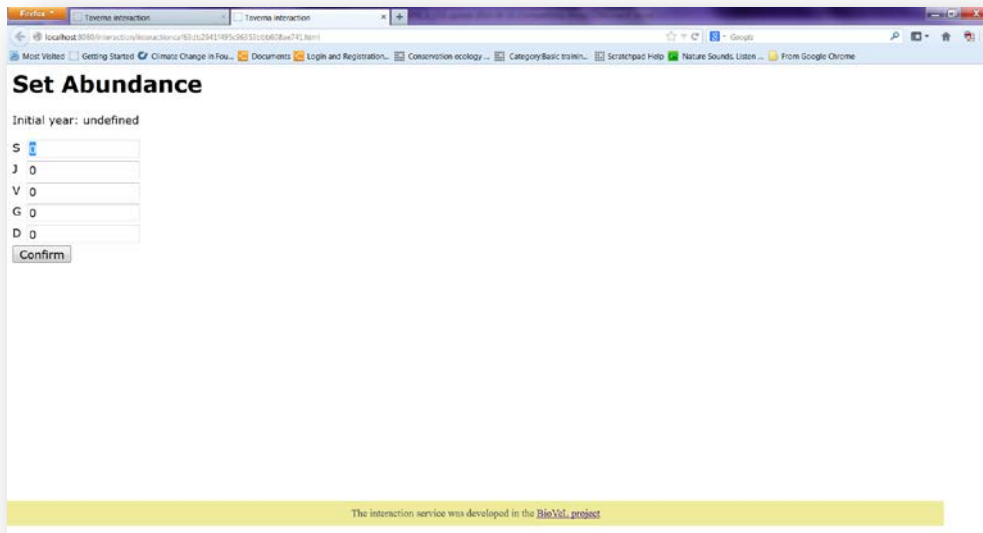


Figure 11. After the user clicks Confirm, the confirmation “Returned results” appears.

2) **Initial abundance:** In this dialogue appear the fields with the initial abundance per stage observed in the field (Fig 12 and 13). As an example *Gentiana pneumonanthe* has 5 stages with its respective abundance. Abundances of the year 1987:

Stage abundance	
S (seedlings)	69
J (Juveniles)	100
V (vegetative)	111
G (reproductive individuals)	21
D (dormant plants)	43

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Firefox - Taverna interaction

localhost:8080/interaction/interaction?id=1229414950963310660&w=741.html

Set Abundance

Initial year: undefined

S 0

J 0

V 0

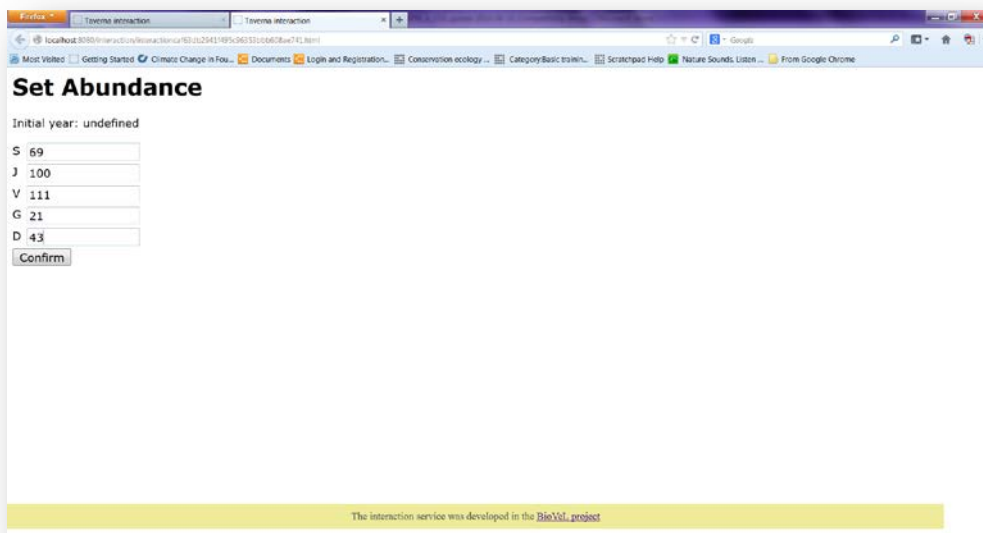
G 0

D 0

Confirm

The interaction service was developed in the [BioVail project](#)

Figure 12. Abundance dialogue. Fill in the abundance per stage appears.



Firefox - Taverna interaction

localhost:8080/interaction/interaction?id=1229414950963310660&w=741.html

Set Abundance

Initial year: undefined

S 69

J 100

V 111

G 21

D 43

Confirm

The interaction service was developed in the [BioVail project](#)

Figure 13. Abundance dialogue. Once the abundances values were submitted. The user confirms the field.

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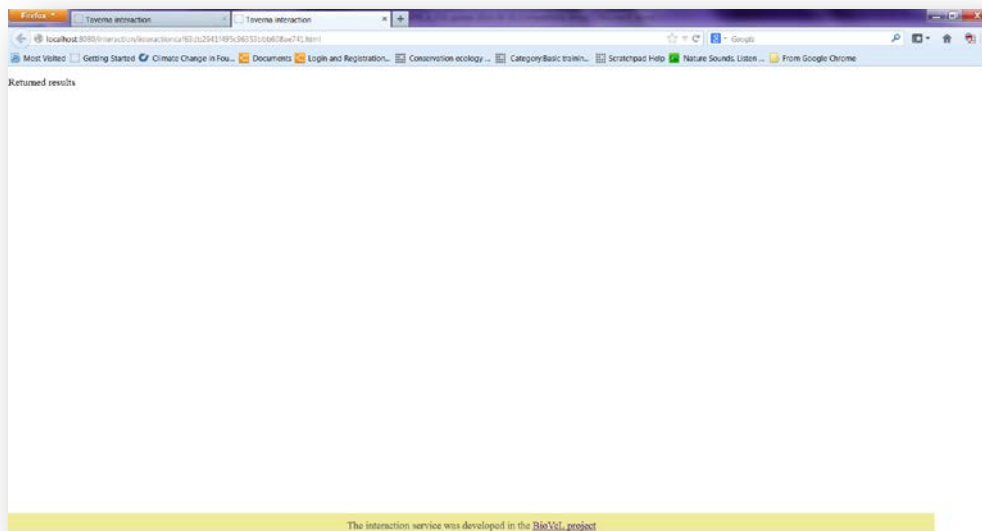


Figure 14. After the user clicks Confirm, the confirmation “Returned results” appears. Refer back to Taverna workbench.

After the user confirms the field, the workflow performs the analysis. To complete all the analysis may take several minutes.

When the analyses are completed, they appear on different windows 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. **eigenanalysis** (green oval in Fig 15). Second, click in the left window on value 1 (blue oval), Third, on the right window click on the save value (red 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 16), Finale, save the file in the chosen map.

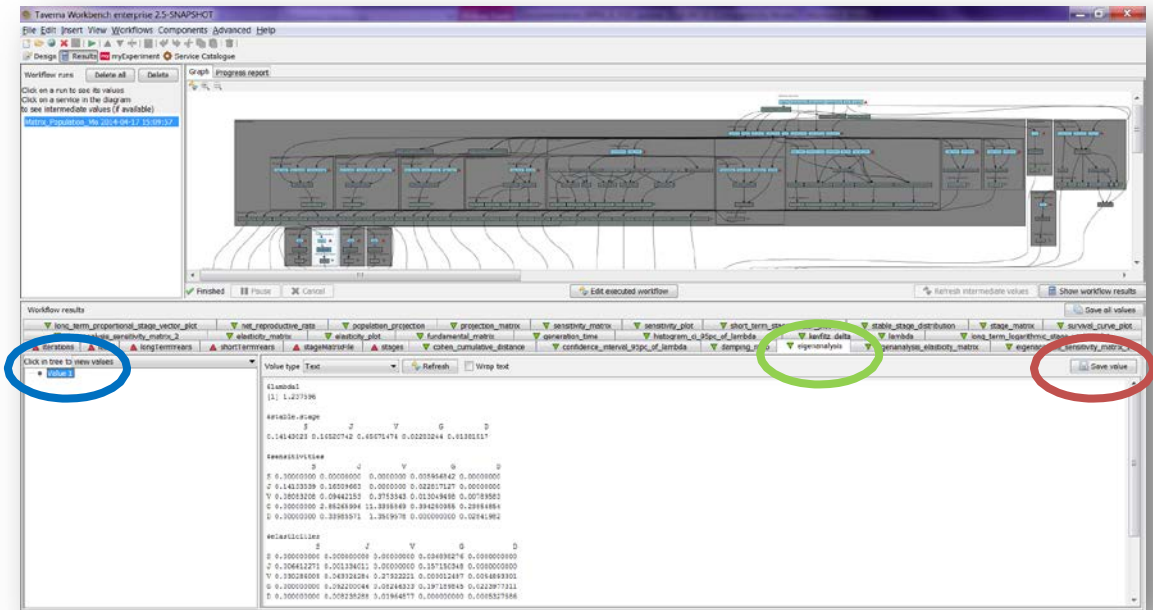


Figure 15. Eigen analysis output window.

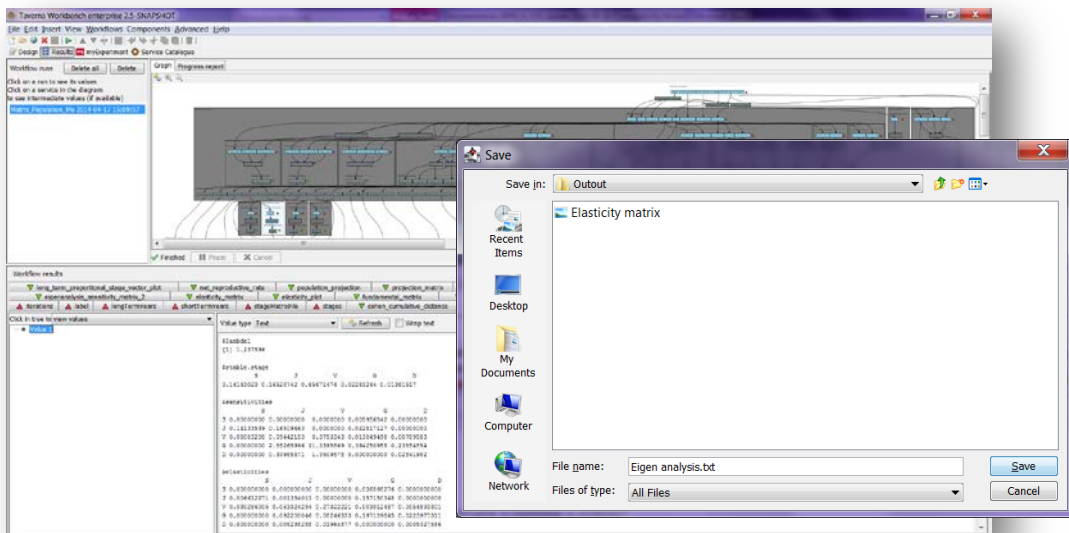


Figure 16. Name the file and determinate the extension file. For a text file: e.g. .csv or .txt. For images: e.g.: .jpg or png.

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1) **Projection_matrix**: This creates a grid of coloured rectangles to display the **stage_matrix** (Fig 17).

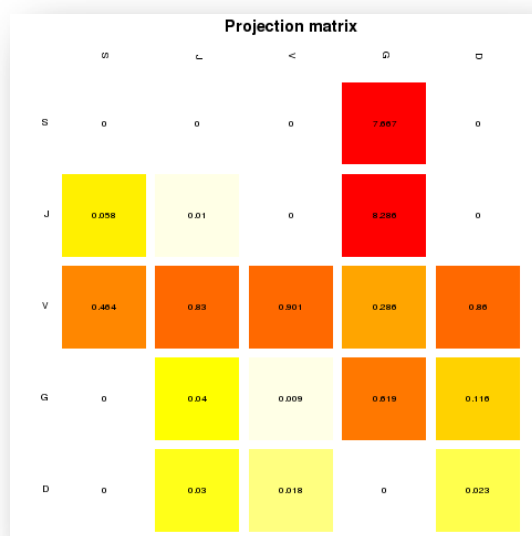


Figure 17. **Projection_matrix** opens as a coloured graph.

2) **Eigen_analysis** (Fig 18)

- 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).
- 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

Elasticity and Sensitivity: Sensitivity and elasticity analyses are prospective analyses.

- The sensitivity matrix**: The sensitivity gives the effect on λ of changes in any entry of the matrix, including those that may, at a given context, be regarded as fixed at zero or some other value. The derivative tells what would happened to λ if a_{ij} was to change, not whether, or in what direction, or how much, a_{ij} actually change. The hypothetical results of such impossible perturbations may or may not be of interest, but they are not zero. It is up to you to decide whether they are useful (Caswell 2001).

When comparing the λ -sensitivity values for all matrix elements one can find out in what element a certain increase has the biggest impact on λ . However, a 0.01 increase in a survival matrix element is hard to compare to a 0.01 increase in a reproduction matrix element, because the latter is not bound between 0 and 1 and can sometimes take high values. Increasing matrix element a_{14} (number of S (seedlings) the next year produced by a G (Reproductive individuals)) with 0.01 from 7.666 to 7.676 does not have a noticeable effect on λ . For comparison between matrix elements it can therefore be more insightful to look at the impact of proportional changes in elements: by what percentage does λ change if a matrix element is changed by a certain

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percentage? This proportional sensitivity is termed elasticity (Description based on Oostermeijer data, based on Jongejans & de Kroon 2012).

- d) **The Elasticity matrix:** The elasticities of λ with respect to the stage are often interpreted as the “contributions” of each of the stages to λ . This interpretation relies on the demonstration, by de Kroon et al (1986) that the elasticities of the λ with respect to the stage, always sum to 1. For further information see: de Kroon, et al., 1986. and Caswell 2001.
- e) **Reproductive value (v):** scaled so $v[1]=1$. To what extent will a plant or animal of a determinate category or stage , contribute to the ancestry of future generation.
- f) **The damping ratio:** 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 p , the quicker the population converges.

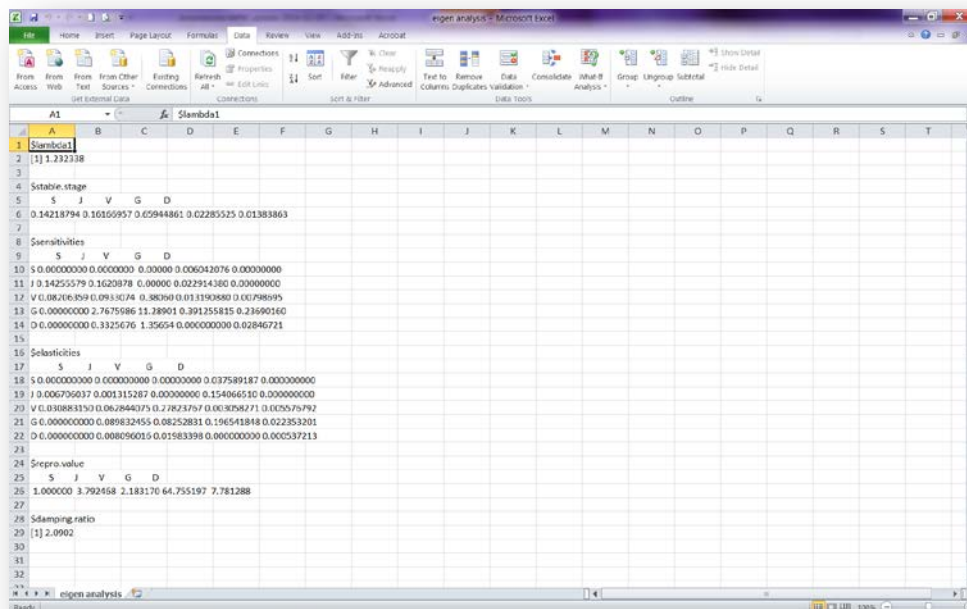


Figure 18. Eigen analysis output file open in excel.

3) **Bartplot:** A bar plot which shows the stable stage distribution (w) of the analysed matrix. In other words, it plots the proportion of individuals per stage (Fig 19).

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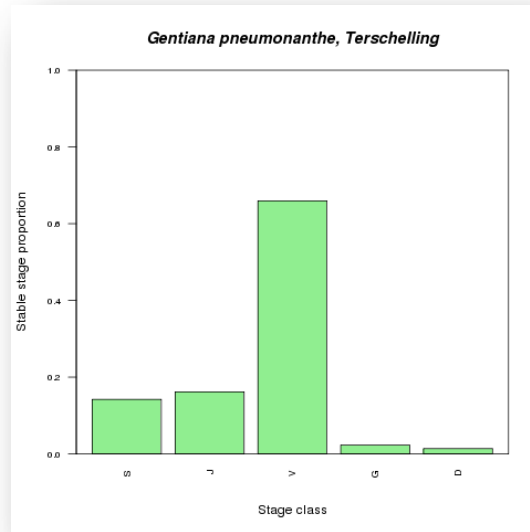


Figure 19. *Bartplot* output file.

4) **Elasticity, Sensitivity 1 and Sensitivity 2 matrices:** Creates a grid of coloured rectangles to display the *elasticity_matrix* (Fig 20), *sensitivity_matrix 1* calculates the sensitivity values of non-zero elements and *sensitivity_matrix 2* calculates the sensitivities of all elements in the matrix (Fig 21 and 22).

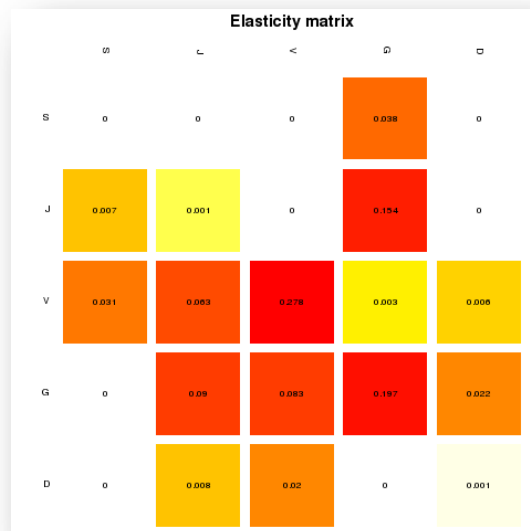


Figure 20. *elasticity_matrix* opens as a coloured graph.

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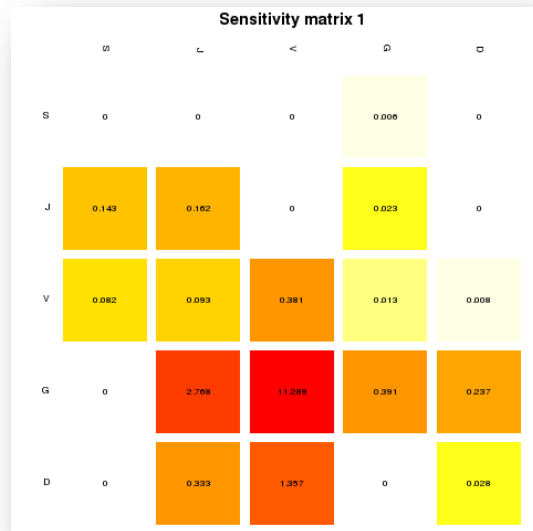


Figure 21. *sensitivity_matrix1* opens as a colour graph.

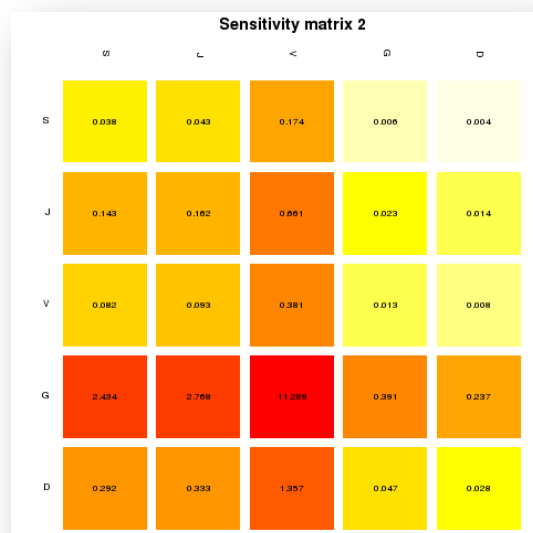


Figure 22. *sensitivity_matrix2* opens as a coloured graph.

5) Age specific survival

The age specific survival workflow gives the basic information on age-specific survival (Fig 23):

- Fundamental matrix (N):** is the mean of the time spent in each stage class. e.g.: For our *Gentiana* example means a J plants will spends, on average, about 1 year as a Juvenile, 11 as vegetative plant, less than a year a reproductive and dormant plant.
- Variance (var):** is the variance in the amount of time spent in each stage class.

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- c) **Coefficient of variation (cv):** is the coefficient of variation of the time spent in each class (sd/mean- the ratio of the standard deviation to the mean).
- d) **Meaneta:** is the mean of time to death, of life expectancy of each stage. e.g. The mean age at death is the life expectancy; the life expectancy of a new individual seedling is
 - 8 years.
- e) **Vareta:** is the variance of time to death.

The screenshot shows an Excel spreadsheet with the following data:

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	
1																						
2	SN																					
3	S		J	V	G	D																
4	J	0,058557	1,010101	0	0	0	0															
5	V	6,890559	11,99681	13,35817	10,01862	12,9606																
6	G	0,208448	0,466788	0,391118	2,918338	0,691977																
7	D	0,128909	0,25233	0,246418	0,184814	1,262894																
8																						
9	Svar																					
10	S		J	V	G	D																
11	S	0	0	0	0	0																
12	J	0,056311	0,010203	0	0	0																
13	V	129,7201	184,5905	165,0824	157,2694	165,3219																
14	G	0,964745	2,039812	1,738736	5,598359	2,868037																
15	D	0,18007	0,321332	0,31526	0,247831	0,332007																
16																						
17	Scv																					
18	S		J	V	G	D																
19	S	0	NaN	NaN	NaN	NaN																
20	J	4,052468	0,1	NaN	NaN	NaN																
21	V	1,65291	1,069391	0,961842	1,25174	0,992065																
22	G	4,712035	3,059674	3,371394	0,810765	2,447376																
23	D	3,291836	2,246508	2,278565	2,693662	0,456254																
24																						
25	Smeaneta																					
26	S		J	V	G	D																
27	S	8,286472	13,72603	13,9957	13,12178	14,91547																
28																						
29	Svareta																					
30	S		J	V	G	D																
31	S	143,4207	181,1844	181,6537	177,2333	181,2319																
32																						
33																						
34																						

Figure 23. Age specific survival opens in excel.

Generation time (T)

6) **Generation time:** Generation time is the time T required for the population to increase by a factor of R_0 (net reproductive rate).

Net reproductive rate (R_0)

7) **Net reproductive rate:** The net reproductive rate is mean number of offspring by which a new-born individual will be replaced by the end of its life, and thus the rate by which the population increases from one generation to the next.

e.g. for Generation time and Net reproductive rate: If $T = 8.13$ and $R_0 = 5.46$.

The average plant of the species *Gentiana pneumonanthe* in Terschelling in the year 1987 replaced itself with five new plants and took approximately 8.13 years to do so.

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Transient dynamic analysis

8) Population projection (Fig 24).

- 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.
- The stable stage distribution** (stable.stage): It is the proportion of the number of individuals per stage and it is given by (w).
- 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).
- Population sizes** (pop.sizes): it is the total population size per year in the long- term (e.g. 50 years).
- Population change** (pop.changes): are the lambda values per year in the long-term
 - (e.g. 50 years).

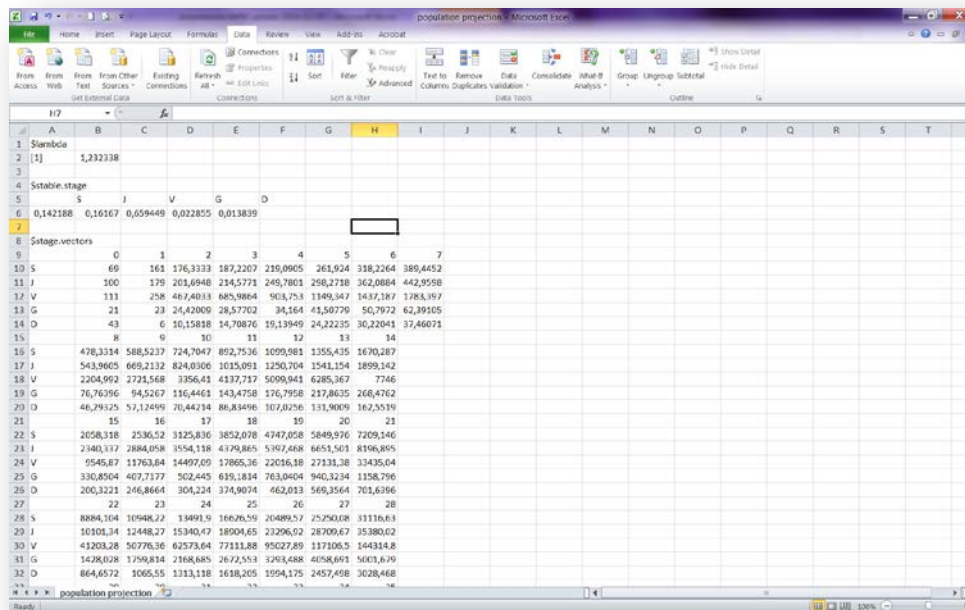


Figure 24. Population projection opens in excel.

9) **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

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reached fairly soon.

e.g. damping ratio= 2.0901.

10) **stageVectorPlotLongTermProportional**: Is the proportion of individuals per stage in the long term (e.g.: 50 years) (Fig 25)

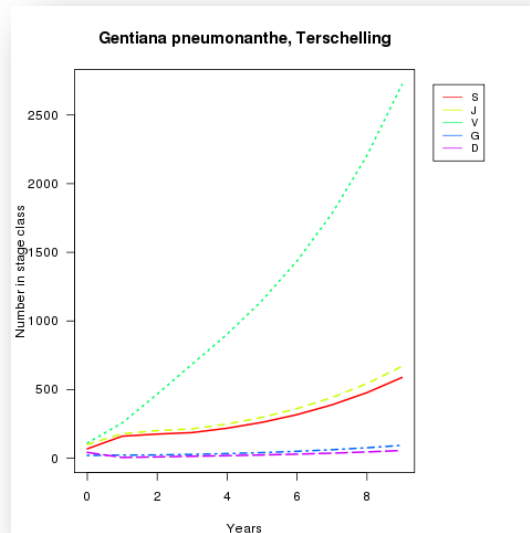


Figure 25. **Stage vector plot long term proportional** opens as a graph.

11) **stageVectorPlotLongTermLogarithmic**: Is the number of individuals per stage in the long term (e.g.: 50 years) (Fig 26).

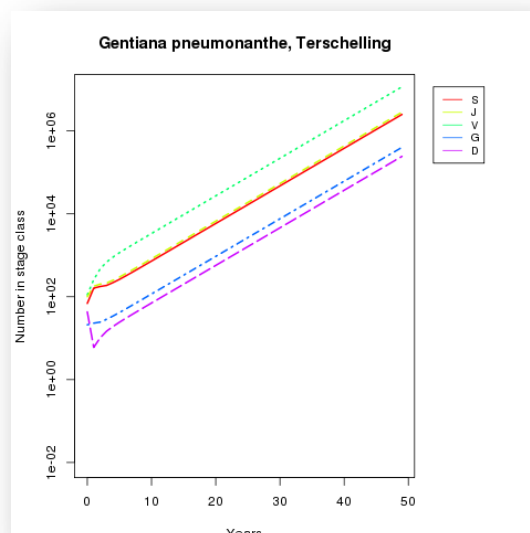


Figure 26. **Stage vector plot long term logarithmic** opens as a graph.

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12) **stageVectorPlotShortTerm**: It is a plot that charts the number of individuals per stage vs. years in the short-term (e.g. 5, 10 years). This value (5 or 10 years) is related to the short-term years input value. (Fig 27).

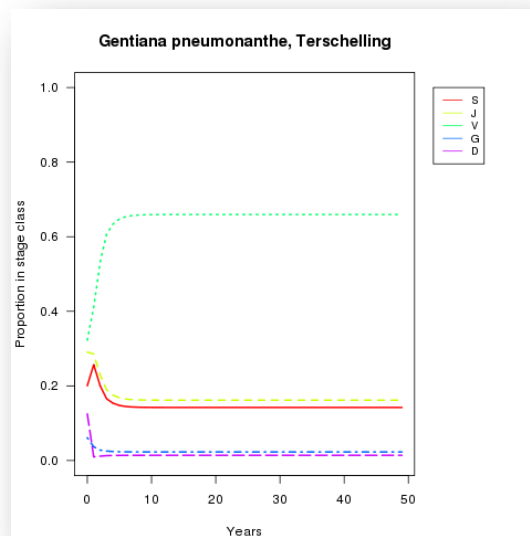


Figure 27. **Stage vector plot short term** opens as a graph.

Bootstrap analysis

13) **Confidence_interval**: 95% Confidence interval of Lambda. In statistics, a confidence interval (CI) is a type of interval estimate of a population parameter and is used to indicate the reliability of an estimate. It is an observed interval (i.e. it is calculated from the observations), in principle different from sample to sample, that frequently includes the parameter of interest if the experiment is repeated. How frequently the observed interval contains the parameter is determined by the confidence level or confidence coefficient

e.g.:	2.5%	97.5%
	0.9566	1.4648

14) **CI_histogram**: Histogram plotting the frequencies of the lambda values and the 95% confidence intervals resulting from the bootstrap analysis (Fig 28).

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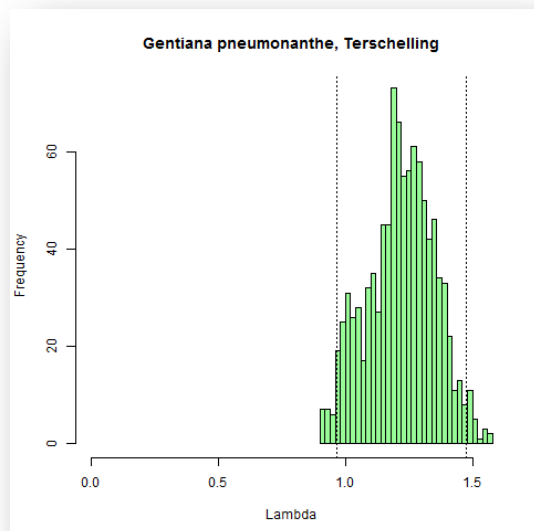


Figure 28. *The confidence interval histogram* opens as a graph.

15) **Survival curve:** A plot of survival curve, where the probability of survival is plotted per stage. (Fig. 29)

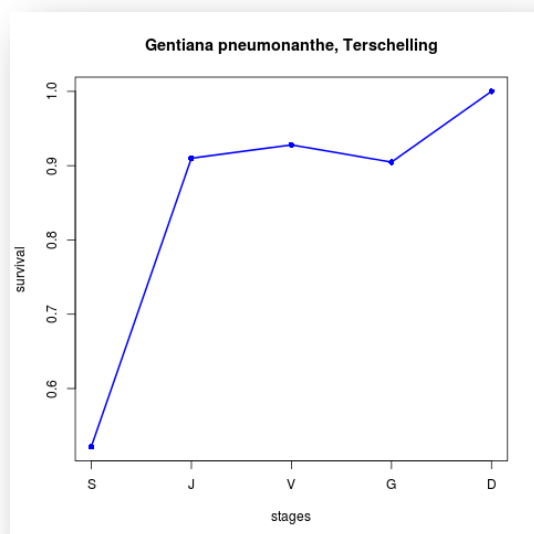


Figure 29. *Survival curve.*

16) **Keyfitz's Δ :** Keyfitz's delta is a measure of the distance between n (Observed Stage Distribution) and w (Stable Stage Distribution). Its maximum value is 1 and its minimum is 0 (when the vectors are identical).

e.g. 0.3367

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17) **Cohen's cumulative distance** Cohen's cumulative distance measures the difference between observed and expected vectors along the matrix path that the population would take to reach the expected population vector.

e.g. 2.6732

For further details see: References

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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 References

This workflow was created using and based on Packages 'popbio' in R. (Stubben & Milligan 2007; Stubben, Milligan & Nantel 2011) and popdemo (Stott, Hodgson and Townley, 2013)

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7.1 Acknowledgements

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7.2 Publications