

BioVeL – Biodiversity Virtual e-Laboratory

Workflow Documentation

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

July 2014

Capacities Programme of Framework 7: EC e-Infrastructure Programme –
e-Science Environments - INFRA-2011-1.2.1

Grant Agreement No:
Project Co-ordinator:
Project Homepage:
Duration of Project:

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



Matrix Population Models construction and analyses (Integrated) Workflow for local execution

1 Description

The Matrix Population Models construction and analyses Workflow provides an environment for create a stage-matrix with no density dependence and perform several analyses on it.

Analyses:

- Eigen analysis.
- Age specific survival.
- Generation time (T).
- Net reproductive rate (R_0).
- Transient Dynamics.
- Bootstrap of observed census transitions (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 construction and analyses (Integrated) Workflow for local execution

Download: The workflow pack can be downloaded at myExperiment under the following address:
<http://www.myexperiment.org/packs/483.html> or only the workflow:
<http://www.myexperiment.org/workflows/3684.html>

To see this documentation online:

<https://wiki.biovel.eu/display/doc/Matrix+Population+Models+Workflow>

2.2 Date, version and licensing

Last updated: 4th July 2013

Version: 20

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 Gerard Oostermeijer unpublished results and publication: Oostermeijer, J.G.B. M.L. Brugman, E.R. de Boer; H.C.M. Den Nijs. 1996.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 construction and 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, Bootstrap of observed census transitions (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 for construct a stage matrix and analyse it. 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 seven distinct parts and/or analyses (Fig 1a and B):

1. Construction of a stage matrix model from demographic monitoring of individuals in an animal or plant population with not density dependence. This section of the workflow create a stage matrix based on two years census data that contains transitions probabilities from each stage to the next, of tagged or mapped individuals of an animal or plant population. The resulting stage matrix is then used to perform the other components of the workflow: the Eigen analyses, age specific survival, generation time (T), net reproductive rate (R_0) and transient dynamics.

2. 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.

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

- c) The sensitivity matrix
- d) The Elasticity matrix.
- e) Reproductive value.
- f) The damping ratio.

3. 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 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) Varetta: is the variance of time to death.

4. 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 .

5. 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.

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

7. Bootstrap of observed census transitions: This workflow calculates bootstrap distributions of population growth rates (λ), stage vectors, and projection matrix elements by randomly sampling with replacement from a stage-fate data frame of observed transitions. The goal of a demographic analysis is very often to estimate lambda, because lambda is estimated from imperfect data, such estimation are uncertain. Therefore, when the results have policy implications it is important to quantify that uncertainty. Confidence interval is one of the traditional tools to doing so.

8. Survival curve: Plots the survival curve.

9. 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).

10. 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).

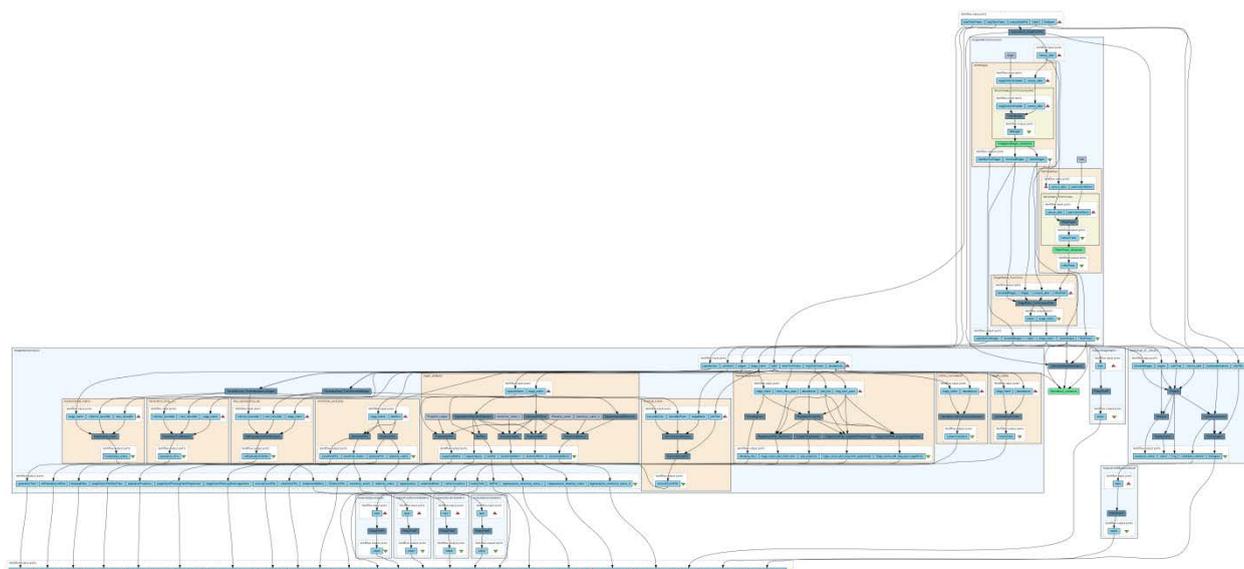


Figure 1. Stage matrix construction and analysis workflow in Taverna workbench.

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+

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

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")`
- 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.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

In this tutorial, you will use an input file `Gentiana87-91.txt`, called in `myexperiment.org`: Demographic data *Gentiana pneumonanthe* 1987-1991 from Terschelling File to construct a stage matrix without density dependence and 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 input data (a `.txt`-file) has to have the format of a table containing the demographic data on a series of individuals in two or more years. Each individual has a table row for each year and is identified by a number (plant column in example). For the year specified in the column 'year', each individual has a certain life stage ('stage'). The stage codes can be chosen by the user, but they have to be specified with a string. For all individuals, the number of offspring is specified in a chosen way (in the example, 'repstr' gives the number of flowers/fruits for each plant. In the example, it can be seen that only generative

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

adults (stage=G) had flowers. Individuals without offspring have to be indicated by filling in '0' in this column, which cannot have empty cells. The column 'recruitment' specifies those individuals that are new in the second year census to the population by means of a code. In the example, 'RS' is a new seedling, and 'RJ' a new juvenile plant. As can be seen in the example, no code is needed in this column for individuals that were already present (Table 1).

Table 1. Input file in a .txt format to create a stage matrix.

plant	year	stage	reprstr	recruitment
2	1987	D	0	
4	1987	J	0	
5	1987	D	0	
31	1987	V	0	
36	1987	D	0	
37	1987	J	0	
41	1987	J	0	
43	1987	S	0	
46	1987	V	0	
47	1987	S	0	
2	1988	V	0	
4	1988	D	0	
5	1988	V	0	
9	1988	J	0	RJ
14	1988	J	0	RJ
15	1988	J	0	RJ
16	1988	J	0	RJ
17	1988	J	0	RJ
18	1988	J	0	RJ
24	1988	S	0	RS
25	1988	S	0	RS
31	1988	V	0	
32	1988	S	0	RS
33	1988	J	0	RJ
35	1988	S	0	RS
36	1988	V	0	

The workflow accepts input data (Table 1) in a .txt format, All examples data input for the tutorial are available in the PACK: <http://www.myexperiment.org/packs/483.html> The example data Gentiana87-91.txt for the tutorial is available as well at: <http://www.myexperiment.org/files/850.html> or here below. The second data Dt1.txt is available at: <http://www.myexperiment.org/files/853.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

- [Gentiana87-91.txt](#) (This table contain data from 87 to 91)
- [Dt1.txt](#) (This table only contain data from 87 to 88)

For this tutorial we use the [Gentiana87-91.txt](#) file.

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) **CensusDataFile:** The input data (a .txt-file) has to have the format of a table containing the demographic data on a series of individuals in two or more years. Each individual has a table row for each year and is identified by a number (plant column in example). For the year specified in the column 'year', each individual has a certain life stage ('stage'). The stage codes can be chosen by the user, but they have to be specified with a string. For all individuals, the number of offspring is specified in a chosen way (in the example, 'repstr' gives the number of flowers/fruits for each plant. In the example, it can be seen that only generative adults (stage=G) had flowers. Individuals without offspring have to be indicated by filling in '0' in this column, which cannot have empty cells. The column 'recruitment' specifies those individuals that are new in the second year census to the population by means of a code. In the example, 'RS' is a new seedling, and 'RJ' a new juvenile plant. As can be seen in the example, no code is needed in this column for individuals that were already present (Table 1).

Click in Set file location (red arrow in Fig 2), a window dialog appears and the user selects the file (e.g. [Gentiana87-91.txt](#)) and then clicks the Open button. Then the link to the file will appear on the Taverna window.

Example of Input page:

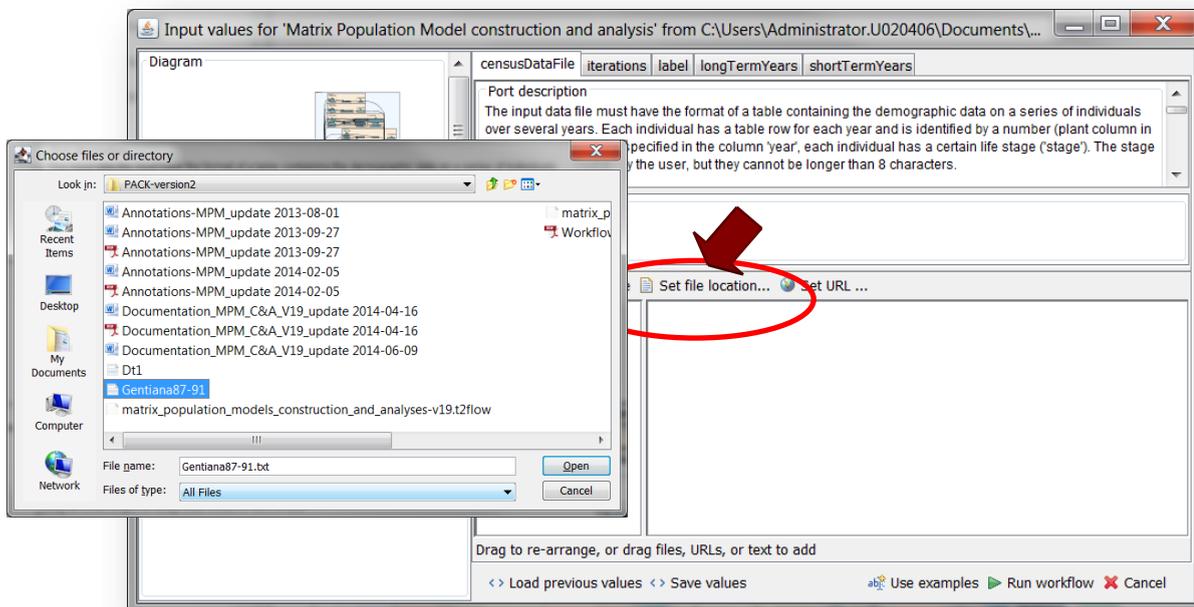


Figure 2. Inputs file to be filled in.

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

2) **BootstrapIterations**: Number of iterations for calculation of bootstrap distributions. Press add value, fill a number and press enter.

e.g.: 1000

3) **Label**: Descriptive title for labelling generated outputs (graphs). Press add value, fill a title and press enter.

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

4) **LongTermYears**: It is the maximal number of iteration or repetitions in the transient dynamic analysis. Press add value, fill a number and press enter.

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.

5) **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. Press add value, fill a number and press enter.

e.g.: 10

This value represents the years of axis X of the output graph: StageVectorPlotShortTerm (see output port):

1) StageVectorPlotShortTerm.

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 appears the names of the stages or categories of the census data file. When the dialogue appears, the stages are in disorder (Fig 3), so the user drags and organizes the stages according to the order in the life cycle. Then, the author chooses if the stage belongs to the recruited, reproductive category or it should be excluded (Fig 4 and 5). 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). In the census data file *Gentiana87-91.txt*, x is use to denote when a plant has died in the second year, so the user must selected in the excluded column.

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

Then the user clicks in confirm and you will read stages submitted (Fig 3, 4 and 5).

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

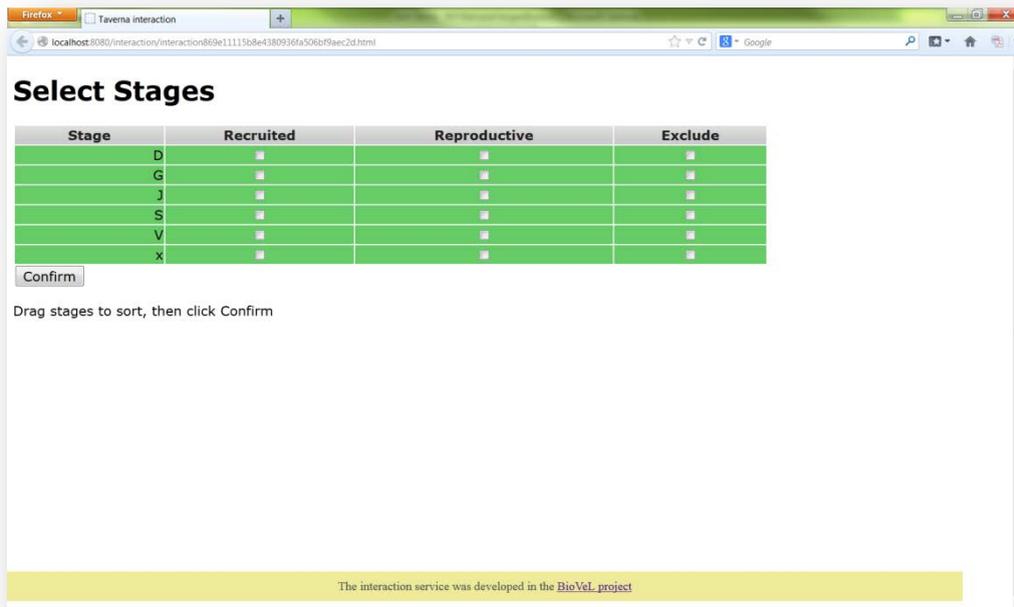


Figure 3. Stages dialogue. When the dialogue appears, the stages are in disorder.

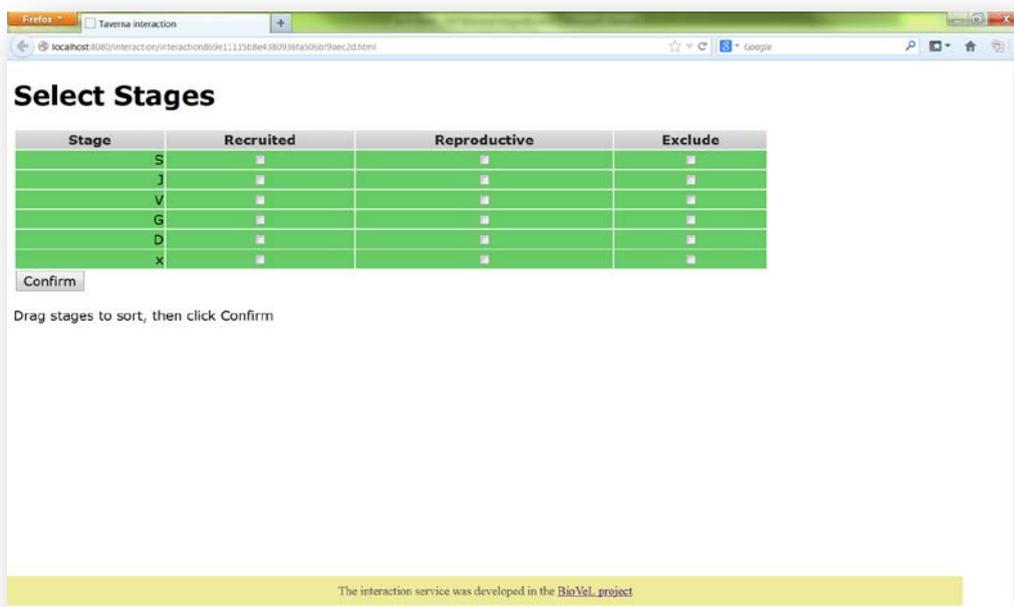


Figure 4. Stages dialogue. Drag each stage to the proper order. The stages should be organized as in the

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

life cycle by the user (e.g. S, J, V, G, D, x).

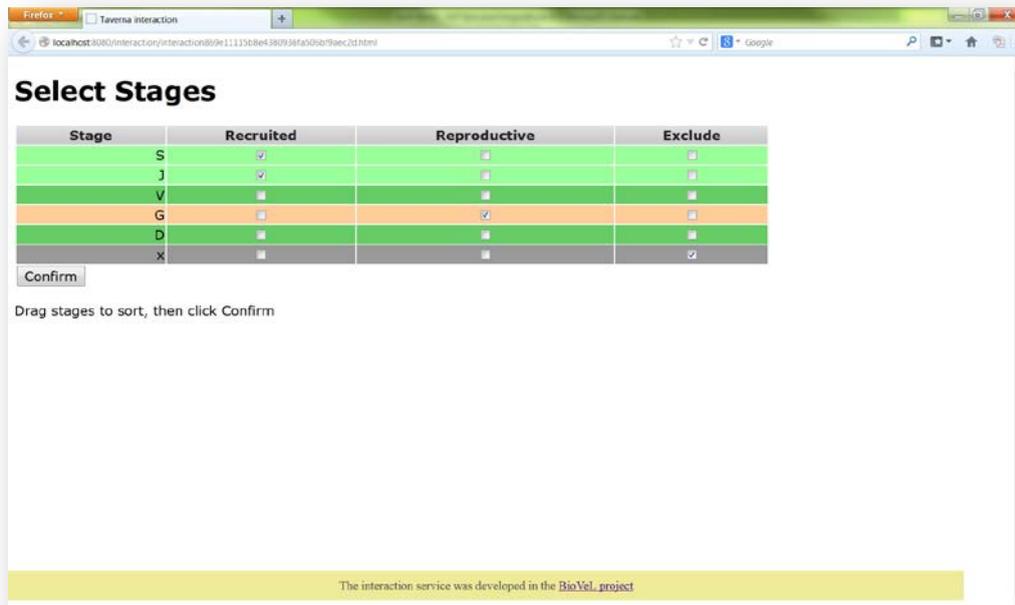


Figure 5. Stages dialogue. Choose if the stage belongs to the recruited or reproductive category, or should be excluded.

2) **Year:** In this dialogue view the years of the census data file (Fig 6, example file from 1987 to 1991). Select one or multiple census years. In this example the years 1987 - 1988 and 1988 - 1989 have been chosen (Fig 7 and 8). That means that the analysis will create two matrices, one for the interval 1987 - 1988 and a second one for 1988 - 1989. After this step, the user should confirm the selection (Fig 8).

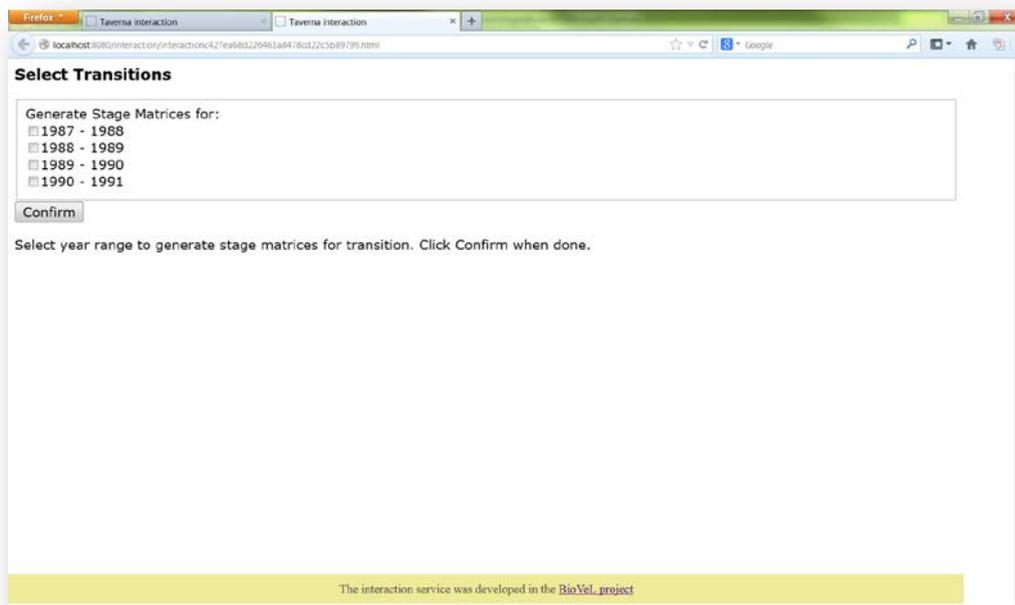


Figure 6. Year's dialogue. When the dialogue appears, the user selects the year interval of one or more year matrices.

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

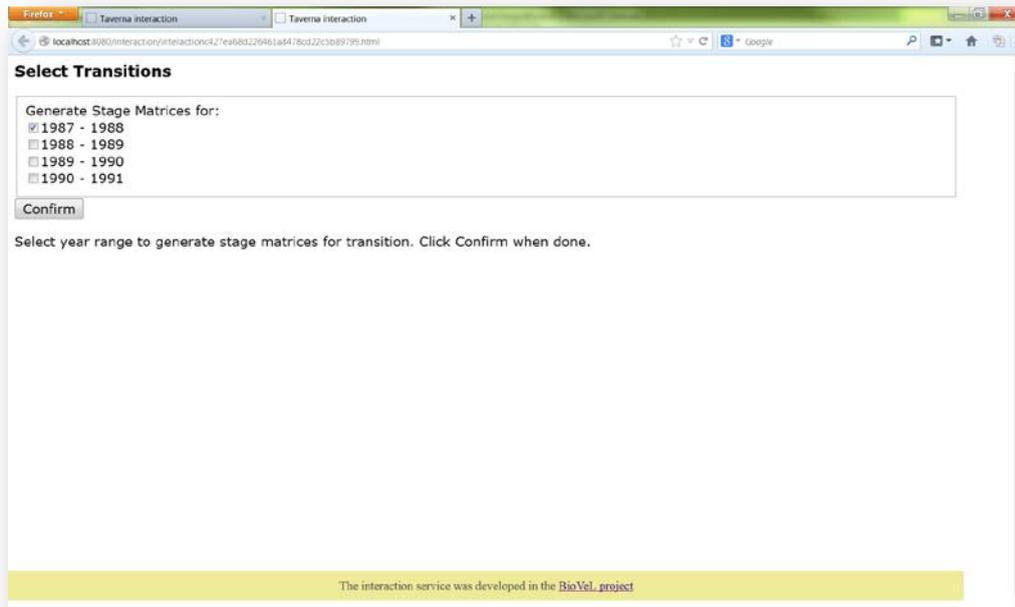


Figure 7. Year dialogue. The user selects the year interval, in this case 1987-1988, for a year matrix 1987-1988.

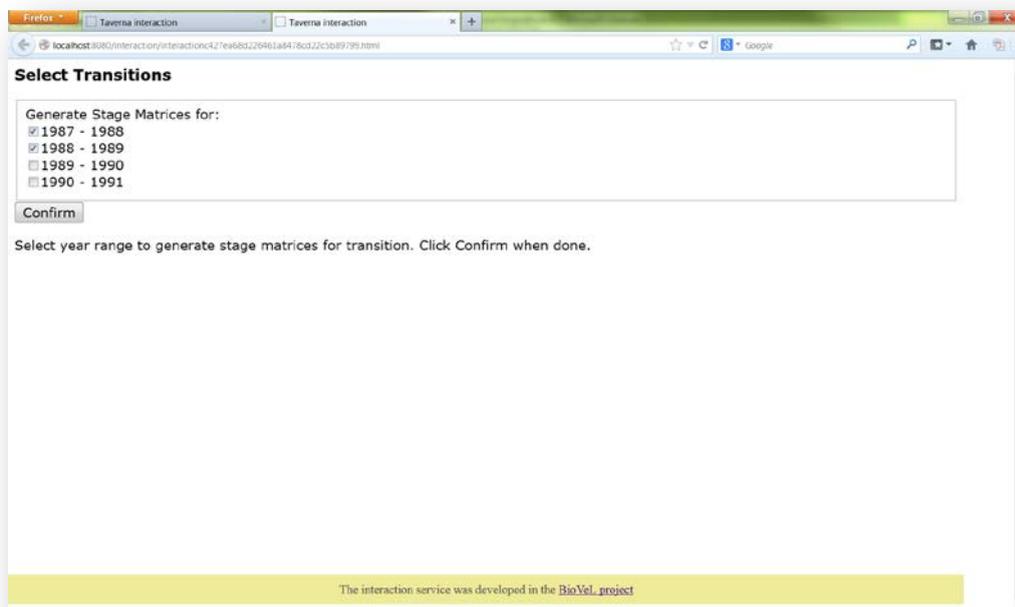


Figure 8. Year dialogue. The user can select other year, in this case 1988 -1989, to generate one more matrix, a matrix from the year 1988-1989. The user confirms the choice.

3) **Initial abundance:** In this dialogue appears the fields with the initial abundance per stage observed in the field (Fig 9). As an example *Gentiana pneumonanthe* has 5 stages with its respective abundance. Abundances of the year 1987:

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

Stage abundance:

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

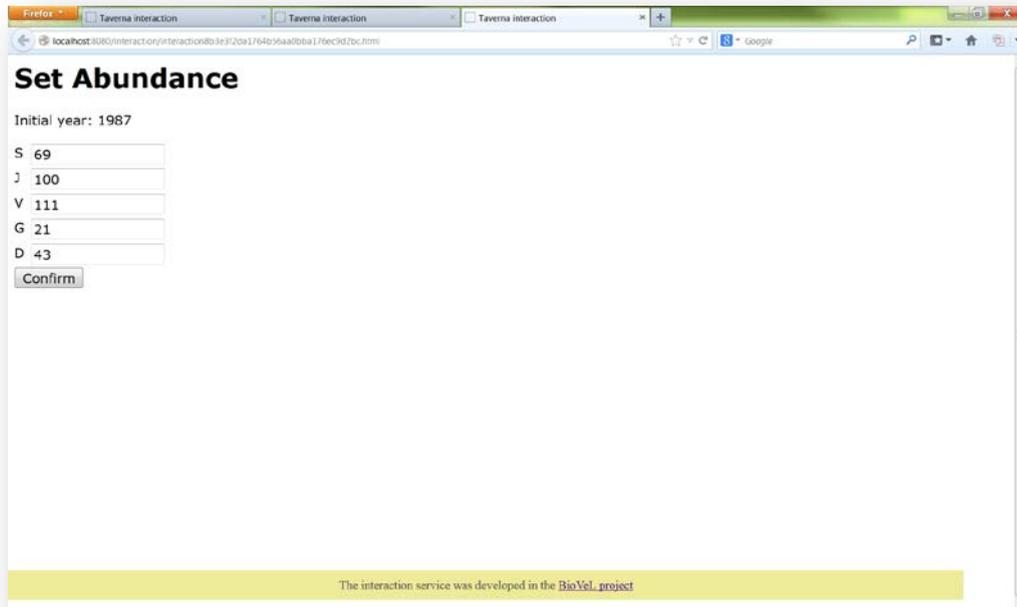


Figure 9. Abundance dialogue. The abundance per stage appears. This dialogue will appear for each selected year. The user confirms the field.

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. **stage_matrix** (Fig 10). Second, click in the left window on value 1 (Fig 11), Third, on the right window click on the save value (Fig 12). Fourth, name the file and determinate the extension file. For a text file: e.g. .csv or .txt. For images: .jpg or png (Fig 13), Finale, save the file in the chosen map.

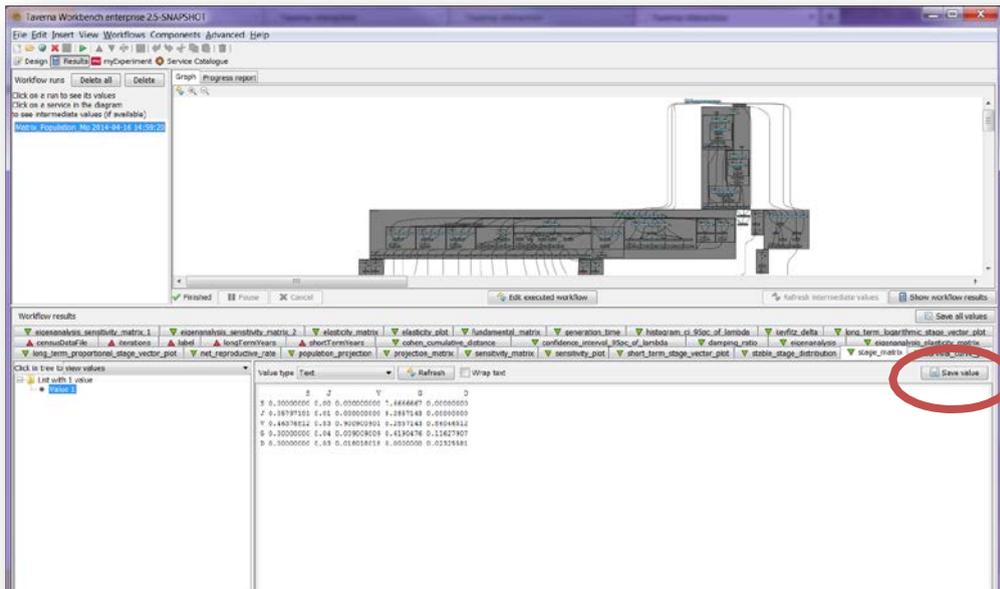


Figure 10. Stage-matrix output window.

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

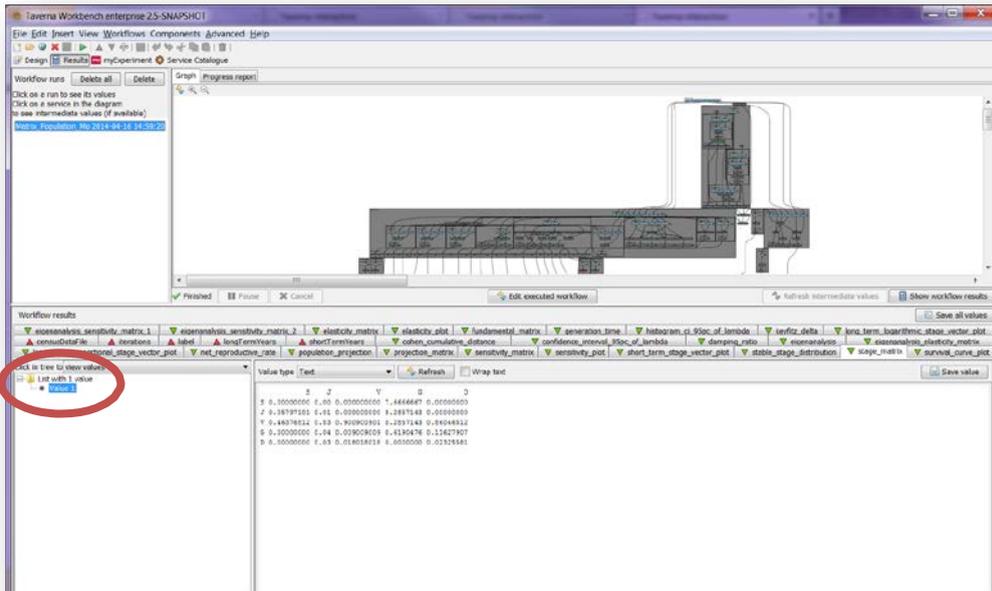


Figure 11. Value 1 on the left window of the stage_matrix output results.

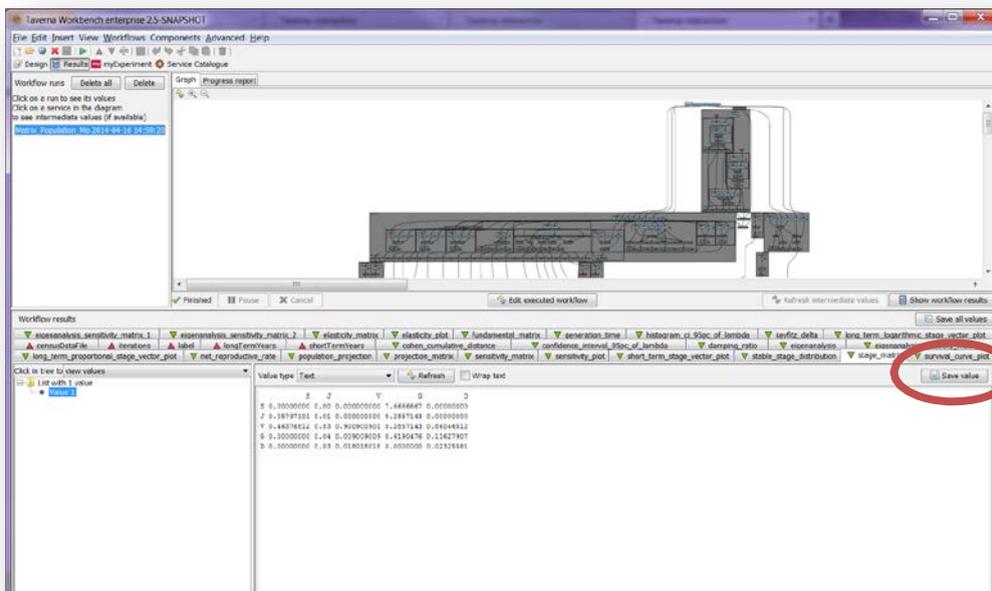


Figure 12. Save value on the right window of the stage_matrix output results.

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

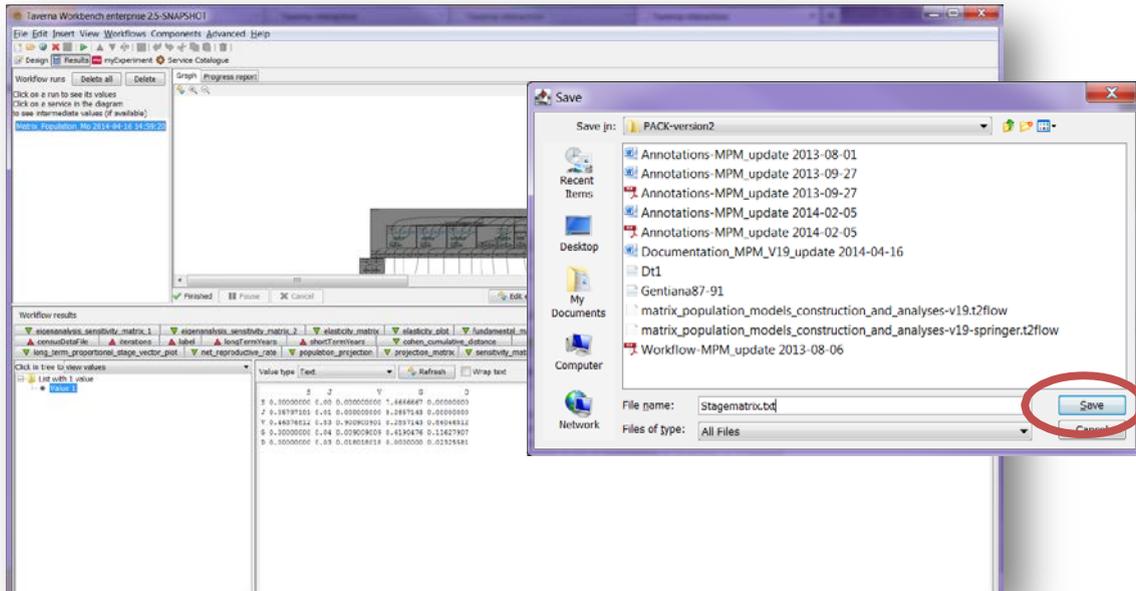


Figure 13. Name the file and determine the extension file. For a text file: e.g. .csv or .txt. For images: e.g.: .jpg or png.

Construction matrix

1) **Stage_matrix**: a stage matrix contains transitions probabilities from each stage to the next. In this example the selected species is *Gentiana pneumonanthe* has a matrix of 5 x 5 stages (Fig. 14; Oostermeijer et al., 1996).

	S	J	V	G	D
S	0	0	0	7.666667	0
J	0.057971	0.01	0	8.285714	0
V	0.463768	0.83	0.909091	0.285714	0.850465
G	0	0.04	0.009091	0.619048	0.116279
D	0	0.03	0.018018	0	0.023256

Figure 14. *stage_matrix* output file open in excel.

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

Furthermore this workflow creates the:

2) **Projection_matrix**: This creates a grid of coloured rectangles to display the **stage_matrix** (Fig 15).

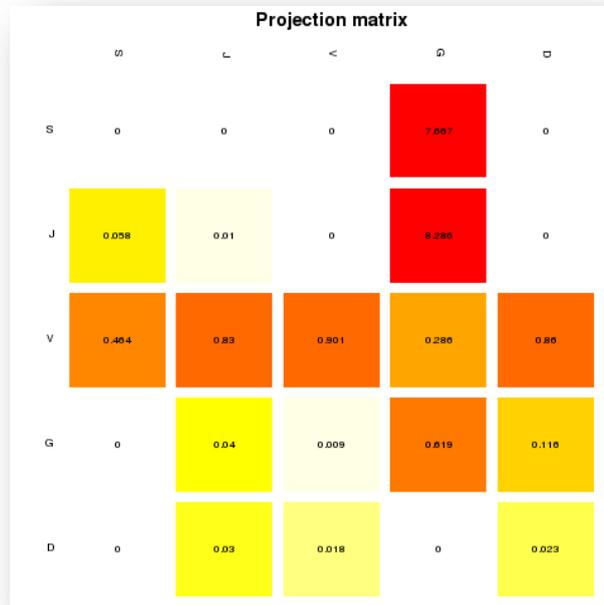


Figure 15. **Projection_matrix** opens as a coloured graph.

3) **Eigen_analysis**

- 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

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

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 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.

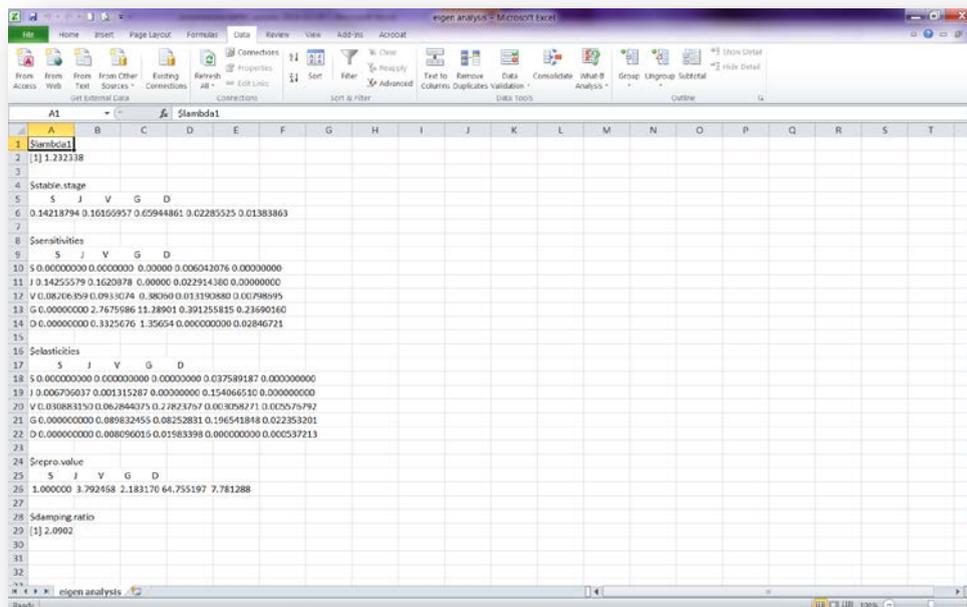


Figure 16. Eigen analysis output file open in excel.

4) **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 17).

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

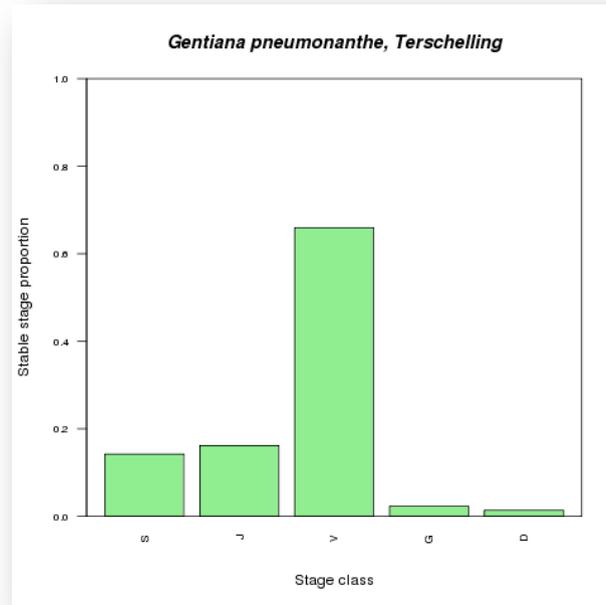


Figure 17. *Bartplot* output file.

5) **Elasticity, Sensitivity 1 and Sensitivity 2 matrices:** Creates a grid of coloured rectangles to display the *elasticity_matrix* (Fig 15), *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 18, 19 and 20).

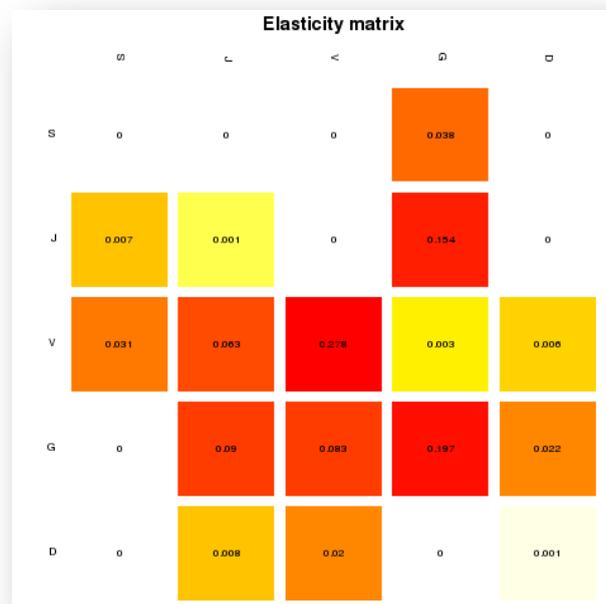


Figure 18. *elasticity_matrix* opens as a coloured graph.

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

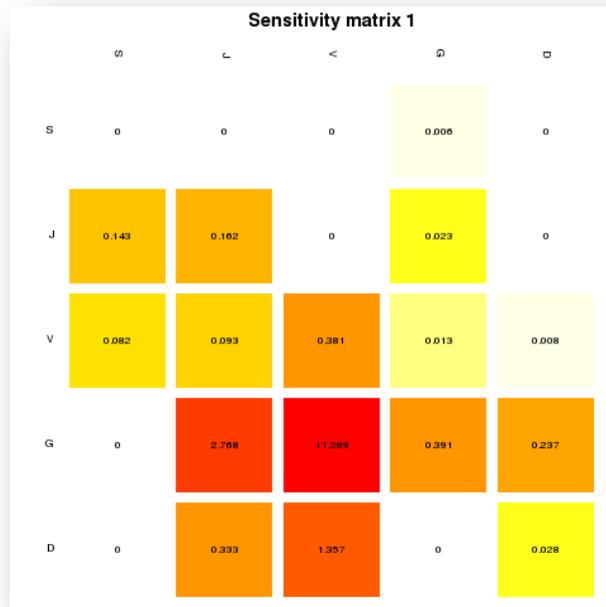


Figure 19. *sensitivity_matrix1* opens as a colour graph.

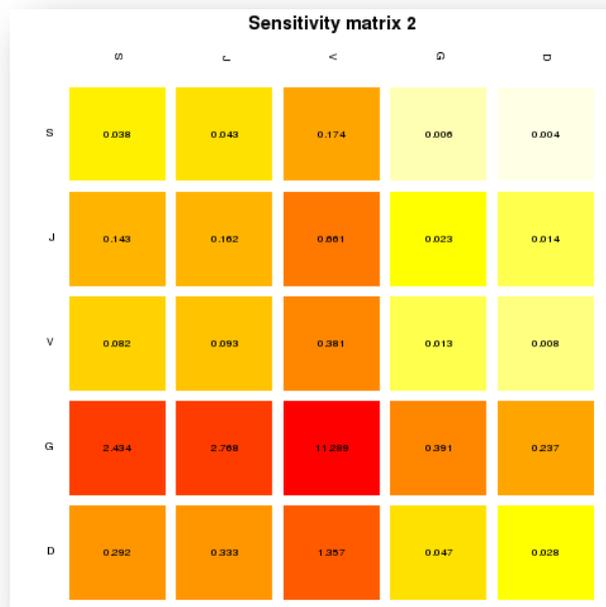


Figure 20. *sensitivity_matrix2* opens as a coloured graph.

6) Age specific survival

The age specific survival workflow gives the basic information on age-specific survival (Fig 21):

- a) **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

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

vegetative plant, less than a year a reproductive and dormant plant.

- 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.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.

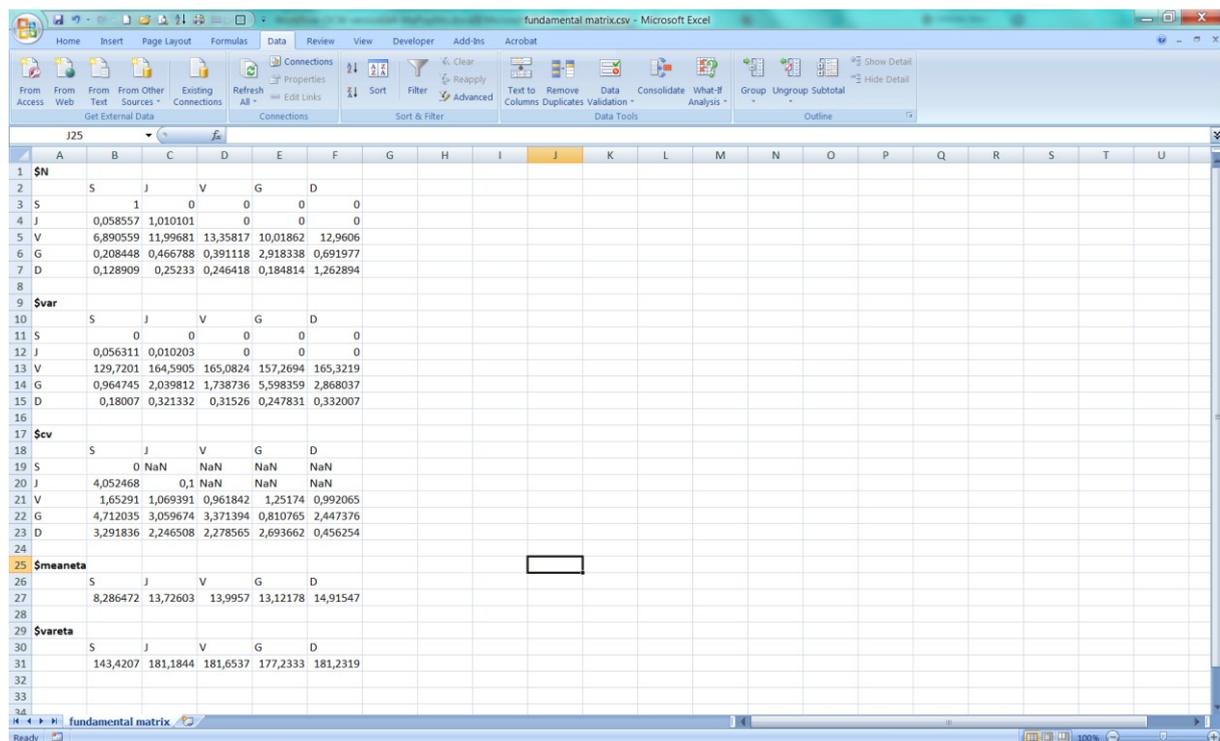


Figure 21. Age specific survival opens in excel.

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

e.g. 8.055186

8) **Net reproductive rate (Ro):** 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 $T = 8.05$ 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 8.05 years to do so.

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

9) *Transient dynamic analysis*

Population projection (Fig 22).

- 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).

10) **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.

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

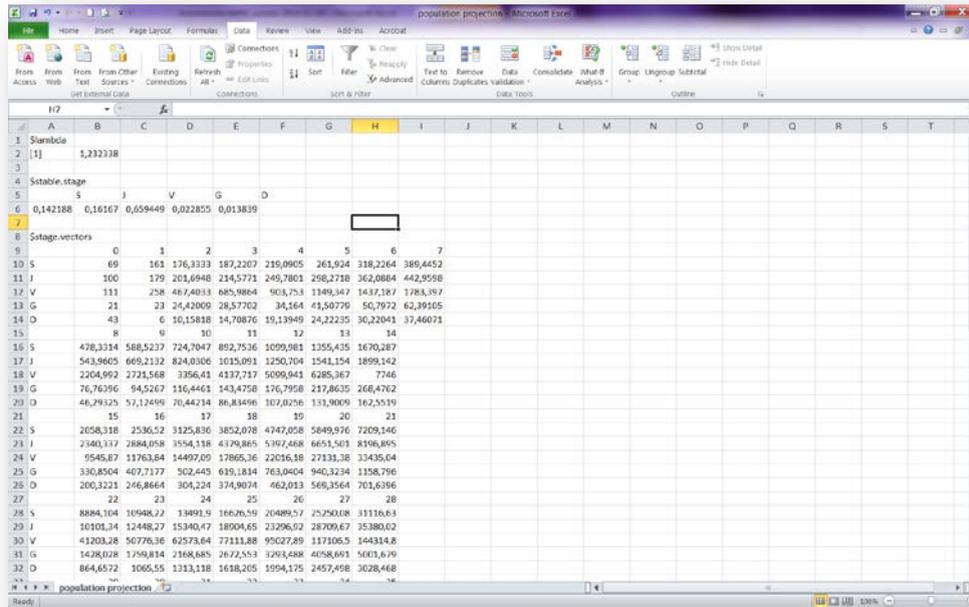


Figure 22. *Population projection* opens in excel.

11) *stageVectorPlotLongTermProportional*: Is the proportion of individuals per stage in the long term (e.g.: 50 years) (Fig 23)

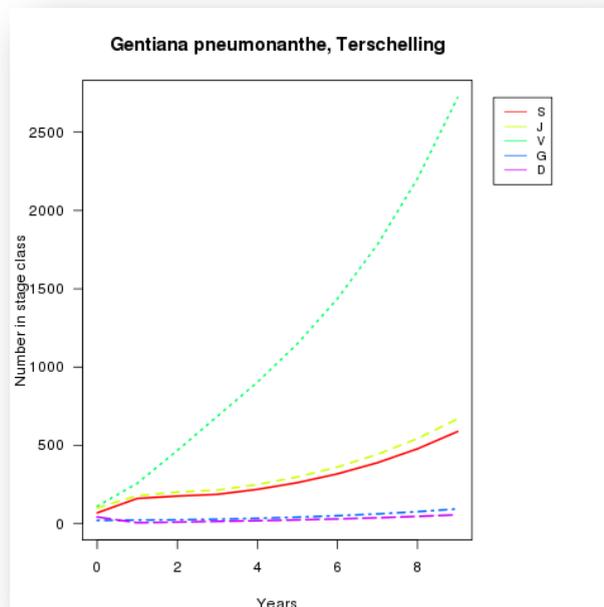


Figure 23. *Stage vector plot long term proportional* opens as a graph.

12) *stageVectorPlotLongTermLogarithmic*: Is the number of individuals per stage in the long term (e.g.: 50 years) (Fig 24).

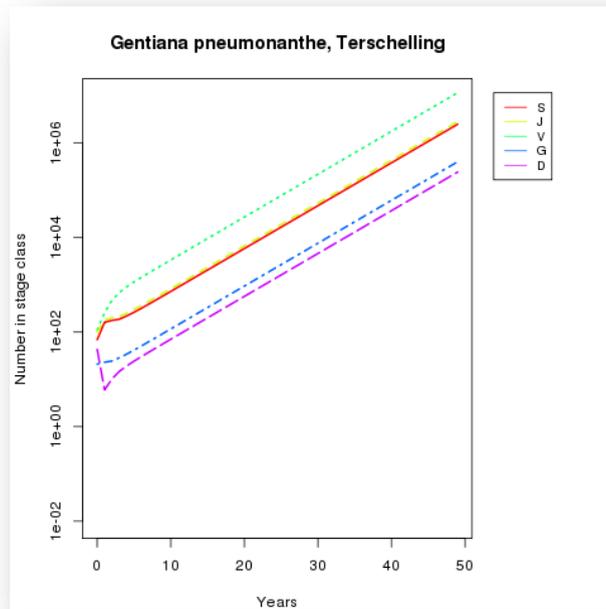


Figure 24. Stage vector plot long term logarithmic opens as a graph.

13) 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 25).

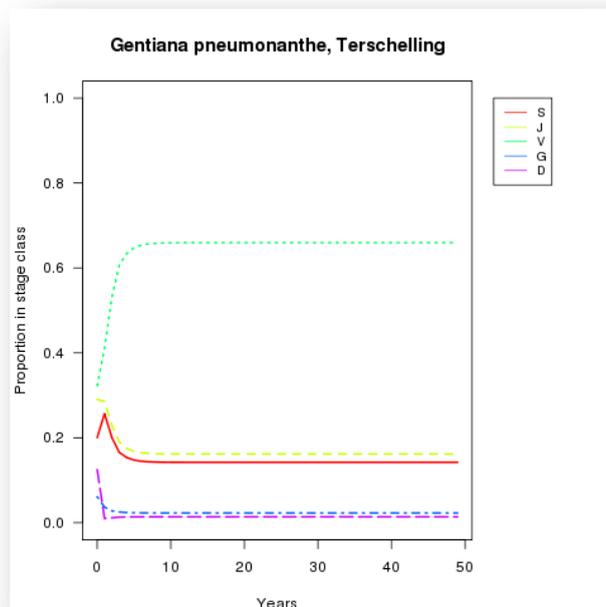


Figure 25. Stage vector plot short term opens as a graph.

Bootstrap analysis

14) **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

15) **CI_histogram**: Histogram plotting the frequencies of the lambda values and the 95% confidence intervals resulting from the bootstrap analysis (Fig 26).

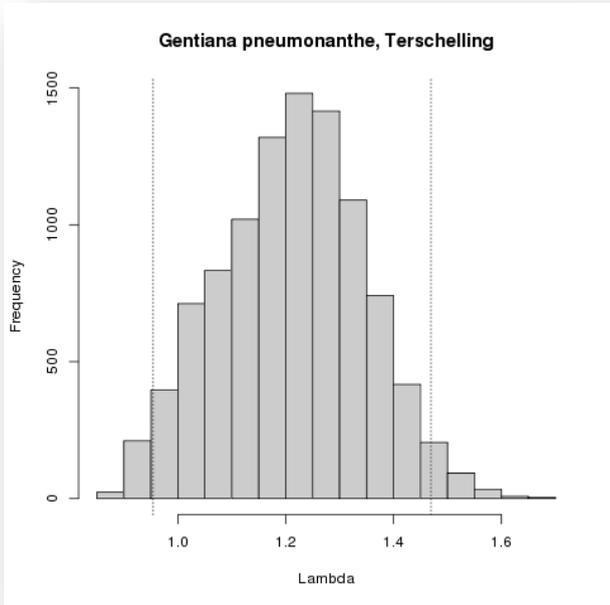


Figure 26. The confidence interval histogram opens as a graph.

16) **Survival curve**: A plot of survival curve, where the probability of survival is plotted per stage. (Fig. 27)

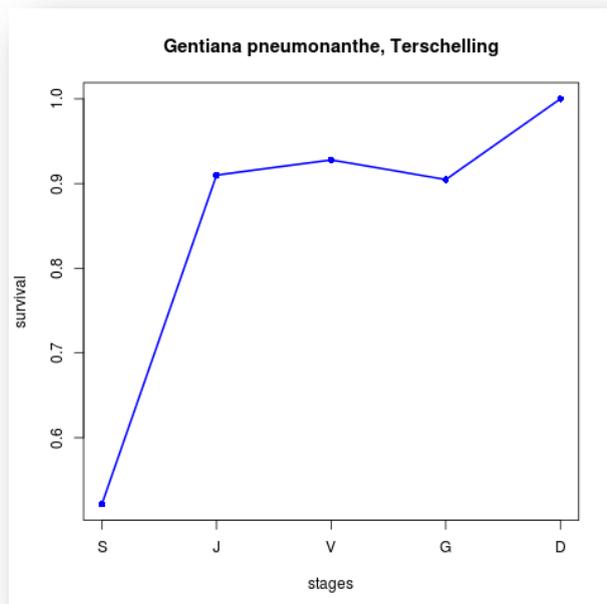


Figure 27. *Survival curve.*

17) 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

18). 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

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)

Caswell, H. 1986. Life cycle models for plants. *Lectures on Mathematics in the Life Sciences* 18: 171-233.

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

Cohen, J.E. 1979. The cumulative distance from an observed to a stable age structure. *SIAM Journal on Applied Mathematics*, 36:169–175.

de Kroon, H. J., A. Plaiser, J. van Groenendael, and H. Caswell. 1986. Elasticity: The relative contribution of demographic parameters to population growth rate. *Ecology* 67: 1427-1431.

Horvitz, C., D.W. Schemske, and Hal Caswell. 1997. The relative "importance" of life-history stages to population growth: Prospective and retrospective analyses. In S. Tuljapurkar and H. Caswell. *Structured population models in terrestrial and freshwater systems*. Chapman and Hall, New York.

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

Keyfitz, N. 1968. *Introduction to the Mathematics of Populations*. Addison-Wesley, Reading, MA, USA.

Mesterton-Gibbons, M. 1993. Why demographic elasticities sum to one: A postscript to de Kroon et al. *Ecology* 74: 2467-2468.

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

Matrix Population Models construction and analyses (Integrated) Workflow for local execution

Stott, I., D.J. Hodgson and S. Townley. 2013. popdemo: Provides Tools For Demographic Modelling Using Projection Matrices. Version 0.1-3.

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

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.

Williams, J.L., M.M. Ellis, M.C. Bricker, J.F. Brodie and E.W. Parsons. 2011. Distance to stable stage distribution in plant populations and implications for near-term population projections. *Journal of Ecology*, 99, 1171–1178.

7.1 Acknowledgements

7.1.1 Authors

1. **Maria Paula Balcazar-Vargas** Instituut voor Biodiversiteit en Ecosysteem Dynamica (IBED), Universiteit van Amsterdam.
2. **Jonathan Giddy** Cardiff School of Computer Science and Informatics, Cardiff University, Cardiff CF24 3AA, United Kingdom.
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 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