

BioVeL – Biodiversity Virtual e-Laboratory

Workflow Documentation

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

November 2012

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

Grant Agreement No: 283359
Project Co-ordinator: Mr Alex Hardisty
Project Homepage: <http://www.biovel.eu>

1 Description¹

The Matrix Population Models 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).

2 General

2.1 Name of the workflow and MyExperiment identifier

Name: Matrix Population Models construction and analyses (Integrated) Workflow

Download: The workflow pack can be downloaded at myExperiment under the following address: <http://www.myexperiment.org/packs/345.html>

2.2 Date, version and licensing

Last updated: 1st November 2012

Version: 11

Licensing: CC-BY-SA

2.3 How to cite this workflow

¹ This is the description that should appear in myExperiment

Matrix Population Models construction and analyses (Integrated) Workflow

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

The 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 Gerard Oostermeijer unpublished results and publication: Oostermeijer, J.G.B. M.L. Brugman, E.R. de Boer; H.C.M. Den Nijs. 1996.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.) through BioVeL workflows and services (www.biovel.eu). The Matrix Population Models construction and analyses 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).

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:

- 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).

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- b) The stable stage distribution.
 - 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) Vareta: 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 *Ro* (net reproductive rate). In other words, *T* calculates how much time takes to a plant/animal to replace itself by a factor of *Ro*.
- 5. Net reproductive rate (*Ro*):** This section of the workflow calculates the net reproductive rate (*Ro*). *Ro* 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.

Population Modelling Workflow

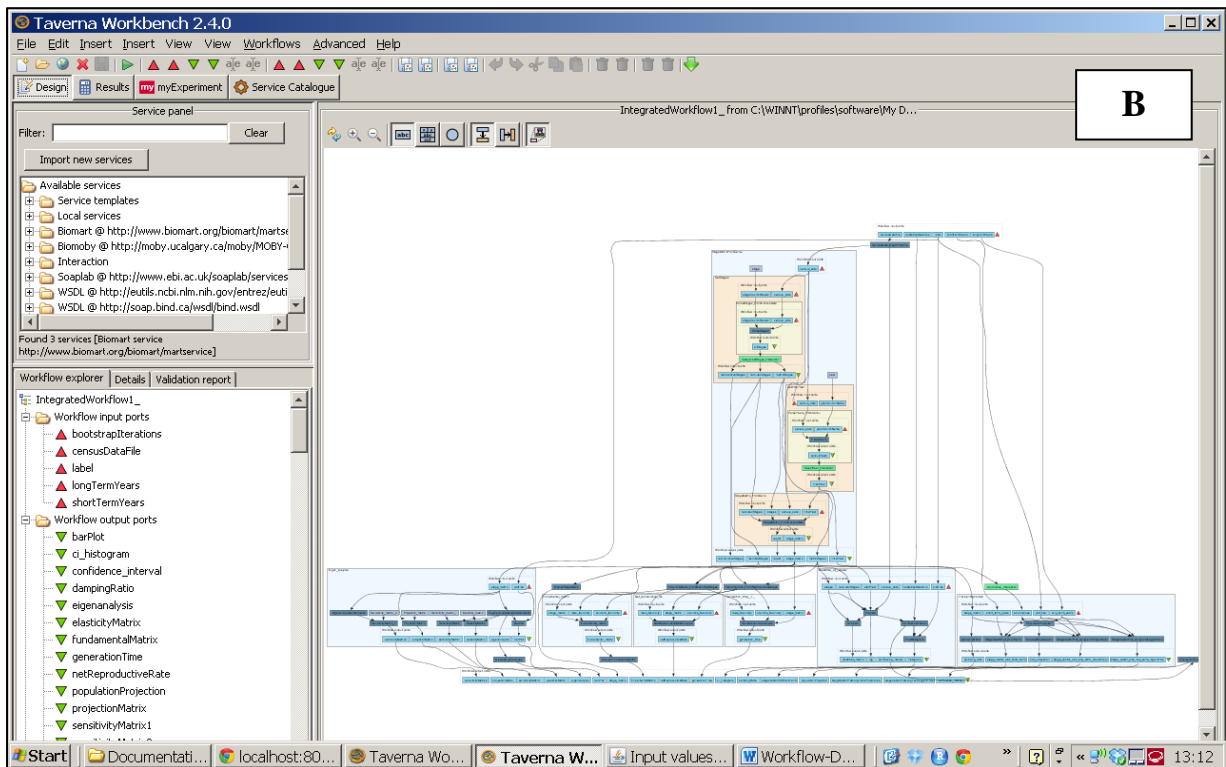
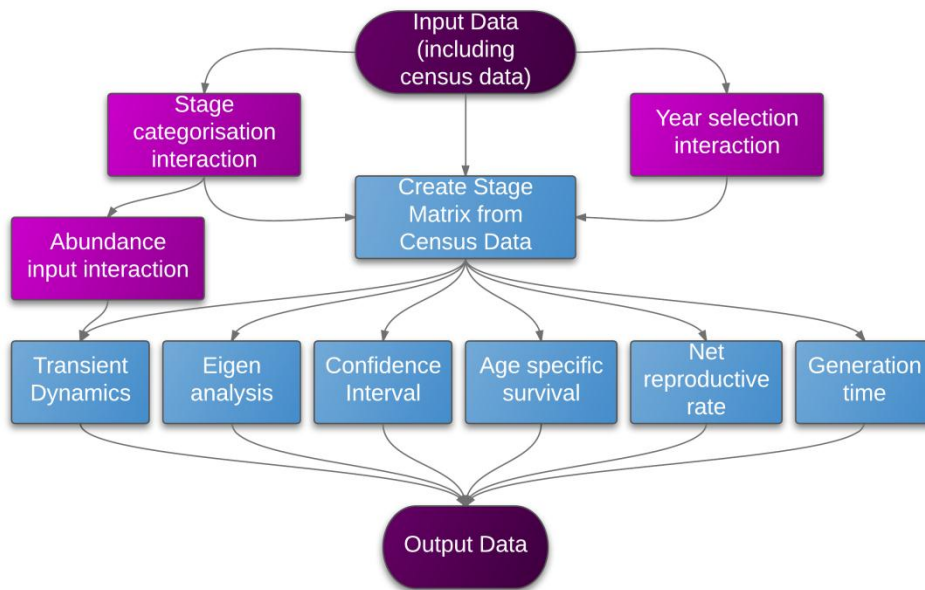


Fig 1. A) Stage matrix workflow in Taverna, B) Graph simplification of the stage matrix workflow.

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 Workbench installation

You need to have the Taverna workbench (v2.4) installed on your computer. For installation files and instructions, please go to <http://www.taverna.org.uk/download/workbench/2-4/>

Please make sure you install the updates under Advanced -> Updates and plugins.

4.2.2 Interaction Plug-in

In addition, you need to install the Taverna Interaction plug-in, version 0.1.15 or higher. Please note that the Plugin is a "work in progress". Comments, suggestions and especially bug reports are welcomed.

4.2.2.1 Installation of the plug-in:

Add <http://www.mygrid.org.uk/taverna/internal/biovel/240/> as a plugin site - see <http://www.mygrid.org.uk/dev/wiki/display/taverna/Plugins>

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Install the Interaction Service Plugin

Restart Taverna

4.2.2.2 Configuring the Interaction preferences:

Once you restart Taverna

Goto Preferences (under File or Taverna) -> Interaction

Specify port on which you want Jetty (the feed and HTML server) to run, or the URL for another machine and the relative webdav and Atom feed.

Restart Taverna

If you are already running a web server on port 8080 (the default port for the Interaction Service) then you need to change the port under preferences

4.2.3 Taverna Dependencies

The dependencies on the Taverna side include,

[Interaction Plugin](#), which handles the interaction between browser applications and Taverna.

5 Tutorial

5.1 General

In this tutorial, you will use an input file Dt1.txt and other input data to construct a stage matrix with out density dependence and perform several analyses on it. Finally you will be able to export your results to diferents formats.

Please note that the workflow as well as the tutorial is a beta version, and is likely to have failures. Furthermore, we only explain a few analyses here, while many new analyses will be added and also made easier in the coming months. We hope you will still find it interesting to work with this workflow and not give up in despair, and looking forward to your feedback.

5.2 Annotation Construct a stage matrix and analyse it.

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The first step is to fill out the input ports:

5.2.1 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 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, 'reprstr' 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).

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	
37	1988	V	0	
38	1988	S	0	RS
39	1988	J	0	RJ
40	1988	J	0	RJ
41	1988	V	0	
42	1988	S	0	RS
43	1988	J	0	
44	1988	S	0	RS
45	1988	S	0	RS
46	1988	V	0	
47	1988	V	0	

- 2) **BootstrapIterations:** Number of iterations for calculation of bootstrap distributions.

e.g.: 1000

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- 3) **Label**: Descriptive title for labelling generated outputs (graphs).

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.

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 use 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 ouput port):

- 1) StageVectorPlotShortTerm.

After the user has filled out the input ports and has clicked in run the workflow, three dialogue pages appear in the user's internet browser, see Dialogue:

5.2.2 Dialogue

- 1) **Stages**: With this dialogue authomatically appears the names of the stages or categories of the census data file. When the dialogue appears, the stages are in disorder (Fig 2), 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 3). 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 Dt1.txt, x is use to denote when a plant has died in the second year, so the user must selected in the excluded column. Then the user clicks in confirm and you will read stages submitted (Fig 4).

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

- 1) Seedlings S
- 2) Juveniles J

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- 3) Vegetative V
- 4) Reproductive individuals G
- 5) Dormant plants D

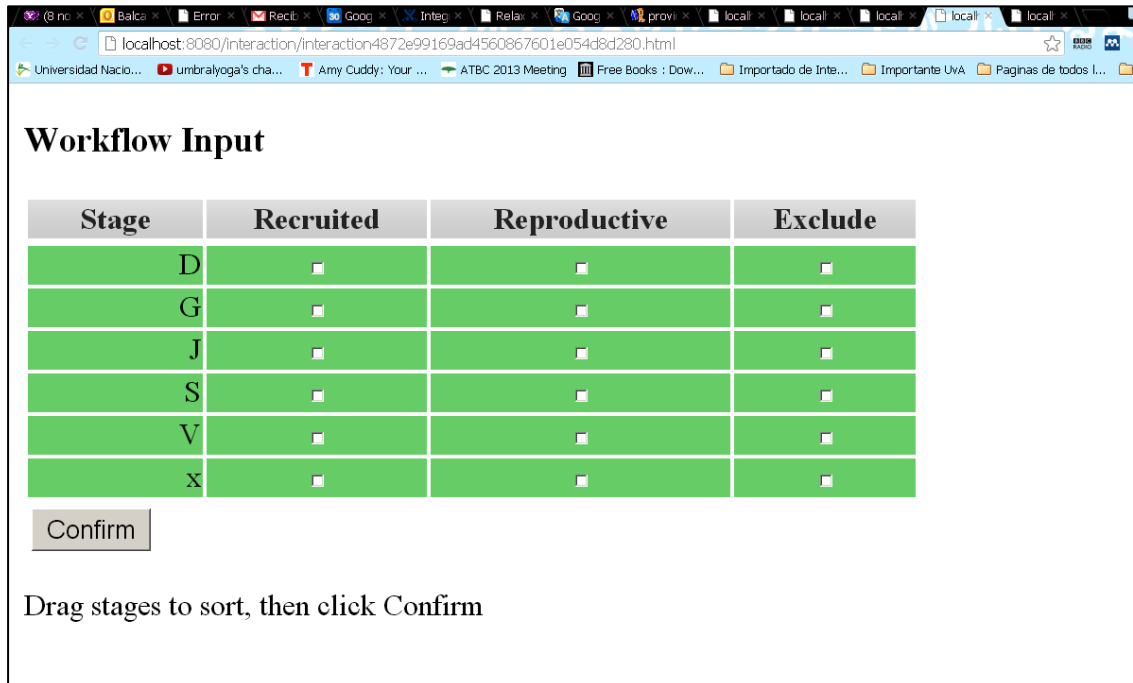


Figure 2. Stages dialogue. When the dialogue appears, the stages are in disorder.

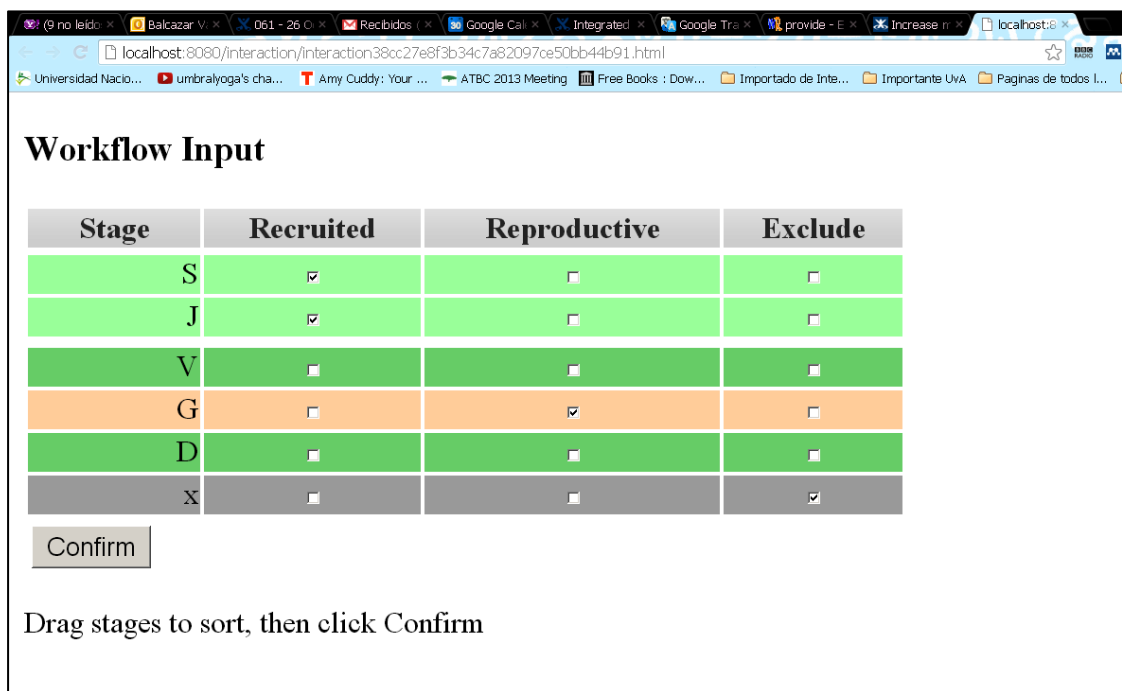


Figure 3. Stages dialogue. The stages are organized as in the life cycle by the user.

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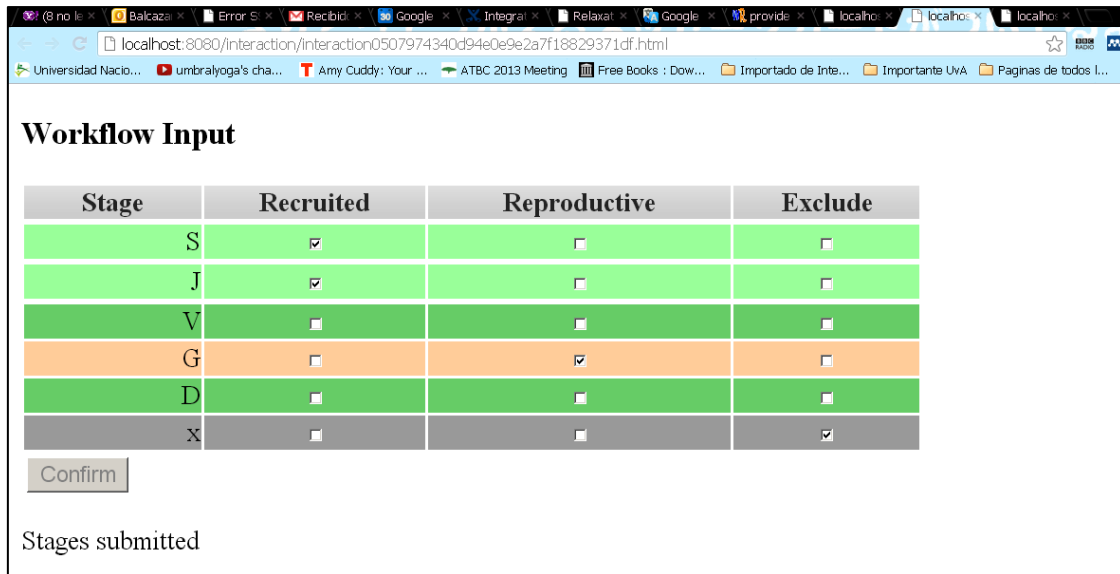


Figure 4. Stages dialogue. The stages are in order and it has been chosen if the stage belongs to the recruited, reproductive category or it should be excluded.

- 2) **Year:** In this dialogue automatically comes the years of the census data file (Fig 5), the user selects the first census year. In this example the census was 1987 -1988, therefore the user selects 1987 (Fig 6). After this step, the user should confirm the selection (Fig 7).

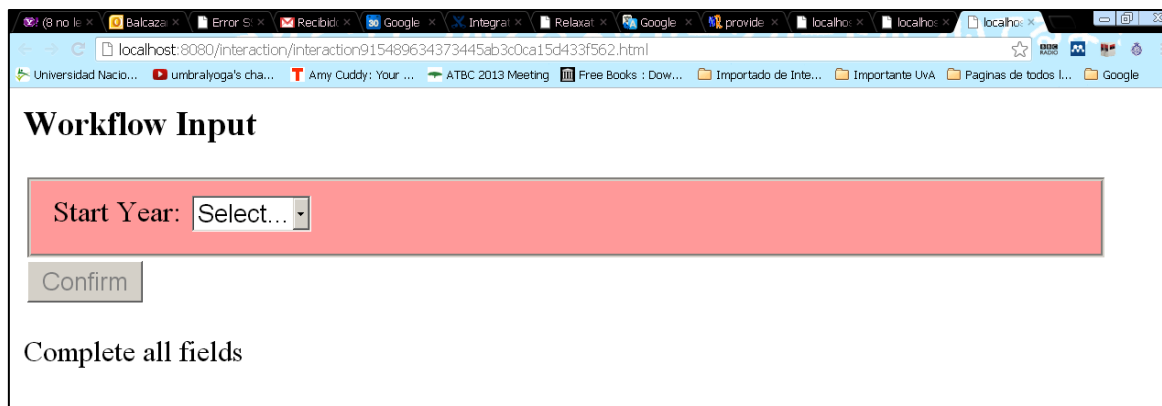


Figure 5. Year dialogue. When the dialogue appears, the user selects the initial year.

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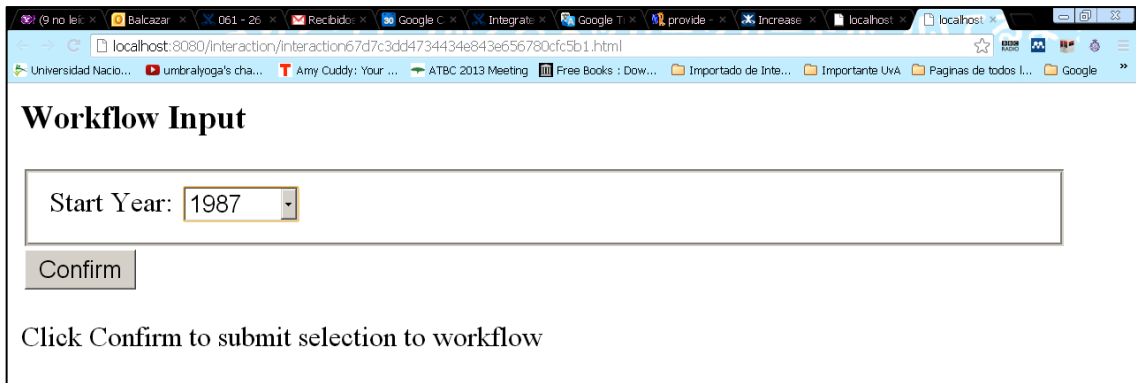


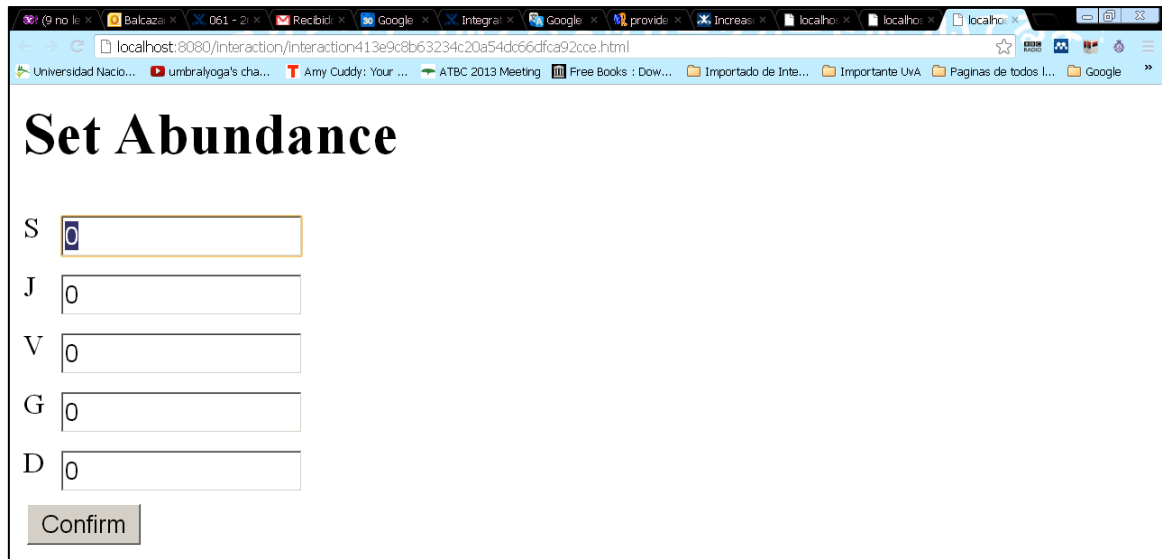
Figure 5. Year dialogue. The user selects the initial year, in this case 1987.



Figure 5. Year dialogue. The user confirms the choice.

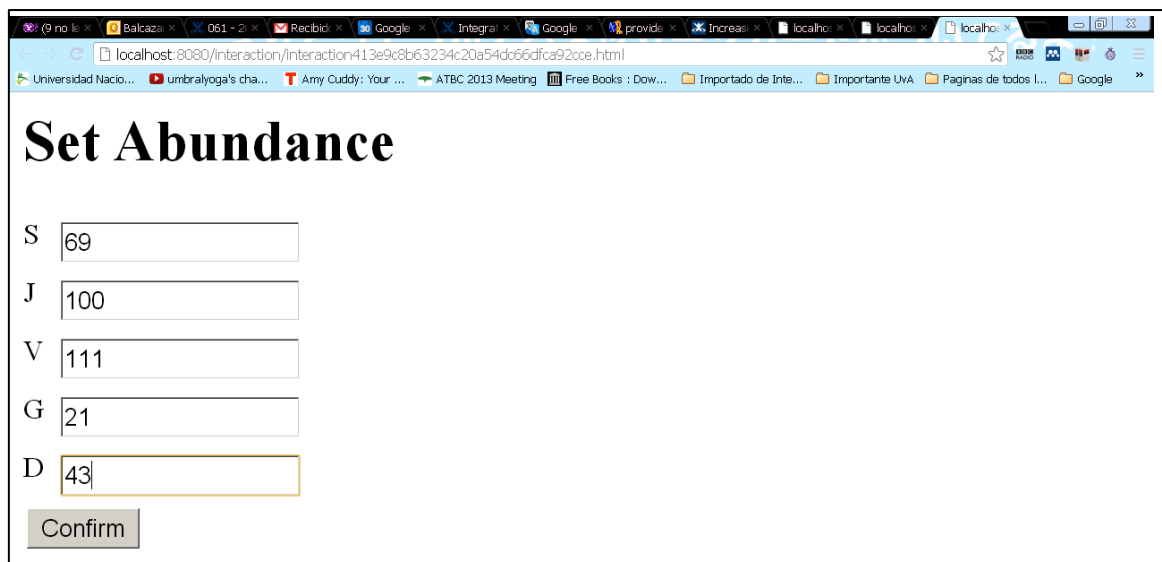
- 3) ***Initial abundance:*** In this dialogue automatically appears the fields to fill out the initial abundance per stage observed in the field (Fig 6). After fill out the abundances (Fig 7), the user confirms the numbers (Fig. 8). As a example *Gentiana pneumonanthe* has 5 stages with its respective abundance:

stage	abundance
1) S (seedlings)	69
2) J (Juveniles)	100
3) V (vegetative)	111
4) G (reproductive individuals)	21
5) D (dormant plants)	43



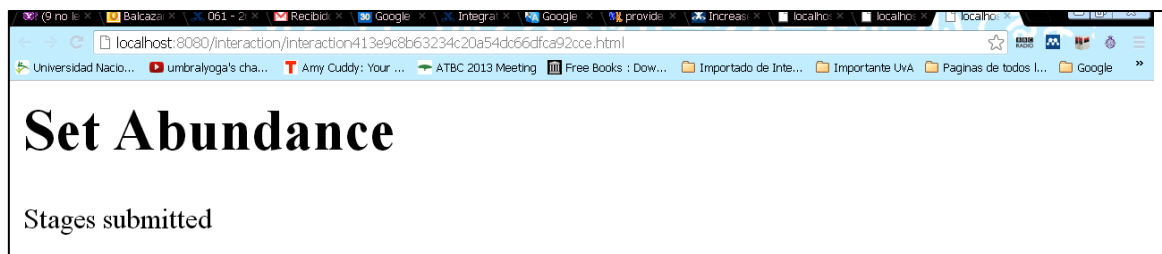
The screenshot shows a web browser window with the title "Set Abundance". The browser's address bar shows the URL "localhost:8080/interaction/interaction413e9c8b63234c20a54dc66dfca92cce.html". The browser's tab bar shows several tabs, including "Balcaza", "061 - 2", "Recibid...", "Google", "Integral", "Google", "provide", "Increas...", "localho...", "localho...", and "localho...". The browser's bookmark bar shows several bookmarks, including "Universidad Nacio...", "umbralayoga's cha...", "Amy Cuddy: Your ...", "ATBC 2013 Meeting", "Free Books : Dow...", "Importado de Inte...", "Importante UvA", "Paginas de todos I...", and "Google". The main content area of the browser displays the "Set Abundance" dialog box. The dialog box has a title "Set Abundance" and five input fields labeled S, J, V, G, and D. The S field is highlighted with a blue border and contains the number "0". The J, V, G, and D fields are empty and contain "0". Below the input fields is a "Confirm" button.

Figure 6. Abundance dialogue. The abundance fields per stage appears.



The screenshot shows the same web browser window as Figure 6, but the input fields in the "Set Abundance" dialog box are now filled with values. The S field contains "69", the J field contains "100", the V field contains "111", the G field contains "21", and the D field contains "43". The "Confirm" button is still visible below the input fields.

Figure 7. Abundance dialogue. The abundance fields are filled by the user.



The screenshot shows the same web browser window as Figure 7, but the input fields in the "Set Abundance" dialog box are now empty. Below the input fields, the text "Stages submitted" is displayed, indicating that the user has confirmed the filled field.

Figure 8. Abundance dialogue. The user confirms the filled field.

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After the user filled out the dialogue, the workflow performs the analysis. To complete all the analysis, Taverna may take 5 minutes.

5.2.3 Construction of a stage matrix and analyse it.

- 1. Construction of a stage matrix model 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 is a stage matrix model (see outputs: *Construction matrix*).
- 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: Lambda or dominant eigenvalue (λ), the stable stage distribution, sensitivity and elasticity matrix, reproductive value and damping ratio (see outputs: *Eigen_analysis*).
- 3. Age specific survival or fundamental analysis.** This workflow gives the basic information on age-specific survival, this includes the fundamental matrix (N): is the mean of the time spent in each stage class, the Variance (var): is the variance in the amount of time spent in each stage class, the 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), Meaneta: is the mean of time to death, of life expectancy of each stage and Vareta: is the variance of time to death. (see outputs: *Age specific survival*).
- 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 (see outputs: *Generation time*).
- 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 (see outputs: *Net reproductive rate*).
- 6. Transient Dynamics:** This workflow produces plots of the short-term dynamics and convergence to stable stage distribution using stage vector projections (see outputs: *Transient Dynamics*).
- 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

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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 (see outputs: *Bootstrap analysis*).

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

5.2.4 OUTPUTS

First, click in the selected result window e.g. **stage_matrix** (Fig 9). Second, click in the left window on value 1 (Fig 10), Third, on the right window click on the save value (Fig 11). Fourth, name the file and determinate the extension file. For a text file: e.g. .csv or .txt. For images: .jpg or png (Fig 12), Finale, save the file in the choosen map.

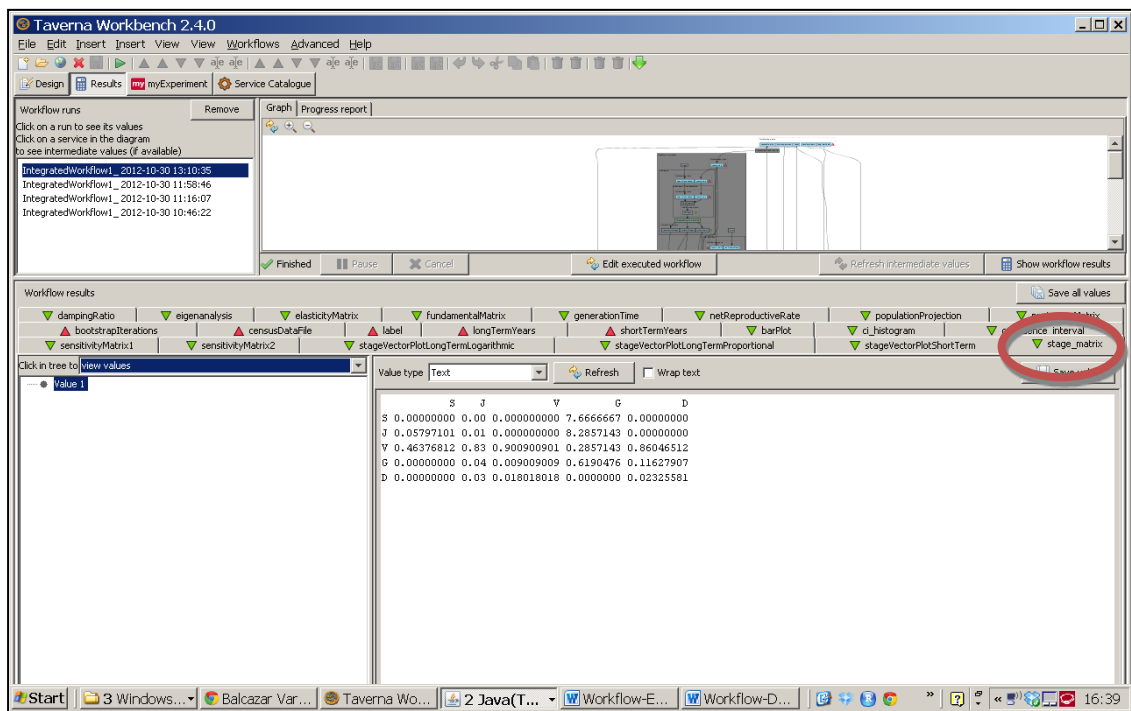


Figure 9. Stage-matrix output window.

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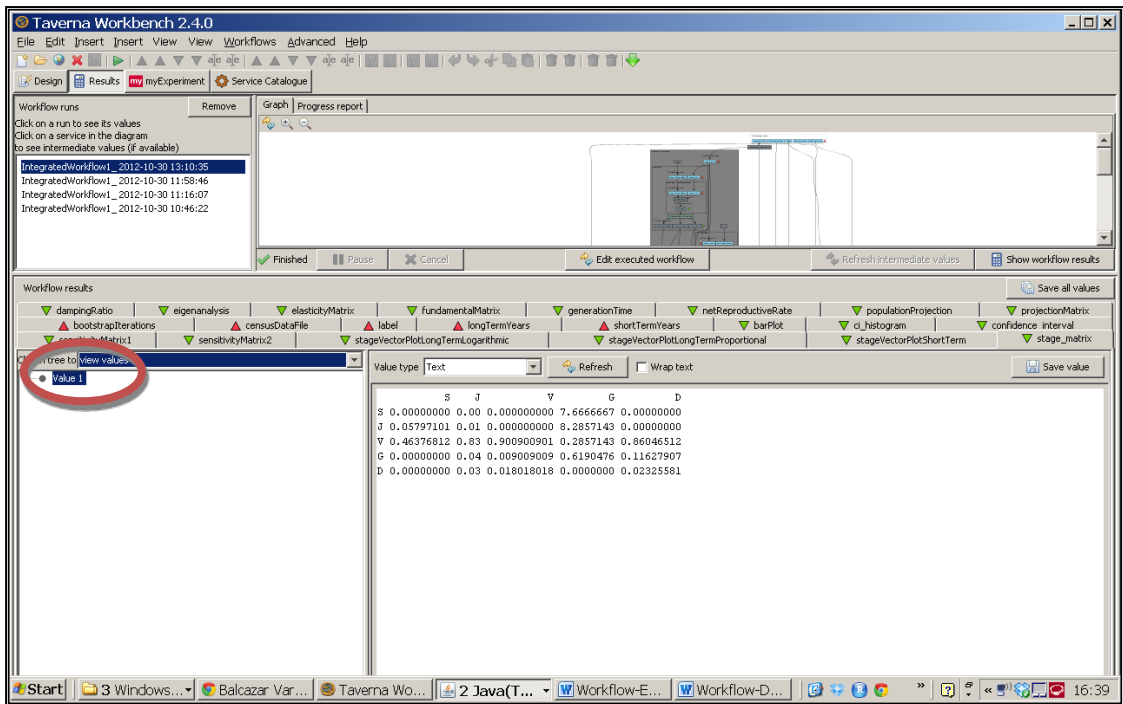


Figure 10. Value 1 on the left window of the stage_matrix output results.

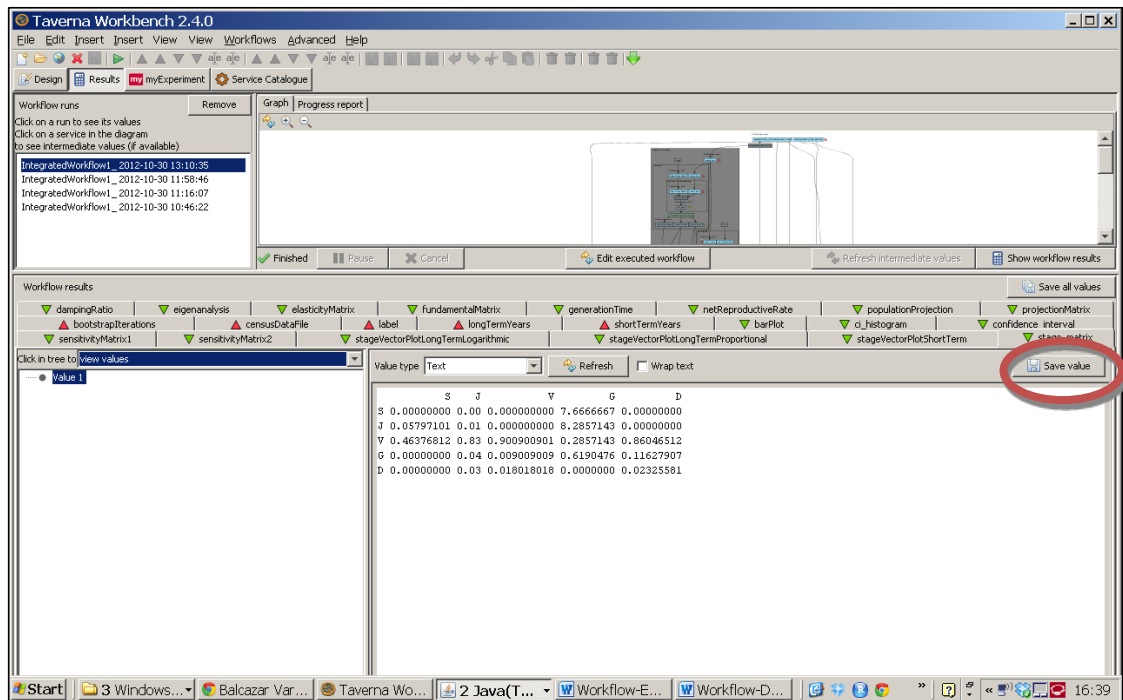


Figure 11. Save value on the right window of the stage_matrix output results.

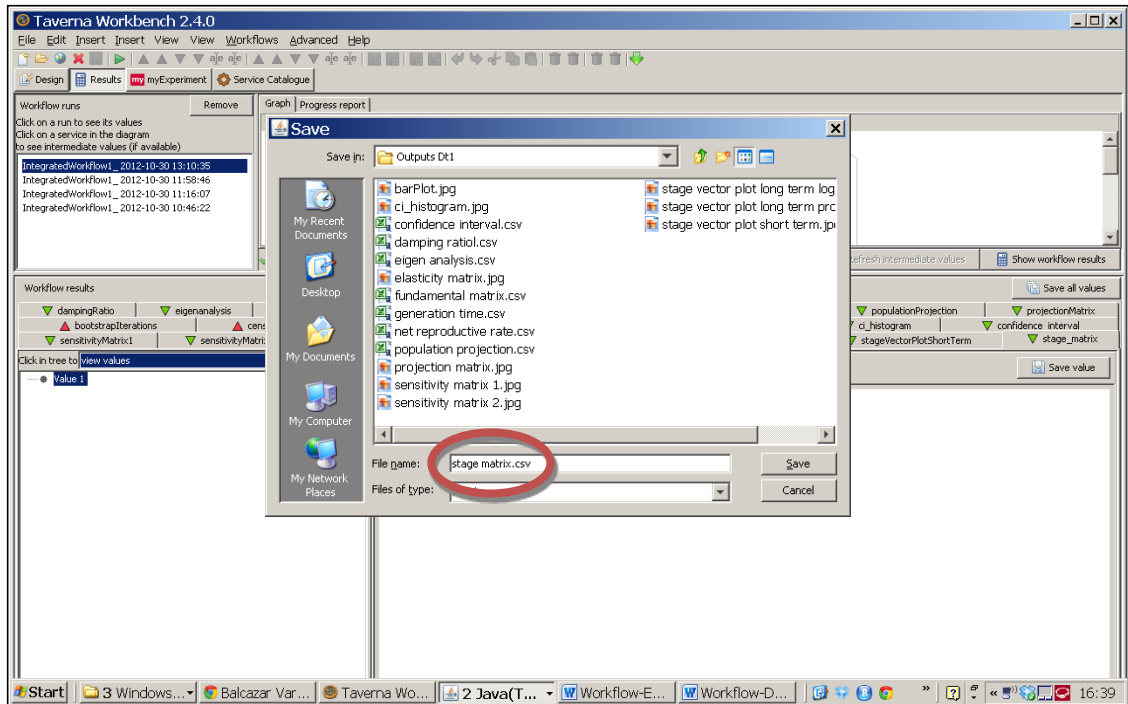


Figure 12. Name the file and determine the extension file. For a text file: e.g. .csv or .txt. For images: e.g.: .jpg or png.

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 (Oostermeijer et al., 1996).

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1														
2	S		0	0	7,6667	0								
3	J	0,0580	0,0100	0	8,2857	0								
4	V	0,4638	0,8300	0,9009	0,2857	0,8605								
5	G		0,0400	0,0090	0,6190	0,1163								
6	D		0,0300	0,0180	0	0,0233								
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Figure 12. **stage_matrix** output file open in excel.

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Furthermore this workflow creates the:

- 2) **Projection_matrix**: This creates a grid of coloured rectangles to display the *stage_matrix* (Fig 13).

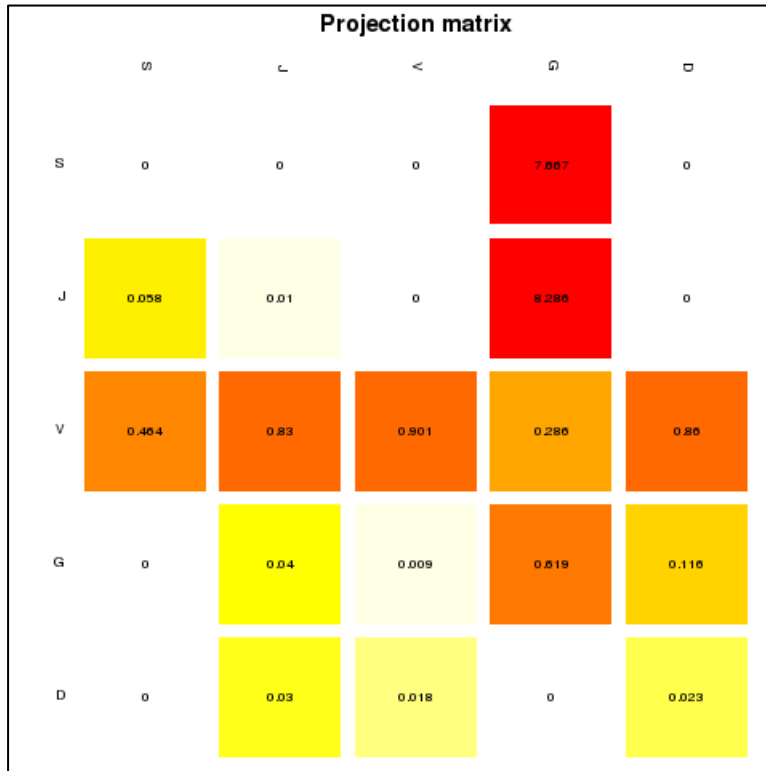


Figure 13. *Projection_matrix* opens as a coloured graph.

Eigen_analysis

- 3) **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).
- 4) **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.

- 5) **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

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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 a14 (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).

- 6) **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.
- 7) **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.
- 8) **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.

	S	J	V	G	D
Stable stage					
S	0,142188	0,16167	0,659449	0,022855	0,013839
Sensitivities					
S	0	0	0	0,006042	0
J	0,142556	0,162088	0	0,022914	0
V	0,082064	0,093307	0,3806	0,013191	0,007987
G	0	2,767599	11,28901	0,391256	0,236902
D	0	0,332568	1,35654	0	0,028467
Elasticities					
S	0	0	0	0,037589	0
J	0,006706	0,001315	0	0,154067	0
V	0,030883	0,062844	0,278238	0,003058	0,005577
G	0	0,089832	0,082528	0,196542	0,022353
D	0	0,008096	0,019834	0	0,000537
Srepro.value					
S	1	3,792468	2,18317	64,7552	7,781288
Sdamping.ratio					
[1]	2,0902				

Figure 14. *Eigen analysis* output file open in excel.

- 9) **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 15).

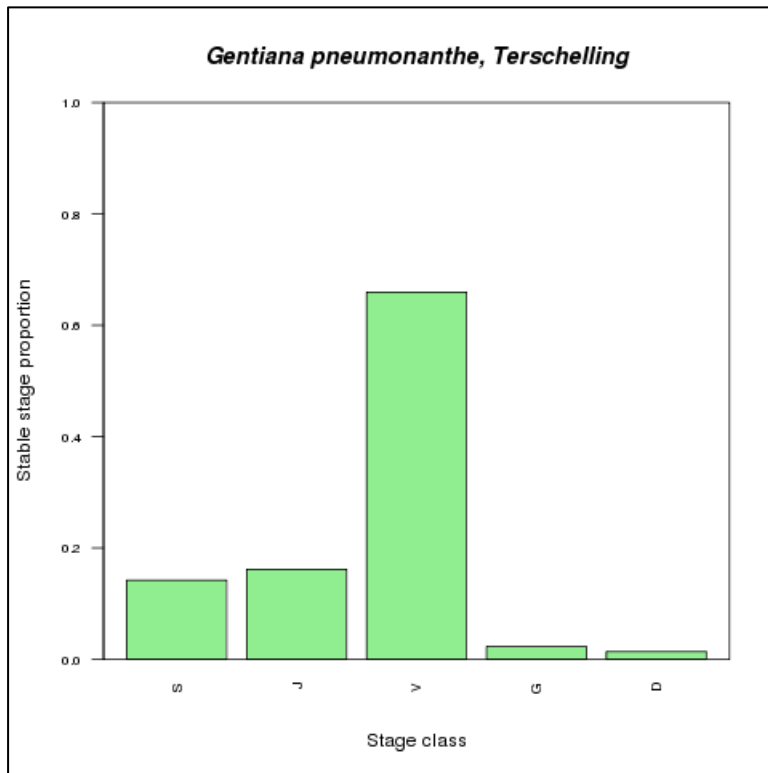


Figure 14. *Bartplot* output file.

- 10) **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 16 & 17).

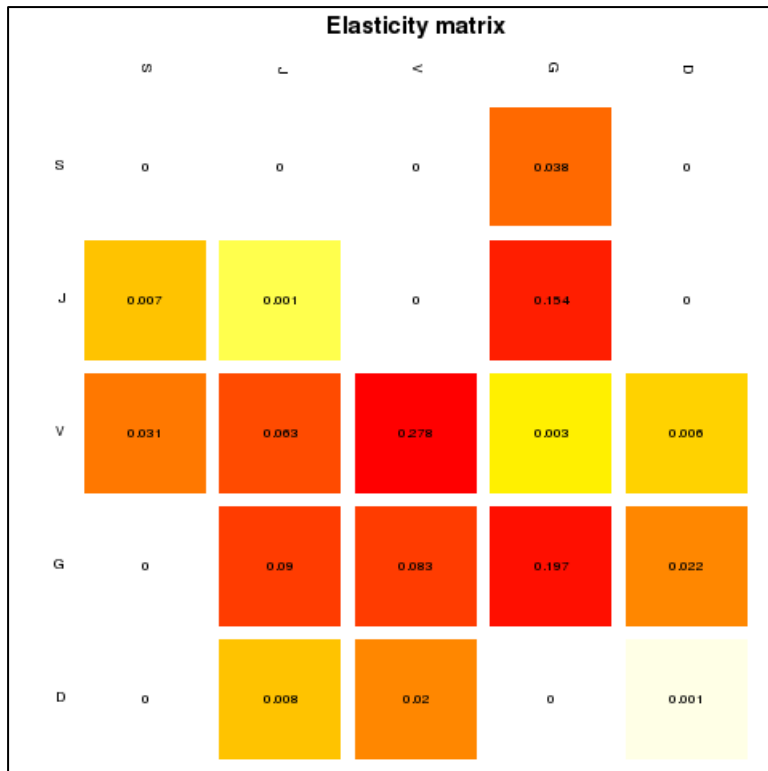


Figure 15. *elasticity_matrix* opens as a coloured graph.

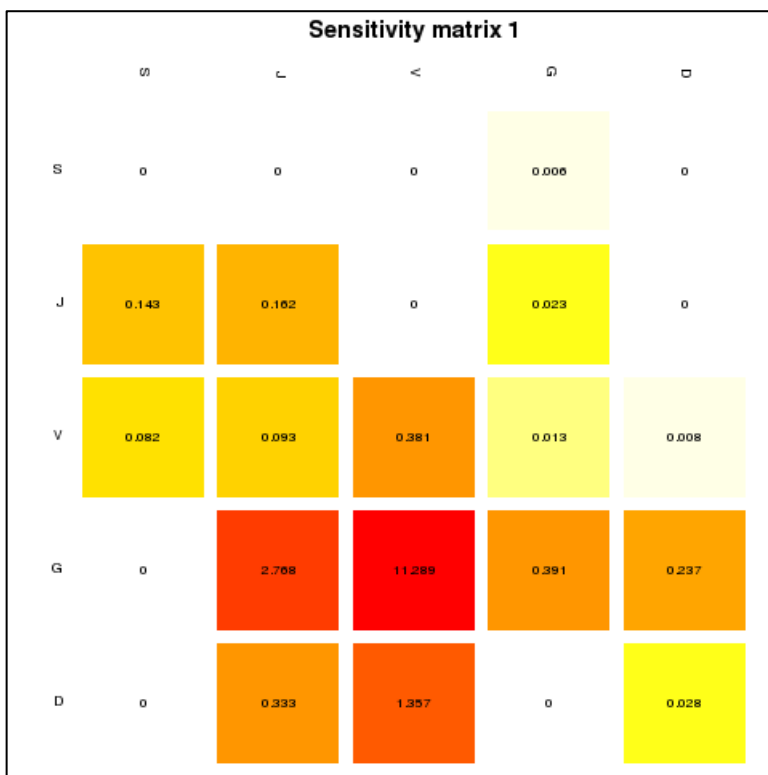


Figure 16. *sensitivity_matrix1* opens as a coloured graph.

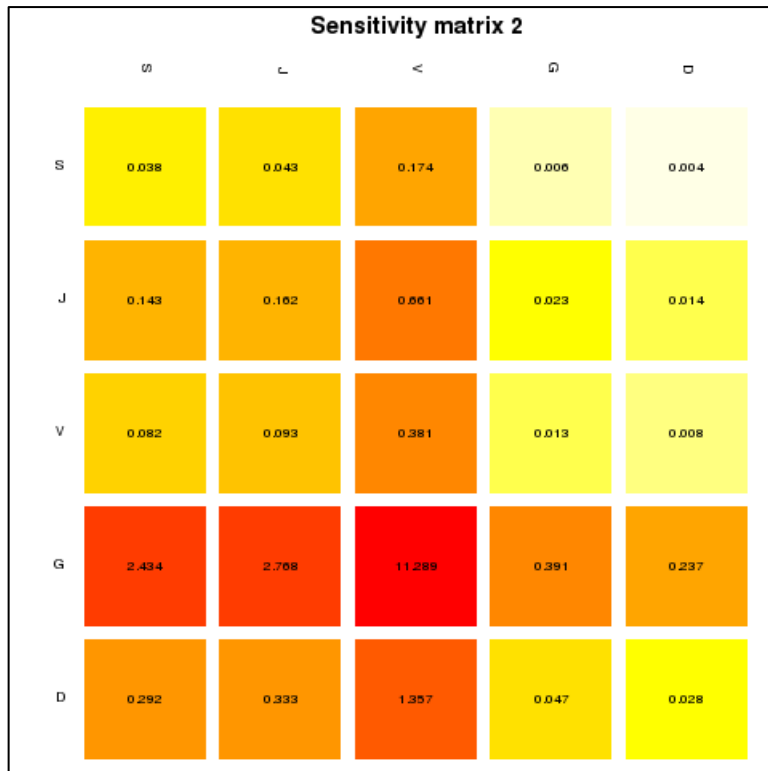


Figure 17. *sensitivity_matrix2* opens as a coloured graph.

Age specific survival

The age specific survival workflow gives the basic information on age-specific survival (Fig 18):

- 11) **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.
- 12) **Variance (var):** is the variance in the amount of time spent in each stage class.
- 13) **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).
- 14) **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.
- 15) **Vareta:** is the variance of time to death.

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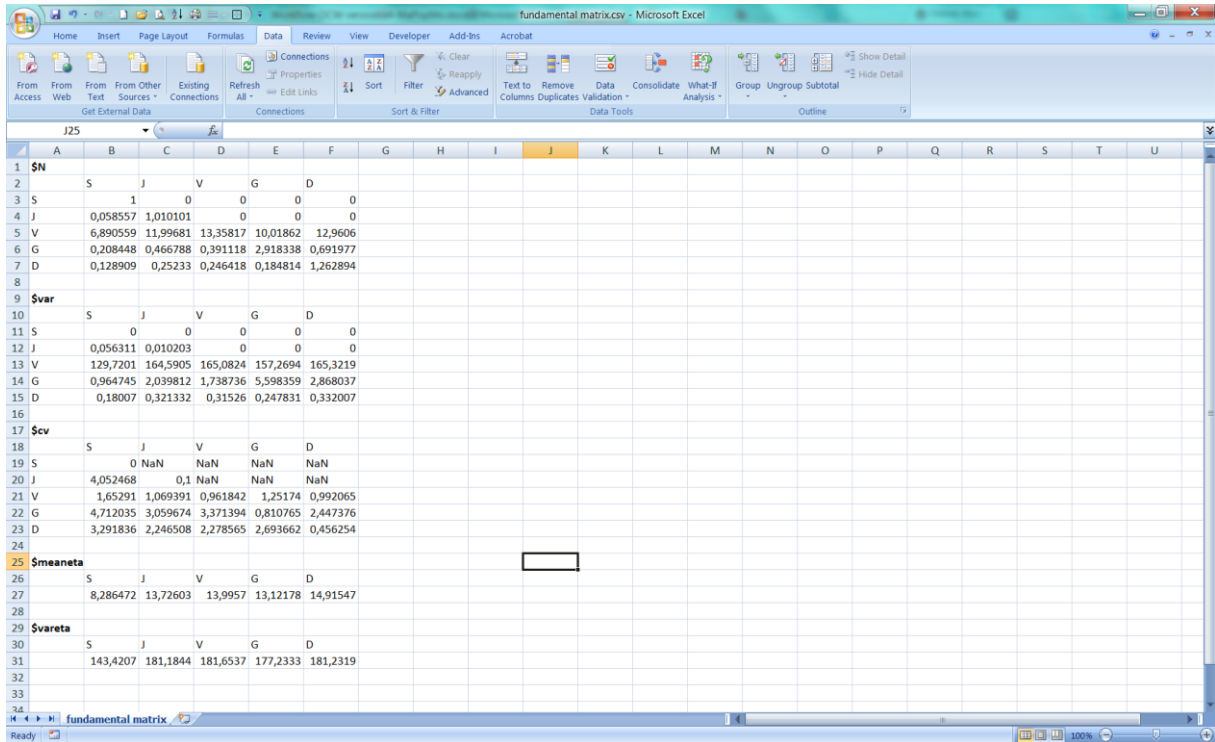


Figure 18. *Eigen analysis* opens in excel.

Generation time (T)

16) **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 (Ro)

17) **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.

Transient dynamic analysis

18) **Population projection** (Fig 19).

- 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).

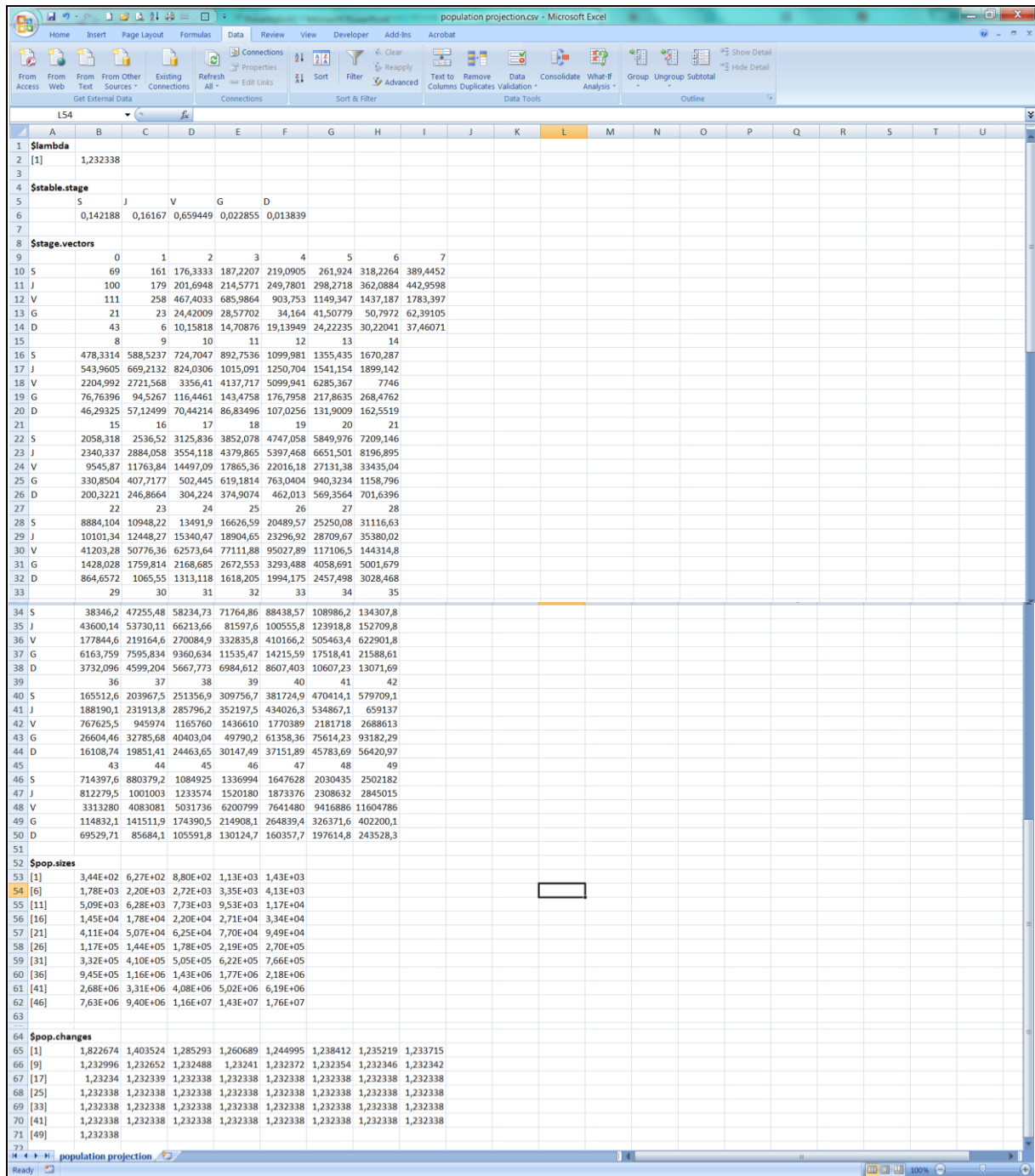


Figure 19. *Population projection* opens in excel.

19) **dampingRatio**: 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

Matrix Population Models construction and analyses (Integrated) Workflow

converges). High damping ratios tell you that the dominant stable stage distribution is reached fairly soon.

e.g. damping ratio= 2.0901.

- 20) **stageVectorPlotLongTermProportional**: Is the proportion of individuals per stage in the long term (e.g.: 50 years) (Fig 20)

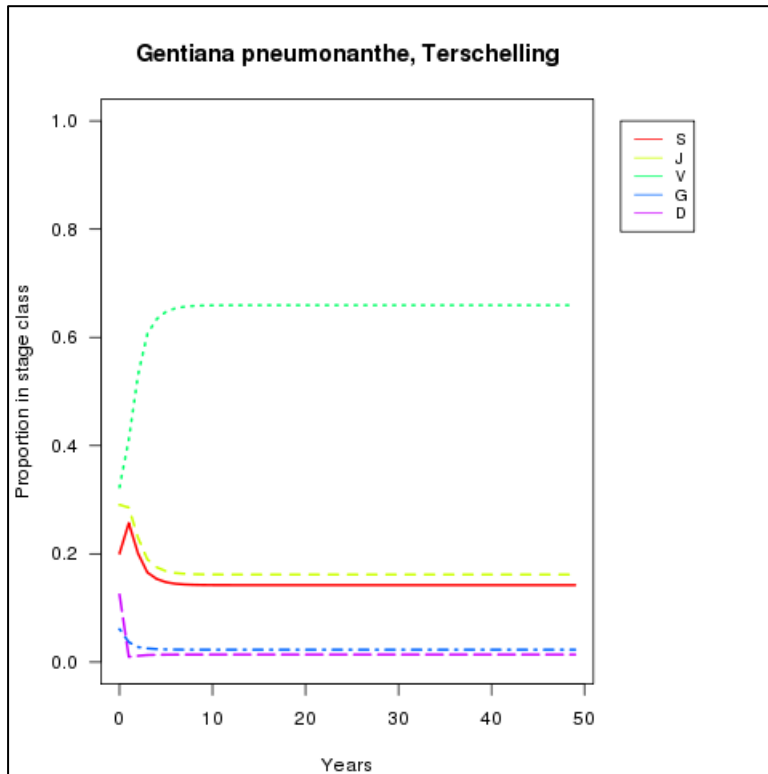


Figure 20. **Stage vector plot long term proportional** opens as a graph.

- 21) **stageVectorPlotLongTermLogarithmic**: Is the number of individuals per stage in the long term (e.g.: 50 years) (Fig 21).

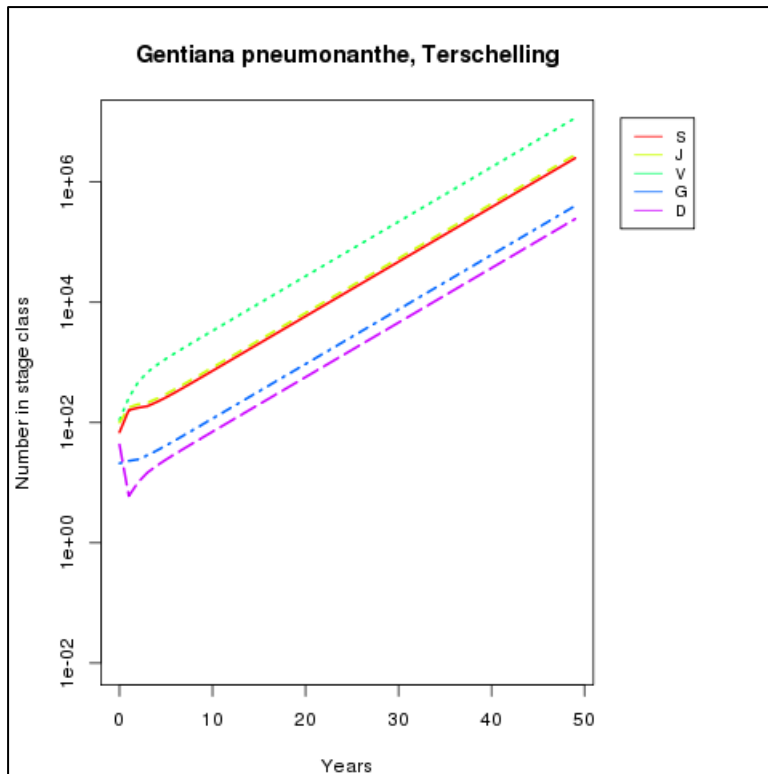


Figure 21. Stage vector plot long term logarithmic opens as a graph.

- 22) 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 22).

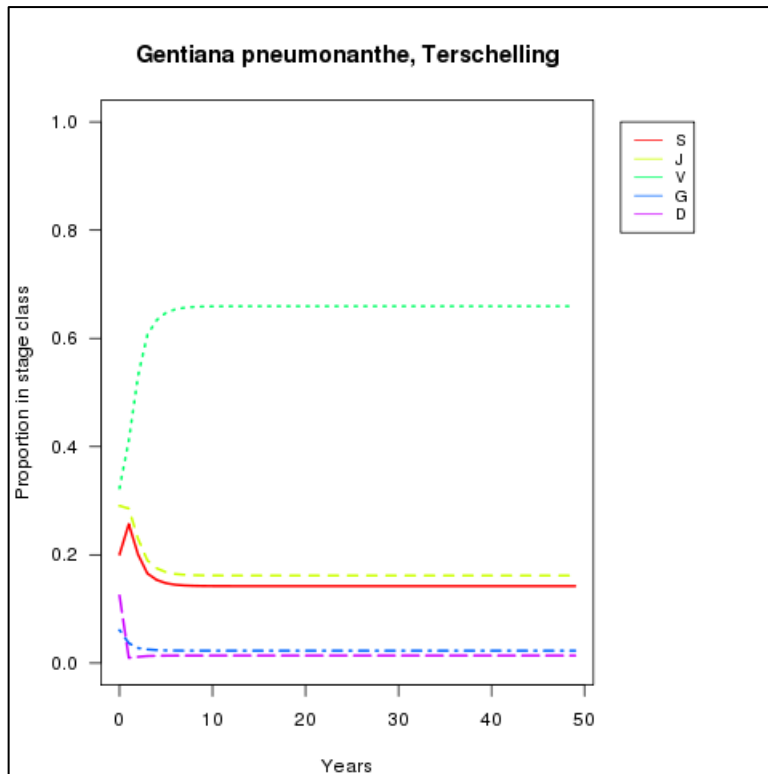


Figure 22. Stage vector plot short term opens as a graph.

Bootstrap analysis

23) **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

24) **ci_histogram**: Histogram plotting the frequencies of the lambda values and the 95% confidence intervals resulting from the bootstrap analysis (Fig 23).

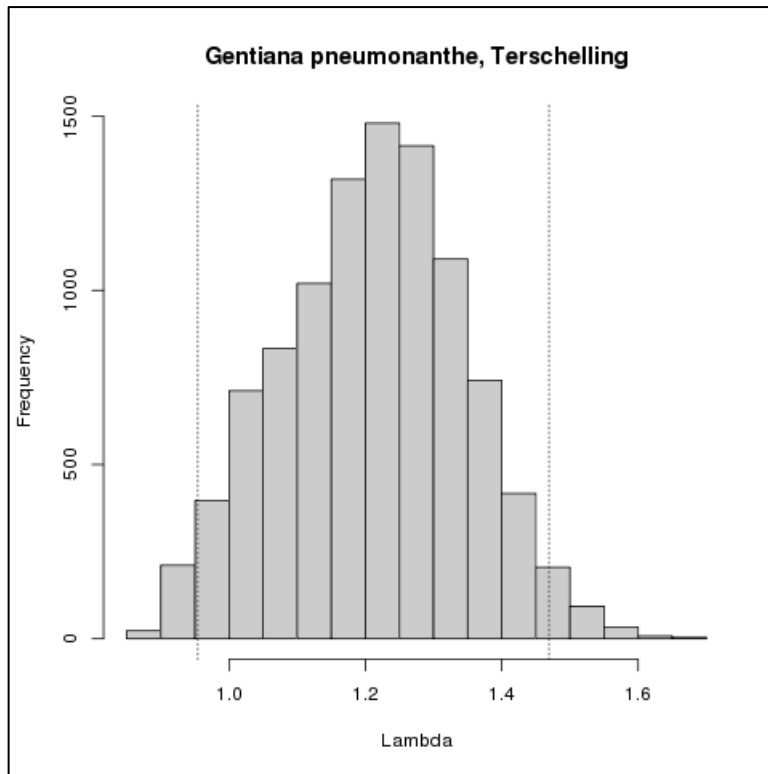


Figure 23. *The confidence interval histogram* opens as a graph.

For further details see: 26 References

5.3 Input file format

The input file is in a .txt format (see Table 1. Section 5.1.1): to download click here Dt1.txt

6 Support

For feedback, suggestions, and comments, please write to 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 Package ‘popbio’ in R. (Stubben & Milligan 2007; Stubben, Milligan & Nantel 2011).

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7.1 Acknowledgements

7.1.1 Authors

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7.2 Publications