

BioVeL – Biodiversity Virtual e-Laboratory

Workflow Documentation

Elasticity and Sensitivity of the Vital rates Workflow for local execution

Augustus 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
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<http://www.biovel.eu>
36 months

1 Description

This workflow calculates the Elasticity and Sensitivity of population growth rate with respect to various vital rates. The goal in both cases is to determine which vital rate(s) has/have the most influence on population growth rate (λ).

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

- a) **The sensitivity matrix:** The sensitivity describes the effect on λ of changes in vital rates of the matrix. 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 (Caswell 2001).
- b) **The Elasticity matrix:** The elasticities of λ with respect to the vital rate are often interpreted as the “relative contributions” of each of the vital rates to λ (de Kroon et al 1986). For further information see: de Kroon, et al., 1986. and Caswell 2001.

2 General

2.1 Name of the workflow in myExperiment.

Name: Elasticity and Sensitivity of the vital rates workflow

Download: The workflow pack can be downloaded at myExperiment under the following address:
<http://www.myexperiment.org/packs/665.html> or only the workflow:
<http://www.myexperiment.org/workflows/4445.html>

2.2 Date, version and licensing

Last updated: 29th Augustus 2014

Version: 1

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:

Elasticity and Sensitivity of the Vital rates Workflow

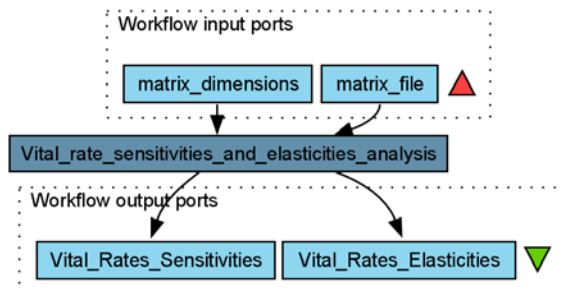
The input data and results reported in this publication (tutorial) come from data (Dr. Gerard Oostermeijer unpublished results and publication: Oostermeijer, J.G.B. M.L. Brugman, E.R. de Boer; H.C.M. Den Nijs. 1996. Temporal and Spatial Variation in the Demography of *Gentiana pneumonanthe*, a Rare Perennial Herb. *The Journal of Ecology*, 84: 153-166.) using BioVeL workflows and services (www.biovel.eu) Elasticity and Sensitivity of the vital rates 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

Analysis, BioVeL, demography, elasticity analysis, fecundity, *Gentiana pneumonanthe*, growth, matrix, matrix population models, package 'popbio' in R, sensitivity analysis, stage matrix, survival, vegetative reproduction, vital rates elasticity analysis, vital rates sensitivity analysis, vital rates. .

3.2 Scientific workflow description



The aim of this workflow is to provide a connected environment to calculate the vital rates elasticities and sensitivities. The workflow accepts input data (decomposed matrices) in a .csv format, with its fields separated by ";" (decimal numbers must be separated by a period e.g.: 0.578). The output is provided as a set of R results and a graphic plot.

Figure 1. A) Graph of the Elasticity and Sensitivity of the vital rates 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 *popbio*, *fBasics*, *Matrix* and *MASS* packages. It is possible to setup the workflow to use a remote Rserve. However, instructions for installing a local Rserve are provided below.

4.2 Taverna installation, including updates and plugins

4.2.1 Taverna installations

- Taverna Workbench: Version 2.4 or 2.5. For installation files and instructions, please go to <http://www.taverna.org.uk/download/workbench>

4.2.2 Taverna Plug-ins

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

4.2.3 Taverna Dependencies

- Install R software in your computer. See: <http://www.r-project.org/>
- Start R, and install package Rserve:
 - `install.packages("Rserve")`
- Install package popbio
 - `install.packages("popbio")`
- Install package fBasics
 - `install.packages("fBasics")`
- Install package Matrix
 - `install.packages("Matrix")`
- Install package MASS
 - `install.packages("MASS")`
- Local R Server: (Rserve) running at port 6311. See <https://wiki.biodel.eu/x/3ICD> for additional information.

4.2.4 How it works

- First, open R, once R is opened, type `library(Rserve)` and press enter; then type `Rserve()` and press enter again. You will see then the following message: Starting Rserve...
"C:\PROGRA~1\R\R-30~1.1\library\Rserve\libs\x64\Rserve.exe"

After this operation you can open Taverna and run the workflow.

5 Tutorial

5.1 Introduction

This tutorial requires a decomposed matrix of *Gentiana pneumonanthe*; demographic data 1987-1988, from Terschelling, The Netherlands.

The input data must be (a .csv-file), with its fields separated by ";" and decimal numbers must be separated by a period e.g.: 0.578. This table has 4 initial columns with general information and a decomposed matrix (matrices U, F and C):

1. Name of the species: (species),
2. Classes (classOrganized)
 - a. "veg": photosynthetically active but not sexually reproductive (and not dormant).
 - b. "rep": photosynthetically active and sexually reproductive (including classes of which only a part of the individual is sexually reproductive)
 - c. "dorm": dormant.
 - d. "seed": bank seeds, etc.
3. Name of the stages (classAuthor), the stage codes can be chosen by the user,
4. Class Number: numerical order of the stages,
5. Columns U.1 to U.n: survival/growth/shrink matrix starts in the column number 5 (**matrix U**),
6. Columns F.1 to F.n: fecundity matrix (**matrix F**),
7. Columns C.1 to C.n: vegetative reproduction matrix (**matrix C**, Fig 2). If the species does not produce ramets all the values will be 0.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
1	species	classOrganized	classAuthor	classNumber	U1	U2	U3	U4	U5	F1	F2	F3	F4	F5	C1.1	C1.2	C1.3	C1.4	C1.5	
2	Gentiana pneumonanthe	veg	S	1	0	0	0	0	0	0	0	0	0	0	7.666	0	0	0	0	0
3	Gentiana pneumonanthe	veg	J	2	0.0579	0.01	0	0	0	0	0	0	0	8.523	0	0	0	0	0	0
4	Gentiana pneumonanthe	veg	V	3	0.4637	0.83	0.9009	0.2857	0.8604	0	0	0	0	0	0	0	0	0	0	0
5	Gentiana pneumonanthe	rep	G	4	0	0.04	0.009	0.619	0.1162	0	0	0	0	0	0	0	0	0	0	0
6	Gentiana pneumonanthe	dorm	D	5	0	0.03	0.018	0	0.0232	0	0	0	0	0	0	0	0	0	0	0

Figure 2. Input file in a .csv format.

5.2 Input data.

5.2.1 Data preparation/format

The workflow accepts input data (decomposed matrices) in a .csv format, with its fields separated by ";". Decimal numbers must be separated by a period e.g.: 0.578. An example of a decomposed matrix for

Elasticity and Sensitivity of the Vital rates Workflow

the tutorial is available in <http://www.myexperiment.org/files/1268.html> or below.

5.2.2 Input data

The input files are in a .csv format: to download click here in each file:

Terschelling matrices

- [MTers 87 88 decomposed-matrix.csv](#)

5.3 Select input data dialogue boxes.

The first step is to fill out the input ports:

5.3.1 INPUTPORTS

1) ***Matrix dimensions***: it is the number of categories that the matrix contains. First press add value (see arrow in Fig 3), fill a number and press enter.

In the following example, the matrix has 5 stages or categories (see classAuthor in input data):

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

e.g. 5

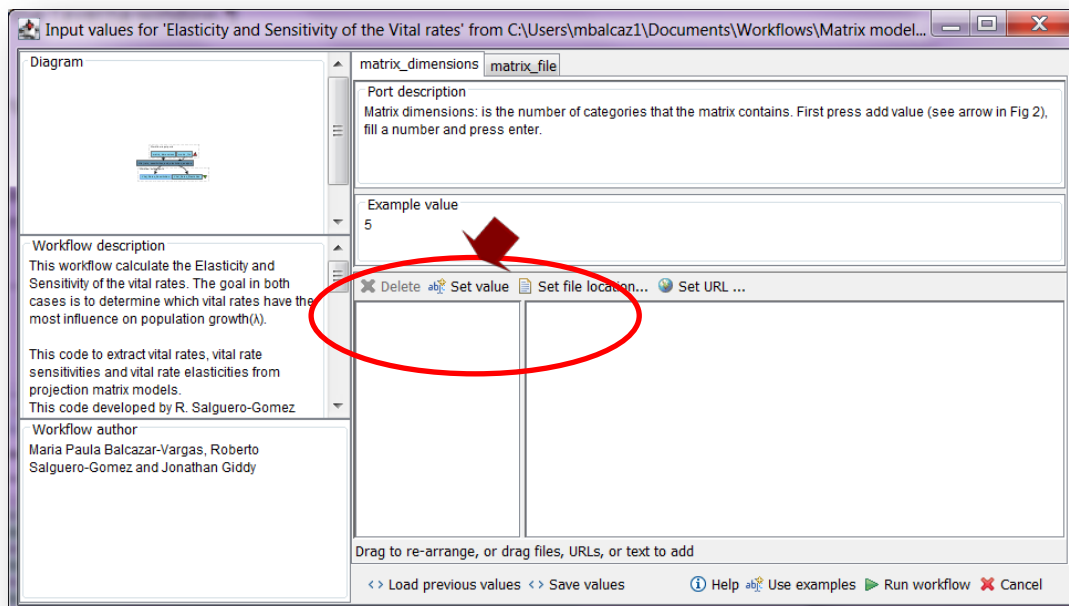


Figure 3. Inputs Matrix dimensions: numbers of stages to be filled in (example).

Elasticity and Sensitivity of the Vital rates Workflow

2) **Matrix file:** the decomposed matrix (a .csv-file) has to have the format described in section 5. Click in Set file location (Fig 4), a window dialog appears and the user selects the file (e.g. MTers_87_88_decomposed-matrix.csv) and then clicks the Open button. Then the link to the file will appear on the Taverna window.

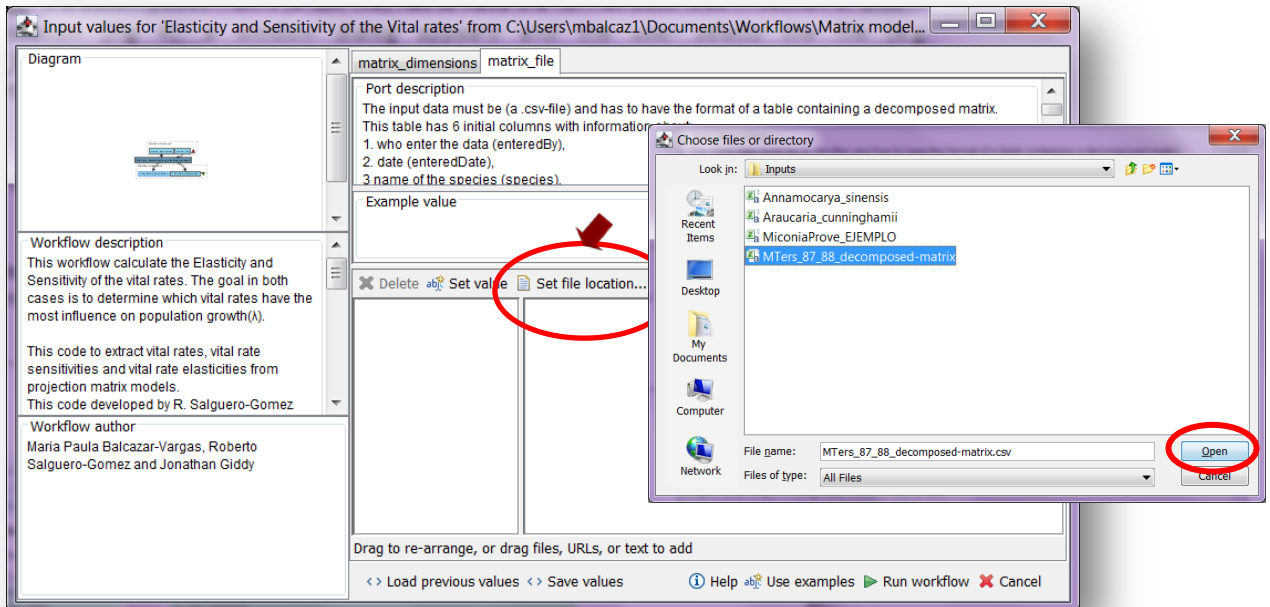


Figure 4. Input file (decomposed matrix file).

After the user has filled out the input ports, click **Run Workflow** button. 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. *Vital_rate_elasticity* (Fig 5, red oval). Second, click in the left window on value 1 (Fig 5, blue oval) and you will see the numeric results. Third, on the right window click on save value (Fig 5, green oval). Fourth, name the file and determinate the extension file. For a text file: e.g. .csv or .txt. Finally, save the file in the chosen map (Fig 6). Repeat the procedure for other output.

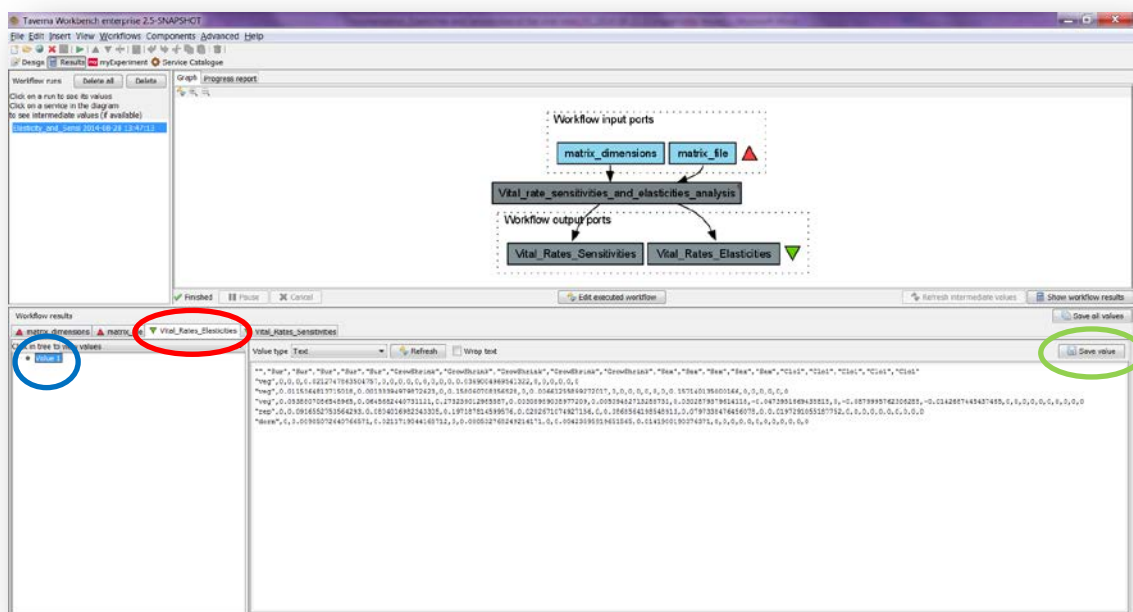


Figure 5. Taverna workbench results. When the analysis is completed, they appear on different windows under results in Taverna.

Elasticity and Sensitivity of the Vital rates Workflow

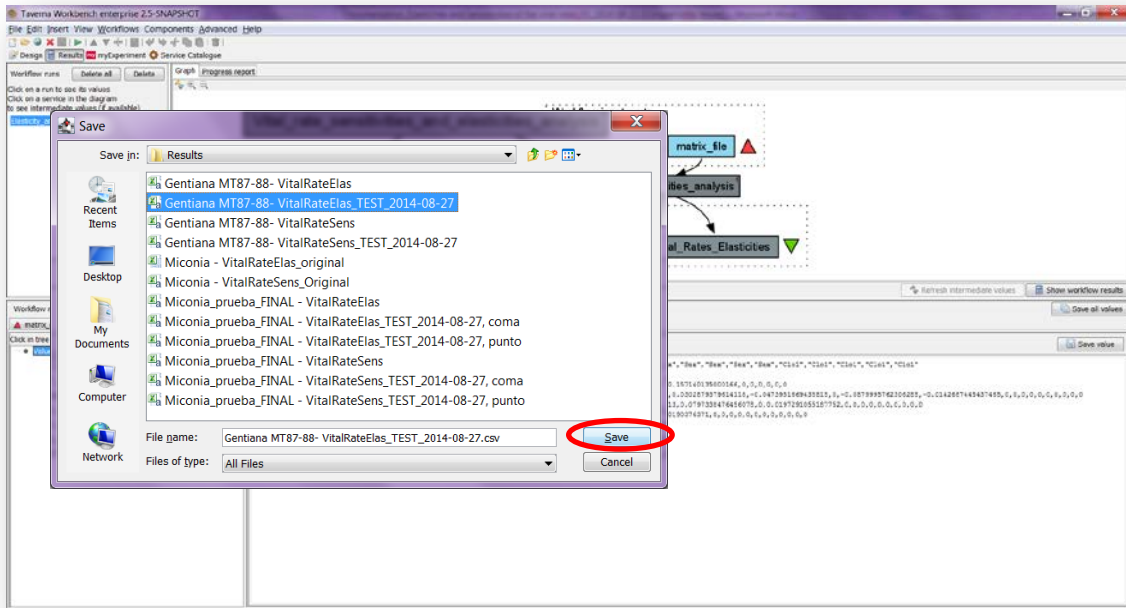


Figure 6. Name the file. Click on Save value, name the file and add the extension for the file. For a text file: e.g. .csv or .txt.

1) *Vital_rate_elasticity*

Decomposed vital rates elasticities (Fig 7).

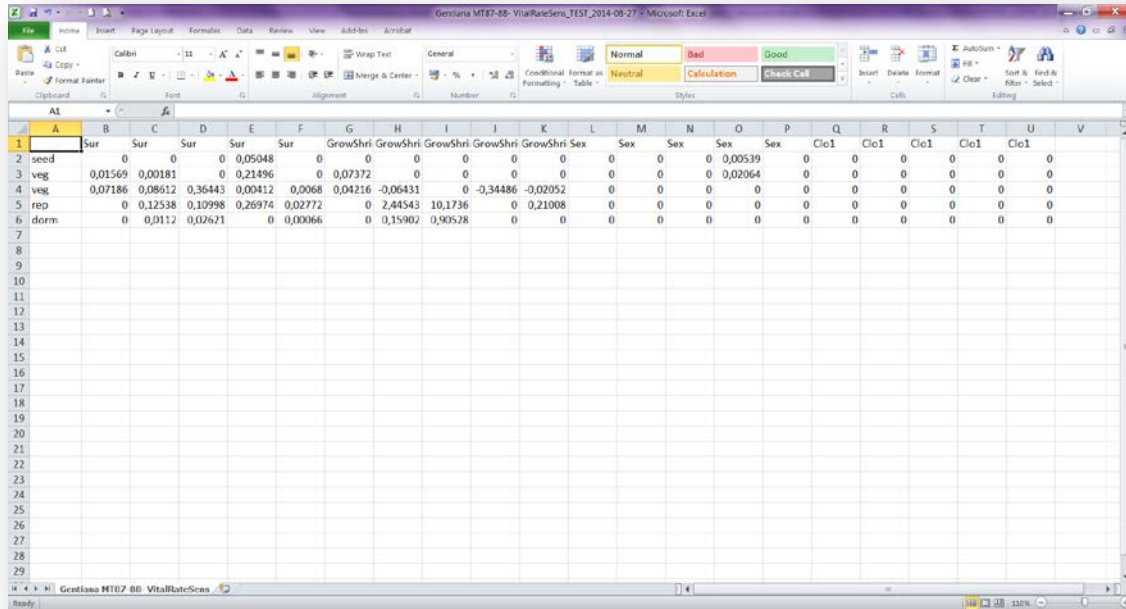
	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V
1	seed	0	0	0	0,02127	0	0	0	0	0	0	0	0	0	0,0369	0	0	0	0	0	0	0
2	veg	0,01154	0,00133	0	0,15806	0	0,00661	0	0	0	0	0	0	0	0,15714	0	0	0	0	0	0	0
3	veg	0,05388	0,06457	0,27324	0,00309	0,00509	0,03029	-0,0474	0	-0,088	-0,01427	0	0	0	0	0	0	0	0	0	0	0
4	rep	0	0,09166	0,0804	0,19719	0,02027	0	0,08686	0,07973	0	0,01973	0	0	0	0	0	0	0	0	0	0	0
5	dorm	0	0,00905	0,02117	0	0,00053	0	0,00424	0,01419	0	0	0	0	0	0	0	0	0	0	0	0	0

Figure 7. *Vital_rate_elasticity* (.csv files).

Elasticity and Sensitivity of the Vital rates Workflow

2) *Vital_rate_sensitivity*

Decomposed vital rates sensitivities (Fig 7).



The screenshot shows a Microsoft Excel spreadsheet titled 'Gensiana MT07-08: VitalRateSens_TEST_2014-08-27'. The spreadsheet displays sensitivity coefficients for five life stages (seed, veg, rep, dorm) across various parameters. The parameters include survival (Sur), growth (GrowShri), sex (Sex), and clover (Clo1) for both males (M) and females (F). The data is organized in columns A through V and rows 1 through 29.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V
1		Sur	Sur	Sur	Sur	Sur	GrowShri	GrowShri	GrowShri	GrowShri	GrowShri	Sex	Sex	Sex	Sex	Sex	Clo1	Clo1	Clo1	Clo1	Clo1	
2	seed	0	0	0	0,05048	0	0	0	0	0	0	0	0	0	0,00539	0	0	0	0	0	0	0
3	veg	0,01569	0,00181	0	0,21496	0	0,07372	0	0	0	0	0	0	0	0,02064	0	0	0	0	0	0	0
4	veg	0,07186	0,08612	0,36443	0,00412	0,0068	0,04216	-0,06431	0	-0,34486	-0,02052	0	0	0	0	0	0	0	0	0	0	0
5	rep	0	0,12538	0,10998	0,26974	0,02772	0	2,44543	10,1736	0	0,21008	0	0	0	0	0	0	0	0	0	0	0
6	dorm	0	0,0112	0,02621	0	0,00066	0	0,15902	0,90528	0	0	0	0	0	0	0	0	0	0	0	0	0
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Figure 7. *Vital_rate_sensitivity* (.csv files).

6 Support

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

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

7 Bibliography

This workflow was created using and based on Package '*popbio*' (Stubben & Milligan 2007; Stubben, Milligan & Nantel 2011), fBasics, Matrix and MASS in R.

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

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.

Stubben, C & B. Milligan. 2007. Estimating and Analysing Demographic Models Using the *popbio* Package in R. Journal of Statistical Software 22 (11): 1-23

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

7.1 Acknowledgements

The Rscript was provided by: **Roberto Salguero Gomez**, Evolutionary Biodemography Laboratory, Max Planck Institute for Demographic Research. Konrad-Zuse-Straße 1, Rostock, DE-18057, Germany.

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Elasticity and Sensitivity of the Vital rates Workflow

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