

BioVeL – Biodiversity Virtual e-Laboratory

Workflow Documentation

Log-log plots of variance vs. sensitivity and CV vs. elasticity in matrix elements 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 Mr Alex Hardisty <u>http://www.biovel.eu</u> 36 months



1 Description

This workflow creates log-log plots of both variance vs. sensitivity and CV vs. elasticity in matrix elements. Plots are based on Figure 2 in Pfister (1998). This workflow calculates as well the summary mean, variance, CV, sensitivities and elasticities of each matrix element of the submitted matrices.

Please if you want to know more about this analyses please refer to: Pfister, C.A. 1998. Patterns of variance in stage-structured populations: Evolutionary predictions and ecological implications. Proc. Natl. Acad. Sci. USA, 95: 213–218.

2 General

2.1 Name of the workflow in myExperiment.

Name: Log-log plots of variance vs. sensitivity and CV vs. elasticity in matrix elements workflow

Download: The workflow pack can be downloaded at myExperiment under the following address:http://www.myexperiment.org/packs/661.htmloronlytheworkflow:http://www.myexperiment.org/workflows/4438.htmloronlytheworkflow:

2.2 Date, version and licensing

Last updated: 21Th 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:

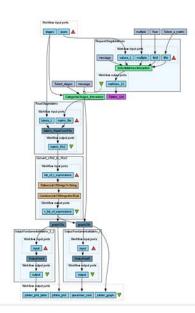
The input data and results reported in this publication (tutorial) come from data (Dr. Gerard Oostermeijer unpublished results and publication: Oostermeijer, J.G.B. M.L. Brugman, E.R. de Boer; H.C.M. Den Nijs. 1996. Temporal and Spatial Variation in the Demography of *Gentiana pneumonanthe*, a Rare Perennial Herb. *The Journal of Ecology*, 84: 153-166.) using BioVeL workflows and services (www.biovel.eu Log-log plots of variance vs. sensitivity and CV vs. elasticity in matrix elements workflow was run on *<date of the workflow run>*. BioVeL is funded by the EU's Seventh Framework Program, grant no. 283359.

3. Scientific specifications

3.1 Keywords

BioVeL, demography, Gentiana pneumonanthe, log-log plot cv vs. elasticity in matrix elements, log-log plot of variance vs. sensitivity, matrix, matrix population models, package 'popbio' in r, stage matrix.

3.2 Scientific workflow description



The aim of the log-log plots workflow is to provide a connected environment to create two log-log plots 1) variance vs. sensitivity and 2) CV vs. elasticity in matrix elements. The workflow accepts input data (matrices) in a .txt format (decimal numbers indicated by dots e.g.: 0.578). The output is provided as a set of R results and a graphic plot.

Figure 1. A) Graph of the log-log plots Workflow in Taverna workbench.

For more detailed description of the functions, please visit the Tutorial section.

4 Technical specifications

4.1 Execution environment and installation requirements

The Workflow requires a Taverna Engine including the Interaction Service plugin. The simplest way to install a Taverna Engine is to install Taverna Workbench, and then install the Interaction Service plugin.

The workflow also requires an Rserve installation with the *popbio* package installed. It is possible to setup the workflow to use a remote Rserve. However, instructions for installing a local Rserve are provided below.

4.2 Taverna installation, including updates and plugins

4.2.1 Taverna installations

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

4.2.2 Taverna Plug-ins

• Please install the <u>Interaction</u> plugin: version 1.0.2+

4.2.3 Taverna Dependencies

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

4.2.4 How it works

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

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

5 Tutorial

5.1 Introduction

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

5.2 Input data.

5.2.1 Data preparation/format

The workflow accepts input data (matrices) in a .txt format, all decimal numbers in each matrix must be indicated by dots e.g.: 0.578. All examples matrices for the tutorial are available in the PACK: http://www.myexperiment.org/packs/661.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
 - <u>MTers87_88.txt</u>
 - <u>MTers88_89.txt</u>
 - <u>MTers89_90.txt</u>
 - <u>MTers90_91.txt</u>
 - <u>MTers91_92.txt</u>
 - <u>MTers92_93.txt</u>

5.3 Select input data dialogue boxes.

The first step is to fill out the input ports:

5.3.1 INPUTPORTS

1) **Stages:** the names of the stages or categories of the input matrices. In the following example, the matrices has 5 stages or categories. The respective name stages must be filled one by one. First press add value (see arrow in Fig 2), fill a stage name and press enter; then press add value and fill once again the next stage name, repeat the action until you have fill all the stages names.

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

The stages of this matrix are called:

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

e.g. [S, J, V, G, D]

Diagram	stages years							
	Port description The names of the stages or categories of the input matrix. In the following example, the matrix has 5 stages.							
	The stages of this matrix are called:							
	1) Seedlings S							
	- Example value [S, J, V, G, D]							
Workflow description								
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	(1) Help → Use examples ► Run workflow X Cancel							

Figure 2. Inputs stages names to be filled in (example).

2) <u>Years</u>: each year represents a matrix and therefore characterizes a period of transition (Fig. 3). In this tutorial, we have 6 matrices (see **5.2.2 Input data**) that represent 6 years (e.g.: **1987** =data interval between 1987 - 1988 and **1988**= data interval between 1988 - 1989). The respective years must be filled one by one. First press add value (see arrow in Fig 3), fill a year (e.g. 1987) and press enter; then press add value and fill once again the next year (1988), repeat the action until you have fill all the years.

e.g. [1987, 1988, 1989, 1990, 1991, 1992]

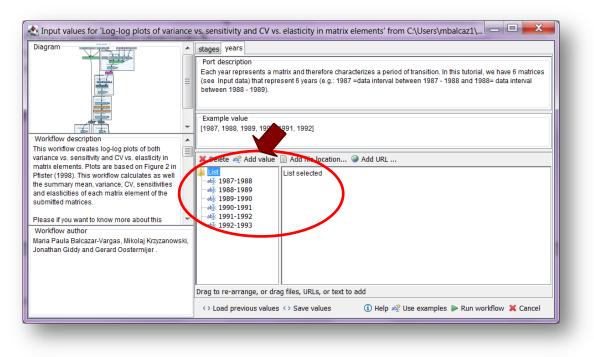


Figure 3. Inputs years to be filled in (example).

After the user has filled out the input ports, click *Run Workflow* button, a dialogue pages appear in the user's internet browser.

5.3.2 INTERACTION

1) <u>Select a matrix for each year</u>: all the matrices must be in the same folder. The interaction page will show the submitted years. When the dialogue appears (Fig 4), click Browse for the first year (e.g. 1987). A file dialog appears. Select the file (one matrix that belong to that year) and clicks Open (Fig 5). Then the selected matrix appears in the browser (Fig 6). Repeat the procedure for each year (Fig 7). Once all the matrices are submitted, click the Confirm button (Fig 7). After clicking Confirm, the confirmation "Returned Results" appears (Fig 8).

In the following example, the	ere are 6 years:
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1) 1987	3) 1989	5) 1991
2) 1988	4) 1990	6) 1992

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90-1991	Browse No file selec	ted.		
91-1992	Browse No file selec	ted.		
92-1993	Browse No file selec	ted.		
Confirm				
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Figure 4. Select a matrix for each year dialogue appears.

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Figure 5. Select a matrix for each year dialogue browse. Click in browse (1987), and select the file (one file e.g. MTer87-88.txt) and then click in Open button.

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Figure 6. Select a matrix for each year dialogue. The selected matrices appear. Repeat the procedure for each year.

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Figure 7. Select a matrix for each year dialogue. Once all the matrices are submitted, click in Confirm.

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Figure 8. Select a matrix for each year dialogue. After the user clicks Confirm. Then the interaction of fecundity transitions appears in another tab.

2) <u>Select fecundity transitions</u>: This interaction page will show the submitted stage matrix. When the dialogue appears (Fig 9), click in the fecundity stages transitions (e.g. column/row, G/S and G/J; Fig 10). Once all the fecundity stages transitions are selected, click the Confirm button (Fig 10). After clicking Confirm, the confirmation "Returned Results" appears (Fig 11).

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Figure 9. Select fecundity transitions dialogue. The dialog appears with the stage matrix submitted.

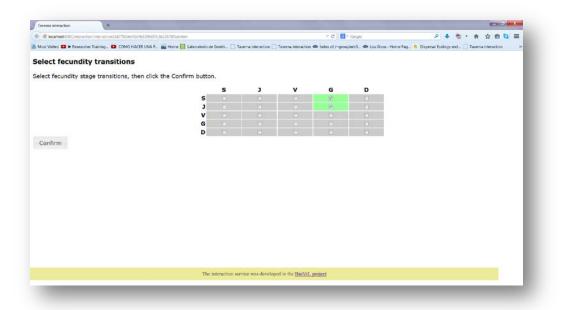


Figure 10. Select fecundity transitions dialogue. Select the fecundity stages transitions and click in confirm.

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Figure 11. Select fecundity transitions dialogue. After the user clicks Confirm. .

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. *pfister_graph* (Fig 12, red oval). Second, click in the left window on value 1 (Fig 12, blue oval) and you will see a plot. Third, on the right window click on save value (Fig 12, green oval). Fourth, name the file and determinate the extension file. For a text file: e.g. .csv or .txt., for images: .jpg or .png. Finally, save the file in the chosen map (Fig 13). Repeat the procedure for other outputs.

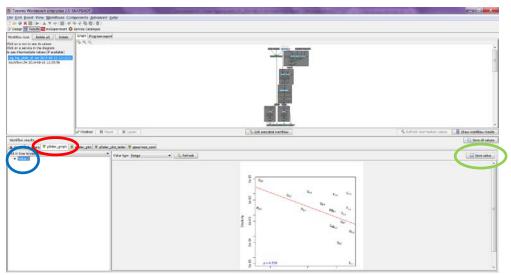


Figure 12. Taverna workbench results. When the analysis is completed, they appear on different windows under results in Taverna. *pfister_graph* window (red oval). Do click on Value 1 on the left window of the *pfister_graph* output results (blue oval). Save value on the right window of the *pfister_graph* output results (green oval).

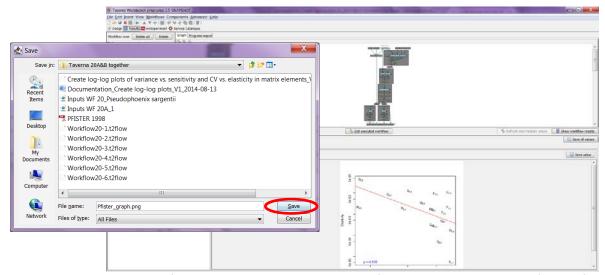


Figure 13. Name the file, click on Save value, name the file and add the extension for the file. For a text file: e.g. .csv or .txt. For images: e.g.: .jpg or png.

1) Pfister_graph

Graph plotting CV vs. Elasticity in matrix elements, showing the regression line (red line) and the Spearman correlation value (ρ) between these two values (Fig 14).

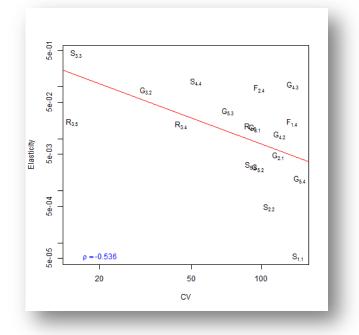


Figure 14.Pfister_graph (.jpg or png files).

2) Spearman rank

Spearman correlation results of the CV vs. Elasticity in matrix elements (Fig 15).

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Figure 15. Spearman rank results (.csv or txt files).

3) *Pfister_plot:* Graphs of the calculated values of Sensitivity vs. Variance and CV vs. Elasticity in matrix elements. (Fig 16).

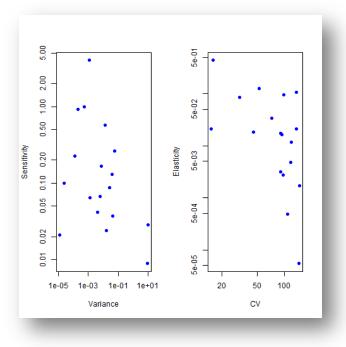


Figure 16. Sensitivity vs. Variance and CV vs. Elasticity in matrix elements graphs (.png or .jpg).

4) *Pfister_plot_table:* A table of calculated values of mean, variance, CV, sensitivity and elasticity of the matrix elements. (Fig 17).

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Figure 17. Table of calculated values of mean, variance, CV, sensitivity and elasticity of the matrix elements (.csv or txt files).

6 Support

For questions with using the workflow, please write support @biovel.eu

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

7 Bibliography

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

- 1) *Maria Paula Balcázar-Vargas* Instituut voor Biodiversiteit en Ecosysteem Dynamica (IBED), Universiteit van Amsterdam.
- 2) *Mikołaj Krzyżanowski* Cardiff School of Computer Science and Informatics, Cardiff University, Cardiff CF24 3AA, United Kingdom.
- 3) Jonathan Giddy Cardiff School of Computer Science and Informatics, Cardiff University, Cardiff CF24 3AA, United Kingdom.
- 4) *Francisco Quevedo* Cardiff School of Computer Science and Informatics, Cardiff University, Cardiff CF24 3AA, United Kingdom.
- 5) *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.

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7.2 Publications