

BioVeL – Biodiversity Virtual e-Laboratory

Workflow Documentation

Life Table Response Experiments (LTRE) Fixed design Place effect 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: 283359

Project Co-ordinator: Mr Alex Hardisty
Project Homepage: http://www.biovel.eu
Duration of Project: 36 months





1 Description

The Life Table Response Experiments place effect workflow provides an environment to analyse one or more stage matrices (e.g. matrices of different years from the same place) from two or more places. The objective of this workflow is to determine the effects of the research places or localities (2 or more) on λ . This workflow performs a fixed LTRE, one way design (Caswell 2001).

LTRE is a retrospective analysis (Caswell 1989), beginning with data on the vital rates and on λ under two or more sets of environmental conditions (in this case plots, places or localities) (Horvitz, Schemske and Caswell 1997). The goal of the analysis is to quantify the contribution of each of the vital rates to the variability in λ . (Caswell 1989, 1996, 2001 in Horvitz, Schemske and Caswell 1997).

Fixed Treatments: Decomposing Plot, place or locality Treatment Effects

A fixed-effect analysis treats the matrices as representative of particular conditions, either experimental or natural (high vs. low nutrients in a one-way model, for example, or year and spatial location in a two-way model). The goal is to determine how much a treatment level (in this case plot, place or locality) on λ is contributed by each of the vital rates. The analysis uses a linear approximation in which the sensitivities appear as slopes. The effect of a treatment on λ depends on its effect on each matrix entry and on the sensitivity of λ to that entry. (Horvitz, Schemske and Caswell 1997).

For more details of the analysis see: Retrospective Analyses: Fixed Treatments (page 262 in Horvitz, Schemske and Caswell 1997) and Chapter 10 Life Table Response Experiments (page 258 in Caswell 2001).

2 General

2.1 Name of the workflow in myExperiment.

Name: Life Table Response Experiments (LTRE) fixed design place effect workflow

Download: The workflow pack can be downloaded at myExperiment under the following address: http://www.myexperiment.org/packs/574.html or only the workflow: http://www.myexperiment.org/workflows/4433.html

2.2 Date, version and licensing

Last updated: 13Th 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:

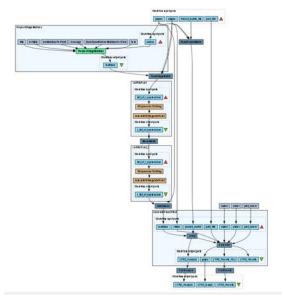
The input data and results reported in this publication (tutorial) come from data (Dr. Gerard Oostermeijer unpublished results and publication: Oostermeijer, J.G.B. M.L. Brugman, E.R. de Boer; H.C.M. Den Nijs. 1996. Temporal and Spatial Variation in the Demography of *Gentiana pneumonanthe*, a Rare Perennial Herb. *The Journal of Ecology*, 84: 153-166.) using BioVeL workflows and services (www.biovel.eu). The Life Table Response Experiments place effect 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, fixed design, Life Table Response Experiments, Matrix Population Models, Place effect, Population Models, Retrospective analysis, stage matrix.

3.2 Scientific workflow description



The aim of the LTRE - Place Effect Workflow is to provide a connected environment to perform LTRE analysis of two or more matrices from two or more places. 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 graphic plots.

Figure 1. A) Graph of the LTRE – place effect 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 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
 - o install.packages("popbio")
- Local R Server: (Rserve) running at port 6311. See https://wiki.biovel.eu/x/3ICD for additional information.

4.2.4 How it works

• First, open R, once R is opened, type library(Rserve) and press enter; then type Rserve() and press enter again. You will see then the following message: Starting Rserve...

"C:\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 11 input files; 10 matrices, 2 per place for two consecutive years (88-89 and 89-90) and a pooled matrix (or a weighted main matrix).

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/574.html or here below. All the files must be saved in the same directory.

5.2.2 Input data

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

Dwingeloo 1

- MDwin1 88 89.txt
- MDwin1 89 90.txt

Dwingeloo 2

- MDwin2 88 89.txt
- MDwin2 89 90.txt

Dwingeloo 3

- MDwin3 88 89.txt
- MDwin3 89 90.txt

Lochem

- MLochem88 89.txt
- MLochem89 90.txt

Terschelling

- MTers88_89.txt
- MTers89 90.txt

Pooled matrix

• Pooled matrix Gentiana.txt

To understand how to calculate a pooled matrix or a weighted main Matrix, please see: *Choice of a reference matrix* (pag: 253, in Horvitz, Schemske and Caswell 1997). This list of matrices will be used to perform a fixed Life Table Response Experiments Place effect analysis.

5.3 Select input data dialogue boxes.

The first step is to fill out the input ports:

5.3.1 INPUTPORTS

1) <u>Places:</u> The list of places (two or more) where the research has being carried out. The respective name places must be filled one by one. First, press add value (see arrow in Fig. 2), fill a place name (not longer than 12 characters) and press enter; then press add value and fill once again the next place name, repeat the action until you have filled all the place names.

Example of Input page:

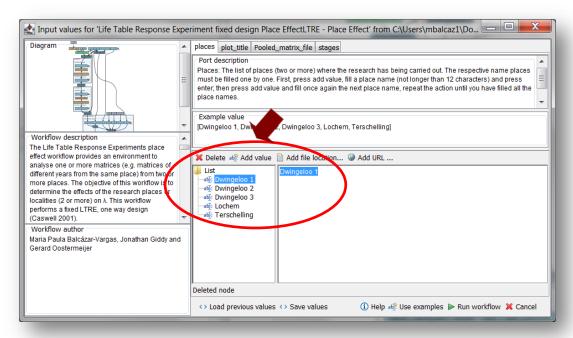


Figure 2. Inputs name of the places to be filled in (example).

- 2) <u>Plot Title</u>: Descriptive main title for labelling generated outputs (graphs). Press add value, fill a title and press enter.
- e.g: LTRE, Gentiana pneumonanthe (name of the analysis, species taxonomic name)
- 3) <u>Pooled matrix file</u>: Weighted main Matrix in a .txt file format what popbio (R package) calls pooled matrix (to see more details: Horvitz, Schemske and Caswell 1997; Horvitz, and Schemske 1995). Click in Set file location (red arrow in Fig 3), a window dialog appears and the user selects the file (e.g. Pooled_matrix_Gentiana.txt) and then clicks the Open button. Then the link to the file will appear on the Taverna window.

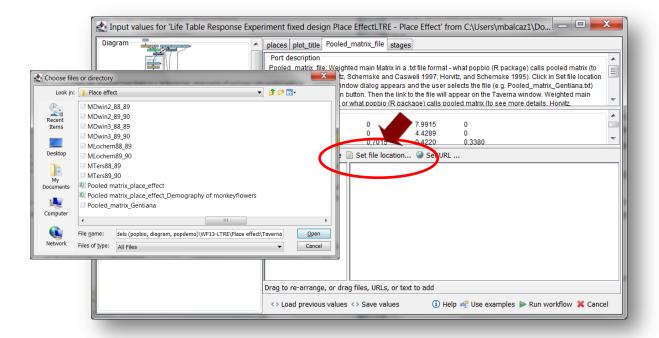


Figure 3. Input Pooled matrix to be filled in. Click in Set file location (red arrow), a window dialog appears and the user selects the file (e.g. Pooled_matrix_Gentiana.txt) and then clicks the Open button.

4) **Stages:** the names of the stages or categories of the input matrix. In the following example, the matrix has 5 stages or categories. The respective name stages must be filled one by one. First press add value (see arrow in Fig 4), fill a stage name (not longer than 8 characters) and press enter; then press add value and fill once again the next stage name, repeat the action until you have fill all the stages names.

In the following example, the 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

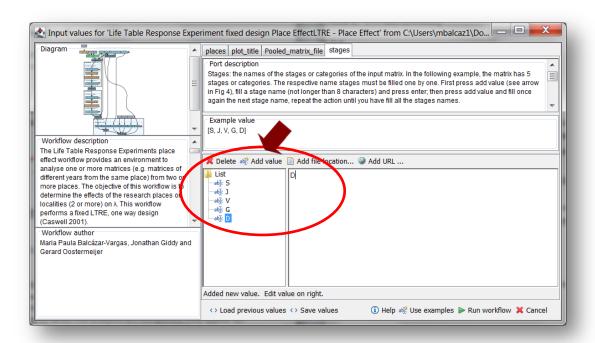


Figure 4. Inputs stages names to be filled in (example).

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) <u>Places:</u> Please be shore that all the files are saved in the same directory. Select multiple stage matrices from different years for each location. This interaction page will show the names of the places. When the dialogue appears (Fig 5), click Browse for the first place (Dwingeloo 1). A file dialog appears. Select the files (one or more matrices that belong to that place) and click Open (Fig 6). The selected matrices appear in the browser. Repeat the procedure for each place (Fig 7). Once all the matrices are submitted, click the Confirm button (Fig 8). After clicking Confirm, the confirmation "Matrices submitted" appears (Fig 9). When the analyses are completed, they appear on different windows under results in Taverna, the user can save each output separately. The workflow controls whether each location have submitted at least 1 matrix.

In the following example, there are 5 places:

- 1) Dwingeloo 1
- 2) Dwingeloo 2
- 3) Dwingeloo 3
- 4) Lochem
- 5) Terschelling

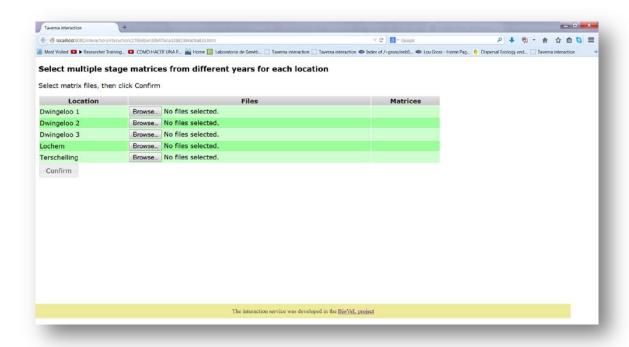


Figure 5. Places dialogue appears.

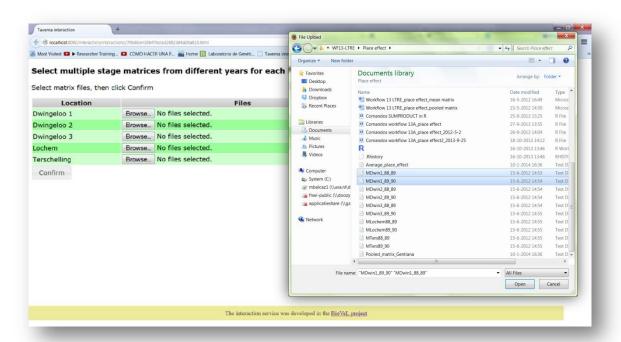


Figure 6. Places dialogue browse. Click in browse (Dwingeloo 1), and select the files (one or more) and then click the Open button.

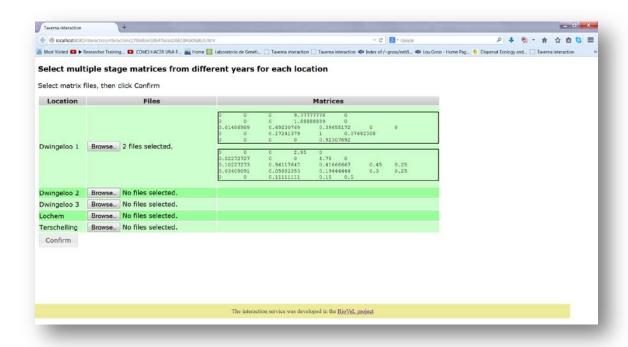


Figure 7. Places dialogue. The selected matrices appear. Repeat the procedure for each place.

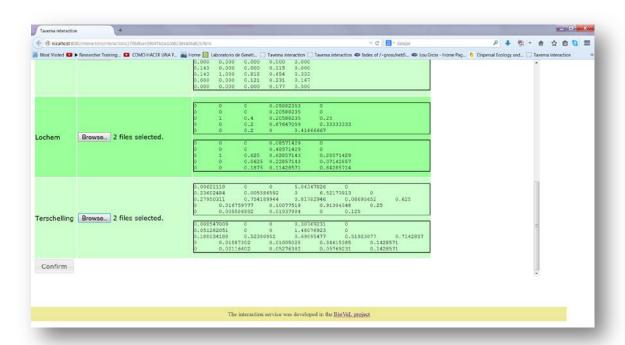


Figure 8. Places dialogue. Once all the matrices are submitted, click in Confirm.

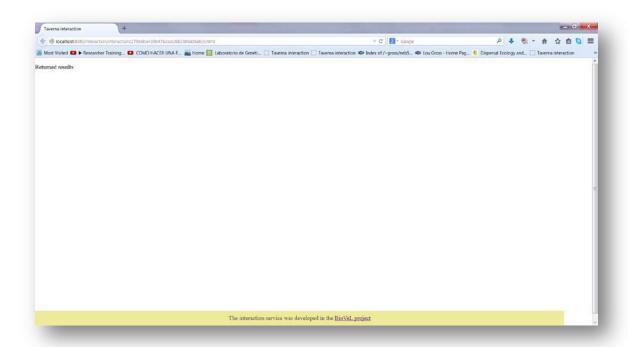


Figure 9. Places dialogue. After the user clicks Confirm, the confirmation "Returned results" appears. Refer back to Taverna workbench.

5.4 Save data/results

5.4.1 OUTPUTS

First, click in the selected result window e.g. LTRE_Analysis (Fig 10, red circle). Second, click in the left window on value 1 (Fig 10, blue circle), you will see the LTRE_Analysis results in the right window. Third, on the right window click on save value (Fig 10, 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 (Fig 10 and 11). Finally, save the file in the chosen map (Fig 11).

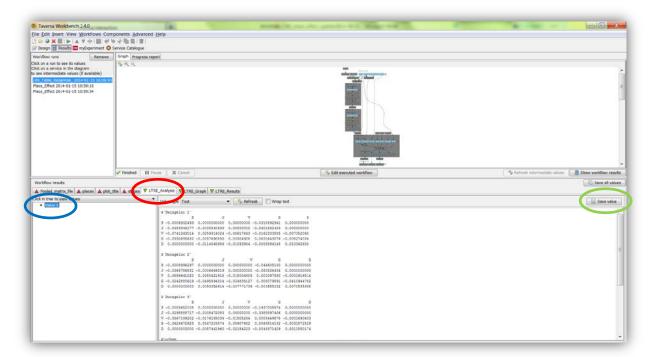


Figure 10. Taverna workbench results. When the analyses are completed, they appear on different windows under results in Taverna.

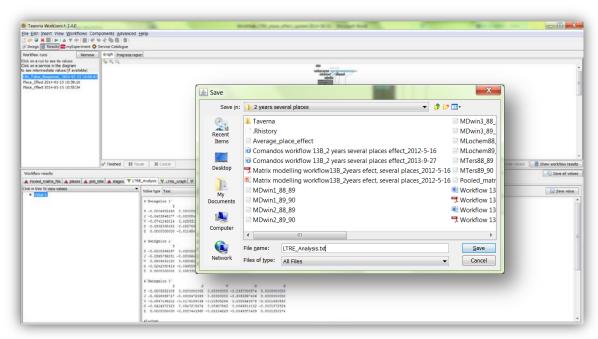
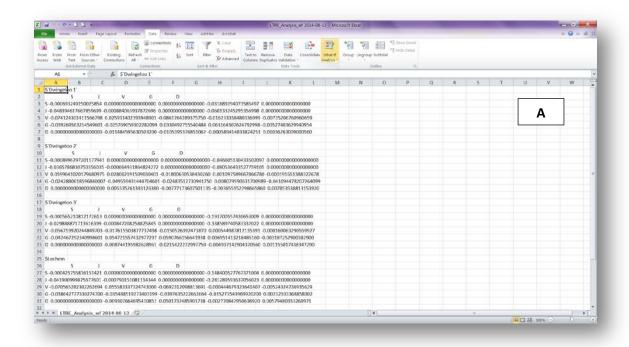


Figure 11. Name the file, adding the extension for the file. For a text file: e.g. .csv or .txt. For images: e.g.: .jpg or png.

LTRE fixed design place effect

1) *LTRE_Analysis*: Intermediary results showing the matrices calculated on the LTRE analysis per place. After this step the workflow sums up all the values per matrix giving us the final result: *LTRE_ Results* (Fig 12).



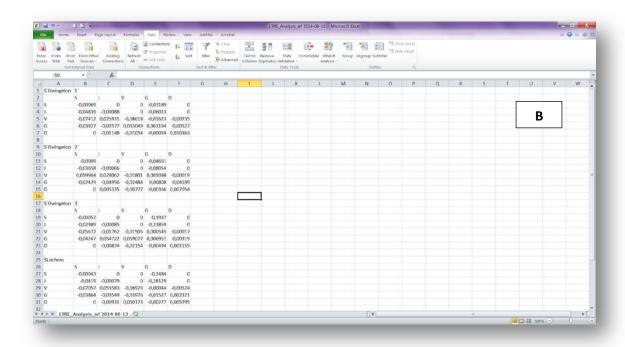


Figure 12. *LTRE_Analysis* output file open in excel, A) Original data before apply text to columns, B) After apply text to columns (.csv).

2) **LTRE_Graph**: a histogram to display the **LTRE_Results** (Fig 13). The place effect is shown in the Figure. In this example: The localities Dwingeloo 3 and Lochem had the largest negative effect on λ , and no place had a positive effect.

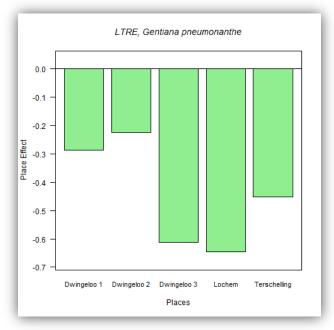


Figure 12. LTRE_Graph opens as a coloured graph.

3) *LTRE_ Results*: The results of the LTRE per location or place. These are the generated values of the plotted LTRE graph (Fig 14).

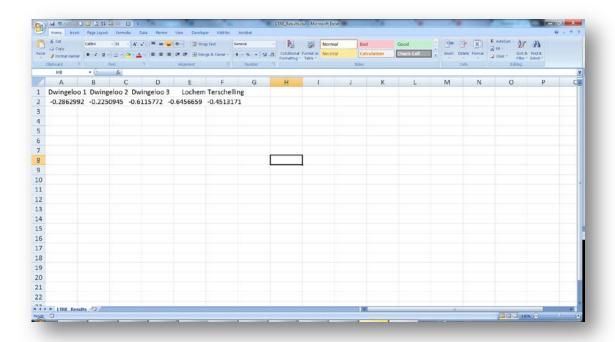


Figure 14. LTRE_Results output file open in excel (.csv).

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: https://wiki.biovel.eu/display/BioVeL/Glossary

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

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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