Analysing Mesocosm Experiments - Principal Response Curves

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Mesocosm studies

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How to

- ▶ Between laboratory and field studies (relevance and control)
- ▶ Higher Tier Tests in ecological risk assessment
- ▶ Effects on community structure and functioning

IGB, LakeLab, Lake Stechlin, Brandenburg

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How to

Mesocosm data

General experimental setup:

- ► Mesocosms treated with test item
- ► Communities sampled before and after exposure
- ► Multiple timepoints (recovery?)

This yields:

- ► large and complex data sets
- ► multiple species
- ► many time points

Multivariate techniques are needed:

- ► analyse
- ► summarise
- ► interpret

Mesocosm data

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Multivariate analysis of stress in experimental ecosystems by Principal Response Curves and similarity analysis

Paul J. Van den Brink[1] and Cajo J. F. Ter Braak[2]
[1]*DLO Winand Staring Centre for Integrated Land, Soil and Wa*
gen, The Netherlands (Fax: +31–317–424812; E-mail: p.j.van
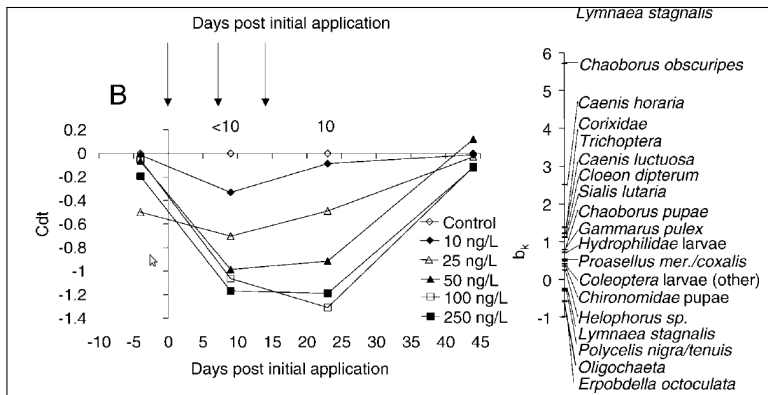*Wageningen, CPRO-DLO, P.O. Box 16, 6700 AA Wageningen, Th*

Abstract

Experiments in microcosms and mesocosms, which can be carried out in an advanced tier of risk assessment,
usually result in large data sets on the dynamics of biological communities of treated and control cosms. Multi-

Results

RDA?

RDA:

- ▶ treatment, time , treatment x time
- ▶ cluttered biplot
- ▶ can spot effects, but not obvious
- ▶ effect of time?

Need a better way to represent the treatment effects!
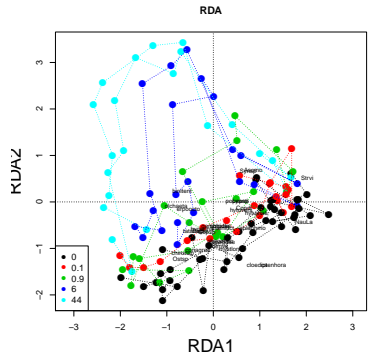
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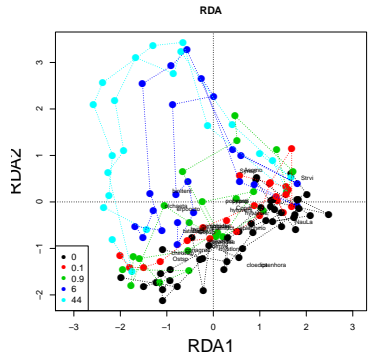Mesocosms
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How to

partial RDA?

partial RDA:

- ▶ Not interested in the pure time effect
- ▶ remove time effect (*partial out*)

partial RDA?

partial RDA:

▶ Not interested in the pure time effect

▶ remove time effect (*partial out*)

▶ treatment + treatment x time on first axis

▶ first axis better separates treatments

▶ still cluttered

▶ time course?

partial RDA

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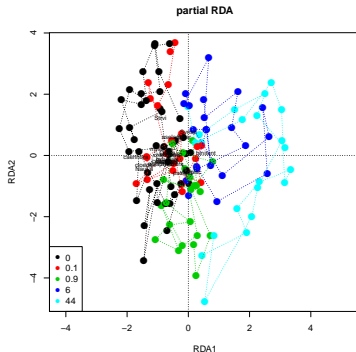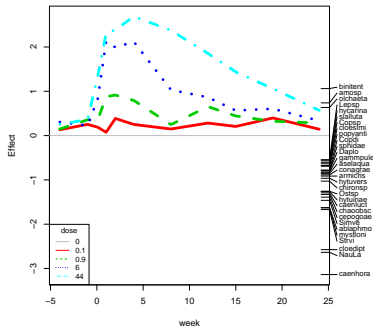
Alternatives

How to

PRC!

PRC:

- ▶ **1st axis**
- ▶ site scores as contrast to control
- ▶ species scores
- ▶ easy plot
- ▶ easy to interpret

Summary

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How to

Raw data
(mesocosm x species)

Transform

downweight species with
high abundances

Transformed data
(mesocosm x species)

Explanatory variables
Time
Treatment
Treatment x Time
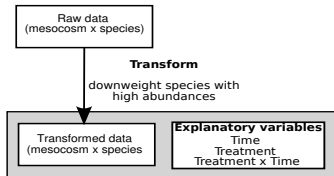
Partial RDA:

1) 'partial out' time effect
2) Fit RDA model

= axes display effect of
Treatment and
Treatment x Time

A) Site scores

Site scores on first axis as
contrast to control

= Effect of treatment along time

B) Species scores

Species scores on first axis

= species responsible for
the pattern in A)

C) Significance test

Permutation tests
of first axis

= axis displays statistically
significant amount
of variation

Numerical output

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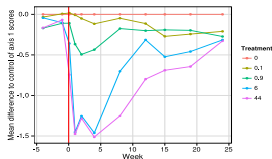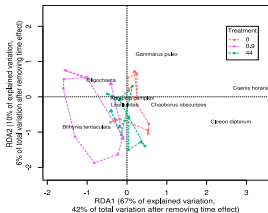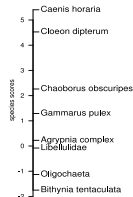How to

► How much variation is displayed on first axis?

► Significance testing:
   ► of first axis
   ► of predictors (treatment x time)
   ► need to take repeated measures into account

► Recovery?
   ► separate RDA per time point

► NOEC?
   ► poorly replicated
   ► cannot use permutations

Numerical output

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Interpretation

Site scores:

- ▶ Date on **x-axis**
- ▶ deviations in composition between treatments and control on the **y-axis**
- ▶ spot recovery (treatment x time)

Species scores

- ▶ species responsible for the pattern
- ▶ increase / decrease

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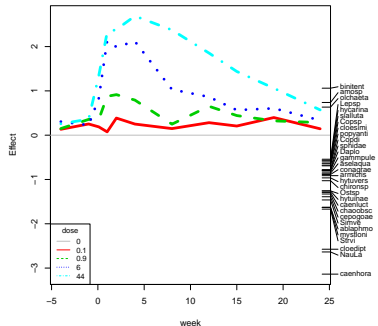Data

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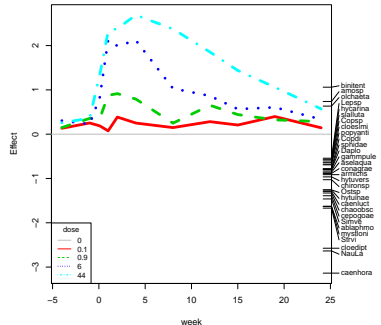Alternatives

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Caveats

- ▶ low species scores not necessarily mean low response!
    - ▶ species associated with main pattern
    - ▶ special responses (no recovery)
- ▶ Need to transform abundance data (often ln(Ax + 1))

Caveats

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Alternatives

- ▶ (multivariate) GLM (Warton 2012)
    - ▶ new method, can model counts
    - ▶ advantages, but also some disadvantages (e.g. computation time, complexity)
- ▶ Univariate indicators?
    - ▶ SPEAR, diversity, ...
    - ▶ univariate solution to a multivariate problem
    - ▶ what about species responses?

Alternatives

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Lets do it in R!

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