Bias due to autocorrelation where no one expects it: the relationship between community-weighted mean traits and environmental variables

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the relationship between community-weighted mean traits
and environmental variables

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Weighted mean of species attributes

\[ \text{R} \ldots \text{matrix of sample attributes (e.g. environmental variables)} \]
\[ \text{L} \ldots \text{matrix of species composition} \]
\[ \text{Q}' \ldots \text{matrix of species attributes (e.g. traits, species indicator values)} \]

(notation of matrices follow that in the RLQ and fourth-corner analysis)
Weighted mean of species attributes

\[ M = L_s Q \]

\[ m_n = \sum_{p=1}^{n} a_{np} \times t_p \]

R ... matrix of sample attributes (e.g. environmental variables)
L ... matrix of species composition (\( L_s \) ... standardized by sample totals)
Q ... matrix of species attributes (e.g. traits, species indicator values)
M ... matrix of weighted means of species attributes (e.g. CWM)
Weighted mean of species attributes

\[ M = L_s Q \]

\[ m_n = \sum_{p=1}^{n} a_{np} \times t_p \]

We should expect inflated Type I error rate

testing the relationship

correlation, regression, ANOVA, parametric or nonparametric versions
Relationship between community weighted mean for SLA and cover of overstory

Data:
- forest vegetation in Vltava valley
- wide range of vegetation types
- SLA for herb species
- 97 samples, 233 herb species

\[ r^2 = 0.123, P < 0.001 \]
Weighted mean of species attributes: compositional autocorrelation

- Samples with the same species composition will have the same value of WM
- Samples with similar species composition will have similar value of WM
Weighted mean of species attributes: compositional autocorrelation

- Samples with the same species composition will have the same value of WM
- Samples with similar species composition will have similar value of WM
Weighted mean of species attributes: compositional autocorrelation

- Samples with the same species composition will have the same value of WM
- Samples with similar species composition will have similar value of WM
Relationship of two compositionally autocorrelated variables

Issues:
- inflated type I error rate
- biased estimation of $r$ or $r^2$

$CWM$ of SLA of herb species

$\text{Cover of overstorey (trees and shrubs)}$ [%]

$\text{weighted mean of SLA (herbs)}$

$r^2 = 0.123, P < 0.001$
The fourth-corner approach

\[ R \] ... matrix of sample attributes (e.g. environmental variables)
\[ L \] ... matrix of species composition
\[ Q' \] ... matrix of sample attributes (e.g. traits, species indicator values)
\[ D \] ... fourth-corner matrix
The fourth-corner approach: testing the significance

Figure 10.25 Permutations of matrix A may be performed in different ways which correspond to different null ecological models.

1. The occurrence of a species in the study area is constant, but positions are random; permute at random within columns.

2. Positions of species assemblages are random; permute whole rows (assemblages).

3. Lottery hypothesis: the species that arrived first occupied a site; permute at random within rows.

4. Species have random attributes; permute whole columns.

Legendre & Legendre (2012)
Solution for weighted-mean approach: modified permutation test

• Modified permutation test:
  – null distribution of test statistic is created by calculating weighted mean from permuted species attributes
  – this test has correct type I error rate in case that there is a link between R and L (sample attributes and species composition matrix)
  – but it’s overly conservative in case that there is no R <-> L link

  – possible to calculate in R package weimea (available on r-forge, beta version)
Solution for weighted-mean approach: modified permutation test
MoPeT: program (R-based) for calculation of modified permutation test

www.bit.ly/ellenberg
Conclusions

• test of the relationship between weighted mean of species attributes and sample attributes has inflated Type I error rate

• applies to community weighted mean of species functional traits, mean Ellenberg indicator values, diatom index etc.

• solution: modified permutation test (based on permuting species instead of sample attributes)

Thank you for your attention!