

Analysing multivariate ecological data with Generalized Linear Latent Variable Models

Bert van der Veen

Jenni Niku

Sam Wenaas Perrin

Robert Brian O'Hara



Wrap-up

You now know:

- 1) What ecological gradient analysis is
- 2a) That JSDMs and ordination are both used to study co-occurrence patterns of species
- 2b) And that these are the same in terms of GLLVM implementation
- 3) How to use the **gllvm** R-package Niku et al. 2019

You might want to

- Include random-effects
- Assume sites are not independent
- Assume species are not independent
- Perform constrained ordination
- Assume species associations depended on the environment
- Model multiple time points
 - Some of these will hopefully come to **gllvm** in the future

GLLVM extensions

- Spatial autocorrelation: $\mathbf{u}_i \sim \mathcal{N}(0, s(\mathbf{H}))$
 - Spatially structure latent variables
- Species are related: $\boldsymbol{\theta}_j \sim \mathcal{N}(0, \mathbf{G})$
 - Where \mathbf{G} is a matrix of relatedness (e.g. phylogeny)
- Constrained ordination: $\mathbf{u}_i \sim \mathcal{N}(\boldsymbol{\mu}_i, \mathbf{I})$
 - Regress the mean of latent variables: $\boldsymbol{\mu}_i = \boldsymbol{\alpha} + \mathbf{X}_i\boldsymbol{\beta}$
- Species associations as function of the environment:
 - $\boldsymbol{\theta}_j = \boldsymbol{\alpha}_j + \mathbf{X}\boldsymbol{\beta}_j$ Perrin et al. in review
- Spatial-temporal JSDM/ordination: species associations through time and/or space

Bayesian Ordination and Regression

- For GLLVMs (ordination) with spatial effects
- Bayesian, with MCMC (i.e. can be **slow**)

Methods in Ecology and Evolution



British Ecological Society

Methods in Ecology and Evolution 2016, **7**, 744–750

doi: 10.1111/2041-210X.12514

APPLICATION

BORAL – Bayesian Ordination and Regression Analysis of Multivariate Abundance Data in R

Francis K.C. Hui*

Mathematical Sciences Institute, The Australian National University, Canberra, ACT 0200, Australia

Hierarchical Modeling of Species


- For other cool GLLVM (JSMD) stuff
- Bayesian, with MCMC (i.e. can be **slow**)

Methods in Ecology and Evolution



APPLICATION |  Open Access |   

Joint species distribution modelling with the R-package HMSC

Gleb Tikhonov, Øystein H. Opedal, Nerea Abrego, Aleksi Lehikoinen, Melinda M. J. de Jonge, Jari Oksanen, Otso Ovaskainen 

First published: 25 December 2019 | <https://doi.org/10.1111/2041-210X.13345> | Citations: 19

Thanks for your attention

 On twitter: #**GLLVMs**, @**vdVeenB** or @**J__Niku** or @**samperrinNTNU** or @**BobOHara**

 On github: <https://github.com/BertvanderVeen/BES2020GLLVMworkshop/discussions>

