

# Some other R packages for model-based multispecies analysis

Bert van der Veen

Department of Mathematical Sciences, NTNU

## Questions so far?

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## Different packages

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I will briefly go through the different model-based ordination packages

I will contrast each package to `gllvm`

Each of these packages really warrants its own presentation

## Examples with Bird counts (from CANOCO 5)

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```
Y <- read.csv("../data/birdY.csv", header = TRUE, skip = 1, row.names = 1)
Y[is.na(Y)] <- 0;
Y <- Y[,order(colSums(ifelse(Y==0,0,1)),decreasing=TRUE)] #reorder by freq
Y <- as.matrix(Y)
row.names(Y)<-1:nrow(Y) # for VGAM
X <- read.csv("../data/birdX.csv", header = TRUE, skip = 1, row.names = 1)
X[,c(1:3,5:9)] <- scale(X[,c(1:3,5:9)])
X[,~c(1:3,5:9)] <- data.frame(lapply(X[,~c(1:3,5:9)], as.factor))
```

# Bayesian Ordination and regression AnaLysis

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## Methods in Ecology and Evolution



*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*

## boral

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- ▶ The first model-based ordination package for community ecology
- ▶ For unconstrained (or residual) ordination (and JSDM)
- ▶ Based on JAGS (Plummer, 2012)
- ▶ Writes the model to a file, loads it into JAGS, returns results
- ▶ Runs on a single MCMC chain

### Features

- ▶ Covariates
- ▶ 4th corner model
- ▶ Row intercepts
- ▶ Structured LVs
- ▶ Natively includes gold-standard residuals

# boral

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This is boral version 2.0.2.

Please note that as of version 2.0, boral will no longer be regularly maintained and updated. However, if you spot any bugs/typos or have a specific feature requests, please contact the maintainer.

## boral: code

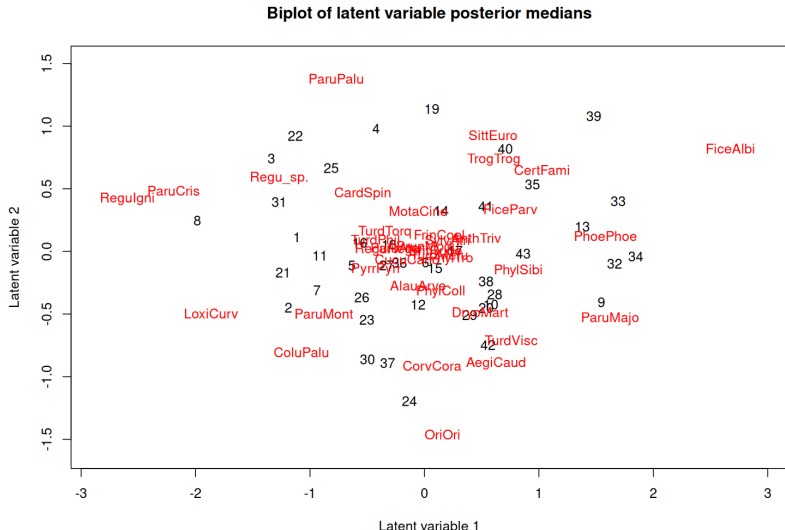
```
model <- boral::boral(Y, X, formula.X = ~ Forest + Altit, lv.control=list(
```

```
## Compiling model graph
##   Resolving undeclared variables
##   Allocating nodes
## Graph information:
##   Observed stochastic nodes: 1591
##   Unobserved stochastic nodes: 270
##   Total graph size: 9883
##
## Initializing model
```

```
boral::lvplot(model)
```

vignette: see paper





## boral

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### Article

## Comparison of distance-based and model-based ordinations

David W. Roberts 

First published: 10 October 2019 | <https://doi.org/10.1002/ecy.2908>

Corresponding Editor: Helene H. Wagner.

## boral: MCMC

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- ▶ MCMC is (kind of) like optimisation, you need to check convergence
- ▶ MCMC needs “burn-in”, i.e., forget the initial state
- ▶ But samples of parameters are stored; so we can expect them
- ▶ MCMC needs to mix well (explore whole parameter space)
- ▶ The chain is stationary if we have reached a good state
- ▶ We can check this visually, or with statistics
- ▶ If it has not converged, it needs to be run longer (or your model is poorly formulated)

## boral: calc.varpart

### Partition variance per species over model terms

```
boral::calc.varpart(model)
```

```
## $varpart.X
## EritRube FrinCoel ParuAter PrunModu SylvAtri TurdMeru PhylColl
## 0.35006766 0.74912303 0.07519307 0.53298447 0.38115978 0.34059272 0.13704461
## CucuCano PyrrPyrr TurdTorg ReguRegu PhylTro TrogTrog PhylSibi
## 0.40878207 0.23032008 0.49760030 0.10155732 0.63947307 0.06725817 0.46875038
## AnthTriv TurdPhil ParuMont CardSpin PhoePhoe ColuPalu FiceAlbi
## 0.74033945 0.16197548 0.11772341 0.19533027 0.33087932 0.08736864 0.04953287
## ParuMajo Regu_sp. CorvCora SittEuro LoxiCurv ParuCris ReguIgni
## 0.12302430 0.16045273 0.40675317 0.58142295 0.12779628 0.24466981 0.16043077
## AlauArve FiceParv MotaCine OriOri AegiCaud CertFami DryoMart
## 0.71026338 0.58186722 0.49177664 0.35784980 0.31973772 0.58934078 0.36350553
## TurdVisc ParuPalu
## 0.28510942 0.29575336
##
## $varpart.lv
## EritRube FrinCoel ParuAter PrunModu SylvAtri TurdMeru PhylColl CucuCano
## 0.6499323 0.2508770 0.9248069 0.4670155 0.6188402 0.6594073 0.8629554 0.5912179
## PyrrPyrr TurdTorg ReguRegu PhylTro TrogTrog PhylSibi AnthTriv TurdPhil
## 0.7696799 0.5023997 0.8984427 0.3605269 0.9327418 0.5312496 0.2596605 0.8380245
## ParuMont CardSpin PhoePhoe ColuPalu FiceAlbi ParuMajo Regu_sp. CorvCora
## 0.8822766 0.8046697 0.6691207 0.9126314 0.9504671 0.8769757 0.8395473 0.5932468
```

## boral

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Has a few other helpful functions:

- ▶ `get.enviro.cor` and `get.residualcor`
- ▶ `predict.boral` and `plot.boral`
- ▶ `coefspplot` and `ranefspplot`

## boral: compared to glvm

boral	glvm
Bayesian	Frequentist
MCMC	Likelihood approximation
Slow	Fast
Correlated LVs	Correlated LVs
Single row effect	Multiple row effects
Stochastic Variable Selection	Adaptive shrinkage?

There is little reason to use `boral` at this point, except for the SVSS.



# Hierarchical Modeling of Species Communities

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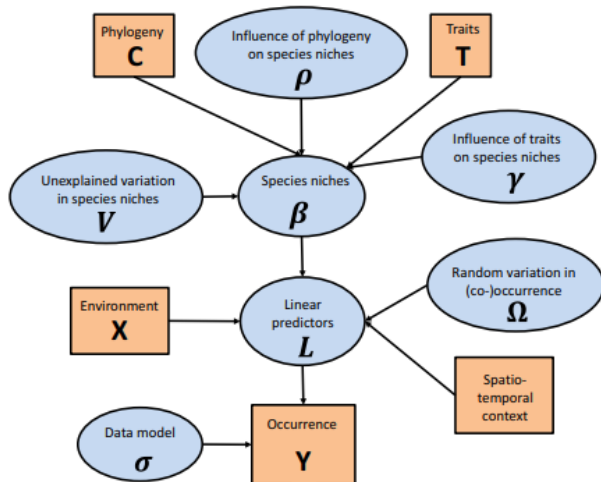
## APPLICATION

Methods in Ecology and Evolution 

## Joint species distribution modelling with the R-package HMSC

Gleb Tikhonov<sup>1,2</sup> | Øystein H. Opedal<sup>2,3</sup>  | Nerea Abrego<sup>4</sup> | Aleksi Lehikoinen<sup>5</sup> |  
Melinda M. J. de Jonge<sup>6</sup> | Jari Oksanen<sup>7</sup> | Otso Ovaskainen<sup>2,3</sup> 

## HMSC





## HMSC

HMSC was introduced by Ovaskainen et al. (2017) but has been expanded a lot since then

### Methods in Ecology and Evolution



Technological Advances at the Interface Between Ecology and Statistics | [Free Access](#)

**Using joint species distribution models for evaluating how species-to-species associations depend on the environmental context**

Gleb Tikhonov, Nerea Abrego, David Dunson, Otso Ovaskainen

### Methods in Ecology and Evolution



APPLICATION | [Open Access](#) |

**Joint species distribution modelling with the R-package Hmsc**

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

First published: 25 December 2019 | <https://doi.org/10.1111/2041-210X.13345> | Citations: 178

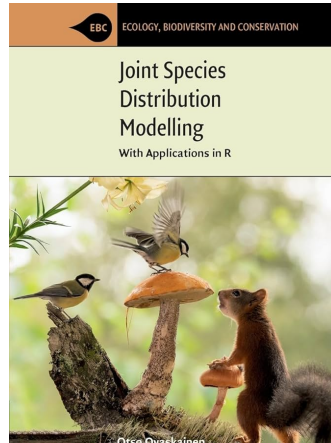
ECOLOGICAL SOCIETY OF AMERICA

Statistical Reports | [Open Access](#) |

**Computationally efficient joint species distribution modeling of big spatial data**

Gleb Tikhonov, Li Duan, Nerea Abrego, Graeme Newell, Matt White, David Dunson, Otso Ovaskainen

First published: 14 November 2019 | <https://doi.org/10.1002/rev.2929> | Citations: 39



## HMSC

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- ▶ Bayesian; fits with MCMC
- ▶ Custom Gibbs samplers
- ▶ Flexible package for multispecies hierarchical modeling
- ▶ Focuses on prediction and species associations
- ▶ Phylogenetic effects
- ▶ Efficiently implements spatial models with nearest neighbors
- ▶ 4th corner model
- ▶ Various extra random effects (intercepts and such)
- ▶ Effects can be specified at different sampling levels, including sets of LVs
- ▶ The “infinite factor model”
- ▶ Have a preprint on parallelisation
- ▶ Very little support for ordination
- ▶ Supports mixed response types

## HMSC: code

*# need to set-up LVs*

```
studyDesign = data.frame(sample=as.factor(1:nrow(Y)))
rL <- Hmsc::HmscRandomLevel(units = studyDesign$sample)
model <- Hmsc::Hmsc(Y, XFormula = ~Forest+Altit, XData= X,
distr = "lognormal poisson", studyDesign = studyDesign,
ranLevels = list(sample = rL))
# Run mcmc
run = Hmsc::sampleMcmc(model, samples = 1000, nChains = 3,
transient = 2500)
```

```
## Computing chain 1
## Chain 1, iteration 20 of 3500 (transient)
## Chain 1, iteration 40 of 3500 (transient)
## Chain 1, iteration 60 of 3500 (transient)
## Chain 1, iteration 80 of 3500 (transient)
## Chain 1, iteration 100 of 3500 (transient)
## Chain 1, iteration 120 of 3500 (transient)
```



## HMSC

HMSC	gllvm
Bayesian	Frequentist
MCMC	Likelihood approximation
Slow (but parallel package)	Fast
normal, Bernoulli, Poisson, lognormal Poisson	Wide range of response types
Different effects at different sampling levels	One effect at a sampling level
Infinite factor model	Number of LVs fixed <u>a-priori</u>
Efficient spatial implementation	Spatial is a work in progress
Few tools for ordination	many tools for ordination

Ultimately, the focus of these two packages is very different. HMSC focuses on prediction and JSDMs, gllvm can do that, but its main focus is different (IMO).

# ecoCopula

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## RESEARCH ARTICLE

Methods in Ecology and Evolution



## Fast model-based ordination with copulas

Gordana C. Popovic<sup>1</sup>  | Francis K. C. Hui<sup>2</sup>  | David I. Warton<sup>1</sup> 

- ▶ Employs graphical models for determining species associations
- ▶ Requires a secondary model
- ▶ Is -very- fast for ordination (faster than NMDS!)
- ▶ Can estimate “direct associations” (not as quick)
- ▶ Supports mixed response types

## ecoCopula: code

---

```
preModel <- ecoCopula::stackedsdm(Y, formula_X =~1, data = X)
model <- ecoCopula::cord(preModel)
plot(model, biplot=TRUE)
```

vignette

## ecoCopula

ecoCopula	gllvm
Frequentist	Frequentist
Gaussian Copula	Likelihood approximation
Faster	Fast
A decent number of distributions	Wide range of response types
Direct species associations	Correlative
None	Many other random effects
Secondary model in parallel	Working on parallel computation
Native residuals	Native residuals
Biplot function	Biplot function
Marginal interpretation	Conditional interpretation

ecoCopula has a lot of potential due to its speed, but lacks in support, maintenance, and perhaps some maturity.



# Vector Generalised Linear and Additive Models



*Journal of Statistical Software*

January 2010, Volume 32, Issue 10.

<http://www.jstatsoft.org/>

## The VGAM Package for Categorical Data Analysis

Thomas W. Yee  
University of Auckland

## Vector Generalised Linera and Additive Models

- ▶ Package with a wide range of model types **VGLMs**
- ▶ Massive package with a lot of functionality
- ▶ An incredible range of response distributions
- ▶ Unconstrained and constrained ordination (fixed effects formulation)
- ▶ Quadratic and additive ordinations
- ▶ Supposed to fit quickly with IWLS
- ▶ In my experience, fitting is often difficult (errs often) and can be unstable
- ▶ Has some residuals
- ▶ Plotting functions are a bit different
- ▶ No random effects
- ▶ Now (recently) has doubly-constrained ordination!

Centers around `vglm()`, `vgam()`, `rrvglm()`, `cqo()`, `cao()`, `rcim()`

# VGAM

---

## The first (model-based) constrained ordination method

*Ecological Monographs*, 74(4), 2004, pp. 685–701  
 © 2004 by the Ecological Society of America

### A NEW TECHNIQUE FOR MAXIMUM-LIKELIHOOD CANONICAL GAUSSIAN ORDINATION

THOMAS W. YEE<sup>1</sup>

*Department of Statistics, University of Auckland, Private Bag 92019, Auckland, New Zealand, and  
 Department of Statistics and Applied Probability, 6 Science Drive 2, National University of Singapore, Singapore 117546*

## VGAM: code

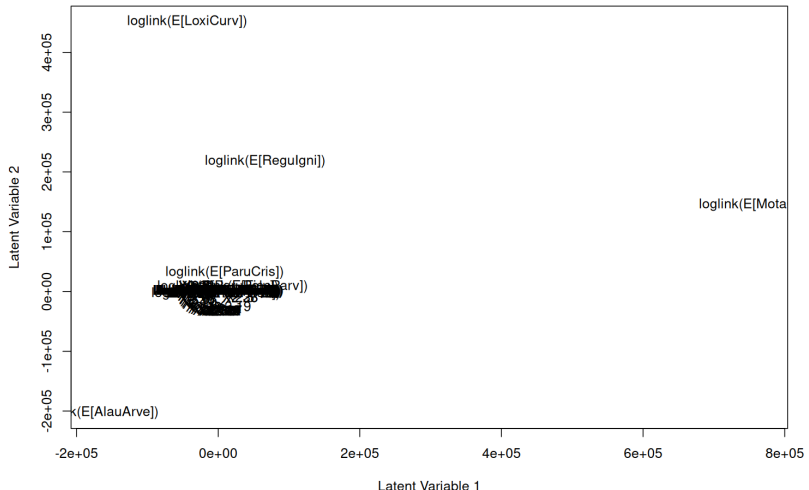
---

```
model1 <- VGAM::rcim(Y, Rank = 2, family = VGAM::poissonff)
VGAM::lvplot(model1)
```

```
# Could not get this to work :(
# model2 <- VGAM::rruglm(Y ~ model.matrix(~.,X[,1:4])[, -1], Rank = 2, fami
```

vignette: see reference card

## VGAM: plot



## VGAM

VGAM	gllvm
Frequentist	Frequentist
ML via IWLS	Approximate marginal likelihood
Fast	Fast
Incredible range of responses	Wide range of response types
Not robust fitting	Relatively robust
No random effects	Many other random effects
UQO, CQO, CAO	UQO, CQO
VGAMs	No smooths
Native residuals	Native residuals
Biplot function	Biplot function

VGAM has a lot of potentially useful tools, but I do not find it very usable.

## glmmTMB

# glmmTMB Balances Speed and Flexibility Among Packages for Zero-inflated Generalized Linear Mixed Modeling

by Mollie E. Brooks, Kasper Kristensen, Koen J. van Benthem, Arni Magnusson, Casper W. Berg,  
Anders Nielsen, Hans J. Skaug, Martin Mächler, Benjamin M. Bolker





*Journal of Statistical Software*


March 2025, Volume 112, Issue 1.


doi: 10.18637/jss.v112.i01

## Parsimoniously Fitting Large Multivariate Random Effects in glmmTMB

Maeve McGillicuddy   
UNSW Sydney

Gordana Popovic   
UNSW Sydney

Benjamin M. Bolker   
McMaster University

David I. Warton   
UNSW Sydney

## glmmTMB: functionality

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- ▶ Kind of similar to gl1vm in that it uses approximate methods
- ▶ Laplace approximation with TMB (state-of-the-art)
- ▶ Great usability
- ▶ Can include many random-effects
- ▶ (Un)constrained random effects ordination
- ▶ Slower than gl1vm's VA (usually)
- ▶ Structured random effects (e.g., spatial), Phylogenetic intercepts
- ▶ Little support for ordinations
- ▶ Big on zero-inflated modelling



## glmmTMB: code

---

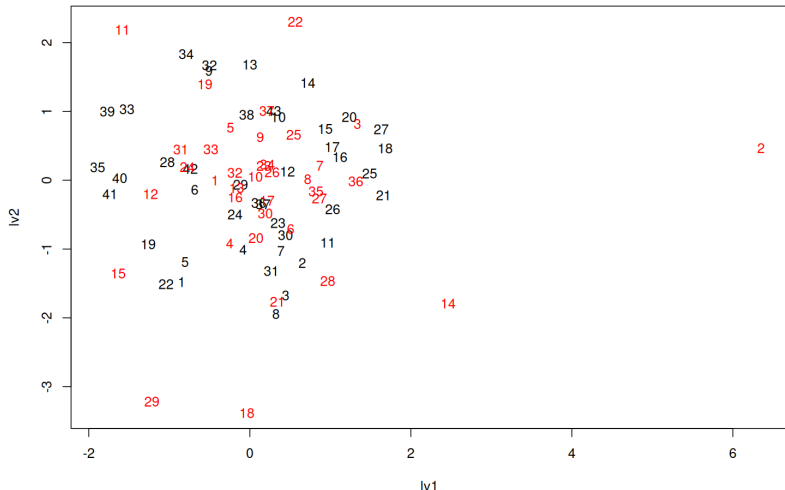
Note: data needs to be in long format

```

# organize data into long format
tmp <- data.frame(Y)
tmp$id <- 1:nrow(tmp)
glmmDat <- reshape(tmp,
                    idvar = "id",
                    timevar = "col",
                    times = colnames(Y),
                    varying = list(colnames(Y)),
                    v.names = "y",
                    direction = "long")

model <- glmmTMB::glmmTMB(y ~ col + rr(col + 0|id, d = 2), data = glmmDat,
rrstuf <- extract_rr(model) # see here: https://github.com/glmmTMB/glmmTMB
plot(rbind(rrstuf$b,rrstuf$f1), type = "n");
text(rrstuf$b);text(rrstuf$f1, col = "red")
  
```

## glmmTMB: plot



## glmmTMB

glmmTMB	gllvm
Frequentist	Frequentist
Laplace	VA (default) or Laplace
Fast	Fast(er)
Wide range of response types	Wide range of response types
Many (structured) random effects	Many random effects
Can also fit with MCMC	No
Zero-inflated modeling	Work in progress
No residuals	Native residuals
No plotting function	Biplot function
Large community	Small community
Excellent developers	No comment :)

glmmTMB is especially useful if you want user friendliness and many other random effects.



## gmf: code

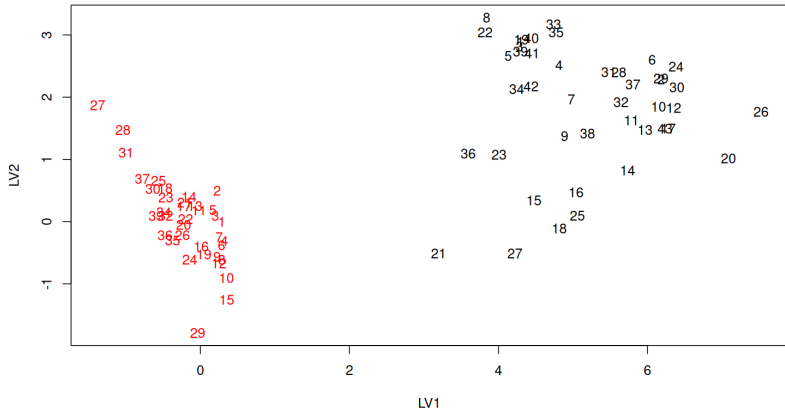
---

```

# devtools::install_github("kidzik/gmf")
model <- gmf::gmf(Y, family = poisson(), p = 2)
plot(rbind(model$u,model$v), type = "n", xlab="LV1", ylab="LV2")
text(model$u)
text(model$v, col="red")

```

## gmf: plot



## gmf

---

gmf	gllvm
Frequentist	Frequentist
Penalized likelihood	VA or LA approximation
Fast(er) but unstable	Fast
A few response types	Wide range of response types
Fitting is fine	Relatively robust
No random effects	Many other random effects

A skeleton of a package, not very useful at this point.

## RCM

# A unified framework for unconstrained and constrained ordination of microbiome read count data

**Stijn Hawinkel**<sup>1\*</sup>, **Frederiek-Maarten Kerckhof**<sup>2</sup>, **Luc Bijmans**<sup>3,4</sup>, **Olivier Thas**<sup>1,4,5</sup>

**1** Department of Data Analysis and Mathematical Modelling, Ghent University, Ghent, Belgium, **2** Center for Microbial Ecology and Technology, Ghent University, Ghent, Belgium, **3** Quantitative Sciences, Janssen Pharmaceutical companies of Johnson and Johnson, Beerse, Belgium, **4** Center for Statistics, Hasselt University, Hasselt, Belgium, **5** National Institute for Applied Statistics Research Australia (NIASRA), University of Wollongong, Wollongong, Australia

\* [stijn.hawinkel@ugent.be](mailto:stijn.hawinkel@ugent.be)

- ▶ Does both unconstrained and unconstrained ordination
- ▶ Even additive constrained ordination
- ▶ All based on fixed effects formulations, no random effects
- ▶ Only the negative binomial distribution
- ▶ Not a “true” statistical model (according to the authors)
- ▶ Permanova functionality
- ▶ Residual plots



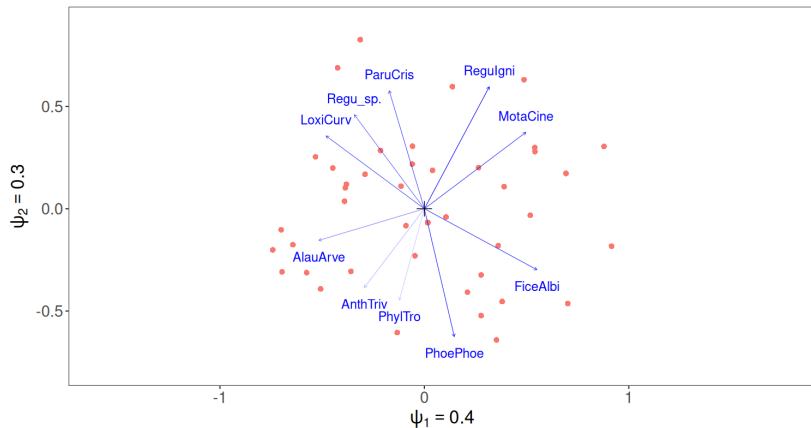
## RCM: code

---

```
# devtools::install_github("CenterForStatistics-UGent/RCM")
model <- RCM::RCM(Y, k = 2)
plot(model)
```

vignette

## RCM: plot



## RCM

RCM	gl1vm
Frequentist	Frequentist
Maximum likelihood	Approximate marginal likelihood
Fast	Fast
Only NB	Wide range of response types
UO, CO, CQO, CAO	UO, CO, CQO
No random effects	Many other random effects

RCM seems good at what it does, but functionality is limited.

# Experimental: latent INLA

## README


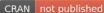
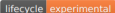
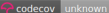
Bob O'Hara 8/29/2021

### LatentINLA Readme

This package is made to play around with latent variable models in INLA.

### To Do

- look at speeding it up
- are initial values going to help with speed or convergence?
- Try a constrained model
- Try a spatial model, making the site scores spatial rather than iid.
- plant some trees to offset the atmospheric warning created by running these models

- ▶ Relatively fast; Bayesian with Laplace approximation
- ▶ Unconstrained, concurrent, ~~and hierarchical ordination~~
- ▶ Fast fitting of large spatial effects
- ▶ **Very much a work in progress, cannot be used at the**

## latent INLA: code

---

don't try, this crashed :(

```
# devtools::install_github("oharar/LatentINLA")  
model <- LatentINLA::FitGLLM(Y=Y, Family="poisson", nLVs = 2  
LatentINLA::biplot(model)
```

vignettes

## Community-level basis function models

### RESEARCH ARTICLE

Methods in Ecology and Evolution

### Spatiotemporal joint species distribution modelling: A basis function approach

Francis K. C. Hui<sup>1</sup> | David I. Warton<sup>2</sup> | Scott D. Foster<sup>3</sup> | Christopher R. Haak<sup>4</sup>

- ▶ Most recent developments: GAM for multiple species
- ▶ Specifically targeted on spatio,temporal or spatio-temporal analysis
- ▶ This is something GLLVMs are not -terribly- good at yet (but very much an area of interest)
- ▶ Based on the idea of LVMs, but not with LVs
- ▶ Fitting using TMB
- ▶ I.e., JSMD-oriented, not ordination

## CBFM

CBFM	gllvm
Frequentist	Frequentist
Penalized Quasi-likelihood	Approximate marginal likelihood
For large spatio-temporal problems	Not an option (yet?)
Wide range of response types	Wide range of response types
Post-hoc ordination	Is an ordination method
Can include extra "random effects" as smooths	Many other random effects
Parallelisation	Parallelisation
No traits or Phylogeny	Traits and Phylogeny

Sorry, no example yet. Bird data does not have coordinates, and CBFM only fits models with space it seems?

## Summary

Package	cran <sup>1</sup>	UO <sup>2</sup>	CO <sup>3</sup>	CN <sup>4</sup>	RE <sup>5</sup>	CI <sup>6</sup>	traits	Phylogeny	Space	framework <sup>7</sup>
glvm	yes	yes	yes	yes	yes	yes	yes	yes	sort of	F
Boral	yes	yes	no	no	some	yes	yes	no	yes	B
HMSC	yes	yes	no	no	yes	yes	yes	yes	yes	B
ecoCopula	yes	yes	no	no	no	no	kind of	no	no	F
VGAM	yes	yes	yes	no	no	some	new?	no	no	F
glmmTMB	yes	yes	no	no	yes	yes	yes	sort of	Kind of	F
gmf	no	yes	no	no	no	no	no	no	no	F
RCM	no	yes	yes	no	no	no	no	no	no	F
latent INLA	no	no	no	yes	yes	yes	soon	no	yes	B
CBFM	no	no	no	no	yes	yes	no	no	yes	F

<sup>1</sup>cran: Package available on CRAN. <sup>2</sup>UO: Unconstrained ordination. <sup>3</sup>CO: Constrained. <sup>4</sup>CN: Concurrent. <sup>5</sup>RE: Random effects. <sup>6</sup>CI: Confidence/Credible intervals. <sup>7</sup>framework: The underlying framework of the model (F: Frequentist, B: Bayesian).



## When to use what package?

- ▶ HMSC for extensive support for JSDMs
- ▶ glmmTMB for many (structured) random effects
- ▶ ecoCopula if you have a **huge** dataset and glvm is too slow
- ▶ CBFM for large spatial/temporal models

gllvm for all your ordination needs

## Summary

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New software implementations are continuously being developed.  
 Dimension reduction methods for ecology have entered a new era.

Most of existing implementations are based on the GLLVM  
 framework (sjSDM, BayesComm, VGAM, RCM excluded)

## Summary

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New software implementations are continuously being developed.  
 Dimension reduction methods for ecology have entered a new era.

Most of existing implementations are based on the GLLVM  
 framework (sjSDM, BayesComm, VGAM, RCM excluded)

## Summary

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- ▶ It is important that we continue to explore new and better methods
- ▶ Especially the application of ordination methods is stuck in the past
- ▶ There is still a lot of work to be done on multivariate methods for community ecology
- ▶ There are more packages for model-based analysis that I have not mentioned
- ▶ E.g., jSDM, sjSDM, BayesComm