# Better GDM

## The Problem

The idea of GDM, modelling matrices of dissimilarity, was suggested by Ferrier (2002). Recently, White et al. (2023) suggested improvements to generalized dissimilarity modelling. Here we will develop an alternative, based on modelling the data rather than the distances between data.

The ecological problem is to explain how beta diversity, i.e. variation between sites, is affected by predictors, such as the environment. This can be done using GDM, which regresses distances between communities against teh environemntal covariates. Here we suggest an alternative approach.

## The Model

We assume we have a site by species matrix, $Y$, with each row being observations of species (abundance, presentece etc.), and each column being a site. So $Y_{ij}$ is the observation for the $i^t h$ species ($i = 1, ..., S$) and $j^t h$ species ($j = 1, ..., N$). For each site we have $P$ covariates, $x_{jk}$ ($k = 1, ..., P$), so these are in a $N \times P$ matrix $X$.

We assume we model this data using a GLM, i.e. we assume $Y_{ij}$ follows some distribution in the exponential family, with expected value $\mu = g(\eta)$, where $g()$ is a link function, and $\eta$ is a linear predictor:

$$\eta_{ij} = \alpha_i + \kappa_j + \beta_{ij}$$

For identifiability we assume $\sum_j \kappa_j = 0$ and $\sum_j \beta_j = 0$

So $\alpha_i$ is the mean commonness of a species, and $\kappa$ is the abundance at a site: we will assume this is not interesting, as it is affected by the sampling process. $\beta_{ij}$ is where beta diversity lies (at least compositional beta diversity). The total beta diversity can be measured as $\text{Var}(\beta) = \sigma_\beta^2$. We can clearly model $\beta_{ij}$ further, e.g. for a single covariate $x_j$

$$\beta_{ij} = \beta_0 + \delta_i x_j + \epsilon_{ij}$$

i.e. each species has its own response to $x$.

Then,

$$\text{Var}(\beta) = \text{Var}(\beta_0 + \delta_i x_j + \epsilon_{ij})$$

$$= \frac{1}{(S-1)(N-1)} \sum_{i=1}^{S} \sum_{j=1}^{N} (\delta_i(x_j - \bar{x}) + \epsilon_{ij})^2$$

$$= \frac{1}{(S-1)(N-1)} \left( \sum_{i=1}^{S} \sum_{j=1}^{N} \delta_i^2 (x_j - \bar{x})^2 + \sum_{i=1}^{S} \sum_{j=1}^{N} \epsilon_{ij}^2 \right)$$

$$= \frac{1}{(S-1)} \sum_{i=1}^{S} \delta_i^2 \frac{1}{(N-1)} \sum_{j=1}^{N} (x_j - \bar{x})^2 + \frac{1}{(S-1)(N-1)} \sum_{i=1}^{S} \sum_{j=1}^{N} \epsilon_{ij}^2$$

$$= \frac{1}{(S-1)} \sum_{i=1}^{S} \delta_i^2 \text{Var}(x) + \text{Var}(\epsilon_{ij})$$

$$= \frac{\text{Var}(x)}{(S-1)} \sum_{i=1}^{S} (\delta_i - \bar{\delta} + \bar{\delta})^2 + \text{Var}(\epsilon_{ij})$$

$$= \frac{\text{Var}(x)}{(S-1)} \sum_{i=1}^{S} (\delta_i - \bar{\delta})^2 - S\bar{\delta}^2 + \text{Var}(\epsilon_{ij})$$

$$= \text{Var}(\delta_i)\text{Var}(x_j) + \frac{S}{S-1} \bar{\delta}^2 \text{Var}(x) + \text{Var}(\epsilon_{ij})$$

because $\sum_i (\delta_i - \bar{\delta} + \bar{\delta})^2 = \sum_i (\delta_i - \bar{\delta})^2 + \sum_i (\delta_i - \bar{\delta})\bar{\delta} + \sum_i \bar{\delta})^2 = \sum_i (\delta_i - \bar{\delta})^2 + \bar{\delta}(\sum_i \delta_i - S\bar{\delta}) + S\bar{\delta}^2 = \sum_i (\delta_i - \bar{\delta})^2 + S\bar{\delta}^2$.

So, we can model the species abundance as a function of the environment. We can extend this to more than one covariate, if they are assumed to have independent effects between species (i.e. $\delta_{ik}$ is independent of $\delta_{il}$ for species $i$ and covariates $k$ and $l$).

## Relationship to Distance

If we have two vectors of biodiversity, $\eta_1$ and $\eta_2$ then the distance between then the distance between them is just the Euclidean distance:

$$D_{12} = \|\eta_1 - \eta_2\| = \sqrt{\sum_{i=1}^{S} (\eta_{i1} - \eta_{i2})^2}$$

So that

$$D_{12}^2 = \sum_{i=1}^{S} (\eta_{i1} - \eta_{i2})^2$$

$$= \sum_{i=1}^{S} (\alpha_i + \kappa_1 + \beta_{i1} - (\alpha_i + \kappa_2 + \beta_{i2}))^2$$

$$= \sum_{i=1}^{S} ((\kappa_1 - \kappa_2) + (\beta_{i1} - \beta_{i2}))^2$$

$$= \sum_{i=1}^{S} ((\kappa_1 - \kappa_2)^2 + (\kappa_1 - \kappa_2)(\beta_{i1} - \beta_{i2}) + (\beta_{i1} - \beta_{i2})^2)$$

$$= S(\kappa_1 - \kappa_2)^2 + (\kappa_1 - \kappa_2) \sum_{i=1}^{S} (\beta_{i1} - \beta_{i2}) + \sum_{i=1}^{S} (\beta_{i1} - \beta_{i2})^2$$

$$= S(\kappa_1 - \kappa_2)^2 + \sum_{i=1}^{S} (\beta_{i1} - \beta_{i2})^2$$

$$= S(\kappa_1 - \kappa_2)^2 + \sum_{i=1}^{S} \beta_{i1}^2 - 2 \sum_{i=1}^{S} \beta_{i1}\beta_{i2} + \sum_{i=1}^{S} \beta_{i1}^2$$

$$= S(\kappa_1 - \kappa_2)^2 + (S-1) \left( \mathrm{Var}(\beta_{\cdot 1}) + \mathrm{Var}(\beta_{\cdot 2}) - 2\mathrm{Cov}(\beta_{\cdot 1}\beta_{\cdot 2}) \right)$$

Where the $(\kappa_1 - \kappa_2) \sum_{i=1}^{S} (\beta_{i1} - \beta_{i2})$ term disappears because, by construction, $\sum_{i=1}^{S} \beta_{ij} = 0$. $\mathrm{Var}_{ij}(X)$ is the variance of $X$ in populations $i$ and $j$.

If we are interested in compositional diversity, we can ignore the terms involving the $\kappa$s, so the distance is just a function of the second moments of $\beta$.

## Examples

We use two of the three examples from White et al. (2023). The third is presence/absence data, so is less interesting, as $\epsilon_{ij}$ is the residual, which is thoroughly uninteresting in Bernoulli trials.

First we need some bookkeeping, to list the libraries and create a function to ...

```
library(zen4R) # usedto download SA data
library(INLA)
library(gdm)
library(taxize)
```

3

```r
# Define PC priors, to stop the models exploding horribly
PCHyper <- list(prec = list(prior="pc.prec", param=c(0.1,0.001)))
PCHyper2 <- list(prec = list(prior="pc.prec", param=c(0.2,0.01)))

# Number of simulations from posterior to calculate statistics
nsim <- 1000

# Function to calculate variance components
CalcPostVar <- function(INLAsamp, data) {
  # Extract main effects of covariates
  LatentNames <- attr(INLAsamp$latent, "dimnames")[[1]]
  RFnames <- paste(c(gsub("Precision for ", "", names(INLAsamp$hyperpar)),
                   "(Intercept)", "Predictor"), collapse="|")
  FxNames <- LatentNames[!grepl(RFnames, LatentNames)]
  RFNames <- gsub(":.", "", FxNames)
  # Calculate/extract parts of variance terms
  VarHyper <- 1/INLAsamp$hyperpar
  wh.delta <- sapply(RFNames, function(wh, nm) grep(wh, nm), nm=names(VarHyper))
  VarDelta <- VarHyper[wh.delta]
  VarOth <- VarHyper[!seq_along(VarHyper)%in%wh.delta]

  VarX <- var(data[, RFNames])
  S <- nlevels(data$Species)

  # Deltabar
  Fx.wh <- which(attr(INLAsamp$latent, "dimnames")[[1]]%in%FxNames)
  Deltabar <- INLAsamp$latent[Fx.wh]
  names(Deltabar) <- attr(INLAsamp$latent, "dimnames")[[1]][Fx.wh]


  AllVars <- c(MeanDelta = t(Deltabar)%*%VarX%*%Deltabar,
               VarDelta = sum(VarDelta*diag(VarX)), # not sure this is right
               VarOth)
  return(AllVars)
}
```

### Example 1: South African flora

This is data with 288 species and 413 sites. The data is given in wide format, so we need to convert it to long. The data can be downloaded from Zenodo.

```
#|output: false

# Download the data, if it hasn't already been done.
if(!dir.exists("data/philawhite-spGDMM-code-d8279ee/data/")) {
  download_zenodo("10.5281/zenodo.10091441", path="data")
  unzip("data/spGDMM-code-spGDMM_v1.zip", exdir="data")
}


Data <- read.csv("data/philawhite-spGDMM-code-d8279ee/data/sa_species_data.csv")


# SpNames <- gsub("\\.", " ", names(Data)[grep("\\.", names(Data))])
SpNames <- names(Data)[grep("\\.", names(Data))]
# FamNames <- names(FamData)[!names(FamData)%in%names(Data)]

# Discover that not all family names from GBIF are he same as the family data
# FamData <- read.csv("philawhite-spGDMM-code-d8279ee/data/sa_family_data.csv")
# FamNames <- names(FamData)[!names(FamData)%in%names(Data)]
# Family[!Family%in%FamNames]

SpData.wide <- Data[, SpNames]
IsZero <- apply(SpData.wide, 2, function(x) mean(x==0))

UseNames <- names(IsZero)[IsZero<0.99]
RemoveNames <- SpNames[!SpNames%in%UseNames]
NamesToLong <- names(Data)[!names(Data)%in%RemoveNames]

SAData.long <- reshape(Data[,NamesToLong], direction = "long", varying = UseNames,
                       v.names = "Percent", timevar="SpeciesID")
SAData.long$Species <- SpNames[SAData.long$SpeciesID]
SAData.long$Percent2 <- pmax(0.1, SAData.long$Percent)
SAData.long$Abund <- log(SAData.long$Percent2/(100-SAData.long$Percent2))

SA.EnvCov <- c("gmap", "RFL_CONC", "HeatLoadIndex30m", "tmean13c",
            # "Elevation30m",
            "SoilConductivitymSm", "SoilTotalNPercent")

ScCov <- apply(SAData.long[,SA.EnvCov], 2, scale)
colnames(ScCov) <- paste0(colnames(ScCov), ".sc")

SAData <- cbind(SAData.long, ScCov)
```

```
# Get family names from GBIF
Classification <- classification(SpNames, db = 'gbif', rows=1)
```

== 288 queries =============


Retrieving data for taxon 'Adenogramma.glomerata'

   Found:   Adenogramma.glomerata


Retrieving data for taxon 'Albuca.concordiana'

   Found:   Albuca.concordiana


Retrieving data for taxon 'Albuca.sp.'

   Found:   Albuca.sp.


Retrieving data for taxon 'Aloe.microstigma'

   Found:   Aloe.microstigma


Retrieving data for taxon 'Amphiglossa.tomentosa'

   Found:   Amphiglossa.tomentosa


Retrieving data for taxon 'Amphiglossa.triflora'

   Found:   Amphiglossa.triflora


Retrieving data for taxon 'Anginon.fruticosum'

```
   Found:   Anginon.fruticosum


Retrieving data for taxon 'Anisodontea.triloba'

   Found:   Anisodontea.triloba


Retrieving data for taxon 'Anthospermum.aethiopicum'

   Found:   Anthospermum.aethiopicum


Retrieving data for taxon 'Anthospermum.spathulatum'

   Found:   Anthospermum.spathulatum


Retrieving data for taxon 'Antimima.triquetra'

   Found:   Antimima.triquetra


Retrieving data for taxon 'Aptosimum.indivisum'

   Found:   Aptosimum.indivisum


Retrieving data for taxon 'Aptosimum.spinescens'

   Found:   Aptosimum.spinescens


Retrieving data for taxon 'Arctopus.echinatus'

   Found:   Arctopus.echinatus
```

```
Retrieving data for taxon 'Arctotheca.calendula'

   Found:   Arctotheca.calendula


Retrieving data for taxon 'Arctotis.acaulis'

   Found:   Arctotis.acaulis


Retrieving data for taxon 'Aridaria.noctiflora'

   Found:   Aridaria.noctiflora


Retrieving data for taxon 'Aristida.vestita'

   Found:   Aristida.vestita


Retrieving data for taxon 'Asparagus.capensis'

   Found:   Asparagus.capensis


Retrieving data for taxon 'Asparagus.retrofractus'

   Found:   Asparagus.retrofractus


Retrieving data for taxon 'Asparagus.rubicundus'

   Found:   Asparagus.rubicundus


Retrieving data for taxon 'Asparagus.striatus'
```

```
   Found:   Asparagus.striatus


Retrieving data for taxon 'Atriplex.lindleyi'

   Found:   Atriplex.lindleyi


Retrieving data for taxon 'Atriplex.semibaccata'

   Found:   Atriplex.semibaccata


Retrieving data for taxon 'Augea.capensis'

   Found:   Augea.capensis


Retrieving data for taxon 'Babiana.sambucina.var.longibracteata'

   Found:   Babiana.sambucina.var.longibracteata


Retrieving data for taxon 'Berkheya.glabrata'

   Found:   Berkheya.glabrata


Retrieving data for taxon 'Bromus.pectinatus'

   Found:   Bromus.pectinatus


Retrieving data for taxon 'Brunsvigia.bosmaniae'

   Found:   Brunsvigia.bosmaniae
```

```
Retrieving data for taxon 'Bulbine.nutans'

   Found:   Bulbine.nutans


Retrieving data for taxon 'Bulbine.succulenta'

   Found:   Bulbine.succulenta


Retrieving data for taxon 'Cannomois.parviflora'

   Found:   Cannomois.parviflora


Retrieving data for taxon 'Chaenostoma.caeruleum'

   Found:   Chaenostoma.caeruleum


Retrieving data for taxon 'Cheiridopsis.namaquensis'

   Found:   Cheiridopsis.namaquensis


Retrieving data for taxon 'Chlorophytum.undulatum'

   Found:   Chlorophytum.undulatum


Retrieving data for taxon 'Chrysocoma.ciliata'

   Found:   Chrysocoma.ciliata


Retrieving data for taxon 'Cladoraphis.spinosa'
```

```
    Found:   Cladoraphis.spinosa


Retrieving data for taxon 'Cleretum.bellidiforme'

    Found:   Cleretum.bellidiforme


Retrieving data for taxon 'Cliffortia.arborea'

    Found:   Cliffortia.arborea


Retrieving data for taxon 'Cliffortia.ruscifolia'

    Found:   Cliffortia.ruscifolia


Retrieving data for taxon 'Colchicum.crispum'

    Found:   Colchicum.crispum


Retrieving data for taxon 'Colchicum.volutare'

    Found:   Colchicum.volutare


Retrieving data for taxon 'Convolvulus.capensis'

    Found:   Convolvulus.capensis


Retrieving data for taxon 'Conyza.scabrida'

    Found:   Conyza.scabrida
```

```
Retrieving data for taxon 'Corymbium.africanum.subsp.scabridum'

    Found:   Corymbium.africanum.subsp.scabridum


Retrieving data for taxon 'Cotula.microglossa'

    Found:   Cotula.microglossa


Retrieving data for taxon 'Cotula.nudicaulis'

    Found:   Cotula.nudicaulis


Retrieving data for taxon 'Cotyledon.orbiculata'

    Found:   Cotyledon.orbiculata


Retrieving data for taxon 'Crassula.barbata'

    Found:   Crassula.barbata


Retrieving data for taxon 'Crassula.muscosa'

    Found:   Crassula.muscosa


Retrieving data for taxon 'Crassula.rupestris'

    Found:   Crassula.rupestris


Retrieving data for taxon 'Crassula.umbella'
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```
    Found:   Crassula.umbella


Retrieving data for taxon 'Cymbopogon.marginatus'

    Found:   Cymbopogon.marginatus


Retrieving data for taxon 'Cyphia.digitata'

    Found:   Cyphia.digitata


Retrieving data for taxon 'Cyphia.volubilis'

    Found:   Cyphia.volubilis


Retrieving data for taxon 'Didelta.spinosa'

    Found:   Didelta.spinosa


Retrieving data for taxon 'Dimorphotheca.cuneata'

    Found:   Dimorphotheca.cuneata


Retrieving data for taxon 'Dimorphotheca.pinnata'

    Found:   Dimorphotheca.pinnata


Retrieving data for taxon 'Dimorphotheca.pluvialis'

    Found:   Dimorphotheca.pluvialis
```

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Retrieving data for taxon 'Dimorphotheca.sinuata'

   Found:   Dimorphotheca.sinuata


Retrieving data for taxon 'Diospyros.austro.africana'

   Found:   Diospyros.austro.africana


Retrieving data for taxon 'Dodonaea.viscosa.var..angustifolia'

   Found:   Dodonaea.viscosa.var..angustifolia


Retrieving data for taxon 'Drosanthemum.floribundum'

   Found:   Drosanthemum.floribundum


Retrieving data for taxon 'Ehrharta.bulbosa'

   Found:   Ehrharta.bulbosa


Retrieving data for taxon 'Ehrharta.calycina'

   Found:   Ehrharta.calycina


Retrieving data for taxon 'Ehrharta.melicoides'

   Found:   Ehrharta.melicoides


Retrieving data for taxon 'Ehrharta.ramosa.subsp.ramosa'
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    Found:   Ehrharta.ramosa.subsp.ramosa


Retrieving data for taxon 'Erepsia.saturata'

    Found:   Erepsia.saturata


Retrieving data for taxon 'Erica.inaequalis'

    Found:   Erica.inaequalis


Retrieving data for taxon 'Erica.plumosa'

    Found:   Erica.plumosa


Retrieving data for taxon 'Eriocephalus.africanus'

    Found:   Eriocephalus.africanus


Retrieving data for taxon 'Eriocephalus.decussatus'

    Found:   Eriocephalus.decussatus


Retrieving data for taxon 'Eriocephalus.ericoides'

    Found:   Eriocephalus.ericoides


Retrieving data for taxon 'Eriocephalus.microphyllus'

    Found:   Eriocephalus.microphyllus
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Retrieving data for taxon 'Eriocephalus.namaquensis'

   Found:   Eriocephalus.namaquensis


Retrieving data for taxon 'Eriocephalus.pauperrimus'

   Found:   Eriocephalus.pauperrimus


Retrieving data for taxon 'Eriocephalus.punctulatus'

   Found:   Eriocephalus.punctulatus


Retrieving data for taxon 'Eriocephalus.purpureus'

   Found:   Eriocephalus.purpureus


Retrieving data for taxon 'Eriocephalus.spinescens'

   Found:   Eriocephalus.spinescens


Retrieving data for taxon 'Eriospermum.capense'

   Found:   Eriospermum.capense


Retrieving data for taxon 'Erodium.cicutarium'

   Found:   Erodium.cicutarium


Retrieving data for taxon 'Euchlora.hirsuta'
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    Found:   Euchlora.hirsuta


Retrieving data for taxon 'Euphorbia.decussata'

    Found:   Euphorbia.decussata


Retrieving data for taxon 'Euphorbia.mauritanica'

    Found:   Euphorbia.mauritanica


Retrieving data for taxon 'Euryops.lateriflorus'

    Found:   Euryops.lateriflorus


Retrieving data for taxon 'Euryops.multifidus'

    Found:   Euryops.multifidus


Retrieving data for taxon 'Felicia.australis'

    Found:   Felicia.australis


Retrieving data for taxon 'Felicia.filifolia'

    Found:   Felicia.filifolia


Retrieving data for taxon 'Felicia.hirta'

    Found:   Felicia.hirta
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Retrieving data for taxon 'Felicia.macrorrhiza'

   Found:   Felicia.macrorrhiza


Retrieving data for taxon 'Felicia.ovata'

   Found:   Felicia.ovata


Retrieving data for taxon 'Felicia.rogersii'

   Found:   Felicia.rogersii


Retrieving data for taxon 'Festuca.scabra'

   Found:   Festuca.scabra


Retrieving data for taxon 'Ficinia.bulbosa'

   Found:   Ficinia.bulbosa


Retrieving data for taxon 'Ficinia.deusta'

   Found:   Ficinia.deusta


Retrieving data for taxon 'Ficinia.indica'

   Found:   Ficinia.indica


Retrieving data for taxon 'Ficinia.nigrescens'
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   Found:  Ficinia.nigrescens


Retrieving data for taxon 'Fingerhuthia.africana'

   Found:  Fingerhuthia.africana


Retrieving data for taxon 'Foveolina.dichotoma'

   Found:  Foveolina.dichotoma


Retrieving data for taxon 'Galenia.africana'

   Found:  Galenia.africana


Retrieving data for taxon 'Galenia.filiformis'

   Found:  Galenia.filiformis


Retrieving data for taxon 'Galenia.fruticosa'

   Found:  Galenia.fruticosa


Retrieving data for taxon 'Galenia.namaensis'

   Found:  Galenia.namaensis


Retrieving data for taxon 'Galenia.sarcophylla'

   Found:  Galenia.sarcophylla
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Retrieving data for taxon 'Gazania.krebsiana'

   Found:  Gazania.krebsiana


Retrieving data for taxon 'Gazania.lichtensteinii'

   Found:  Gazania.lichtensteinii


Retrieving data for taxon 'Gazania.rigida'

   Found:  Gazania.rigida


Retrieving data for taxon 'Gnidia.scabra'

   Found:  Gnidia.scabra


Retrieving data for taxon 'Gorteria.diffusa'

   Found:  Gorteria.diffusa


Retrieving data for taxon 'Gymnodiscus.capillaris'

   Found:  Gymnodiscus.capillaris


Retrieving data for taxon 'Helichrysum.asperum'

   Found:  Helichrysum.asperum


Retrieving data for taxon 'Helichrysum.hamulosum'
```

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   Found:   Helichrysum.hamulosum


Retrieving data for taxon 'Helichrysum.moeserianum'

   Found:   Helichrysum.moeserianum


Retrieving data for taxon 'Helichrysum.obtusum'

   Found:   Helichrysum.obtusum


Retrieving data for taxon 'Helichrysum.revolutum'

   Found:   Helichrysum.revolutum


Retrieving data for taxon 'Helichrysum.stellatum'

   Found:   Helichrysum.stellatum


Retrieving data for taxon 'Heliophila.amplexicaulis'

   Found:   Heliophila.amplexicaulis


Retrieving data for taxon 'Heliophila.collina'

   Found:   Heliophila.collina


Retrieving data for taxon 'Heliophila.crithmifolia'

   Found:   Heliophila.crithmifolia
```

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Retrieving data for taxon 'Heliophila.pinnata'

   Found:  Heliophila.pinnata


Retrieving data for taxon 'Hermannia.althaeifolia'

   Found:  Hermannia.althaeifolia


Retrieving data for taxon 'Hermannia.coccocarpa'

   Found:  Hermannia.coccocarpa


Retrieving data for taxon 'Hermannia.cuneifolia'

   Found:  Hermannia.cuneifolia


Retrieving data for taxon 'Hermannia.spinosa'

   Found:  Hermannia.spinosa


Retrieving data for taxon 'Hirpicium.alienatum'

   Found:  Hirpicium.alienatum


Retrieving data for taxon 'Hoodia.gordonii'

   Found:  Hoodia.gordonii


Retrieving data for taxon 'Ifloga.ambigua'
```

```
   Found:   Ifloga.ambigua


Retrieving data for taxon 'Ifloga.glomerata'

   Found:   Ifloga.glomerata


Retrieving data for taxon 'Indigofera.nigromontana'

   Found:   Indigofera.nigromontana


Retrieving data for taxon 'Ixia.rapunculoides'

   Found:   Ixia.rapunculoides


Retrieving data for taxon 'Lapeirousia.jacquinii'

   Found:   Lapeirousia.jacquinii


Retrieving data for taxon 'Lapeirousia.plicata'

   Found:   Lapeirousia.plicata


Retrieving data for taxon 'Lasiopogon.muscoides'

   Found:   Lasiopogon.muscoides


Retrieving data for taxon 'Lasiospermum.brachyglossum'

   Found:   Lasiospermum.brachyglossum
```

```
Retrieving data for taxon 'Leipoldtia.schultzei'

   Found:  Leipoldtia.schultzei


Retrieving data for taxon 'Leucadendron.brunioides'

   Found:  Leucadendron.brunioides


Retrieving data for taxon 'Leucadendron.remotum'

   Found:  Leucadendron.remotum


Retrieving data for taxon 'Leucadendron.salignum'

   Found:  Leucadendron.salignum


Retrieving data for taxon 'Leysera.gnaphalodes'

   Found:  Leysera.gnaphalodes


Retrieving data for taxon 'Leysera.gnaphaloides'

   Found:  Leysera.gnaphaloides


Retrieving data for taxon 'Leysera.tenella'

   Found:  Leysera.tenella


Retrieving data for taxon 'Limeum.aethiopicum'
```

```
    Found:   Limeum.aethiopicum


Retrieving data for taxon 'Linum.africanum'

    Found:   Linum.africanum


Retrieving data for taxon 'Lycium.cinereum'

    Found:   Lycium.cinereum


Retrieving data for taxon 'Malephora.crassa'

    Found:   Malephora.crassa


Retrieving data for taxon 'Massonia.depressa'

    Found:   Massonia.depressa


Retrieving data for taxon 'Melianthus.comosus'

    Found:   Melianthus.comosus


Retrieving data for taxon 'Melolobium.candicans'

    Found:   Melolobium.candicans


Retrieving data for taxon 'Mesembryanthemum.guerichianum'

    Found:   Mesembryanthemum.guerichianum
```

```
Retrieving data for taxon 'Mesembryanthemum.stenandrum'

   Found:   Mesembryanthemum.stenandrum


Retrieving data for taxon 'Microloma.sagittatum'

   Found:   Microloma.sagittatum


Retrieving data for taxon 'Monoculus.monstrosus'

   Found:   Monoculus.monstrosus


Retrieving data for taxon 'Montinia.caryophyllacea'

   Found:   Montinia.caryophyllacea


Retrieving data for taxon 'Moraea.bifida'

   Found:   Moraea.bifida


Retrieving data for taxon 'Moraea.brachygyne'

   Found:   Moraea.brachygyne


Retrieving data for taxon 'Moraea.ciliata'

   Found:   Moraea.ciliata


Retrieving data for taxon 'Moraea.falcifolia'
```

```
    Found:   Moraea.falcifolia


Retrieving data for taxon 'Muraltia.divaricata'

    Found:   Muraltia.divaricata


Retrieving data for taxon 'Muraltia.spinosa'

    Found:   Muraltia.spinosa


Retrieving data for taxon 'Nemesia.cheiranthus'

    Found:   Nemesia.cheiranthus


Retrieving data for taxon 'Nemesia.leipoldtii'

    Found:   Nemesia.leipoldtii


Retrieving data for taxon 'Oedera.genistifolia'

    Found:   Oedera.genistifolia


Retrieving data for taxon 'Oedera.sedifolia'

    Found:   Oedera.sedifolia


Retrieving data for taxon 'Oedera.squarrosa'

    Found:   Oedera.squarrosa
```

```
Retrieving data for taxon 'Olea.europaea'

   Found:   Olea.europaea


Retrieving data for taxon 'Ornithogalum.tanquanum'

   Found:   Ornithogalum.tanquanum


Retrieving data for taxon 'Osteospermum.acanthospermum'

   Found:   Osteospermum.acanthospermum


Retrieving data for taxon 'Osteospermum.incanum.subsp.incanum'

   Found:   Osteospermum.incanum.subsp.incanum


Retrieving data for taxon 'Osteospermum.leptolobum'

   Found:   Osteospermum.leptolobum


Retrieving data for taxon 'Osteospermum.scariosum'

   Found:   Osteospermum.scariosum


Retrieving data for taxon 'Osteospermum.sinuatum'

   Found:   Osteospermum.sinuatum


Retrieving data for taxon 'Otholobium.candicans'
```

```
    Found:   Otholobium.candicans


Retrieving data for taxon 'Othonna.auriculifolia'

    Found:   Othonna.auriculifolia


Retrieving data for taxon 'Othonna.hederifolia'

    Found:   Othonna.hederifolia


Retrieving data for taxon 'Othonna.rechingeri'

    Found:   Othonna.rechingeri


Retrieving data for taxon 'Othonna.undulosa'

    Found:   Othonna.undulosa


Retrieving data for taxon 'Oxalis.flava'

    Found:   Oxalis.flava


Retrieving data for taxon 'Oxalis.luteola'

    Found:   Oxalis.luteola


Retrieving data for taxon 'Oxalis.massoniana.var.massoniana'

    Found:   Oxalis.massoniana.var.massoniana
```

```
Retrieving data for taxon 'Oxalis.obtusa'

   Found:   Oxalis.obtusa


Retrieving data for taxon 'Oxalis.pes.caprae'

   Found:   Oxalis.pes.caprae


Retrieving data for taxon 'Oxalis.pocockiae'

   Found:   Oxalis.pocockiae


Retrieving data for taxon 'Paranomus.bracteolaris'

   Found:   Paranomus.bracteolaris


Retrieving data for taxon 'Passerina.truncata'

   Found:   Passerina.truncata


Retrieving data for taxon 'Pelargonium.articulatum'

   Found:   Pelargonium.articulatum


Retrieving data for taxon 'Pelargonium.crithmifolium'

   Found:   Pelargonium.crithmifolium


Retrieving data for taxon 'Pelargonium.magenteum'
```

```
   Found:   Pelargonium.magenteum


Retrieving data for taxon 'Pelargonium.praemorsum'

   Found:   Pelargonium.praemorsum


Retrieving data for taxon 'Pelargonium.rapaceum'

   Found:   Pelargonium.rapaceum


Retrieving data for taxon 'Pelargonium.reflexum'

   Found:   Pelargonium.reflexum


Retrieving data for taxon 'Pelargonium.scabrum'

   Found:   Pelargonium.scabrum


Retrieving data for taxon 'Pelargonium.triste'

   Found:   Pelargonium.triste


Retrieving data for taxon 'Pentameris.pallida'

   Found:   Pentameris.pallida


Retrieving data for taxon 'Pentameris.rupestris'

   Found:   Pentameris.rupestris
```

```
Retrieving data for taxon 'Pentzia.incana'

   Found:   Pentzia.incana


Retrieving data for taxon 'Pentzia.spinescens'

   Found:   Pentzia.spinescens


Retrieving data for taxon 'Pharnaceum.aurantium'

   Found:   Pharnaceum.aurantium


Retrieving data for taxon 'Pharnaceum.ciliare'

   Found:   Pharnaceum.ciliare


Retrieving data for taxon 'Phylica.agathosmoides'

   Found:   Phylica.agathosmoides


Retrieving data for taxon 'Phylica.rigidifolia'

   Found:   Phylica.rigidifolia


Retrieving data for taxon 'Plantago.cafra'

   Found:   Plantago.cafra


Retrieving data for taxon 'Poa.bulbosa'
```

```
   Found:  Poa.bulbosa


Retrieving data for taxon 'Polycarena.aurea'

   Found:  Polycarena.aurea


Retrieving data for taxon 'Polygala.myrtifolia'

   Found:  Polygala.myrtifolia


Retrieving data for taxon 'Polygala.scabra'

   Found:  Polygala.scabra


Retrieving data for taxon 'Protea.laurifolia'

   Found:  Protea.laurifolia


Retrieving data for taxon 'Protea.repens'

   Found:  Protea.repens


Retrieving data for taxon 'Pteronia.adenocarpa'

   Found:  Pteronia.adenocarpa


Retrieving data for taxon 'Pteronia.divaricata'

   Found:  Pteronia.divaricata
```

```
Retrieving data for taxon 'Pteronia.empetrifolia'

   Found:   Pteronia.empetrifolia


Retrieving data for taxon 'Pteronia.glabrata'

   Found:   Pteronia.glabrata


Retrieving data for taxon 'Pteronia.glauca'

   Found:   Pteronia.glauca


Retrieving data for taxon 'Pteronia.glomerata'

   Found:   Pteronia.glomerata


Retrieving data for taxon 'Pteronia.incana'

   Found:   Pteronia.incana


Retrieving data for taxon 'Pteronia.pallens'

   Found:   Pteronia.pallens


Retrieving data for taxon 'Pteronia.paniculata'

   Found:   Pteronia.paniculata


Retrieving data for taxon 'Pteronia.villosa'
```

```
    Found:   Pteronia.villosa


Retrieving data for taxon 'Restio.capensis'

    Found:   Restio.capensis


Retrieving data for taxon 'Restio.longiaristatus'

    Found:   Restio.longiaristatus


Retrieving data for taxon 'Restio.macer'

    Found:   Restio.macer


Retrieving data for taxon 'Restio.monanthos'

    Found:   Restio.monanthos


Retrieving data for taxon 'Restio.rudolfii'

    Found:   Restio.rudolfii


Retrieving data for taxon 'Restio.vimineus'

    Found:   Restio.vimineus


Retrieving data for taxon 'Romulea.sabulosa'

    Found:   Romulea.sabulosa
```

```
Retrieving data for taxon 'Rosenia.glandulosa'

   Found:  Rosenia.glandulosa


Retrieving data for taxon 'Rosenia.oppositifolia'

   Found:  Rosenia.oppositifolia


Retrieving data for taxon 'Ruschia.cradockensis'

   Found:  Ruschia.cradockensis


Retrieving data for taxon 'Ruschia.intricata'

   Found:  Ruschia.intricata


Retrieving data for taxon 'Salsola.aphylla'

   Found:  Salsola.aphylla


Retrieving data for taxon 'Salsola.kali'

   Found:  Salsola.kali


Retrieving data for taxon 'Salvia.disermas'

   Found:  Salvia.disermas


Retrieving data for taxon 'Sarcocaulon.crassicaule'
```

```
    Found:  Sarcocaulon.crassicaule


Retrieving data for taxon 'Satyrium.erectum'

    Found:  Satyrium.erectum


Retrieving data for taxon 'Schismus.schismoides'

    Found:  Schismus.schismoides


Retrieving data for taxon 'Scirpoides.dioecus'

    Found:  Scirpoides.dioecus


Retrieving data for taxon 'Searsia.angustifolia'

    Found:  Searsia.angustifolia


Retrieving data for taxon 'Searsia.burchellii'

    Found:  Searsia.burchellii


Retrieving data for taxon 'Searsia.lancea'

    Found:  Searsia.lancea


Retrieving data for taxon 'Searsia.longispina'

    Found:  Searsia.longispina
```

```
Retrieving data for taxon 'Searsia.undulata'

   Found:   Searsia.undulata


Retrieving data for taxon 'Selago.albida'

   Found:   Selago.albida


Retrieving data for taxon 'Selago.articulata'

   Found:   Selago.articulata


Retrieving data for taxon 'Selago.glabrata'

   Found:   Selago.glabrata


Retrieving data for taxon 'Senecio.arenarius'

   Found:   Senecio.arenarius


Retrieving data for taxon 'Senecio.burchellii'

   Found:   Senecio.burchellii


Retrieving data for taxon 'Senecio.cardaminifolius'

   Found:   Senecio.cardaminifolius


Retrieving data for taxon 'Senecio.erosus'
```

```
    Found:   Senecio.erosus


Retrieving data for taxon 'Senecio.radicans'

    Found:   Senecio.radicans


Retrieving data for taxon 'Septulina.glauca'

    Found:   Septulina.glauca


Retrieving data for taxon 'Silene.clandestina'

    Found:   Silene.clandestina


Retrieving data for taxon 'Stachys.rugosa'

    Found:   Stachys.rugosa


Retrieving data for taxon 'Stipagrostis.ciliata'

    Found:   Stipagrostis.ciliata


Retrieving data for taxon 'Stipagrostis.namaquensis'

    Found:   Stipagrostis.namaquensis


Retrieving data for taxon 'Stipagrostis.obtusa'

    Found:   Stipagrostis.obtusa
```

```
Retrieving data for taxon 'Stipagrostis.zeyheri'

   Found:   Stipagrostis.zeyheri


Retrieving data for taxon 'Struthiola.ciliata.subsp.incana'

   Found:   Struthiola.ciliata.subsp.incana


Retrieving data for taxon 'Sutherlandia.frutescens'

   Found:   Sutherlandia.frutescens


Retrieving data for taxon 'Tenaxia.dura'

   Found:   Tenaxia.dura


Retrieving data for taxon 'Tenaxia.stricta'

   Found:   Tenaxia.stricta


Retrieving data for taxon 'Tetragonia.fruticosa'

   Found:   Tetragonia.fruticosa


Retrieving data for taxon 'Tetragonia.microptera'

   Found:   Tetragonia.microptera


Retrieving data for taxon 'Tetragonia.nigrescens'
```

```
    Found:   Tetragonia.nigrescens


Retrieving data for taxon 'Thamnochortus.platypteris'

    Found:   Thamnochortus.platypteris


Retrieving data for taxon 'Thesium.hispidulum'

    Found:   Thesium.hispidulum


Retrieving data for taxon 'Thesium.lineatum'

    Found:   Thesium.lineatum


Retrieving data for taxon 'Trachyandra.divaricata'

    Found:   Trachyandra.divaricata


Retrieving data for taxon 'Trachyandra.falcata'

    Found:   Trachyandra.falcata


Retrieving data for taxon 'Tribolium.hispidum'

    Found:   Tribolium.hispidum


Retrieving data for taxon 'Tribolium.uniolae'

    Found:   Tribolium.uniolae
```

```
Retrieving data for taxon 'Tylecodon.paniculatus'

   Found:   Tylecodon.paniculatus


Retrieving data for taxon 'Tylecodon.reticulatus'

   Found:   Tylecodon.reticulatus


Retrieving data for taxon 'Tylecodon.wallichii'

   Found:   Tylecodon.wallichii


Retrieving data for taxon 'Ursinia.anthemoides'

   Found:   Ursinia.anthemoides


Retrieving data for taxon 'Ursinia.cakilefolia'

   Found:   Ursinia.cakilefolia


Retrieving data for taxon 'Ursinia.chrysanthemoides'

   Found:   Ursinia.chrysanthemoides


Retrieving data for taxon 'Ursinia.pilifera'

   Found:   Ursinia.pilifera


Retrieving data for taxon 'Viscum.capense'
```

```
   Found:   Viscum.capense


Retrieving data for taxon 'Wiborgia.monoptera'

   Found:   Wiborgia.monoptera


Retrieving data for taxon 'Wiborgiella.leipoldtiana'

   Found:   Wiborgiella.leipoldtiana


Retrieving data for taxon 'Willdenowia.arescens'

   Found:   Willdenowia.arescens


Retrieving data for taxon 'Willdenowia.incurvata'

   Found:   Willdenowia.incurvata


Retrieving data for taxon 'Zaluzianskya.cohabitans'

   Found:   Zaluzianskya.cohabitans


Retrieving data for taxon 'Zaluzianskya.pusilla'

   Found:   Zaluzianskya.pusilla


Retrieving data for taxon 'Zaluzianskya.violacea'

   Found:   Zaluzianskya.violacea
```

```
Retrieving data for taxon 'Zygophyllum.foetidum'

  Found:  Zygophyllum.foetidum


Retrieving data for taxon 'Zygophyllum.lichtensteinianum'

  Found:  Zygophyllum.lichtensteinianum


Retrieving data for taxon 'Zygophyllum.pygmaeum'

  Found:  Zygophyllum.pygmaeum


Retrieving data for taxon 'Zygophyllum.retrofractum'

  Found:  Zygophyllum.retrofractum
==  Results  =================
```

- Total: 288
- Found: 288
- Not Found: 0

```r
Family <- unlist(lapply(Classification, function(lst) lst$name[lst$rank=="family"]))

SAData$Family <- unlist(sapply(SAData$Species, function(Sp, fam) {
#  cat(Spp, "\n")
  ff <- which(Sp==names(fam))
  if(length(ff)==0) {
    res <- "AAAAAGH"
  } else {
    res <- fam[ff]
  }
  res
}, fam=Family))

# any(SAData$Family=="AAAAAGH")
```

```
SAData$Family <- factor(SAData$Family)
SAData$Species <- factor(SAData$Species)
SAData$plot <- factor(SAData$plot)
```

Covariates:

- gmap: mean annual precipitation
- RFL_CONC: rainfall concentration
- Elevation30m: elevation (at 30m resolution)
- HeatLoadIndex30m: heat load index (at 30m resolution)
- tmean13c: mean annual temperature
- SoilConductivitymSm: soil conductivity
- SoilTotalNPercent: Nitrogen concentration in soil (%)

We remove elevation because of the high correlation with tmean13c (-0.94), and all species that occur in <1% of sites, giving 146 species out of the original 288.

We fit the model with INLA, and use relatively tight PC priors to control the estimates of the environmental effects (without doing this everything is horribly unstable).

```
# Create formula for INLA
SA.Formula <- formula(
  paste0("Abund ~ f(Species, hyper = PCHyper) + f(plot, hyper = PCHyper) + ",
         paste(
           c(paste0(SA.EnvCov, ".sc"),
             sapply(paste0(SA.EnvCov, ".sc"), function(eu) {
               paste0("f(Species.", eu, ", ", eu, ", hyper = PCHyper)")
             })), collapse=" + "))
)



SAenvInd <- data.frame(sapply(SA.EnvCov, function(nm, dat) assign(nm, dat),
                              dat=SAData$Species))
names(SAenvInd) <- paste0("Species.", names(SAenvInd), ".sc")


SAData <- cbind(SAData, SAenvInd)



# int.strategy = "ccd" or int.strategy = "grid"
# Fit the model
SAinla <- inla(SA.Formula, data=SAData, control.compute=list(config = TRUE),
               control.inla=list(int.strategy = "ccd"))
SASumm <-summary(SAinla)
```
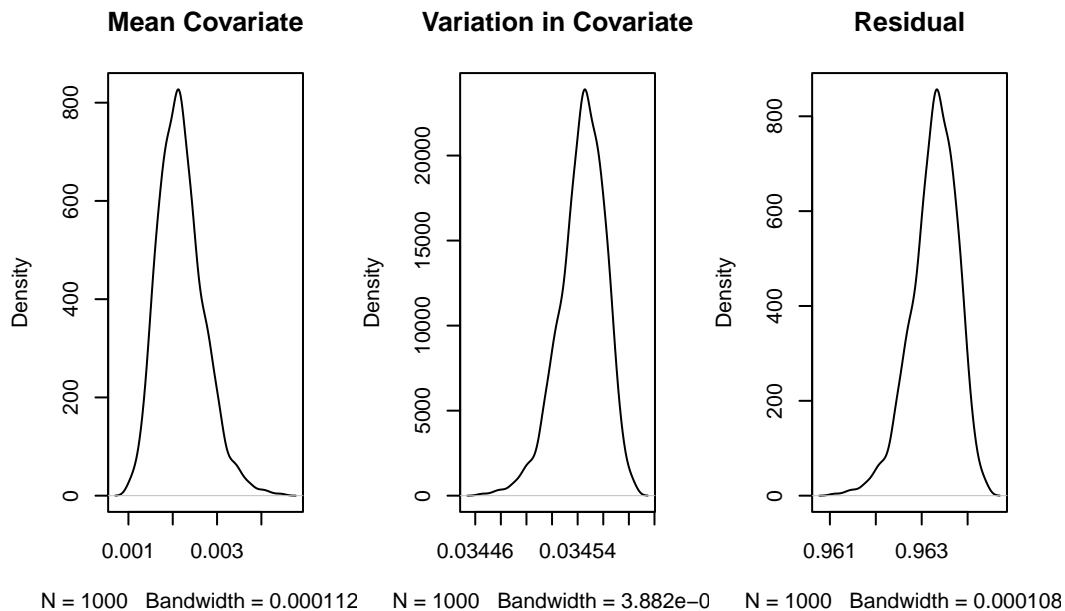
This will calculate the statistics

```
SAsamps <- inla.posterior.sample(nsim, SAinla)

SAPosts <- data.frame(t(sapply(SAsamps, CalcPostVar, data=SAData)))
Use <- !names(SAPosts)%in%paste0("Precision.for.", c("Species", "plot"))
SA.PropVar <- sweep(SAPosts[,Use], 1, rowSums(SAPosts[,Use]), "/")
names(SA.PropVar) <- gsub("Precision.for.the.Gaussian.observations", "VarEps",
                          names(SA.PropVar), fixed=TRUE)

par(mfrow=c(1,3))
plot(density(SA.PropVar$MeanDelta), main="Mean Covariate")
plot(density(SA.PropVar$VarDelta), main="Variation in Covariate")
plot(density(SA.PropVar$VarEps), main="Residual")
```



```
# Summary
SA.SummVars <- cbind(
  Mode=MCMCglmm::posterior.mode(coda::as.mcmc(SA.PropVar)),
  coda::HPDinterval(coda::as.mcmc(SA.PropVar), prob = 0.95)
)
```

We find that 3.67% of the variation in beta diversity is explained by the covariates, with a 95% HPDI of 3.58% - 3.77%.

## Example 2: The Inevitable BCI Data

This is counts of trees on an island that only exists to let ecologists take a holiday in the jungle. The data can be downloaded from Condit et al. (2002).

```r
BCI.Env <- read.csv("philawhite-spGDMM-code-d8279ee/data/Panama_env.csv")
BCI.Sp <- read.csv("philawhite-spGDMM-code-d8279ee/data/Panama_species.csv")

# Stupid naming
# "species" is actually site. And the format of the names is different between files
# This is why "data scientist" has a lower job satisfaction than "statistician"
BCI.Sp$site.no. <- sprintf("P%02d", as.numeric(gsub("P", "", BCI.Sp$species)))
BCI.Sp$species <- NULL

BCI.EnvCov <- c("precip", "elev", "age")
Pres <- apply(BCI.Sp, 2, function(x) sum(x>0))
sp.tmp <- BCI.Sp[,which(Pres>10)]
dat.tmp <- cbind(BCI.Env, sp.tmp)
SpNames <- names(sp.tmp)[!names(sp.tmp)%in%c("species", "site.no.")]
BCIData <- reshape(dat.tmp, direction = "long", varying = SpNames, v.names = "Count")
BCIData$Species <- factor(SpNames[BCIData$time])
BCIData$Site <- factor(BCIData$site.no.)
BCIData$SiteSpecies <- paste0(BCIData$Site, BCIData$Species)
# Scale env
Scale.tmp <- apply(BCIData[,BCI.EnvCov], 2, scale)
colnames(Scale.tmp) <- paste0(colnames(Scale.tmp), ".sc")
BCIData <- cbind(BCIData, Scale.tmp)
```

We can fit the model in INLA:

```r
BCI.Formula <- formula(
  paste0("Count ~ f(Species, hyper = PCHyper) + f(Site, hyper = PCHyper) + ",
         paste(
           c(paste0(BCI.EnvCov, ".sc"),
             sapply(paste0(BCI.EnvCov, ".sc"), function(eu) {
               paste0("f(Species.", eu, ", ", eu, ", hyper = PCHyper)")
             })), collapse=" + "), " + f(OD, hyper = PCHyper)")
)

BCIenvInd <- data.frame(sapply(BCI.EnvCov, function(nm, dat) assign(nm, dat),
                               dat=BCIData$Species))
names(BCIenvInd) <- paste0("Species.", names(BCIenvInd), ".sc")
```

```
BCIData <- cbind(BCIData, BCIenvInd)
BCIData$OD <- factor(1:nrow(BCIData))

# Fit the model
BCIinla <- inla(BCI.Formula, data=BCIData, control.compute=list(config = TRUE),
                family="poisson")
BCISumm <-summary(BCIinla)
```
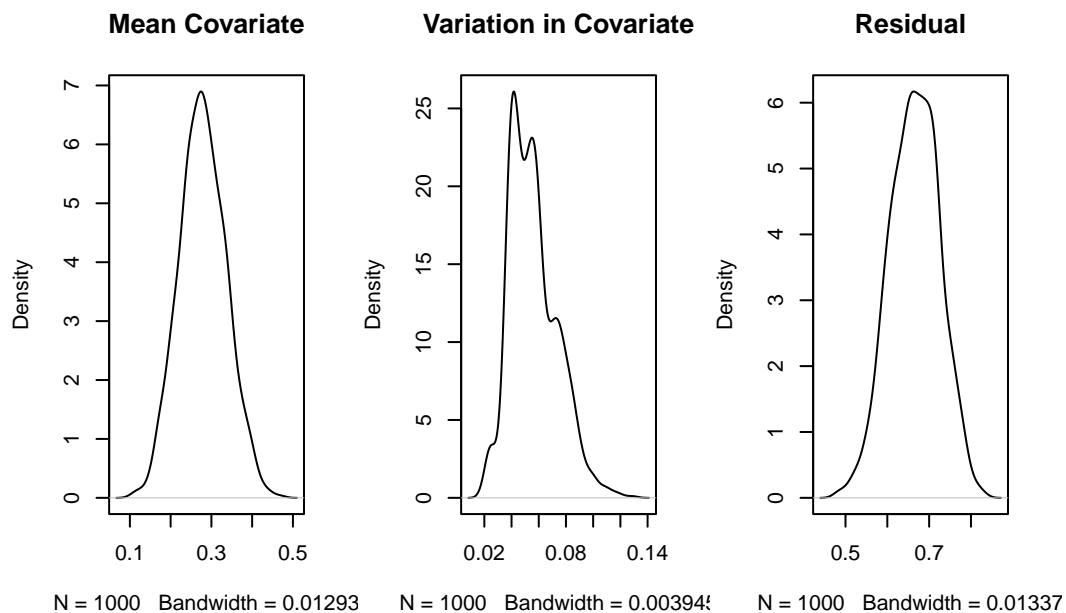
```
BCIsamps <- inla.posterior.sample(nsim, BCIinla)

BCI.Posts <- data.frame(t(sapply(BCIsamps, CalcPostVar, data=BCIData)))
Use <- !names(BCI.Posts)%in%paste0("Precision.for.", c("Species", "Site"))
BCI.PropVar <- sweep(BCI.Posts[,Use], 1, rowSums(BCI.Posts[,Use]), "/")
names(BCI.PropVar)[3] <- "VarEps"

par(mfrow=c(1,3))
plot(density(BCI.PropVar$MeanDelta), main="Mean Covariate")
plot(density(BCI.PropVar$VarDelta), main="Variation in Covariate")
plot(density(BCI.PropVar$VarEps), main="Residual")
```



```
BCI.SummVars <- cbind(
  Mode=MCMCglmm::posterior.mode(coda::as.mcmc(BCI.PropVar)),
  coda::HPDinterval(coda::as.mcmc(BCI.PropVar), prob = 0.95)
)
```

We find that 29.63% of the variation in beta diversity is explained by the covariates, with a 95% HPDI of 21.59% - 44.13%.

**Example 3: Australian Plants**

This is occurrence of plants in Southwest Australia, the `southwest` data in the `gdm` package. The data are not well documented, with several presences per species per site. Absence data is not given. Fortunately, the environmental data does not vary within a site.

```
data("southwest")

SW.EnvCov <- names(southwest)[!names(southwest)%in%c("species","site", "Lat", "Long")]

Pres <- table(southwest$species)
sp.keep <- names(Pres[Pres>50]) #reduce to 10?

southwest.small <- southwest[southwest$species%in%sp.keep,]
southwest.small$species <- factor(southwest.small$species)
SW.pres <- expand.grid(species=unique(southwest.small$species),
                       site=unique(southwest.small$site))
SW.pres$Presence <- apply(SW.pres, 1, function(wh, dat) {
 any(dat$site==wh["site"] & dat$species==wh["species"])
}, dat=southwest.small)

# Extract environmental variables
SWenv <- data.frame(apply(southwest.small[,SW.EnvCov], 2, function(x, dat) {
  tapply(x, list(dat$site), function(xx) xx[1])
}, dat=southwest.small))
env.site <- rownames(SWenv)
SWenv <- data.frame(apply(SWenv, 2, scale))
names(SWenv) <- paste0(colnames(SWenv), ".sc")
SWenv$site <- env.site

SW.data <- merge(SW.pres, SWenv)
SW.data$Presence <- as.numeric(SW.data$Presence)

# Check to see if there is variation in environment between sites. There isn't.
# SDs <- by(southwest.small, list(southwest.small$site), function(df, vars) {
#   apply(df[,vars], 2, sd)
```

```
# }, vars=SW.EnvCov)
# table(unlist(SDs))
```

We can fit the model in INLA:

```
SW.Formula <- formula(
  paste0("Presence ~ f(species, hyper = PCHyper) + f(site, hyper = PCHyper) + ",
         paste(
           c(paste0(SW.EnvCov, ".sc"),
             sapply(paste0(SW.EnvCov, ".sc"), function(eu) {
               paste0("f(Species.", eu, ", ", eu, ", hyper = PCHyper)")
             })), collapse=" + "))
)

SWenvInd <- data.frame(sapply(SW.EnvCov, function(nm, dat) assign(nm, dat),
                              dat=SW.data$species))
names(SWenvInd) <- paste0("Species.", names(SWenvInd), ".sc")
SW.data <- cbind(SW.data, SWenvInd)

# Fit the model
SWinla <- inla(SW.Formula, data=SW.data, control.compute=list(config = TRUE),
               family="binomial", Ntrials = 1)
SWSumm <-summary(SWinla)
```
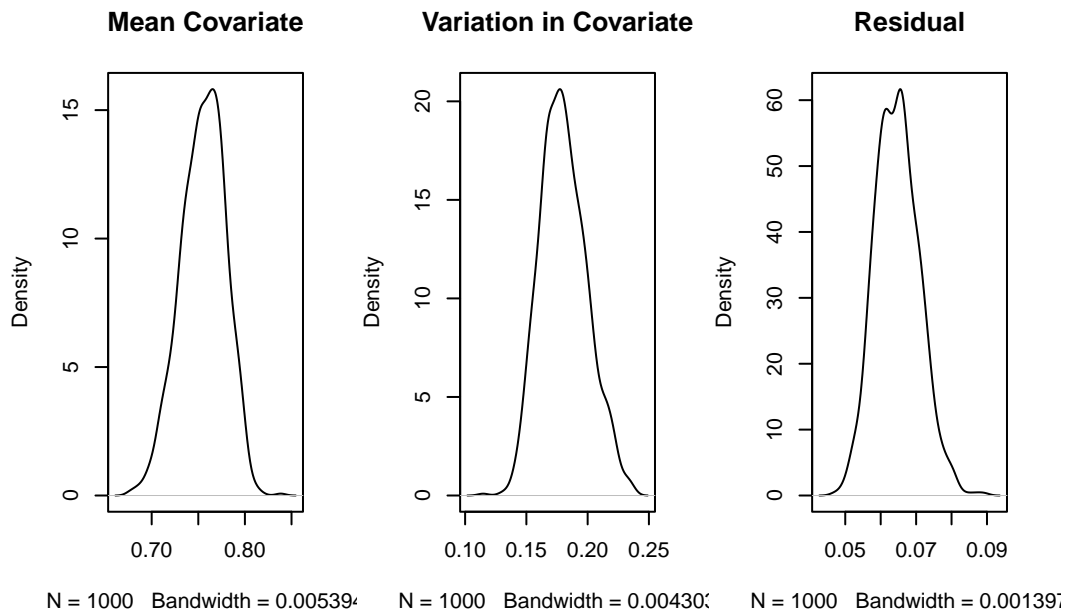
And now…

```
SWsamps <- inla.posterior.sample(nsim, SWinla)

SW.Posts <- data.frame(t(sapply(SWsamps, CalcPostVar, data=SW.data)))
SW.Posts$logitVar <- pi/3
Use <- !names(SW.Posts)%in%paste0("Precision.for.", c("species", "site"))
SW.PropVar <- sweep(SW.Posts[,Use], 1, rowSums(SW.Posts[,Use]), "/")
names(SW.PropVar)[3] <- "VarEps"

par(mfrow=c(1,3))
plot(density(SW.PropVar$MeanDelta), main="Mean Covariate")
plot(density(SW.PropVar$VarDelta), main="Variation in Covariate")
plot(density(SW.PropVar$VarEps), main="Residual")
```

| **Mean Covariate** | **Variation in Covariate** | **Residual** |

N = 1000   Bandwidth = 0.005394          N = 1000   Bandwidth = 0.004303          N = 1000   Bandwidth = 0.001397

```r
SW.SummVars <- cbind(
  Mode=MCMCglmm::posterior.mode(coda::as.mcmc(SW.PropVar)),
  coda::HPDinterval(coda::as.mcmc(SW.PropVar), prob = 0.95)
)
```

We find that 93.4% of the variation in beta diversity is explained by the covariates, with a 95% HPDI of 92.4% - 94.77%.

## References

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