# Bayesian nonparametric dependent model for the study of diversity for species data

Journées jeunes probabilistes et statisticiens

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Moncalieri, Italy

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Collegio Carlo Alberto

# Project's bio

### **Authors**

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- Kerrie L. Mengersen (Mathematical Sciences, Queensland University of Technology, Brisbane)
- Cath King (Australian Antarctic Division, Kingston, Tasmania 7050)
- Ben Raymond (Australian Antarctic Division, Kingston, Tasmania 7050)

### Status

Chapter of my PhD thesis. Two submitted manuscripts Arbel et al. (2013b) and Arbel et al. (2013a).









J. Arbel et al.

Dependent model for species data

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Ecological data and diversity

2 Dependent model for species data and diversity

Applications

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Ecological data and diversity

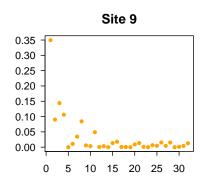
2 Dependent model for species data and diversity

Applications

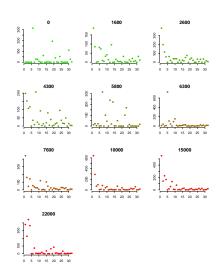
 Series of measurements at different places around Casey Station, permanent base in Antarctica



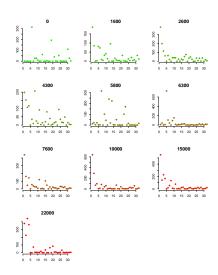
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- Series of measurements at different places around Casey Station, permanent base in Antarctica
- At each site: pollution level (total petroleum hydrocarbon (TPH) in mg/kg of soil), and abundance of microbes.
- Goals: Assess the impact of a pollutant on the soil composition / biodiversity, e.g. compute effective concentration values at level x%, ECx



### Data collection

Soil samples were collected from a range of sites across a fuel contamination gradient at Australias Casey Station in East Antarctica (110° 32′ E, 66° 17′ S). The data comprise counts of a large number (of the order of 1 800) of microbial taxa, referred to as OTUs (operational taxonomic units; see Schloss et al., 2009), collected at 60 sites, across a range of hydrocarbon contamination (Siciliano et al., 2014). Genomic DNA extracted from samples was sequenced on a 454 Titanium FLX+ instrument (Roche, Brandford, CT, USA) at the Research and Testing facility (Lubbock, TX, USA) using the universal bacterial primers 28F and 519R (Dowd et al., 2008). Pyrosequencing data were processed using the mother software package (Schloss et al., 2009). This involved removal of short reads (<150bp), excessive homoploymeric reads (>8bp repeats) and denoising with AmpliconNoise (min/max flows 360/720) (Quince et al., 2011). Preclustering at 1% was performed to negate the per base error rate of the 454 platforms. Seed sequences were then aligned to the SILVA 16S rRNA gene database alignment using a NAST alignment algorithm (Pruesse et al., 2007; Caporaso et al., 2010). Reads were then chimaera-checked (Edgar et al., 2011) and clustered into OTUs at 96% sequence similarity to achieve approximately species-level units as derived by Kim et al. (2011). Seed sequences from each OTU were then classified using a Naïve Bayesian classifier in mothur against the Greengenes 16S reference database (October 2012 version, see McDonald et al., 2012).

# Diversity indices

Shannon index

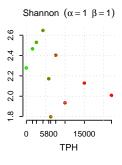
Simpson index

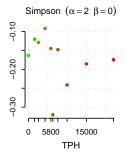
$$H_{\mathsf{Shan}}(\mathbf{p}) = -\sum p_j \log p_j \quad H_{\mathsf{Simp}}(\mathbf{p}) = 1 - \sum p_j^2$$

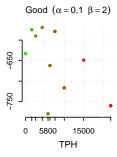
Good index

$$H_{\mathsf{Good},lpha,eta}(\mathbf{p}) = -\sum p_j^lpha \log^eta p_j$$

# Diversity indices of microbial data







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Dependent model for species data and diversity

Applications

Model the distribution of microbes in the soil:

The nth observation at site i is species j with probability  $p_i(X_i)$ 

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### Model

For every site i

$$Y_{n,i} \mid \mathbf{p}(X_i), X_i \stackrel{\text{ind}}{\sim} \sum_{j=1}^{\infty} p_j(X_i) \delta_j$$

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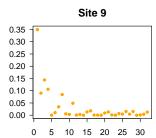
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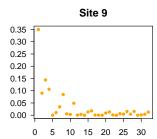
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- Lijoi et al. (2007): Bayesian nonparametric estimation of the probability of discovering new species (Biometrika)



 Use the distribution of the weights in a Dirichlet process, obtained by a stick-breaking construction



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### Stick-breaking construction

$$p_1 = V_1, \quad p_j = V_j \prod_{l < j} (1 - V_l),$$

with  $V_i \stackrel{\text{iid}}{\sim} \text{Beta}(1, M)$ .

# Site 9 0.35 0.30 0.25 0.20 0.15 0.10 0.05 0.00

15

20

10

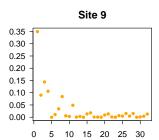
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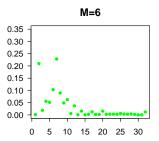
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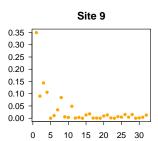
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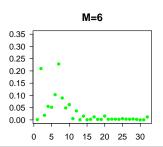
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It is denoted  $\mathbf{p} \sim \mathsf{GEM}(M)$ .





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Limit distribution seems to be Gumbel...

### Construction of the prior

 With the strick-breaking relation, a Dep – GEM prior is obtained from a Beta process.

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- Such a dependent Beta process is obtained by a transformed Gaussian process (Rasmussen and Williams, 2006)
  - $\to$  Denote by  $Z \sim N(0, \sigma^2)$  a Gaussian random variable, by  $\Phi_{\sigma_Z}$  its CDF and by  $F_M$  a Beta(1, M) CDF. Then:

$$\Phi_{\sigma_Z}(Z) \sim \mathsf{Unif}(0,1) \text{ and } V = F_M^{-1} \circ \Phi_{\sigma_Z}(Z) \sim \mathsf{Beta}(1,M),$$

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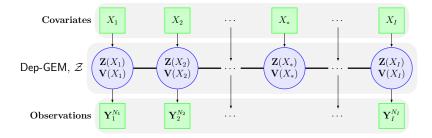
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Dependence specified by covariance function

$$K(X_i, X_j) = Cov(\mathcal{Z}(X_i), \mathcal{Z}(X_j)).$$

Covariance function	$ ilde{\mathcal{K}}_{\lambda}(X_1,X_2)$
Squared Exponential (SE)	$\exp\big(-(X_1-X_2)^2/(2\lambda^2)\big)$
Ornstein-Uhlenbeck (OU)	$\expig(- X_1-X_2 /\lambdaig)$
Rational Quadratic (RQ)	$(1+(X_1-X_2)^2/(2\lambda^2))^{-1}$

# Graphical model representation for the Dep – GEM model



## Algorithm: Metropolis within Gibbs

### $\textbf{Algorithm 1} \ \mathsf{Dep} - \mathsf{GEM} \ \mathsf{algorithm} \ (\mathsf{Gibbs})$

- 1: Update **Z** given  $(\sigma_{\mathbf{Z}}, \lambda, M)$
- 2: Update  $\sigma_{\mathbf{Z}}$  given  $(\mathbf{Z}, \lambda, M)$
- 3: Update  $\lambda$  given  $(\mathbf{Z}, \sigma_{\mathbf{Z}}, M)$
- 4: Update M given  $(\mathbf{Z}, \sigma_{\mathbf{Z}}, \lambda)$

# Algorithm: Metropolis within Gibbs

### **Algorithm 3** Dep — GEM algorithm (Gibbs)

- 1: Update **Z** given  $(\sigma_{\mathbf{Z}}, \lambda, M)$
- 2: Update  $\sigma_{\mathbf{Z}}$  given  $(\mathbf{Z}, \lambda, M)$
- 3: Update  $\lambda$  given  $(\mathbf{Z}, \sigma_{\mathbf{Z}}, M)$
- 4: Update M given  $(\mathbf{Z}, \sigma_{\mathbf{Z}}, \lambda)$

### Algorithm 4 MH algorithm

- 1: Given  $\theta$ , propose  $\theta' \sim Q_{\theta}(\cdot \mid \theta)$
- 2: Compute  $\rho_{\theta} = \frac{P_{\theta}(\theta')}{P_{\theta}(\theta)} \frac{Q_{\theta}(\theta|\theta')}{Q_{\theta}(\theta'|\theta)}$
- 3: Accept  $\theta'$  wp min $(\rho_{\theta}, 1)$ , otherwise keep  $\theta$

### Predictive distribution

• Predictive distribution of  $\mathbf{Z}_*$  obtained by integrating out  $\mathbf{Z}$  in the conditional distribution according to the posterior distribution  $\pi(\mathbf{Z}|Y,X)$ :

$$\pi(\mathbf{Z}_* \mid X_*, Y) = \int \pi(\mathbf{Z}_* \mid X_*, X, \mathbf{Z}) \pi(\mathbf{Z} \mid Y, X) d\mathbf{Z}.$$

No particular computational burden:

### Algorithm 5 Predictive distribution simulation

- 1: Sample **Z** from the posterior distribution  $\pi(\mathbf{Z}|Y,X)$
- 2: Given **Z**, sample **Z**\* from the conditional distribution  $\pi(\mathbf{Z}_* \mid X_*, X, \mathbf{Z})$

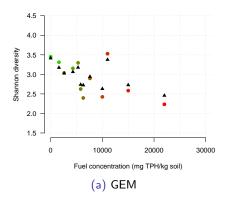
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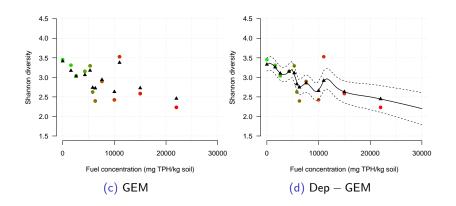
Dependent model for species data and diversity

Applications

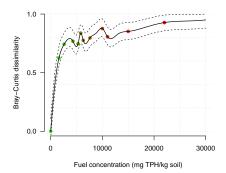
# Comparison of the Dep-GEM and indep. GEM models



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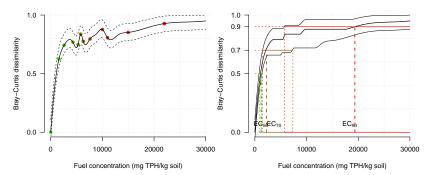


# Effective concentration estimation $EC_x$



(e) Bray-Curtis dissimilarity

# Effective concentration estimation $EC_x$



(g) Bray-Curtis dissimilarity

(h) Illustration of  $EC_x$  estimation

### Future work

- Extension to multiple covariates
  - $\longrightarrow$  by using Gaussian random fields instead of Gaussian processes
  - --- model choice

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- Extension to multiple covariates
  - → by using Gaussian random fields instead of Gaussian processes
  - ---- model choice
- Use of finer stick-breaking distributions
  - $\longrightarrow$  e.g. Beta(a,b) or Gibbs-type priors instead of Beta(1,M)

# Thank you for your attention!

- Arbel, J., Mengersen, K., Raymond, B., and King, C. (2013a). Ecotoxicological data study of diversity using a dependent Bayesian nonparametric model. *Manuscript under preparation*.
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