**Dirichlet-multinomial Empirical Bayesian model of OTU distribution**

In order to further elucidate XXX we implemented a simple alternative modeling strategy using Dirichlet-Multinomial Bayesian framework. The Multinomial likelihood for modeling OTU counts has been proposed in several study previously (Holmes *et al.* 2012; Wadsworth *et al.* 2017).

Observed data (observed OTU’s count):

Where *i* and *j* correspond to *i*-th sample and *j*-th OTU

= vector *i* of observed j OTU counts

= a probability vector that defines expected number of each OTU abundance in *i*-th vector

= expected *j*-th OTU abundance in *i*-th vector

Each parameter includes effects of climate (*c*), genetic distance (*dis*) and a random effect () distributed according to a Gaussian distribution with the corresponding hyperparameters.

represent regression coefficients distributed according to Gaussian distributions with high variance.

The hyperparameters and were estimated from the normalized genetic distance and climatic data, respectively.



**Figure 1** A graphical representation of the Dirichlet-multinomial empirical Bayesian model. The solid line circles denote stochastic nodes whereas squares denote constant nodes. Dashed elements represent deterministic nodes defined by applying a function to another variable. The graphical model was constructed following convention of (Höhna et al. 2014; Wadsworth et al. 2017)

Höhna S, Heath TA, Boussau B*, et al.* (2014) Probabilistic Graphical Model Representation in Phylogenetics. *Systematic Biology* **63**, 753-771.

Holmes I, Harris K, Quince C (2012) Dirichlet Multinomial Mixtures: Generative Models for Microbial Metagenomics. *PLoS One* **7**, e30126.

Wadsworth WD, Argiento R, Guindani M*, et al.* (2017) An integrative Bayesian Dirichlet-multinomial regression model for the analysis of taxonomic abundances in microbiome data. *BMC Bioinformatics* **18**, 94.