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Motivation

Start writing what might be a good introduction for any paper or chapter.

Include citations!

Definitions

- ASV
- OTU
- Zero-Inflation
- Phylogenetic tree
- Compositional
- Covariates/variables/ coefficients

Notation

 \bullet Number of samples: n

• Sample index: $i:i=1,\ldots,n$

 \bullet Number of ASVs: k

• ASV index: $j:j=1,\ldots,k$

 \bullet Number of covariates: q. Note that q does not include the intercept.

• Covariate index: $k: k = 1, \dots, q$

• Responses: Transformed counts into relative abundances.

Note that an alternative transformation to relative abundance might be good.

$$y_{ij}$$

$$\mathbf{y}_{np imes 1} = \begin{pmatrix} y_{i=1,j=1} \\ \vdots \\ y_{i=1,j=p} \\ \vdots \\ y_{i=n,j=1} \\ \vdots \\ y_{i=n,j=p} \end{pmatrix}$$

• Design matrix \mathbf{x} ('little \mathbf{x} ').

$$\mathbf{x}_{n \times q} = \begin{pmatrix} x_{i=1,k=1} & \cdots & x_{i=1,k=q} \\ x_{i=2,k=1} & \cdots & x_{i=2,k=q} \\ \vdots & \ddots & \vdots \\ x_{i=n,k=1} & \cdots & x_{i=n,k=q} \end{pmatrix}$$

We don't have coefficient values measured on each ASV (i.e. no j index), they are only measured on each sample. Thus $x_{ij} = x_i$ for all j = 1, ..., p. Then we convert to design matrix big X:

• Design matrix X:

$$X_{np \times pq} = x \otimes I_{p}$$

$$= \begin{pmatrix} x_{i=1,k=1} & 0 & \cdots & 0 & x_{i=1,k=2} & 0 & \cdots & 0 \\ 0 & x_{i=1,k=1} & \cdots & 0 & x_{i=1,k=2} & \cdots \\ \vdots & & \ddots & \vdots & \vdots & & \ddots & \vdots \\ 0 & \cdots & 0 & x_{i=1,k=1} & 0 & \cdots & 0 & x_{i=1,k=2} \end{pmatrix}$$

$$= \begin{pmatrix} 0 & x_{i=1,k=1} & 0 & \cdots & 0 & x_{i=1,k=2} \\ \vdots & & & \ddots & \vdots & & & & & & & & \\ 0 & \cdots & 0 & x_{i=1,k=1} & 0 & \cdots & 0 & 0 & x_{i=1,k=2} \\ \vdots & & & & & \ddots & & & & & \\ x_{i=2,k=1} & & & 0 & \cdots & 0 & x_{i=1,k=1} \\ \vdots & & & & & \ddots & & & & & \\ x_{i=2,k=1} & & & 0 & \cdots & 0 & x_{i=2,k=2} & \cdots \\ \vdots & & & & \ddots & & & & \\ \vdots & & & & \ddots & & & \\ \vdots & & & & & \ddots & & \\ x_{i=2,k=2} & & & \ddots & & & \\ \vdots & & & & \ddots & & & \\ \vdots & & & & \ddots & & \\ \vdots$$

• Parameter vector β with entries β_{jk}

$$\boldsymbol{\beta}_{pq \times 1} = \begin{pmatrix} \beta_{j=1,k=1} \\ \beta_{j=2,k=1} \\ \vdots \\ \beta_{j=p,k=1} \\ \beta_{j=1,k=2} \\ \vdots \\ \beta_{j=1,k=q} \\ \vdots \\ \beta_{j=p,k=q} \end{pmatrix}$$

• Link:

Link covariates to response.

First assume that **y** has the same mean and covariance structure as if $\mathbf{y}_i \sim Dir(\alpha_{1p}, \dots, \alpha_{ip})$ for all $i = 1, \dots, n$.

Then,

$$g(\alpha) = \log(\alpha) = X\beta$$

 $\log(\alpha_{ij}) = x_i\beta_j$

Where $\beta_j = (\beta_{j,k=1}, ..., \beta_{j,k=q})^t$, and $x_i = (x_{i1}, ..., x_{iq})$

This link function makes sense since $\alpha > 0$.

Dirichlet ideas

Assume $\eta_i = (\eta_{i1}, \dots, \eta_{ip}) \sim Dir(\alpha_{i1}, \dots, \alpha_{ip})$, and $\sum_{j=1}^p \alpha_{ij} = \alpha_{i0}$

Dirichlet Expected value

$$E(\eta_{ij}) = \frac{\alpha_{ij}}{\alpha_{i0}}$$

Dirichlet variance

$$Var(\eta_{ij}) = \frac{\alpha_{ij}(\alpha_{i0} - \alpha_{ij})}{\alpha_{i0}^2(\alpha_{i0} + 1)}$$

Note: $0 \le Var(\eta_{ij}) \le 1$

Dirichlet covariance

For $i \neq j$

$$Cov(\eta_{is}, \eta_{it}) = -\frac{\alpha_{is}\alpha_{it}}{\alpha_{i0}^2(\alpha_{i0} + 1)}$$

Note this matrix is singular. Note this quantity is always negative

Dirichlet correlation

For $i \neq j$

$$Cor(\eta_{is}, \eta_{it}) = \frac{Cov(\eta_{is}, \eta_{it})}{\sqrt{Var(\eta_{is})Var(\eta_{it})}}$$

$$= -\frac{\alpha_{is}\alpha_{it}}{\alpha_{i0}^2(\alpha_{i0} + 1)} \cdot \sqrt{\frac{\alpha_{i0}^2(\alpha_{i0} + 1)}{\alpha_{is}(\alpha_{i0} - \alpha_{is})}} \sqrt{\frac{\alpha_{i0}^2(\alpha_{i0} + 1)}{\alpha_{it}(\alpha_{i0} - \alpha_{it})}}$$

$$= -\sqrt{\frac{\alpha_{is}\alpha_{it}}{(\alpha_{i0} - \alpha_{is})(\alpha_{i0} - \alpha_{it})}}$$

Note this is always negative

GEEs

The collection of measurements taken on a single sample are assumed to be correlated. The entries in \mathbf{y}_i for a given i are correlated.

One such analysis method useful for correlated data are Generalized Estimating Equations. Originally proposed by LIANG and ZEGER 1986 for longitudinal data, this method uses a working correlation structure, which allows

for any specified correlation structure. Even if the correlation structure is misspecified, the resulting estimates are consistent.

The GEE method is a marginal model, only needing the first two moments and a link function to specify the method. In other words, this method does not perform any calculations on the full distribution likelihood. Therefore this method is useful in cases when the likelihood is intractable or very difficult to work with.

We assume that

$$E(y_{ij}) = \mu_{ij} = a'(\theta_{ij})$$
$$Var(y_{ij}) = a''(\theta_{ij})$$

Where $\theta_{ij} =$

 ϕ is then the dispersion parameter.

We link the expected mean to a set of linear predictors by

$$g(\mu_i) = \mathbf{x}\boldsymbol{\beta}$$

Where g is a known invertible link function.

Instead of directly to the mean μ_i , for this parametrization of the Dirichlet distribution, we link the α Dirichlet hyperparameters to a linear predictor. To link α s, the log link is appropriate, since $\alpha > 0$

Thus:

$$\log \alpha_{ij} = x_i \beta_j$$

See above for more details.

The GEE equations are

$$\sum_{i=1}^{n} \left(\frac{\partial \boldsymbol{\mu}_i}{\partial \boldsymbol{\beta}} \right)_{pq \times p}^{t} \mathbf{V}_{i_{p \times p}}^{-1} (\mathbf{Y_i} - \boldsymbol{\mu}_i)_{p \times 1} = 0$$

The estimator $\hat{\beta}$ is the solution to this set of equations.

- $V_i = A_i^{\frac{1}{2}} R_i A_i^{\frac{1}{2}}$: Working covariance matrix
- $diag(A_i) = \sqrt{Var(\eta_i)}$: Square root of Dirichlet variance.
- R_i : working correlation matrix, see below, mixture of Dirichlet and phylogenetic correlation.
- $\left(\frac{\partial \mu_i}{\partial \beta}\right)$: Matrix of partial derivatives, defined below
- Y_i : response ASV proportions $0 < Y_i < 1$
- μ_i : Expected mean: $E(Y_i) = \frac{\alpha_i}{\alpha_{i0}}$

Derivation of $\left(\frac{\partial \boldsymbol{\mu}_i}{\partial \boldsymbol{\beta}}\right)$

GEE algorithm

Let G be the GEE equation, and H be the hessian.

Identifiability issues

Note that we can write the mean:

$$\mu_{ij} = \frac{\alpha_{ij}}{\alpha_{i0}}$$

$$= \frac{e^{x_i\beta_j}}{\sum_{s=1}^p e^{x_i\beta_s}}$$

$$= \frac{e^{x_i\beta_j}}{e^{x_i\beta_1} + \dots + e^{x_i\beta_p}}$$

$$= \frac{e^{\gamma}}{e^{\gamma}} \frac{e^{x_i\beta_j}}{e^{x_i\beta_1} + \dots + e^{x_i\beta_p}}$$

$$= \frac{e^{\gamma}}{e^{\gamma}} \frac{e^{x_i\beta_j}}{e^{x_i\beta_1} + \dots + e^{x_i\beta_p}}$$

Thus μ_{ij} is the same regardless of if $\beta = (\beta_1, \dots, \beta_p)$ or $\beta = (\beta_1 + \gamma, \dots, \beta_p + \gamma)$.

Thus the mean is non-identifiable.

Check if this is the same for the variance.

Penalty

To solve this problem, we first attempt to add a penalty.

Penalty:

$$\lambda \left(\sum_{j=1}^{p} \beta_p \right)^2 = \lambda \beta^t 11^t \beta$$

New GEE eqn

$$G^* = G + \frac{\partial \text{Penalty}}{\partial \beta}$$
$$= G + 2\lambda 11^t \beta$$

New Hessian:

$$H^* = H + \frac{\partial^2 \text{Penalty}}{\partial^2}$$
$$= H + 2\lambda 11^t$$

Approaches from here

References

LIANG, KUNG-YEE and SCOTT L. ZEGER (Apr. 1986). "Longitudinal Data Analysis Using Generalized Linear Models". In: Biometrika 73.1, pp. 13–22. ISSN: 0006-3444. DOI: 10.1093/biomet/73.1.13.