

GEEs in R

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10/24/2012

Longitudinal data

Characteristics:

- ▶ Take multiple observations of K patients
- ▶ Call observations on one patient a cluster
- ▶ Correlation within clusters
- ▶ Independence between clusters

Example (from some website):

| Student Name | 2001 Score | 2002 Score | 2003 Score | 2004 Score |
|--------------|------------|------------|------------|------------|
| Mike | 339 | 350 | 361 | 366 |
| Jasmine | 332 | 343 | 350 | 351 |
| Thomas | 360 | 380 | 400 | 420 |

Generalized estimating equations: setup

K multivariate observations of responses

$$Y_i = (Y_{i1}, \dots, Y_{it}, \dots, Y_{in_i})$$

Let $E(Y_{it}) = \mu_{it}$.

Let $g(\cdot)$ be a monotone link function and

$$g(\mu_{it}) = \eta_{it} = X_{it}^T \beta.$$

Also assume

$$\text{var}(Y_{it}) = \phi a_{it} = \phi a(\mu_{it}).$$

Link function options in R: identity, log, exponential, logit, probit, and so on.

We don't want to be limited by the link function options!

Setup, continued

First, denote $\boldsymbol{\mu}_i = (\mu_{i1}, \dots, \mu_{in_i})^T$.

Next, denote $A_i = \text{diag}(a(\boldsymbol{\mu}_i))$

Finally, let

$$V_i = \phi A_i^{\frac{1}{2}} R_i(\boldsymbol{\alpha}) A_i^{\frac{1}{2}}$$

where $R_i(\boldsymbol{\alpha})$ is a working correlation matrix.

Independence structure

All within cluster observations are independent, as well as all between cluster observations

$$R_i(\alpha) = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix}$$

Exchangeable structure

Correlation between any two observations is always α

$$R_i(\alpha) = \begin{bmatrix} 1 & \alpha & \alpha & \alpha \\ \alpha & 1 & \alpha & \alpha \\ \alpha & \alpha & 1 & \alpha \\ \alpha & \alpha & \alpha & 1 \end{bmatrix}$$

AR-1 structure

Correlation between any two observations is $\alpha^{|i-j|}$

$$R_i(\alpha) = \begin{bmatrix} 1 & \alpha & \alpha^2 & \alpha^3 \\ \alpha & 1 & \alpha & \alpha^2 \\ \alpha^2 & \alpha & 1 & \alpha \\ \alpha^3 & \alpha^2 & \alpha & 1 \end{bmatrix}$$

M-dependence structure

if $M = 1$, it will look like

$$R_i(\alpha) = \begin{bmatrix} 1 & \alpha & 0 & 0 \\ \alpha & 1 & \alpha & 0 \\ 0 & \alpha & 1 & \alpha \\ 0 & 0 & \alpha & 1 \end{bmatrix}$$

If $M = 2$, then

$$R_i(\alpha) = \begin{bmatrix} 1 & \alpha_1 & \alpha_2 & 0 \\ \alpha_1 & 1 & \alpha_1 & \alpha_2 \\ \alpha_2 & \alpha_1 & 1 & \alpha_1 \\ 0 & \alpha_2 & \alpha_1 & 1 \end{bmatrix}$$

Unstructured structure

Each entry is allowed to be different (still symmetric)

$$R_i(\alpha) = \begin{bmatrix} 1 & \alpha_{12} & \alpha_{13} & \alpha_{14} \\ \alpha_{12} & 1 & \alpha_{23} & \alpha_{24} \\ \alpha_{13} & \alpha_{23} & 1 & \alpha_{34} \\ \alpha_{14} & \alpha_{24} & \alpha_{34} & 1 \end{bmatrix}$$

Estimating equations are:

$$\sum_{i=1}^K X_i^T \Delta_i A_i V_i^{-1} S_i = 0 \quad (1)$$

where

$$\Delta_i = \text{diag} \left(\frac{dg^{-1}(\eta_i)}{d\eta_i} \right)$$

and

$$S_i = Y_i - \mu_i.$$

In the future, let

$$D_i = A_i \Delta_i X_i$$

Example: linear regression

Consider the case: $g(x) = x$, $a(x) = 1$, $R_i(\alpha) = I$

This corresponds to plain vanilla linear regression

Then, $\Delta_i = A_i = I$ and $V_i = \phi I$

So the estimating equation becomes

$$\sum_{i=1}^K X_i^T \Delta_i A_i V_i^{-1} S_i = \sum_{i=1}^K \sum_{t=1}^{n_i} X_{it}^T (\phi I)^{-1} (Y_{it} - X_{it} \beta) = 0$$

A little algebra and putting everything in matrix notation gives

$$X^T X \beta = X^T Y$$

Liang and Zeger recommend calculating by

$$\beta^{(k+1)} = \beta^{(k)} - \left\{ \sum_{i=1}^K D_i^T V_i^{-1} D_i \right\}^{-1} \left\{ \sum_{i=1}^K D_i^T V_i^{-1} S_i \right\} \quad (2)$$

with a robust variance estimate of

$$\left\{ \sum_{i=1}^K D_i^T V_i^{-1} D_i \right\}^{-1} \left\{ \sum_{i=1}^K D_i^T V_i^{-1} S_i S_i^T V_i^{-1} D_i \right\} \left\{ \sum_{i=1}^K D_i^T V_i^{-1} D_i \right\}^{-1}$$

Replace $\sum_{i=1}^K$ with bigger matrices. Define all these things:

$$X = [X_1 \ X_2 \ \cdots \ X_K]^T,$$

$$\mu = [\mu_1^T \ \mu_2^T \ \cdots \ \mu_K^T]^T$$

$$A = \text{diag}(a(\mu)) \quad \Delta = \text{diag}\left(\frac{dg^{-1}(\eta)}{d\eta}\right)$$

$$S = [S_1^T \ S_2^T \ \cdots \ S_K^T]^T$$

and $R(\alpha)$ is a block diagonal matrix with each $R_i(\alpha)$ as blocks.

Matrix-izing it all

Using new matrices, solve (2) by

$$\beta^{(k+1)} = \beta^{(k)} - \left\{ D^T V^{-1} D \right\}^{-1} \left\{ D^T V^{-1} S \right\} \quad (3)$$

with $V = \phi A^{\frac{1}{2}} R(\alpha) A^{\frac{1}{2}}$.

Variance estimate is now

$$\left\{ D^T V^{-1} D \right\}^{-1} \left\{ D^T V^{-1} S^T J S V^{-1} D \right\} \left\{ D^T V^{-1} D \right\}^{-1}$$

where J is block diagonal with ones.

Block diagonals

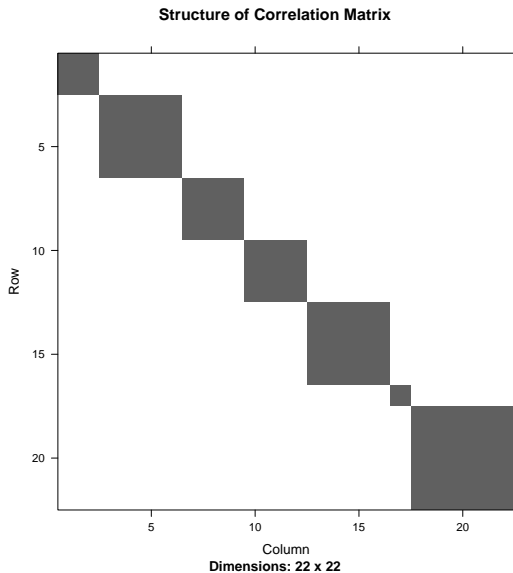
Two big block diagonals are used:

$$R(\alpha) = \begin{bmatrix} R_1(\alpha) & & & \\ & R_2(\alpha) & & \\ & & \ddots & \\ & & & R_K(\alpha) \end{bmatrix}$$
$$J = \begin{bmatrix} J_{n_1} & & & \\ & J_{n_2} & & \\ & & \ddots & \\ & & & J_{n_K} \end{bmatrix}$$

where J_n is a $n \times n$ matrix of ones

Memory allocation for these is the single most expensive thing

Block diagonal structure



Let $N = \sum_{i=1}^K n_i$.

- ▶ X is $N \times p$
- ▶ A and Δ are $N \times N$
- ▶ $R(\alpha)$ is $N \times N$ block diagonal
- ▶ J has same structure as $R(\alpha)$, but with only 1 and 0
- ▶ S , μ and η are $N \times 1$.

The Matrix package in R

Sparse matrix storage:

$$\begin{bmatrix} 1 & . & . & . \\ . & . & . & . \\ . & . & . & . \\ . & . & . & 1 \end{bmatrix}$$

represented as

Formal class 'dgTMatrix' [package "Matrix"] with 6 slots

```
..@ i : int [1:2] 0 3  
..@ j : int [1:2] 0 3  
..@ Dim : int [1:2] 4 4  
..@ Dimnames:List of 2  
.. .. $ : NULL  
.. .. $ : NULL  
..@ x : num [1:2] 1 1  
..@ factors : list()
```

- ▶ So we can build really large matrices and multiply them!
- ▶ However, we still have the problem of V^{-1}
- ▶ $V = \phi A^{\frac{1}{2}} R(\alpha) A^{\frac{1}{2}}$ is block diagonal (sparse, symmetric)
- ▶ Inverse of block diagonal is block diagonal of inverses
- ▶ R doesn't know this
- ▶ The real problem is $R(\alpha)^{-1}$

Analytic inverses are worked out for

- ▶ AR-1
- ▶ Independence
- ▶ Exchangeable

However, this requires that we have no skipped observations!
R package geepack does not have this limitation

For everything else, we have to use the solve function in R.
Consider unstructured matrix

$$R_i(\alpha) = \begin{bmatrix} 1 & \alpha_{12} & \alpha_{13} & \alpha_{14} \\ \alpha_{12} & 1 & \alpha_{23} & \alpha_{24} \\ \alpha_{13} & \alpha_{23} & 1 & \alpha_{34} \\ \alpha_{14} & \alpha_{24} & \alpha_{34} & 1 \end{bmatrix}$$

Then the full $R(\alpha)$ matrix will be roughly K blocks of this matrix

But say we have clusters of size 2,3, and 4 with no skipped observations (only dropouts)

Numeric inverses, continued

In addition to the previous $R_i(\alpha)$, we have

$$\begin{bmatrix} 1 & \alpha_{12} & \alpha_{13} \\ \alpha_{12} & 1 & \alpha_{23} \\ \alpha_{13} & \alpha_{23} & 1 \end{bmatrix} \text{ and } \begin{bmatrix} 1 & \alpha_{12} \\ \alpha_{12} & 1 \end{bmatrix}$$

and that's it!

So we only need to solve a 2×2 , a 3×3 , and a 4×4 matrix, then reassemble appropriately for the full $R(\alpha)$ matrix.

Much easier than $N \times N$ (largest N we use is about 300k)

Speed comparison

$N = 296,218$, clusters of size 2 or 3 (birth outcomes data)

| Independence | | |
|--------------|----------------------|-----------------|
| | Averaged Elapsed (s) | Relative To Min |
| geeM | 3.666 | 1.000 |
| gee | 11.634 | 3.173 |
| geepack | 10.940 | 2.984 |
| AR-1 | | |
| | Averaged Elapsed (s) | Relative To Min |
| geeM | 6.594 | 1.000 |
| gee | 30.590 | 4.639 |
| geepack | 25.578 | 3.879 |
| Unstructured | | |
| | Averaged Elapsed (s) | Relative To Min |
| geeM | 4.820 | 1.000 |
| gee | 19.462 | 4.038 |
| geepack | 31.418 | 6.518 |

Speed comparison, comments

- ▶ Our package is much faster on large data
- ▶ Maybe a little slower on small data
- ▶ We use tons of memory
- ▶ Using large matrices \Rightarrow time/memory tradeoff