Some research in multivariate analysis Stat 542

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Outline

Copula modeling

Covariance regression

Hierarchical models for matrix-variate data

GSS data



Conditional models

Interest is typically in the conditional relationship between pairs of variables, accounting for heterogeneity in other variables of less interest. Standard bivariate rank-based methods are inappropriate.

Model 1

$$\begin{split} \mathrm{INC}_i &= \beta_0 + \beta_1 \mathrm{CHILD}_i + \beta_2 \mathrm{DEG}_i + \beta_3 \mathrm{AGE}_i + \beta_4 \mathrm{PCHILD}_i + \beta_5 \mathrm{PINC}_i + \beta_6 \mathrm{PDEG}_i + \epsilon_i \\ \text{p-value for } \beta_1 \text{ is 0.11: "little evidence" that } \beta_1 \neq 0 \end{split}$$

Model 2

CHILD_i ~ Pois(exp{
$$\beta_0 + \beta_1$$
INC_i+ β_2 DEG_i+ β_3 AGE_i+ β_4 PCHILD_i+ β_5 PINC_i+ β_6 PDEG_i})
p-value for β_1 is 0.01: "strong evidence" that $\beta_1 \neq 0$.

	Predictor										
Response	INC	CHILD	DEG	AGE	PCHILD	PINC	PDEG				
INC	NA NA	1.10 (.11)	7.03 (<.01)	.34 (<.01)	4.07 (<.01)	.28 (.41)	1.40 (.12)				
CHILD	.01 (.01)	NA	07 (.06)	.04 (<.01)	06 (.20)	.02 (.08)	05 (.20)				

Multivariate normal copula model

This idea motivates the following "latent variable" model:

$$(z_1, \ldots, z_p) \sim \text{mvn}(\mathbf{0}, \Sigma)$$

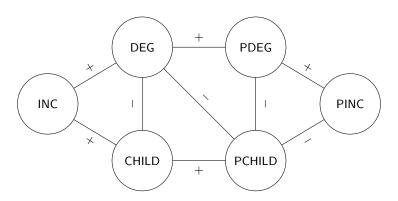
 $(y_1, \ldots, y_p) = (F_1^{-1}(z_1), \ldots, F_p^{-1}(z_p))$

 Σ parameterizes the dependence, $F_1^{-1}, \ldots, F_p^{-1}$ the marginal distributions.

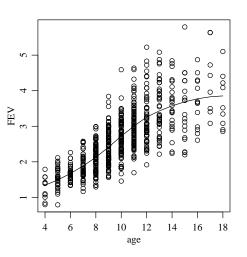
This model

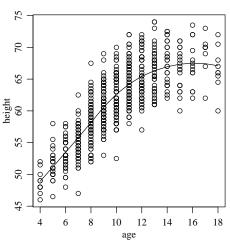
- is scale free
- is appropriate for discrete and continuous data
- gives compatible full conditional distributions

$$E[z_j|z_{-j}] = \sum_{[j,-j]} \sum_{[-j,-j]}^{-1} z_{-j}$$

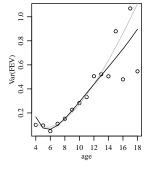


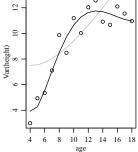
FEV data

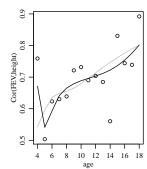




FEV data

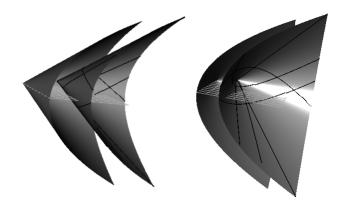




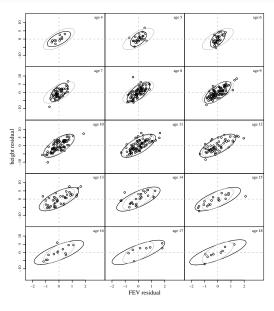


A covariance regression model

$$\mathbf{\Sigma}_{\mathbf{x}} = \mathbf{A} + \mathbf{B} \mathbf{x} \mathbf{x}^{\mathsf{T}} \mathbf{B}^{\mathsf{T}} \tag{1}$$



FEV data by age

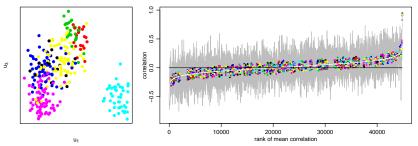


Leukemia data

Gene expression data on 327 cancer patients, each in one of seven groups:

group	BCR	E2A	Hyperdip50	MLL	Т	TEL	other
sample size	15	27	64	20	43	79	79

We look at the 300 genes with highest rank variation across subjects.



 $\mathbf{Y} = \mathbf{U}\mathbf{D}\mathbf{V}^T$ $\mathbf{Y}_k = \mathbf{U}_k \mathbf{D}_k \mathbf{V}_k^T$

Left-singular vectors of \boldsymbol{U} separate the groups.

How do covariances $\mathbf{V}_k \mathbf{D}_k^2 \mathbf{V}_k^T$ differ across groups?

Reduced rank matrix approximation

For high-dimensional data, low rank approximations are useful for describing the main patterns in row/column variability:

Symmetric matrices: $\mathbf{Y} = \mathbf{U}\Lambda\mathbf{U}^T + \mathbf{E}$, $y_{i,j} = \mathbf{u}_i^T\Lambda\mathbf{u}_j + e_{i,j}$

Rectangular matrices: $\mathbf{Y} = \mathbf{U}\mathbf{D}\mathbf{V}^T + \mathbf{E}$, $y_{i,j} = \mathbf{u}_i^T \mathbf{D}\mathbf{v}_j + e_{i,j}$

The column dimension R of U is generally much smaller than that of Y,

$$R \ll \min(m, n)$$

so that $\mathbf{U}\Lambda\mathbf{U}^T$, $\mathbf{U}\mathbf{D}\mathbf{V}^T$ provide low-rank approximations to \mathbf{Y} .

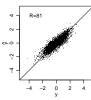
$$\min_{\mathbf{M}: \mathrm{rank}(\mathbf{M}) = R} ||\mathbf{Y} - \mathbf{M}||^2 = ||\mathbf{Y} - \hat{\mathbf{U}}_{[,1:R]} \hat{\mathbf{D}}_{[1:R,1:R]} \hat{\mathbf{V}}_{[,1:R]}^T||^2$$











A hierarchical eigenmodel

$$\mathbf{Y}_{1} = \mathbf{U}_{1}\mathbf{D}_{1}\mathbf{V}_{1}^{T} + \mathbf{E}_{1}$$

$$\vdots \quad \vdots \quad \vdots$$

$$\mathbf{Y}_{K} = \mathbf{U}_{K}\mathbf{D}_{K}\mathbf{V}_{K}^{T} + \mathbf{E}_{K}$$

$$\begin{aligned} \mathbf{U}_1 \sim \mathrm{uniform}(\mathcal{V}_{n_1,R}) & \mathrm{diag}(\mathbf{D}_1) \sim \mathrm{normal}(\mathbf{0},\tau^2 I) & \mathbf{V}_1 \sim \mathrm{Bingham}(\mathbf{A},\mathbf{B},\mathbf{V}) \\ & \vdots \\ \mathbf{U}_K \sim \mathrm{uniform}(\mathcal{V}_{n_K,R}) & \mathrm{diag}(\mathbf{D}_K) \sim \mathrm{normal}(\mathbf{0},\tau^2 I) & \mathbf{V}_K \sim \mathrm{Bingham}(\mathbf{A},\mathbf{B},\mathbf{V}) \end{aligned}$$

$$V \sim \operatorname{uniform}(\mathcal{O}_R)$$