# Separable covariance arrays via the Tucker product <br> by Peter Hoff 

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## Correlated Errors are Bad!



Lecture slide from Biostat 533

## Review of Multivariate Analysis

Multivariate normal model, $\mathbf{y} \in \mathbb{R}^{m}$ :

$$
\begin{aligned}
\mathbf{z}=\left\{z_{j}: j\right. & =1, \ldots, m\} \\
& \stackrel{\text { iid }}{\sim} \text { normal }(0,1) \\
& \mathbf{y}=\boldsymbol{\mu}+\mathbf{A z} \stackrel{\text { iid }}{\sim} \text { multivariate } \operatorname{normal}\left(\boldsymbol{\mu}, \boldsymbol{\Sigma}=\mathbf{A A}^{T}\right)
\end{aligned}
$$

Matrix-variate normal model, $\mathbf{Y} \in \mathbb{R}^{m_{1} \times m_{2}}$ :

$$
\begin{aligned}
\mathbf{Z}=\left\{z_{i, j}\right\}_{i=1 j=1}^{m_{1} m_{j}} & \stackrel{\text { iid }}{\sim} \text { normal }(0,1) \\
\mathbf{Y}=\mathbf{M}+\mathbf{A Z B}^{T} \stackrel{\text { iid }}{\sim} & \text { matrix normal }\left(\mathbf{M}, \boldsymbol{\Sigma}_{1}=\mathbf{A A}^{T}, \boldsymbol{\Sigma}_{2}=\mathbf{B B}^{T}\right) \\
& \sim \text { matrix normal }\left(\mathbf{M}, \boldsymbol{\Sigma}_{1} \circ \boldsymbol{\Sigma}_{2}\right)
\end{aligned}
$$

Note that matrix-variate normal assumes separable covariance structure

## What is separable covariance structure?

$$
\mathbf{Y} \sim \text { matrix normal }\left(0, \boldsymbol{\Sigma}_{1}, \boldsymbol{\Sigma}_{2}\right)
$$

- Covariance is product of row covariance and column covariance

$$
\operatorname{Cov}\left(Y_{i j}, Y_{k l}\right)=\Sigma_{1 i k} \times \Sigma_{2 j l}
$$

- Reduced number of parameters to be estimated
- From $\frac{(n p) \times(n p+1)}{2}$ to $\frac{p(p+1)}{2}+\frac{n(n+1)}{2}$

Made up motivation - linear regression model

$$
\mathbf{Y}=\mathbf{M}+\mathbf{E}
$$

- $\mathbf{M}$ is the mean structure (for instance, $\mathbf{X} \boldsymbol{\beta}$, or ANOVA model)
- $\mathbf{E}$ is the error term


## Made up motivation - Example 1

Suppose $\mathbf{y}_{i} \in \mathbb{R}^{m_{1}}$ is the outcome variable obtained by repeatedly taking measurements from subject $i$ across time $j=\left\{1, \ldots, m_{1}\right\}$.

Appropriate Model:

$$
\mathbf{y}_{i}=\mathbf{x}_{i}^{T} \beta+\boldsymbol{\epsilon}_{i}
$$

$\boldsymbol{\epsilon}_{i} \sim$ multivariate normal $(\mathbf{0}, \boldsymbol{\Sigma})$

## Made up motivation - Example 2

Suppose $Y_{i} \in \mathbb{R}^{m_{1} \times m_{2}}$ and $y_{i, j, k}$ is the $i$ th outcome variable for location $j$ at time $k$.
Naive Model: Assume that the locations are not correlated

$$
\mathbf{y}_{i j}=\mathbf{x}_{i j}^{T} \beta+\boldsymbol{\epsilon}_{i j}
$$

$\boldsymbol{\epsilon}_{i j} \sim$ multivariate normal $(\mathbf{0}, \boldsymbol{\Sigma})$

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Really? Ignoring dependent errors after taking Biostat571?

## More complicated models

Look at Laina Mercer's slides, or alternatively,

## More complicated models

## Look at Laina Mercer's slides, or alternatively,

$$
\mathbf{Y}_{i}=\mathbf{\Theta} \mathbf{X}_{i}+\mathbf{E}_{i}
$$

$\mathbf{E}_{i} \stackrel{\text { iid }}{\sim}$ matrix normal $\left(\mathbf{0}, \boldsymbol{\Sigma}_{1}, \boldsymbol{\Sigma}_{2}\right)$
Closely related to (Knorr-Held and Besag, 1998), it does not allow for space $\times$ time interactions.

Citation: On matrix-variate regression analysis by Cinzia Viroli (2012)

## What is an array?

Gene expression data set
$\mathbf{Y}=\left\{y_{i, j, k}\right\}$.

- $i$ indexes the $i$ th subject
- $j$ indexes the $j$ th gene
- $k$ indexes the $k$ th repeated measurement

Then, $y_{i, j, k}$ is the gene expression level for the $j$ th gene of the $i$ th subject, measured at time $k$.


Citation: Are a set of microarrays independent of each other by Brad Efron (2009)

## Motivation - Example 3

Yearly change in log trade value (in 2000 dollars): $\mathbf{Y}=\left\{y_{i, j, k, l}\right\}$

- $i \in\{1, \ldots, 30\}$ indexes the exporting nation
- $j \in\{1, \ldots, 30\}$ indexes the importing nation
- $k \in\{1, \ldots, 6\}$ indexes the commodity type
- $t \in\{1, \ldots, 10\}$ indexes the year

Interested in modeling the mean $M_{i j k}=\mu_{i, j, k}$ across $t$ measurements

## What can we do?

## Motivation - Example 3 cont

Interested in the model

$$
y_{i, j, k, l}=\mu_{i, j, k}+\epsilon_{i, j, k, l}
$$

- iid error model: $\epsilon_{i, j, k, I} \sim \operatorname{normal}\left(0, \sigma^{2}\right)$
- multivariate error model: $\boldsymbol{\epsilon}_{i, j, k} \sim$ multivariate normal $(\mathbf{0}, \boldsymbol{\Sigma})$
- matrix-variate error model: $\boldsymbol{\epsilon}_{i, j} \sim$ matrix normal $\left(\mathbf{0}, \boldsymbol{\Sigma}_{1}, \boldsymbol{\Sigma}_{2}\right)$


## Motivation - Example 3 cont

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But all four dimensions are correlated!

$$
\mathrm{E} \sim ? ? ?
$$

## Goal of the paper

Propose the Array Normal distribution for array data

- model mean structure
- model covariance structure

Suppose $\mathbf{Y} \in \mathbb{R}^{m_{1} \times \ldots \times m_{k}}$

$$
\mathbf{Y} \sim \text { array normal }\left(\mathbf{M}, \boldsymbol{\Sigma}_{1}, \ldots, \boldsymbol{\Sigma}_{k}\right)
$$

## Take home message until the next talk

- Array data is everywhere


Gene expression


- Most people assume certain dimensions are independent
- Maybe it is a good idea to model the dependencies after all!

Questions?

