Design matrices for models

Analysis of Ecological and Environmental Data QERM 514

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Goals for today

- Understand how to create design matrices for use in linear models
- Recognize the different coding schemes for factor models
- See how to use model.matrix() for creating & extracting design matrices

Models in matrix form

Recall the matrix form for our linear models, where

$$y = X\beta + e$$
$$e \sim MVN(0, \Sigma)$$

Models in matrix form

Let's write out this model in more detail

The columns in ${f X}$ define the *design* of the analysis

Ordinary least squares

Also recall that we can use X to solve for \hat{y}

$$\hat{\mathbf{y}} = \mathbf{X}\hat{\boldsymbol{\beta}}$$

$$= \mathbf{X}\left((\mathbf{X}^{\top}\mathbf{X})^{-1}\mathbf{X}^{\top}\mathbf{y}\right)$$

$$= \underbrace{\mathbf{X}(\mathbf{X}^{\top}\mathbf{X})^{-1}\mathbf{X}^{\top}\mathbf{y}}_{\mathbf{H}}$$

$$= \mathbf{H}\mathbf{y}$$

Understanding the form of ${f X}$ is critical to our inference

A simple starting point

Data = (Deterministic part) + (Stochastic part)

Types of linear models

We classify linear models by the form of their deterministic part

Discrete predictor \rightarrow ANalysis Of VAriance (ANOVA)

Continuous predictor \rightarrow Regression

Both \rightarrow ANalysis of COVAriance (ANCOVA)

Possible models for growth of fish

Model	Description
$\text{growth}_i = \beta_0 + \beta_{1,\text{species}} + \epsilon_i$	1-way ANOVA
$\text{growth}_i = \beta_0 + \beta_{1,\text{species}} + \beta_{2,\text{tank}} + \epsilon_i$	2-way ANOVA
$\text{growth}_i = \beta_0 + \beta_1 \text{ration}_i + \epsilon_i$	simple linear regression
growth _i = $\beta_0 + \beta_1$ ration _i + β_2 temperature _i + ϵ_i	multiple regression
$\text{growth}_i = \beta_0 + \beta_{1,\text{species}} + \beta_2 \text{ration}_i + \epsilon_i$	ANCOVA

Mean only

What would ${\bf X}$ look like for a simple model of the data ${\bf y}$ that included a mean only?

 $\mathbf{y} = \boldsymbol{\mu} + \mathbf{e}$

Mean only

Let's start by rewriting our model as

$$\mathbf{y} = \boldsymbol{\beta}_0 + \mathbf{e}$$
$$= \begin{bmatrix} \boldsymbol{\beta}_0 \\ \boldsymbol{\beta}_0 \\ \vdots \\ \boldsymbol{\beta}_0 \end{bmatrix} + \mathbf{e}$$

Mean only

$$\mathbf{y} = \begin{bmatrix} 1 \\ 1 \\ \vdots \\ 1 \end{bmatrix} \boldsymbol{\beta}_0 + \mathbf{e}$$
$$= \mathbf{X}\boldsymbol{\beta} + \mathbf{e}$$

with $\mathbf{X} = \begin{bmatrix} 1 \ 1 \ \cdots \ 1 \end{bmatrix}^{\top}$ and $\boldsymbol{\beta} = [\boldsymbol{\beta}_0]$

Regression

What would ${f X}$ look like for a regression model with 2 predictors?

$$y_i = \beta_0 + \beta_1 x_{1,i} + \beta_2 x_{2,i} + e_i$$
$$\Downarrow?$$
$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{e}$$

Regression

Regression

What would \mathbf{X} look like for model with an intercept and linear increase over time t?

$$y_t = \beta_0 + \beta_1 t + e_t$$
$$\Downarrow?$$
$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{e}$$

Regression



Defining models with \boldsymbol{X}

Regression



Analysis of variance (ANOVA)

ANOVA was popularized by <u>Ronald Fisher</u> ~100 years ago when he was studying the variance of genetic traits among commercial crops

ANOVA is used to analyze *differences among group means*

Comparing group means

Recall our analysis of fish growth as a function of ration



ANOVA

Here we want to know if the mean growth of fish varies among the 3 ration sizes

$$\bar{\boldsymbol{g}}_{ration_1} \stackrel{?}{=} \bar{\boldsymbol{g}}_{ration_2} \stackrel{?}{=} \bar{\boldsymbol{g}}_{ration_3}$$

How would we write the model for this?

ANOVA

Our model for an observation y_i is something like

 $y_i = \mu_i + e_i$ $\mu_i = \begin{cases} \mu_1 & \text{if fed ration 1} \\ \mu_2 & \text{if fed ration 2} \\ \mu_3 & \text{if fed ration 3} \end{cases}$

ANOVA

We can use binary 0/1 coding to represent if/then constructs

$$y_i = \mu_1 x_{1,i} + \mu_2 x_{2,i} + \mu_3 x_{3,i} + e_i$$

 $x_{1,i} = 1$ if fed ration 1 and 0 otherwise $x_{2,i} = 1$ if fed ration 2 and 0 otherwise $x_{3,i} = 1$ if fed ration 3 and 0 otherwise

ANOVA

How would we specify the model matrix \boldsymbol{X} for this?

ANOVA

Let's rewrite our model as

ANOVA

And define \boldsymbol{X} as

$$\mathbf{X} = \begin{bmatrix} \mathbf{x}_{1,1} & \mathbf{x}_{2,1} & \mathbf{x}_{3,1} \\ \mathbf{x}_{1,2} & \mathbf{x}_{2,2} & \mathbf{x}_{3,2} \\ \vdots & \vdots & \vdots \\ \mathbf{x}_{1,n} & \mathbf{x}_{2,n} & \mathbf{x}_{3,n} \end{bmatrix}$$

Let's now re-order all of the observations into their groups

$$\mathbf{y} = \begin{bmatrix} \mathbf{y}_{1,1} \\ \vdots \\ \mathbf{y}_{1,j_1} \\ \mathbf{y}_{2,1} \\ \vdots \\ \mathbf{y}_{2,j_2} \\ \mathbf{y}_{3,1} \\ \vdots \\ \mathbf{y}_{3,j_3} \end{bmatrix} \text{ with } \mathbf{j}_1 + \mathbf{j}_2 + \mathbf{j}_3 = \mathbf{n}$$

We can then define ${f X}$ and ${m eta}$ as

$$\mathbf{X} = \begin{bmatrix} 1 & 0 & 0 \\ \vdots & \vdots & \vdots \\ 1 & 0 & 0 \\ \hline 0 & 1 & 0 \\ \vdots & \vdots & \vdots \\ 0 & 1 & 0 \\ \hline 0 & 0 & 1 \\ \vdots & \vdots & \vdots \\ 0 & 0 & 1 \end{bmatrix} \quad \boldsymbol{\beta} = \begin{bmatrix} \boldsymbol{\beta}_1 \\ \boldsymbol{\beta}_2 \\ \boldsymbol{\beta}_3 \end{bmatrix}$$

ANOVA

Here are the mean growth rates of our 3 groups of fish

 $\bar{y}_{j=1} = \beta_1 = 19.6$ $\bar{y}_{j=2} = \beta_2 = 25.6$ $\bar{y}_{j=3} = \beta_3 = 35$

ANOVA

And here are the results of our ANOVA model

```
## fit ANOVA w/ `- 1` to remove intercept
m1 <- lm(yy ~ ration - 1)
coef(m1)</pre>
```

ration_1 ration_2 ration_3
19.62001 25.64846 35.01523

This confirms that we have fit a model of means

ANOVA



ANOVA

Suppose we wanted to reframe our model to instead include the effect of ration relative to the overall mean growth rate (μ)

$$y_i = \mu + \beta_1 x_{1,i} + \beta_2 x_{2,i} + \beta_3 x_{3,i} + e_i$$

and calculate the groups means as

$$\bar{y}_{j=1} = \mu + \beta_1$$
$$\bar{y}_{j=2} = \mu + \beta_2$$
$$\bar{y}_{j=3} = \mu + \beta_3$$

We would then define ${f X}$ and ${m eta}$ as

$$\mathbf{X} = \begin{bmatrix} 1 & 1 & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots \\ 1 & 1 & 0 & 0 \\ \hline 1 & 0 & 1 & 0 \\ \vdots & \vdots & \vdots & \vdots \\ 1 & 0 & 1 & 0 \\ \hline 1 & 0 & 0 & 1 \\ \vdots & \vdots & \vdots & \vdots \\ 1 & 0 & 0 & 1 \end{bmatrix} \quad \boldsymbol{\beta} = \begin{bmatrix} \boldsymbol{\mu} \\ \boldsymbol{\beta}_1 \\ \boldsymbol{\beta}_2 \\ \boldsymbol{\beta}_3 \end{bmatrix}$$

ANOVA

And here are the results of our ANOVA model

design matrix
X <- cbind(rep(1,nn*pp), ration)
fit ANOVA w/ `- 1` to remove intercept
m2 <- lm(yy ~ X - 1)
coef(m2)</pre>

##	Х	X_1	X_2	X_3
##	35.015235	-15.395221	-9.366774	NA

Wait-what happened here?!

Can you spot the problem in our design matrix?



ANOVA

solve for beta by hand
beta <- solve(t(X) %*% X) %*% t(X) %*% yy</pre>

Error in solve.default(t(X) %*% X) :

system is computationally singular: reciprocal condition number

X is not *full rank* ($\mathbf{X}_{(\cdot 1)} = \mathbf{X}_{(\cdot 2)} + \mathbf{X}_{(\cdot 3)} + \mathbf{X}_{(\cdot 4)}$)

	1	1	0	0
	•	•	•	• •
	1	1	0	0
	1	0	1	0
X =	•	•	•	• •
	1	0	1	0
	1	0	0	1
	•	•	•	• •
	1	0	0	1

ANOVA

Let's think about our model again

$$y_i = \mu + \beta_1 x_{1,i} + \beta_2 x_{2,i} + \beta_3 x_{3,i} + e_i$$

where we want the group means to be

$$\bar{y}_{j=1} = \mu + \beta_1$$
$$\bar{y}_{j=2} = \mu + \beta_2$$
$$\bar{y}_{j=3} = \mu + \beta_3$$

ANOVA

Consider the overall mean of \boldsymbol{y} in terms of the group means

$$\bar{y} = \frac{\bar{y}_{j=1} + \bar{y}_{j=2} + \bar{y}_{j=3}}{3}$$

ANOVA

Consider the overall mean of \boldsymbol{y} in terms of the group means

$$\bar{y} = \frac{\bar{y}_{j=1} + \bar{y}_{j=2} + \bar{y}_{j=3}}{3}$$

$$\psi$$

$$\mu = \frac{(\mu + \beta_1) + (\mu + \beta_2) + (\mu + \beta_3)}{3}$$

$$\psi$$

$$\beta_1 + \beta_2 + \beta_3 = 0$$

ANOVA

Now we can rewrite our model as

$$y_i = \mu + \beta_1 x_{1,i} + \beta_2 x_{2,i} + (-\beta_1 + -\beta_2) x_{3,i} + e_i$$

and calculate the group means as

$$\bar{y}_{j=1} = \boldsymbol{\mu} + \boldsymbol{\beta}_1$$
$$\bar{y}_{j=2} = \boldsymbol{\mu} + \boldsymbol{\beta}_2$$
$$\bar{y}_{j=3} = \boldsymbol{\mu} - (\boldsymbol{\beta}_1 + \boldsymbol{\beta}_2)$$

We would then define ${f X}$ and ${m eta}$ as

$$\mathbf{X} = \begin{bmatrix} 1 & 1 & 0 \\ \vdots & \vdots & \vdots \\ 1 & 1 & 0 \\ \hline 1 & 0 & 1 \\ \vdots & \vdots & \vdots \\ 1 & 0 & 1 \\ \hline 1 & -1 & -1 \\ \vdots & \vdots & \vdots \\ 1 & -1 & -1 \end{bmatrix} \quad \boldsymbol{\beta} = \begin{bmatrix} \boldsymbol{\mu} \\ \boldsymbol{\beta}_1 \\ \boldsymbol{\beta}_2 \end{bmatrix}$$

ANOVA

```
## empty design matrix
XX <- matrix(NA, nn*pp, pp)
## for mu
XX[i1,] <- matrix(c(1, 1, 0), nn, pp, byrow = TRUE)
## for beta_1
XX[i2,] <- matrix(c(1, 0, 1), nn, pp, byrow = TRUE)
## for beta_2
XX[i3,] <- matrix(c(1, -1, -1), nn, pp, byrow = TRUE)
## fit model & get parameters
Bvec <- coef(lm(yy ~ XX - 1))
names(Bvec) <- c("mu", "beta_1", "beta_2")
Bvec</pre>
```

mu beta_1 beta_2
26.761236 -7.141222 -1.112776

ANOVA

```
## mean of ration 1
Bvec["mu"] + Bvec["beta_1"]
## mean of ration 2
Bvec["mu"] + Bvec["beta_2"]
## mean of ration 3
Bvec["mu"] - (Bvec["beta 1"] + Bvec["beta 2"])
```

##	m	J
##	19.6200	1
##	m	ı
##	25.6484	б
##	m	l
##	35.01523	3

ANOVA

We could also fit our grand mean model after some simple algebra

ANOVA

fit anova with implicit grand mean
m2 <- lm((yy - mean(yy)) ~ ration - 1)
coef(m2)</pre>

ration_1 ration_2 ration_3
-7.141222 -1.112776 8.253998

ANOVA

do we recover our means?
coef(m2) + mean(yy)

ration_1 ration_2 ration_3
19.62001 25.64846 35.01523

coef(m1)

ration_1 ration_2 ration_3
19.62001 25.64846 35.01523

Comparing group means



ANOVA

What if we wanted to treat one group as a control or reference (eg, our low ration) and estimate the other effects relative to it?

$$y_i = \beta_1 x_{1,i} + (\beta_1 + \beta_2) x_{2,i} + (\beta_1 + \beta_3) x_{3,i} + e_i$$

such that

$$\bar{y}_{j=1} = \beta_1$$
$$\bar{y}_{j=2} = \beta_1 + \beta_2$$
$$\bar{y}_{j=3} = \beta_1 + \beta_3$$

We would define ${f X}$ and ${meta}$ as

$$\mathbf{X} = \begin{bmatrix} 1 & 0 & 0 \\ \vdots & \vdots & \vdots \\ 1 & 0 & 0 \\ \hline 1 & 1 & 0 \\ \vdots & \vdots & \vdots \\ 1 & 1 & 0 \\ \hline 1 & 0 & 1 \\ \vdots & \vdots & \vdots \\ 1 & 0 & 1 \end{bmatrix} \quad \boldsymbol{\beta} = \begin{bmatrix} \boldsymbol{\beta}_1 \\ \boldsymbol{\beta}_2 \\ \boldsymbol{\beta}_3 \end{bmatrix}$$

ANOVA

```
## empty design matrix
XX <- matrix(NA, nn*pp, pp)
## for beta_1
XX[i1,] <- matrix(c(1, 0, 0), nn, pp, byrow = TRUE)
## for beta_1 + beta_2
XX[i2,] <- matrix(c(1, 1, 0), nn, pp, byrow = TRUE)
## for beta_1 + beta_3
XX[i3,] <- matrix(c(1, 0, 1), nn, pp, byrow = TRUE)
## fit anova with implicit grand mean
Bvec <- coef(lm(yy ~ XX - 1))
names(Bvec) <- c("beta_1", "beta_2", "beta_3")
Bvec</pre>
```

beta_1 beta_2 beta_3
19.620014 6.028446 15.395221

ANOVA

```
## mean of ration 1
Bvec["beta_1"]
## mean of ration 2
Bvec["beta_1"] + Bvec["beta_2"]
## mean of ration 3
Bvec["beta_1"] + Bvec["beta_3"]
```

beta_1
19.62001
beta_1
25.64846
beta_1
35.01523

Comparing group means





Here is our model with the categorical effect of lineage & the continuous effect of ration

 $\operatorname{growth}_{i} = \alpha + \beta_{1,\operatorname{lineage}} + \beta_{2}\operatorname{ration}_{i} + \epsilon_{i}$

Dropping the global intercept & writing out the lineage effects yields

growth_i =
$$\beta_1 x_{1,i} + \beta_2 x_{2,i} + \beta_3 x_{3,i} + \beta_4 x_{4,i} + e_i$$

lineage

We would then define ${f X}$ and ${m eta}$ as

$$\mathbf{X} = \begin{bmatrix} 1 & 0 & 0 & r_1 \\ \vdots & \vdots & \vdots & \vdots \\ 1 & 0 & 0 & r_{j_1} \\ \hline 0 & 1 & 0 & r_{j_1+1} \\ \vdots & \vdots & \vdots & \vdots \\ 0 & 1 & 0 & r_{j_2+j_2} \\ \hline 0 & 0 & 1 & r_{j_1+j_2+1} \\ \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & 1 & r_n \end{bmatrix} \quad \boldsymbol{\beta} = \begin{bmatrix} \boldsymbol{\beta}_1 \\ \boldsymbol{\beta}_2 \\ \boldsymbol{\beta}_3 \\ \boldsymbol{\beta}_4 \end{bmatrix}$$

beta_1 beta_2 beta_3 beta_4
10.205959 15.286507 19.435551 1.950062



57/67

We have been building our design matrices by hand, but we could instead use

model.matrix() with factor()

factor(x) tells R to treat x as categorical

2 groups with 2 obs each
groups <- factor(c(1, 1, 2, 2))
inspect them
groups</pre>

[1] 1 1 2 2
Levels: 1 2

model.matrix(~ x) uses a right-hand side formula ~ x

create design matrix from `groups`
model.matrix(~ groups)

```
## (Intercept) groups2
## 1 1 0
## 2 1 0
## 3 1 1
## 4 1 1
## 4 1 1
## attr(,"assign")
## [1] 0 1
## attr(,"contrasts")
## attr(,"contrasts")$groups
## [1] "contr.treatment"
```

```
What if we don't use factor()?
```

```
## 2 groups with 2 obs each
groups <- c(1, 1, 2, 2)
## create design matrix from `groups`
model.matrix(~ groups)</pre>
```

```
## (Intercept) groups
## 1 1 1
## 2 1 1
## 3 1 2
## 4 1 2
## attr(,"assign")
## [1] 0 1
```

You can drop the intercept term with – 1

```
## 2 groups with 2 obs each
groups <- factor(c(1, 1, 2, 2))
## create design matrix from `groups`
model.matrix(~ groups - 1)</pre>
```

```
## groups1 groups2
## 1 1 0
## 2 1 0
## 3 0 1
## 4 0 1
## attr(,"assign")
## [1] 1 1
## attr(,"contrasts")
## attr(,"contrasts")$groups
## [1] "contr.treatment"
```

The names/categories are irrelevant for factor()

```
## 2 groups with 2 obs each
groups <- factor(c("ref", "ref", "exp", "exp"))
## create design matrix from `groups`
model.matrix(~ groups)</pre>
```

```
## (Intercept) groupsref
## 1 1 1
## 2 1 1
## 2 1 1
## 3 1 0
## 4 1 0
## attr(,"assign")
## [1] 0 1
## attr(,"contrasts")
## attr(,"contrasts")$groups
## [1] "contr.treatment"
```

R assigns factors in alphabetical order; the *reference* is first

```
## 2 groups with 2 obs each
groups <- factor(c("ref", "ref", "exp", "exp"))
## create design matrix from `groups`
model.matrix(~ groups)</pre>
```

```
## (Intercept) groupsref
## 1 1 1
## 2 1 1
## 2 1 1
## 3 1 0
## 4 1 0
## attr(,"assign")
## [1] 0 1
## attr(,"contrasts")
## attr(,"contrasts")$groups
## [1] "contr.treatment"
```

We can change the reference case with relevel()

```
## 2 groups with 2 obs each
groups <- relevel(groups, "ref")
## create design matrix from `groups`
model.matrix(~ groups)</pre>
```

```
##
    (Intercept) groupsexp
## 1
           1
                    0
## 2 1
                   0
## 3 1
                   1
## 4
    1
                   1
## attr(,"assign")
## [1] 0 1
## attr(,"contrasts")
## attr(,"contrasts")$groups
## [1] "contr.treatment"
```

We can add multiple factors with +

```
diet <- factor(c(1, 1, 2, 2))
sex <- factor(c("f", "m", "f", "m"))</pre>
model.matrix(~ diet + sex)
## (Intercept) diet2 sexm

    ##
    1
    0
    0

    ##
    2
    1
    0
    1

             1 0 1
## 3 1 1 0
## 4 1 1 1
## attr(,"assign")
## [1] 0 1 2
## attr(,"contrasts")
## attr(,"contrasts")$diet
## [1] "contr.treatment"
##
## attr(,"contrasts")$sex
## [1] "contr.treatment"
```

You can also extract the design matrix from a fitted model

```
## ANCOVA model from above
mod_fit <- lm(yy ~ XX - 1)
## get design matrix
mm <- model.matrix(mod_fit)
head(mm)</pre>
```

##		XXL1	XXL2	XXL3	XXRA
##	1	1	0	0	11.944444
##	2	1	0	0	3.835147
##	3	1	0	0	3.376075
##	4	1	0	0	4.112188
##	5	1	0	0	2.721664
##	6	1	0	0	1.779256