An Introduction to the R Statistical Computing Environment

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Outline

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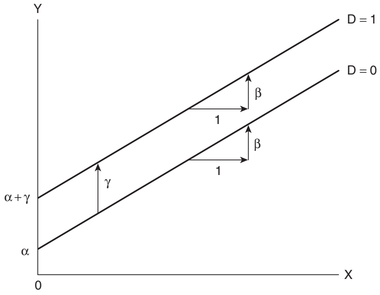

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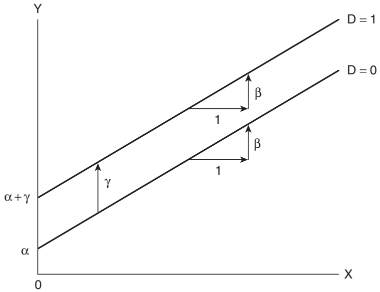

- In R notation with data in `Data`:

```
model <- lm(income ~ education
                + gender, data=Data).
```

- Different slopes for women and men ("different slopes for different folks") can be modelled by introducing an interaction regressor, the product of X and D, into the model:

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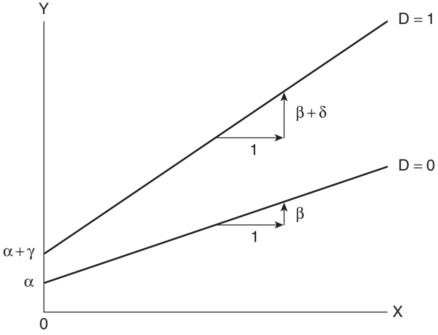

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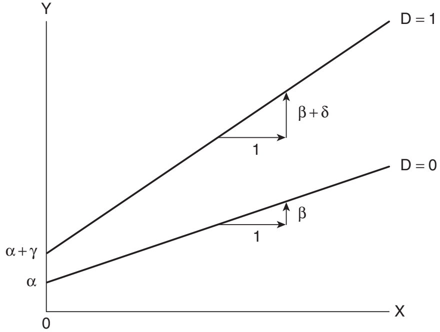

- In R (compact) notation:
`model <- lm (income ~ education*gender, data=Data).`

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- For example, for gender with levels female, male, and nonbinary, we can code two dummy regressors:

Gender	D_1	D_2
female	0	0
male	1	0
nonbinary	0	1

- Then we can fit the model

$$Y = \alpha + \beta X + \gamma_1 D_1 + \gamma_2 D_3 + \delta_1 (X \times D_1) + \delta_2 (X \times D_2) + \varepsilon$$

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- and

$$\begin{aligned}
\text{female} : E(Y) &= \alpha + \beta X + \gamma_1 \times 0 + \gamma_2 \times 0 + \delta_1 (X \times 0) + \delta_2 (X \times 0) \\
&= \alpha + \beta X \\
\text{male} : E(Y) &= \alpha + \beta X + \gamma_1 \times 1 + \gamma_2 \times 0 + \delta_1 (X \times 1) + \delta_2 (X \times 0) \\
&= (\alpha + \gamma_1) + (\beta + \delta_1) X \\
\text{nonbinary} : E(Y) &= \alpha + \beta X + \gamma_1 \times 0 + \gamma_2 \times 1 + \delta_1 (X \times 0) + \delta_2 (X \times 1) \\
&= (\alpha + \gamma_2) + (\beta + \delta_2) X
\end{aligned}$$

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- Thus, a main effect (e.g., `X`) is tested assuming that the interaction or interactions to which the main effect is marginal (e.g., `X:A`, `X:A:B`) are zero.
- For example, consider the model `y ~ a*b*c` or in longer form
  `y ~ 1 + a + b + c + a:b + a:c + b:c + a:b:c`.

- For Type-II tests of all terms, we implicitly fit the following models (all in longer form):

Model	*Formula*
1	`y ~ 1 + a + b + c + a:b + a:c + b:c + a:b:c`
2	`y ~ 1 + a + b + c + a:b + a:c + b:c`
3	`y ~ 1 + a + b + c + a:c + b:c`
4	`y ~ 1 + a + b + c + a:b + b:c`
5	`y ~ 1 + a + b + c + a:b + a:c`
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8	`y ~ 1 + a + b + c + a:c`
9	`y ~ 1 + a + c + a:c`
10	`y ~ 1 + a + b + c + a:b`
11	`y ~ 1 + a + b + a:b`

- Contrasting pairs of models by subtracting the regression sum of squares for the smaller model from that for the larger model produces the Type-II ANOVA table:

Term	*Models Contrasted*
a	$6 - 7$
b	$8 - 9$
c	$10 - 11$
a:b	$2 - 3$
a:c	$2 - 4$
b:c	$2 - 5$
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- The degrees of freedom for each term are the number of regressors used for that term.
- The estimated error variance used for the denominator of the F-tests comes from the largest model fit to the data, here Model 1, and the denominator degrees of freedom for F are the residual degrees of freedom for this model.

- `lm(formula, data, subset, weights, na.action, method = "qr", model = TRUE, x = FALSE, y = FALSE, qr = TRUE, singular.ok = TRUE, contrasts = NULL, offset, ...)`

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- Operators for the formula argument:

Expression	*Interpretation*	*Example*
A + B	include both A and B	income + education
A - B	exclude B from A	a*b*d - a:b:d
A:B	interaction of A and B	type:education
A*B	A + B + A:B	type*education
B %in% A	B nested within A	education %in% type
A/B	A + B %in% A	type/education
A^k	effects crossed to order k	(a + b + d)^2

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- `offset`: term added to the right-hand-side of the model with a fixed coefficient of 1.

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  - The diagonal entries h_j of $\mathbf{H}$ are the hat-values.
  - The hat-values are bounded between $1/n$ (if the model has an intercept, otherwise 0) and 1, and the average hat-values is $\overline{h} = p/n$.

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  - But because there are n studentized residuals, it's necessary to correct for simultaneous statistical inference—e.g., a Bonferroni correction, which multiplies the two-sided P-value for the t-test by n.

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  - The answer is $\text{dfbeta}_i = \mathbf{b} - \mathbf{b}_{(-i)} = (\mathbf{X}^T\mathbf{X})^{-1}\mathbf{x}_i E_i/(1-h_i)$, where $\mathbf{b}_{(-i)}$ is the vector of least-squares coefficients computed with the ith case deleted, and $\mathbf{x}_i$ is the ith row of $\mathbf{X}$ (written as a column vector).

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  - Because there are a lot $(n \times p)$ of dfbeta_{ij}, it's useful to summarize the p values for each case i. The most common such measure is *Cook's distance*:

$$D_i = \frac{\text{dfbeta}_i^T \mathbf{X}^T\mathbf{X}\ \text{dfbeta}_i}{pS_E^2} = \frac{(\widehat{\mathbf{y}} - \widehat{\mathbf{y}}_{(-i)})^T(\widehat{\mathbf{y}} - \widehat{\mathbf{y}}_{(-i)})}{pS_E^2} \approx \frac{E_{Ti}^2}{p} \times \frac{h_i}{1-h_i}$$
$$= \text{outlyingness} \times \text{leverage}$$

  where $\widehat{\mathbf{y}}_{(-i)}$ is the vector of fitted values computed when the ith case is removed.

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- For example, focusing on the coefficient B_1 of X_1 in the regression $Y = A + B_1X_1 + B_2X_2 + \cdots + B_kX_k + E$ (so $p = k + 1$):

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  - Following John Tukey, we say that $p > 1$ (e.g., X^2, X^3) is a transformation "up the ladder of powers" and $p < 1$ (e.g., $X^{1/2}$, $\log(X)$, $1/X$) is "down the ladder of powers."

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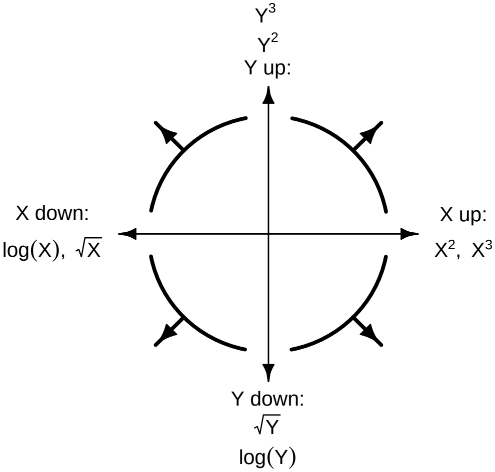

Outline

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   on which the expected value μ_i of Y_i depends.
3. A *link function* $g(\mu_i) = \eta_i$, which transforms the expectation of the response to the linear predictor. The inverse of the link function is called the *mean function*: $g^{-1}(\eta_i) = \mu_i$.

- In the following table, the logit, probit and complementary log-log links are for binomial or binary data:

Link	$\eta_i = g(\mu_i)$	$\mu_i = g^{-1}(\eta_i)$
identity	μ_i	η_i
log	$\log_e \mu_i$	e^{η_i}
inverse	μ_i^{-1}	η_i^{-1}
inverse-square	μ_i^{-2}	$\eta_i^{-1/2}$
square-root	$\sqrt{\mu_i}$	η_i^2
logit	$\log_e \dfrac{\mu_i}{1-\mu_i}$	$\dfrac{1}{1+e^{-\eta_i}}$
probit	$\Phi(\mu_i)$	$\Phi^{-1}(\eta_i)$
complementary log-log	$\log_e[-\log_e(1-\mu_i)]$	$1-\exp[-\exp(\eta_i)]$

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  - The response variable and regressors are given in a model `formula`.
  - `data`, `subset`, and `na.action` arguments determine the data on which the model is fit.
  - The additional `family` argument is used to specify a *family-generator function*, which may take other arguments, such as a link function.

- The following table gives family generators and default links:

Family	*Default Link*	*Range of* Y_i	$V(Y_i \mid \eta_i)$
`gaussian`	`identity`	$(-\infty, +\infty)$	ϕ
`binomial`	`logit`	$\frac{0, 1, \ldots, n_i}{n_i}$	$\mu_i(1-\mu_i)$
`poisson`	`log`	$0, 1, 2, \ldots$	μ_i
`Gamma`	`inverse`	$(0, \infty)$	$\phi\mu_i^2$
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- For distributions in the exponential families, the variance is a function of the mean and a dispersion parameter ϕ (fixed to 1 for the binomial and Poisson distributions).

- The following table shows the links available (✓) for each family in R, with the default link marked by ★:

	link							
family	identity	inverse	sqrt	1/mu^2	log	logit	probit	cloglog
gaussian	★	✓			✓			
binomial					✓	★	✓	✓
poisson	✓		✓		★			
Gamma	✓	★			✓			
inverse.gaussian	✓	✓		★	✓			
quasi	★	✓	✓	✓	✓	✓	✓	✓
quasibinomial						★	✓	✓
quasipoisson	✓		✓		★			

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quasi	★	✓	✓	✓	✓	✓	✓	✓
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- The quasi, quasibinomial, and quasipoisson family generators do not correspond to exponential families.

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  - For binomial data, the response may be
    - a two-column matrix, with the first column giving the count of successes and the second the count of failures for each binomial observation.
    - a vector giving the *proportion* of successes, while the binomial denominators (total counts or numbers of trials) are given by the `weights` argument to `glm()`.

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- The `clm()` function in the **ordinal** package fits a variety of models (including the proportional-odds model) to ordinal polytomous responses.

Outline

The Linear Mixed-Effects Model

- The *Laird-Ware form* of the linear mixed model:

$$
\begin{aligned}
Y_{ij} &= \beta_1 + \beta_2 X_{2ij} + \cdots + \beta_p X_{pij} + B_{1i} Z_{1ij} + \cdots + B_{qi} Z_{qij} + \varepsilon_{ij} \\
B_{ki} &\sim N(0, \psi_k^2), \mathrm{Cov}(B_{ki}, B_{k'i}) = \psi_{kk'} \\
& \quad B_{ki}, B_{k'i'} \text{ are independent for } i \neq i' \\
\varepsilon_{ij} &\sim N(0, \sigma^2 \lambda_{ijj}), \mathrm{Cov}(\varepsilon_{ij}, \varepsilon_{ij'}) = \sigma^2 \lambda_{ijj'} \\
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- where:
  - Y_{ij} is the value of the response variable for the jth of n_i observations in the ith of m groups or clusters.
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    - If the observations in a "group" represent longitudinal data on a single individual, then the structure of the λs may be specified to capture serial (i.e., over-time) dependencies among the errors.

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- There are also Bayesian approaches to modeling hierarchical and longitudinal data that offer certain advantages; see in particular the **rstan**, **rstanarm**, and **blme** packages.

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- Our interest in detecting differences in exercise histories between subjects and controls suggests the level-2 model

$$\alpha_{0i} = \gamma_{00} + \gamma_{01}\text{group}_i + \omega_{0i}$$
$$\alpha_{1i} = \gamma_{10} + \gamma_{11}\text{group}_i + \omega_{1i}$$

where group is a dummy variable coded 1 for subjects and 0 for controls.

- Substituting the level-2 model into the level-1 model produces

$$
\begin{aligned}
\text{log-exercise}_{ij} &= (\gamma_{00} + \gamma_{01}\text{group}_i + \omega_{0i}) + (\gamma_{10} + \gamma_{11}\text{group}_i + \omega_{1i})(\text{age}_{ij} - 8) + \varepsilon_{ij} \\
&= \gamma_{00} + \gamma_{01}\text{group}_i + \gamma_{10}(\text{age}_{ij} - 8) + \gamma_{11}\text{group}_i \times (\text{age}_{ij} - 8) \\
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A Mixed Model for the Blackmore Exercise Data

Laird-Ware form of the Model

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- in Laird-Ware form,

$$Y_{ij} = \beta_1 + \beta_2 X_{2ij} + \beta_3 X_{3ij} + \beta_4 X_{4ij} + \delta_{1i} + \delta_{2i} Z_{2ij} + \varepsilon_{ij}$$

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- Continuous first-order autoregressive process for the errors:

$$\text{Cor}(\varepsilon_{it}, \varepsilon_{i,t+s}) = \rho(s) = \phi^{|s|}$$

where the time-interval between observations, s, need not be an integer.

- Using lme() in the **nlme** package:

```
lme(log.exercise ~ I(age - 8)*group,
            random = ~ I(age - 8) | subject,
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A Mixed Model for the Blackmore Exercise Data

Specifying the Model in lme() and lmer()

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- Using `lmer()` in the **lme4** package, but without autocorrelated errors:

```
lmer(log.exercise ~ I(age - 8)*group + (I(age - 8) | subject),
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- A central goal of the data-oriented Tidyverse packages is to construct, modify, and maintain "tidy data"—rectangular data sets in which the rows represent cases and the columns represent variables.
  - Of course, the idea of a rectangular data set greatly antedates the Tidyverse and is incorporated in the standard R data frame.

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  8. **ggplot2**: A comprehensive alternative graphics system for R (to be discussed when we take up R graphics, and a package that is slightly out-of-place in the Tidyverse).

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Should You Commit to the Tidyverse?

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- Tidyverse tools often don't play well with non-Tidyverse tools.
  - For example, the **data.table** package implements a data frame alternative that is superior to tibbles for large data sets, but data.tables aren't well supported by Tidyverse functions.

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- For an interesting general critique of the Tidyverse (with which I don't entirely agree), see an essay by Norm Matloff at `https://github.com/matloff/TidyverseSkeptic`.

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- Setting the gradient to 0 produces nonlinear estimating equations for $\boldsymbol{\beta}$, which have to be solved iteratively, possibly using the information in the Hessian.

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  3. Step 2 is repeated until $\mathbf{b}_t$ is close enough to $\mathbf{b}_{t-1}$, at which point the MLE $\widehat{\boldsymbol{\beta}} \approx \mathbf{b}_t$. The estimated asymptotic covariance matrix of the coefficients is given by $\widehat{V}(\widehat{\boldsymbol{\beta}}) \approx (\mathbf{X}^T \mathbf{V}_t \mathbf{X})^{-1}$.

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    - Methods are searched from left to right, so if `mod` is produced by a call to `glm()`, and if `generic(mod)` is called, then methods are invoked in the order
      `generic(mod)` ⇒ `generic.glm(mod)` ⇒ `generic.lm(mod)` ⇒ `generic.default(mod)`
      and will fail if none of these three methods are available.

- Generic functions take the form:

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generic <- function(object, other, named, arguments, ...){
    UseMethod("generic")
}
```

where the ellipses (...) "soak up" additional arguments not named in the generic function that may be passed to specific methods when `generic()` is called.

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- For example, the R `summary()` function is defined as

```
summary <- function(object, ...){
    UseMethod("summary")
}
```

and `summary.lm()` is

```
summary.lm <- function (object, correlation=FALSE, symbolic.cor=FALSE, ...){
     etc.
}
```