An Introduction to the R Statistical Computing Environment

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ICPSR 2021

Outline

Outline

Linear Models in R

Review of Dummy-Variable Regression

- Defining a dummy-variable regressor for a dichotomous explanatory variable — e.g., gender in the regression of income Y on gender and education X.
- Let $D = 0$ for women and $D = 1$ for men.
- Then the additive dummy-regression model is

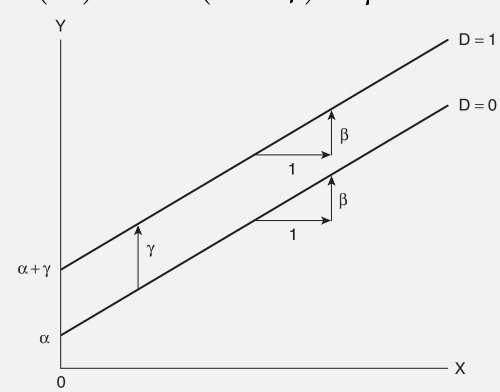
$$Y = \alpha + \beta X + \gamma D + \varepsilon$$

- So, for women (treating X as conditionally fixed)

$$\begin{aligned} Y &= \alpha + \beta X + \gamma \times 0 + \varepsilon \\ E(Y) &= \alpha + \beta X \end{aligned}$$

- And, for men

$$\begin{aligned} Y &= \alpha + \beta X + \gamma \times 1 + \varepsilon \\ E(Y) &= (\alpha + \gamma) + \beta X \end{aligned}$$



- 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:

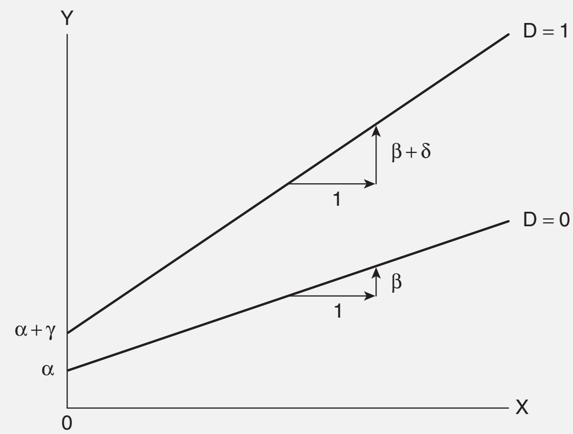
$$Y = \alpha + \beta X + \gamma D + \delta(X \times D) + \varepsilon$$

- Then, for women

$$\begin{aligned} Y &= \alpha + \beta X + \gamma \times 0 + \delta(X \times 0) + \varepsilon \\ E(Y) &= \alpha + \beta X \end{aligned}$$

- And, for men

$$\begin{aligned} Y &= \alpha + \beta X + \gamma \times 1 + \delta(X \times 1) + \varepsilon \\ E(Y) &= (\alpha + \gamma) + (\beta + \delta) X \end{aligned}$$



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

- Polytomous explanatory variables—i.e., factors with more than two levels—are handled by creating a set of dummy regressors, one fewer than the number of levels.
- 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

Linear Models in R

Review of Dummy-Variable Regression

- Then we can fit the model

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

- and

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

Linear Models in R

Type-II Tests for Linear (and Other) Models

- Type II tests are constructed in conformity to the *principle of marginality*: Each term in the model is tested assuming that its higher-order relatives are zero (and hence are ignored).
- 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`.

Linear Models in R

Type-II Tests for Linear (and Other) Models

- 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`
6	`y ~ 1 + a + b + c + b:c`
7	`y ~ 1 + b + c + b:c`
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`

Linear Models in R

Type-II Tests for Linear (and Other) Models

- 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`	$2 - 5$
`a:b:c`	$1 - 2$

- 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.

Linear Models in R

Arguments of the `lm()` Function

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

Linear Models in R

Arguments of the `lm()` Function

- `data`: A data frame containing the data for the model.
- `subset`:
  - a logical vector: `subset = gender == "F"`
  - a numeric vector of observation indices: `subset = 1:100`
  - a negative numeric vector with observations to be omitted: `subset = -c(6, 16)`
- `weights`: for weighted-least-squares regression
- `na.action`: name of a function to handle missing data; default given by the `na.action` option, initially `"na.omit"`
- `method`, `model`, `x`, `y`, `qr`, `singular.ok`: technical arguments
- `contrasts`: specify a list of contrasts for factors; e.g., `contrasts=list(partner.status=contr.sum, fcategory=contr.poly))`
- `offset`: term added to the right-hand-side of the model with a fixed coefficient of 1.

- Influence on the regression coefficients = leverage × outlyingness.
- *Hat-values* measure leverage.
  - The fitted linear regression model in matrix form is $\mathrm{y} = \mathrm{Xb} + \mathrm{e}$, where y is the $(n \times 1)$ response vector, X is the $(n \times p)$ model matrix, and $\mathrm{b} = (\mathrm{X}^T\mathrm{X})^{-1}\mathrm{X}^T\mathrm{y}$ is the $(p \times 1)$ vector of least squares coefficients.
  - The fitted values are then $\widehat{\mathrm{y}} = \mathrm{Xb} = \mathrm{X}(\mathrm{X}^T\mathrm{X})^{-1}\mathrm{X}^T\mathrm{y} = \mathrm{Hy}$, where the $(n \times n)$ *hat-matrix* is $\mathrm{H} = \mathrm{X}(\mathrm{X}^T\mathrm{X})^{-1}\mathrm{X}^T$.
  - The h_{ij} element of H gives the weight of Y_j in determining $\widehat{Y}_i$.
  - The H matrix is symmetric ($\mathrm{H} = \mathrm{H}^T$) and idempotent ($\mathrm{H}^2 = \mathrm{H}$), and it follows that the jth diagonal element of H, $h_j = h_{jj} = \sum_{i=1}^{n} h_{ij}^2$ summarizes the size of all of the elements in the jth column of of H and hence the leverage of the jth case in determining the fit.
  - The diagonal entries h_j of 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 $\overline{h} = p/n$.

- *Studentized residuals* measure outlyingness.
  - The studentized residuals are
$$E_{Ti} = \frac{E_i}{S_{E(-i)}\sqrt{1 - h_i}}$$
    where E_i is the ith element of the least-squares residuals vector e and $S_{E(-i)}$ is the standard deviation of the residuals when the regression is refit with the ith case removed.
  - If the model is correct, then each studentized residual is distributed at t with $n - p - 1$ degrees of freedom, providing a basis for an outlier test based on the the largest absolute studentized residual.
  - 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.

- Measuring influence on the regression coefficients with dfbeta and Cook's D:
  - The most direct measure is to refit the model without the ith case and see how the coefficients change.
  - 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).
  - 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.

- Added-variable plots visualize leverage, outlyingness, and influence on each regression coefficient, reducing the p-dimensional scatterplot of the data to a series of p two-dimensional scatterplots, one for each coefficient.
- 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 $p = k + 1$):
  - Regress Y on $X_2, \ldots, X_k$ (and an intercept), obtaining residuals $E^{(Y_1)}$ (i.e., what remains of Y when the effects of $X_2, \ldots, X_k$ are removed).
  - Regress X_1 on $X_2, \ldots, X_k$ (and an intercept), obtaining residuals $E^{(X_1)}$ (i.e., what remains of X_1 when the effects of $X_2, \ldots, X_k$ are removed).
  - plot $E^{(Y_1)}$ versus $E^{(X_1)}$.
- Repeat for each of $X_2, \ldots, X_k$ (and even, if desired, for the constant regressor, $X_0 = 1$).

Linear Models in R

Regression Diagnostics: Added-Variable (AV) Plots

- The AV plot for X_j has the following remarkable properties:
  - The slope of the least-squares line in the plot is the coefficient B_j of X_j in the multiple regression.
  - The residuals from this line are the same as the residuals E_i in the multiple regression.
  - The horizontal variation of X_j in the plot is its conditional variation holding the other Xs constant: $S^2_{X_j|\text{other } X\text{s}} = \sum E^{(X_j)^2}/(n-k)$.
  - Consequently, the standard error of B_j computed from the simple regression corresponding to the plot, $\text{SE}(B_j) = S_E/\sqrt{\sum E^{(X_j)^2}}$ is the same as the standard error of B_j from the multiple regression.

Linear Models in R

Regression Diagnostics: Component-Plus-Residuals (C+R) Plots

- Component-plus-Residuals plots are even a simpler way of reducing the p-dimensional scatterplot to a series of 2D plots:
  - Add the residuals from the full regression to the linear component representing X_1 to form the *partial residuals*: $E^{(1)} = B_1X_1 + E$.
  - Plot $E^{(1)}$ versus X_1, enhancing the graph with a scatterplot smoother (nonparametric regression line) to judge nonlinearity.
- By construction, the least-squares slope of the C+R plot for X_1 is B_1 from the multiple regression, and the residuals in the C+R plot are just the Es.
- Under certain reasonably general (but not bulletproof) circumstances, if the partial relationship between Y and X_1 is nonlinear but incorrectly modelled as linear, the nature of the nonlinearity will be apparent in the C+R plot for X_1.
- Repeat for each of $X_2, \ldots, X_k$.

Linear Models in R

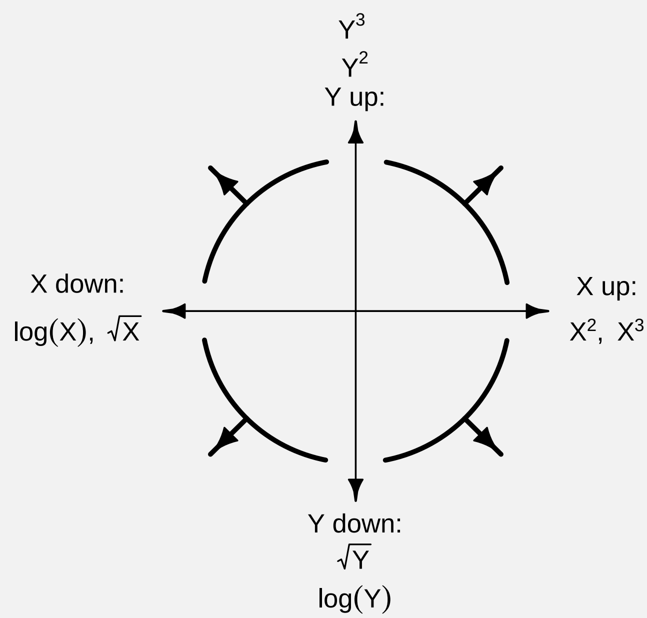
The Bulging Rule for Linearizing a Relationship

- It's often possible to linearize a nonlinear relationship between Y and X by transforming one or the other (or both) by a power transformation.
- By power transformations, I mean $X \rightarrow X^p$ or similarly for Y.
  - The power p may be positive or negative, and need not be a whole number.
  - For example, $X^{1/2} = \sqrt{X}$ and $X^{-1} = 1/X$.
  - $p = 1$ is no transformation: $X^1 = X$.
  - If $p = 0$, we use $\log(X)$.
  - 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."

Linear Models in R

The Bulging Rule for Linearizing a Relationship

- This approach works if
  1. The values of the variable to be transformed are all *positive*.
  2. The relationship between the variables is *monotone* (strictly increasing or decreasing).
  3. The relationship is *simple*, in the sense that the direction of curvature doesn't change.
  4. There are then only four patterns, summarized by Mosteller and Tukey's *bulging rule*:



Outline

Generalized Linear Models in R

Review of the Structure of GLMs

- A generalized linear model consists of three components:

1. A *random component*, specifying the conditional distribution of the response variable, Y_i, given the predictors. Traditionally, the random component is an exponential family — the normal (Gaussian), binomial, Poisson, gamma, or inverse-Gaussian.
2. A linear function of the regressors, called the *linear predictor*,

$$\eta_i = \alpha + \beta_1 X_{i1} + \cdots + \beta_k X_{ik}$$

   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*: $g^{-1}(\eta_i) = \mu_i$.

Generalized Linear Models in R

Review of the Structure of GLMs

- 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	$\log_e[-\log_e(1-\mu_i)]$	$1-\exp[-\exp(\eta_i)]$

Generalized Linear Models in R

Implementation of GLMs in R: The `glm()` Function

- Generalized linear models are fit with the `glm()` function. Most of the arguments of `glm()` are similar to those of `lm()`:
  - 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.

Generalized Linear Models in R

Implementation of GLMs in R: The `glm()` 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`	$(0, \infty)$	$\phi\mu_i^2$
`inverse.gaussian`	`1/mu^2`	$(0, \infty)$	$\phi\mu_i^3$

- 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).

Generalized Linear Models in R

Implementation of GLMs in R: The `glm()` Function

- 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	✓		✓		★			

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

- The response for a binomial GLM may be specified in several forms:
  - For binary data, the response may be
    - a variable or an R expression that evaluates to `0`s ('failure') and `1`s ('success').
    - a logical variable or expression, such as `voted == "yes"` (with `TRUE` representing success, and `FALSE` failure).
    - a factor (in which case the first category is taken to represent failure and the others success).
  - 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()`.

- Poisson generalized linear models are commonly used when the response variable is a count (Poisson regression) and for modeling associations in contingency tables (loglinear models). The two applications are formally equivalent.
- Poisson GLMs are fit in R using the `poisson` family generator with `glm()`.
- Overdispersed binomial and Poisson models may be fit via the `quasibinomial` and `quasipoisson` families.
- The `glm.nb()` function in the **MASS** package fits negative-binomial GLMs to count data.
- The `multinom()` function in the **nnet** package fits multinomial GLMs for nominal polytomous responses.
- The `polr()` function in the **MASS** package fits the proportional-odds logit model and the ordered probit model to ordinal polytomous responses.
- 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:

$$\begin{aligned}
Y_{ij} &= \beta_1 + \beta_2 X_{2ij} + \cdots + \beta_p X_{pij} + B_{1i} Z_{1ij} + \cdots + B_{qi} Z_{qij} + \varepsilon_{ij} \\
B_{ki} &\sim N(0, \psi_k^2), \mathrm{Cov}(B_{ki}, B_{k'i}) = \psi_{kk'} \\
& \quad B_{ki}, B_{k'i'} \text{ are independent for } i \neq i' \\
\varepsilon_{ij} &\sim N(0, \sigma^2 \lambda_{ijj}), \mathrm{Cov}(\varepsilon_{ij}, \varepsilon_{ij'}) = \sigma^2 \lambda_{ijj'} \\
& \quad \varepsilon_{ij}, \varepsilon_{i'j'} \text{ are independent for } i \neq i'
\end{aligned}$$

The Linear Mixed-Effects Model

- 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.
  - $\beta_1, \beta_2, \ldots, \beta_p$ are the fixed-effect coefficients, which are identical for all groups.
  - $X_{2ij}, \ldots, X_{pij}$ are the fixed-effect regressors for observation j in group i; there is also implicitly a constant regressor, $X_{1ij} = 1$.
  - $B_{1i}, \ldots, B_{qi}$ are the random-effect coefficients for group i, assumed to be multivariately normally distributed, independent of the random effects of other groups. The random effects, therefore, vary by group.
    - The B_{ik} are thought of as random variables, not as parameters, and are similar in this respect to the errors ε_{ij}.
  - $Z_{1ij}, \ldots, Z_{qij}$ are the random-effect regressors.
    - The Zs are almost always a subset of the Xs (and may include *all* of the Xs).
    - When there is a random intercept term, $Z_{1ij} = 1$.

The Linear Mixed-Effects Model

- The remaining parameters specify the variance-covariance components (don't get lost!):
  - ψ_k^2 are the variances and $\psi_{kk'}$ the covariances among the random effects, assumed to be constant across groups.
    - In some applications, the ψs are parametrized in terms of a smaller number of fundamental parameters.
  - ε_{ij} is the error for observation j in group i.
    - The errors for group i are assumed to be multivariately normally distributed, and independent of errors in other groups.
  - $\sigma^2 \lambda_{ijj'}$ are the covariances between errors in group i.
    - Generally, the $\lambda_{ijj'}$ are parametrized in terms of a few basic parameters, and their specific form depends upon context.
    - When observations are sampled independently within groups and are assumed to have constant error variance (as is typical in hierarchical models), $\lambda_{ijj} = 1$, $\lambda_{ijj'} = 0$ (for $j \neq j'$), and thus the only free parameter to estimate is the common error variance, σ^2.
    - 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.

Fitting Mixed Models in R
with the **nlme** and **lme4** packages

- In the **nlme** package (Pinheiro, Bates, DebRoy, and Sarkar):
  - `lme()`: linear mixed-effects models with nested random effects; can model serially correlated errors.
  - `nlme()`: nonlinear mixed-effects models.
- In the **lme4** package (Bates, Maechler, Bolker, and Walker):
  - `lmer()`: linear mixed-effects models with nested or crossed random effects; no facility (yet) for serially correlated errors.
  - `glmer()`: generalized-linear mixed-effects models.
- There are many other CRAN packages that fit a variety of mixed-effects models, perhaps most notably **glmmTMB** (see `https://bbolker.github.io/mixedmodels-misc/glmmFAQ.html`).
- There are also Bayesian approaches to modeling hierarchical and longitudinal data that offer certain advantages; see in particular the **rstan**, **rstanarm**, and **blme** packages.

A Mixed Model for the Blackmore Exercise Data
Longitudinal Model

- A level-1 model specifying a linear "growth curve" for log exercise for each subject:

$$\log\text{-exercise}_{ij} = \alpha_{0i} + \alpha_{1i}(\text{age}_{ij} - 8) + \varepsilon_{ij}$$

- 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.

A Mixed Model for the Blackmore Exercise Data

Laird-Ware form of the Model

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

$$\begin{aligned}\log\text{-exercise}_{ij} &= (\gamma_{00} + \gamma_{01}\text{group}_i + \omega_{0i}) + (\gamma_{10} + \gamma_{11}\text{group}_i + \omega_{1i})(\text{age}_{ij} - 8) + \varepsilon_{ij} \\ &= \gamma_{00} + \gamma_{01}\text{group}_i + \gamma_{10}(\text{age}_{ij} - 8) + \gamma_{11}\text{group}_i \times (\text{age}_{ij} - 8) \\ &\quad + \omega_{0i} + \omega_{1i}(\text{age}_{ij} - 8) + \varepsilon_{ij}\end{aligned}$$

- in Laird-Ware form,

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

- 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.

A Mixed Model for the Blackmore Exercise Data

Specifying the Model in `lme()` and `lmer()`

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

```
lme(log.exercise ~ I(age - 8)*group,
            random = ~ I(age - 8) | subject,
            correlation = corCAR1(form = ~ age |subject)
            data=Blackmoore)
```

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

```
lmer(log.exercise ~ I(age - 8)*group + (I(age - 8) | subject),
            data=Blackmoore)
```

Outline

Using the Tidyverse for Data Management

Overview of the Tidyverse

- The "Tidyverse" is an integrated set of R packages developed by Hadley Wickham and his collaborators at RStudio (see `https://www.tidyverse.org/`).
- The packages are meant to provide a straightforward way to import data into R and to manipulate the data.
- There are also Tidyverse tools for R programming and statistical graphics.
- 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.

Using the Tidyverse for Data Management

Core Tidyverse Packages

- There are eight "core" Tidyverse packages, which can be installed and loaded via the master **tidyverse** package:
  1. **readr**: Imports rectangular data sets from plain-text files.
  2. **tibble**: The specific implementation of rectangular data sets in the Tidyverse is called a "tibble," and tibble objects inherit from the `"data.frame"` class.
  3. **tidyr**: Provides functions to create and maintain rectangular data sets (e.g., to transform rectangular data sets between "wide" and "long" form).
  4. **dplyr**: Provides functions for data manipulation (e.g., adding variables to an existing data set).
  5. **stringr**: Provides functions for manipulating text (character-string) data (e.g., searching for text).
  6. **forcats**: Provides functions for manipulating R factors (e.g., changing the order of levels of a factor).
  7. **purrr**: Provides R programming tools (e.g., alternatives to iteration).
  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).

Using the Tidyverse for Data Management

Other Tidyverse Packages

- There are other Tidyverse packages, which can be installed and loaded separately, most notably:
  - **haven**: Imports data from other statistical packages.
  - **readxl**: Imports data from Excel files.
  - **lubridate**: For working with dates.
  - **magrittr**: The style of data manipulation encouraged by the developers of the Tidyverse makes extensive use of the "pipe" operator, %>%, which is provided by the **magritr** package.
    - **magrittr** also includes some other programming-oriented functions.
    - The pipe operator is supplied by several of the core Tidyverse packages.
    - Pipes can be used with standard R functions.

Using the Tidyverse for Data Management
Should You Commit to the Tidyverse?

- There are few, if any, Tidyverse functions that don't have close analogs in the standard R distribution, but the Tidyverse functions are more uniform and many people claim that they are easier to use (possibly because they're unfamiliar with standard R).
  - There are hundreds of functions in the core Tidyverse packages. It isn't obvious that it's easier to learn the Tidyverse than to learn standard R.
- There are both advantages and disadvantages to Tidyverse implementations of ideas.
  - For example, the `print()` method for tibbles is nicer than that for data frames (cf., the `brief()` function in the **car** package), but tibbles don't support row names.
- 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.

Using the Tidyverse for Data Management
Should You Commit to the Tidyverse?

- R is a programming language, and in many cases the simplest and most direct solution to a problem is to write a program.
  - Using the Tidyverse tools effectively requires some programming skills, and a beginner's time might be better spent learning more general basic R programming.
- 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`.

Outline

R Programming

MLE Estimation of the Binary Logit Models by Newton-Raphson

- The binary logit model is

$$\Pr(Y_i = 1) = \phi_i = \frac{1}{1 + exp(-\mathrm{x}_i^T \boldsymbol{\beta})}$$

where
  - X is the model matrix, with x_i^T as its ith row;
  - y is the response vector (containing 0s and 1s) with Y_i as its ith element;
  - $\boldsymbol{\beta}$ is the vector of logistic-regression parameters.

- The log-likelihood for the model is
$$\log_e L(\boldsymbol{\beta}) = \sum y_i \log_e \phi_i + (1 - y_i) \log_e (1 - \phi_i)$$
- The gradient (the vector of partial derivatives) of the log-likelihood with respect to the parameters is
$$\frac{\partial \log_e L}{\partial \boldsymbol{\beta}} = \sum (y_i - \phi_i) \mathrm{x}_i$$
- The Hessian (the matrix of second-order partial derivatives) of the log-likelihood is
$$\frac{\partial \log_e L}{\partial \boldsymbol{\beta} \partial \boldsymbol{\beta}^T} = \mathrm{X}^T \mathrm{V} \mathrm{X}$$
where $\mathrm{V} = \mathrm{diag}\{\phi_i(1 - \phi_i)\}$. The variance-covariance matrix of the estimated regression coefficients is the inverse of the Hessian.
- 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.

R Programming
MLE Estimation of the Binary Logit Models by Newton-Raphson

- Newton-Raphson is a general method for solving nonlinear equations iteratively.
- Here:
  1. Choose initial estimates of the regression coefficients, such as $\mathrm{b}_0 = 0$.
  2. At each iteration t, update the coefficients:
  $$\mathrm{b}_t = \mathrm{b}_{t-1} + (\mathrm{X}^T \mathrm{V}_{t-1} \mathrm{X})^{-1} \mathrm{X}^T (\mathrm{y} - \mathrm{p}_{t-1})$$
  where
     - $\mathrm{p}_{t-1} = \{1/[1 + \exp(-\mathrm{x}_i^T \mathrm{b}_{t-1})]\}$ is the vector of fitted response probabilities from the previous iteration.
     - $\mathrm{V}_{t-1} = \mathrm{diag}\{p_{i,t-1}(1 - p_{i,t-1})\}$.
  3. Step 2 is repeated until b_t is close enough to b_{t-1}, at which point the MLE $\widehat{\boldsymbol{\beta}} \approx \mathrm{b}_t$. The estimated asymptotic covariance matrix of the coefficients is given by $\widehat{V}(\widehat{\boldsymbol{\beta}}) \approx (\mathrm{X}^T \mathrm{V}_t \mathrm{X})^{-1}$.

- Three standard object-oriented programming systems in R: S3, S4, reference classes. Of these, the S3 object system is the one most commonly used in applications.
- How the S3 object system works:
  - Method dispatch of the generic function `generic()` for the object named `object`, which is of of class `"class"` (where ⇒ means "the interpreter looks for and dispatches"):
    `generic(object)` ⇒ `generic.class(object)` ⇒ `generic.default(object)`
    - For example, summarizing an object `mod` of class `"lm"`:
      `summary(mod)` ⇒ `summary.lm(mod)`
  - Objects can have more than one class, in which case the first applicable method is used.
    - For example, objects produced by `glm()` are of class `c("glm", "lm")` and therefore can *inherit* methods from class `"lm"`.
    - 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:

```
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.
- 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.
}
```