outline

- 1. Equivalence Studies
- 2. Missing Data
- 3. The Cross-Over Design
- 4. Clustered Binary Data
 - Hypothesis test
 - Regression Models: GEE model
- 5. Longitudinal Data Analysis

Equivalence Studies

Example Cancer

- Suppose we want to design a clinical trial to compare two surgical treatments for early-stage breast cancer.
 - simple mastectomy (standard treatment, yields a 5-year survival rate of 80%)
 - a more conservative tumor resection (experimental treatment)
- Acceptable: if it can be shown to be no more than 10% inferior to the standard treatment in terms of 5-year survival.
- How can we test whether the experimental treatment is acceptable?

Equivalence study

Remember

- studies in which the null hypothesis is that two treatments are equally effective vs. the alternative hypothesis that the effects of the two treatments are different from each other
- effectiveness in each treatment group is expressed as a binomial proportion.
- These types of studies, which constitute the majority of clinical trials, are referred to as superiority/noninferiority/equivalence studies.

Superiority/Non-inferiority test

- p_1 : the survival rate for the standard treatment
- p_2 : the survival rate for the experimental treatment
- Superiority test
 - Higher means better, $H_1: p_2 > p_1 + \delta, \delta > 0$
 - Higher means worse, $H_1: p_2 < p_1 \delta, \delta > 0$
- Non-inferiority test
 - Higher means better, $H_1: p_2 > p_1 \delta, \delta > 0$
 - Higher means worse, $H_1: p_2 < p_1 + \delta, \delta > 0$

Inference Based on CI Estimation

- The cancer example: $p_1 = 0.8$ (standard)
- Non-inferiority test

$$H_1: p_2 > p_1 - 0.1 = 0.7$$
 and $H_0: p_1 - p_2 \ge 0.1$

• Then $\frac{\hat{p}_1 - \hat{p}_2 - (p_1 - p_2)}{\sqrt{\hat{p}_1 \hat{q}_1 / n_1 + \hat{p}_2 \hat{q}_2 / n_2}} \sim N(0,1)$ and the rejection area is $\hat{p}_1 - \hat{p}_2 - (p_1 - p_2)$

$$\frac{\hat{p}_1 - \hat{p}_2 - (p_1 - p_2)}{\sqrt{\hat{p}_1 \hat{q}_1 / n_1 + \hat{p}_2 \hat{q}_2 / n_2}} < -z_{1-\alpha}$$

• A lower one-sided 100% imes (1 – lpha) CI for p_1-p_2

$$p_1 - p_2 < \hat{p}_1 - \hat{p}_2 + z_{1-\alpha} \sqrt{\hat{p}_1 \hat{q}_1 / n_1 + \hat{p}_2 \hat{q}_2 / n_2}$$

• If the upper bound of this one-sided CI does not exceed δ , where δ is a pre-specified threshold.

Cancer

Non-inferiority Example

- Suppose we have a clinical trial with 100 patients each on the standard treatment and on the experimental treatment.
 - 80% of patients on the standard treatment
 - 75% of the patients on the experimental treatment
- Can the treatments be considered equivalent if the threshold is 10%?

•
$$p_1 - p_2 < 0.80 - 0.75 + z_{0.95} \sqrt{0.80 \times \frac{0.20}{100} + 0.75 \times \frac{0.25}{100}} = 0.147$$

- The upper bound of the lower 95% CI exceeds 10%, so the treatments cannot be considered non-inferior.
 - although the observed survival rates are only 5% apart, the underlying rates may differ by as much as 15%

Sample-Size Estimation (Non-inferiority)

1. Assume the experimental treatment sample size (n_2) is k times as large as the standard treatment sample size (n_1)

$$n_2 = kn_1$$

1. Want to establish equivalence with a probability $1 - \beta$. That is,

$$\Pr\left(\hat{p}_1 - \hat{p}_2 + z_{1-\alpha} \sqrt{\frac{\hat{p}_1 \hat{q}_1}{n} + \frac{\hat{p}_2 \hat{q}_2}{n_2}} \le \delta\right) = 1 - \beta$$

So we require

$$- n_1 = \frac{(p_1 q_1 + p_2 q_2/k)(z_{1-\alpha} + z_{1-\beta})^2}{[\delta - (p_1 - p_2)]^2}$$
 subjects in group 1

 $-n_2=kn_1$ subjects in group 2

Cancer

Revisited

- Estimate the required sample size for the study if
- we want a probability of 80% for establishing equivalence

$$-1 - \beta = 0.80$$

II. the sample sizes are the same in the two groups,

$$n_1 = n_2$$
, $k = 1$

III. the underlying 5-year survival rate in both groups is 80%

$$- p_1 = p_2 = 0.80, q_1 = q_2 = 0.20$$

IV. the threshold for equivalence is 10%

$$-\delta = 0.10$$

$$n_1 = \frac{0.80 \times 0.20 \times 2(z_{0.95} + z_{0.80})^2}{0.10^2} = 197.6 = n_2$$

Missing data

Multiple imputation

Introduction

- As you can see from your project data, most epidemiologic and clinical studies have missing (or incomplete) data, for many different reasons.
- Can not do multivariate analyses?
 - such as multiple regression or multiple logistic regression
- Easy solution:
 - Delete it and use the complete data to analysis.
- Work?
 - Small amount: little bias, so OK
 - Nontrivial ($\geq 10\%$) or nonrandom missing: large bias, so NO

Example Aging

- Determine the longitudinal course of aging and to identify risk factors that affect subsequent mortality
- A multiple logistic regression analysis
 - 2341 elderly participants ages 71–103 in 1988–1989
 - predict mortality through 1991

missing for 550 elderly participants

who were either unwilling or unable to perform the test.

- predictor variables:
 - $-x_1 = age(yrs)$
 - $-x_2 = \frac{\sec(\text{coded as 1 if male and 2 if female})}{2}$
 - $-x_3$ = physical-performance score (a 13-item scale from 0 to 12)
 - $-x_4$ = selfassessed health score (a scale from 1 to 4: excellent to poor)

Descriptive statistics Aging

Descriptive statistics for 2341 older residents of East Boston interviewed in 1988–1989

Completed the physical-performance evaluation

	Y	es	no		
Dead by 12/31/1991	No	Yes	No	Yes	
n	1527	264	416	134	
Age, median (IQR) ^a	77 (74-81)	78 (74–84)	78 (74–83)	85 (78–90)	
Male, %	32.0	45.1	30.3	47.0	
Physical performance median (IQR)	8 (5-10)	6 (2-8)			
Self-assessed health median (IQR)	2 (2–3)	3 (2–3)	2 (2–3)	3 (2–3)	

Analysis with complete data Aging

the logistic-regression analyses for the 1791 elderly participants with complete data

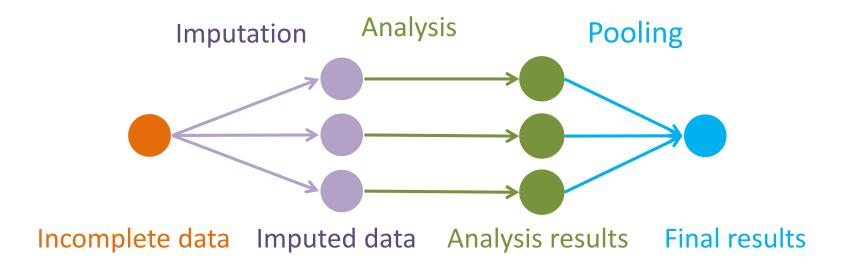
	$\widehat{oldsymbol{eta}}$	$sd(\widehat{oldsymbol{eta}})$	z value	p-value
Intercept	-4.76	1.17		
Age	0.033	0.013	2.538	0.011
Male	0.92	0.15	6.133	<0.001
Self-assessed health	0.38	0.095	4.000	< 0.001
Physical performance	-0.14	0.023	-6.087	<0.001

But, whether excluding these people affected the estimates of the regression parameters?

If yes, how to incorporate participants with missing data into the analysis?

Multiple imputation

- Imputation is defined roughly as the estimation of a missing variable (or variables) as a function of other covariates that are present, including the outcome.
- Multiple imputation is a Monte Carlo technique in which the missing values are replaced by m>1 simulated versions, where m is typically small (e.g. 3-10, m=3 in the figure).



Procedure(I)

- 1. Covariates: x_1, \dots, x_k
 - $-x_1, \dots, x_{k-1}$ are complete (n subjects);
 - $-x_k$ is available for N_{obs} subjects and is missing for N_{mis} subjects A binary outcome variable: y
- 2. Run a multiple regression analysis of x_k on x_1, \dots, x_{k-1} and y based on the complete data

$$x_k = \alpha + \gamma_1 x_1 + \dots + \gamma_{k-1} x_{k-1} + \delta y + \varepsilon$$

3. For $i=1,\ldots,N_{mis}$ subjects with missing data on x_k , calculate an estimated value for x_k , denoted by $x_{i,k,1}$ for ith subject

$$\widehat{x_k} = \widehat{\alpha} + \widehat{\gamma_1} x_1 + \dots + \widehat{\gamma_{k-1}} x_{k-1} + \widehat{\delta} y$$

- Two source of bias compiled in $\widehat{x_k}$: estimation bias of $\widehat{\alpha}$, $\widehat{\gamma_1}$, ..., $\widehat{\gamma_{k-1}}$, $\widehat{\delta}$, and the residual $e = x_k \widehat{x_k}$)
- Estimated value $x_{i,k,1} = \xi(\hat{\alpha}) + \xi(\hat{\gamma}_1)x_1 + \dots + \xi(\hat{\gamma}_{k-1})x_{k-1} + \xi(\hat{\delta})y + \xi \cdot MSE$, where $\xi(X)$ indicates a monte carlo sample representing X and ξ represents N(0,1)

Procedure(II)

4. Run a logistic regression

$$\ln \frac{p}{1-p} = \alpha + \beta_1 x_1 + \dots + \beta_k x_k$$

- 5. Repeat steps 3 and 4 for m-1 additional imputations
- 6. The estimates from the m separate imputations are then combined into an overall estimate for β_i

$$\hat{\beta}_j = \sum_{q=1}^m \hat{\beta}_{j,q} / m$$

and an overall variance given by

$$Var(\hat{\beta}_j) = \sum_{q=1}^m \frac{Var(\hat{\beta}_{j,q})}{m} + \left[\frac{(m+1)}{m}\right] \sum_{q=1}^m \frac{(\hat{\beta}_{j,q} - \hat{\beta}_j)^2}{m-1}$$

Rubin, D. B. (2004). *Multiple imputation for nonresponse in surveys*. New York: Wiley.

Revisited

Summary of linear-regression model predicting physical-performance score, and 5 draws of these regression parameters

Aging

			5 Drawn values of parameters			
Variable	Estimate (SE)	1	2	3	4	5
Age (per year)	-0.22 (0.013)	-0.23	-0.23	-0.23	-0.21	-0.22
Male gender	1.18 (0.15)	1.21	1.08	1.29	1.25	1.22
Self-assessed health	-1.38 (0.089)	-1.33	-1.43	-1.24	-1.43	-1.35
Dead by 1991	-1.30 (0.20)	-1.12	-1.47	-1.37	-1.60	-1.05
Intercept	27.2 (1.1)	27.6	27.7	27.5	26.3	27.2

Overall R2 0.30; Root MSE 2.88

Table 13.42 Comparison of effects of variables on the risk of death from alternative models; shown are logistic-regression parameters (standard errors)

		Analytic method			
	Complete case	No physical performance	Multiple imputation	Indicator method	
n (deaths)	1791 (264)	2341 (398)	2341 (398)	2341 (398)	
Age	0.033 (0.013)	0.088 (0.009)	0.057 (0.011)	0.068 (0.01)	
Male	0.92 (0.15)	0.82 (0.12)	1.00 (0.14)	0.92 (0.12)	
Self-assessed health	0.38 (0.095)	0.60 (0.073)	0.39 (0.087)	0.46 (0.076)	
Physical performance	-0.14 (0.023)	_	-0.15 (0.024)	-0.12(0.022)	
Intercept	-4.76 (1.17)	-10.41 (0.79)	-6.60 (1.04)	-7.42 (0.92)	
Indicator of missing performance				-0.47 (0.13)	

^{*}The indicator method assigns the average performance score (6.8) to those with missing values and includes an indicator variable for this group.

The Cross-Over Design

What is a cross-over design?

A cross-over design is a type of randomized clinical trial

	First period	washout period	Second period
	Group A		Group B
participant randomized	Group B		Group A

Some definition

- A washout period in a cross-over design is a period between active drug periods, during which subjects receive no study medication.
- A carry-over effect in a cross-over design is when the effects of one or both study medications taken during the first active drug period have a residual biological effect during the second active drug period.

Example Sports Medicine

- a cross-over design: comparing Motrin vs. placebo for the treatment of tennis elbow.
- Each participant
- was randomized to receive either Motrin (group A) or placebo (group B) for a 3-week period.
- had a 2-week washout period during which they received no study medication.
- was then "crossed-over" for a second 3-week period to receive the opposite study medication from that initially received.
- How should we compare the efficacy of Motrin vs. placebo?

Assessment of Overall Treatment Effects

- x_{i1} : score of the *i*th patient in group A in the first period x_{i2} : its score in group B in the second period
- y_{i1} : score of the *i*th patient going to group B in the first period y_{i2} : its score going to group B in the second period
- Paired –data method

$$d_{1i} = x_{i1} - x_{i2}, d_{2i} = y_{i2} - y_{i1}$$
 Then $(d_{1i}, i = 1, 2, ... n_1; d_{2i}, i = 1, 2, ... n_2) \sim F$ with mean Δ
$$\overline{d_1} = \sum_{i=1}^{n_1} d_{1i} / n_1, \overline{d_2} = \sum_{i=1}^{n_2} d_{2i} / n_2$$

$$\overline{d} = (\overline{d_1} + \overline{d_2}) / 2$$

$$H_0: \Delta = 0 \ vs. H_1: \Delta \neq 0$$
 (for the details, see page 668-669)

Assessment of Carry-Over Effects

- Assume that $\bar{x}_i = (x_{i1} + x_{i2})/2 \sim N(\mu_1, \sigma^2)$ and $\bar{y}_i = (y_{i1} + y_{i2})/2 \sim N(\mu_2, \sigma^2)$
- To test H_0 : $\mu_1 = \mu_2$ vs. H_1 : $\mu_1 \neq \mu_2$
- The test statistic

$$t = \frac{\bar{x} - \bar{y}}{\sqrt{s^2 \left(\frac{1}{n_1} + \frac{1}{n_2}\right)}}$$

Where

$$\bar{\bar{x}} = \frac{\sum \bar{x_i}}{n_1}, \bar{\bar{y}} = \frac{\sum \bar{y_i}}{n_2},$$

and

$$s^{2} = \frac{(n_{1}-1)s_{1}^{2} + (n_{2}-1)s_{2}^{2}}{n_{1}+n_{2}-2},$$

$$s_{1}^{2} = \sum_{i=1}^{n_{1}} (\bar{x}_{i} - \bar{\bar{x}})^{2} / (n_{1}-1), s_{2}^{2} = \sum_{i=1}^{n_{2}} (\bar{y}_{i} - \bar{\bar{y}})^{2} / (n_{2}-1)$$

Discussion

- What can we do if we identify a significant carry-over effect?
- In this case, the second-period data are not useful to us because they provide a biased estimate of treatment effects
- We can use an ordinary two-sample t test for independent samples based on the first-period data.
- This test usually has less power than the cross-over efficacy test, or requires a greater sample size to achieve a given level of power

Sample-Size Estimation

- A major advantage of cross-over studies is that they usually require many fewer subjects than the usual randomized clinical trials (which have only 1 period), if no carry-over effect is present.
- Use the cross-over efficacy test given before, we have

$$n = \frac{\sigma_d^2 (z_{1-\alpha/2} + z_{1-\beta})^2}{2\Delta^2}$$

- σ_d^2 = variance of difference scores
- only applicable if no carry-over effects are present.

Clustered Binary Data

Correlated binary data

Example (Dependent samples)

- Rowe et al. [26] reported on a clinical trial of topically applied 3% vidarbine vs. placebo in treating recurrent herpes labialis.
 - the characteristics of 53 lesions observed on 31 patients receiving vidarbine
 - the characteristics of 69 lesions observed on 39 patients receiving placebo.
- A question of interest is whether the proportion of lesions showing significant shrinkage in the two groups is the same after 7 days.
- The two-sample test for the comparison of binomial proportions is not appropriate here because
 - dependencies in response among lesions observed on the same patient.

Notation

		# of lesions	# of success	Prob. estimate
Group 1	Patient 1	m_{11}	a_{11}	$\hat{p}_{11} = a_{11}/m_{11}$
_	2	m_{12}	a_{12}	$\hat{p}_{12} = a_{12}/m_{12}$
_	•••	•••		
	n_1	m_{1n_1}	a_{1n_1}	$\hat{p}_{1n_1} = a_{1n_1}/m_{1n_1}$
		M_1	A_1	$\hat{p}_1 = A_1/M_1 = \sum_{j=1}^{n_i} m_{1j} \hat{p}_{1j}/M_1$
Group 2	Patient 1	m_{11}	a_{11}	$\hat{p}_{11} = a_{11}/m_{11}$
_	2	m_{12}	a_{12}	$\hat{p}_{12} = a_{12}/m_{12}$
_				
	n_1	m_{1n_1}	a_{1n_1}	$\hat{p}_{1n_1} = a_{1n_1}/m_{1n_1}$
		M_2	A_2	$\hat{p}_2 = A_2/M_2$

$$N = n_1 + n_2$$
, $M = M_1 + M_2$

Intraclass correlation coefficient

- An estimate of the degree of clustering within individuals/patients is given by the intra-class correlation ρ_I for clustered binary data.
- Definition: the correlation ρ_I between two replicates from the same subject, i.e., between y_{ij} and y_{il} , where y_{ij} is the j-th record of the i-th subject.
- If y_{ij} follows a one-way random-effect ANOVA model,

$$\rho_I = \frac{\sigma_A^2}{\sigma_A^2 + \sigma^2}$$

It can be estimated by

$$\hat{\rho}_I = \max(\frac{\widehat{\sigma_A}^2}{\widehat{\sigma_A}^2 + \widehat{\sigma}^2}, 0) = \max(\frac{MSB - MSW}{MSB + (n_0 - 1)MSW}, 0)$$
(refer to page 6 in lecture 8)

the degree of clustering

- Take each individual/patient as a group in the random-effect ANOVA model, where $y_{ijk} \sim B(1, p_{ij})$ indicates whether or not the k-th lesion shrinks of the j-th patient in the i-th group
- Then

- Within SS=
$$\sum_{i=1}^{2} \sum_{j=1}^{n_1} \sum_{k=1}^{m_{ij}} (y_{ijk} - \hat{p}_{ij})^2 = \dots = \sum_{i=1}^{2} \sum_{j=1}^{n_1} a_{ij} (1 - \hat{p}_{ij})$$

- Between SS= $\sum_{i=1}^{2} \{\sum_{j=1}^{n_1} m_{ij} (\hat{p}_{ij} \hat{p}_i)^2 \}$
- Let MSB = Between SS/(N-2), MSW = Within SS/(M-N)
- The estimate of intra-class correlation is

$$\hat{\rho} = (MSB - MSW)/[MSB + (m_A - 1)MSW]$$

where
$$m_A = \left[M - \sum_{i=1}^{2} \left(\sum_{j=1}^{n_i} m_{ij}^2 / M_i \right) \right] / (N-2)$$

design effect

The clustering correction factor in group i may be defined as

$$C_i = \sum_{j=1}^{n_i} m_{ij} C_{ij}/M_i$$
 where $C_{ij} = 1 + (m_{ij} - 1)\hat{\rho}$ effect

- Note:
 - if the $\hat{\rho}=0$, then no clustering is present and $C_i=1,\ i=1,2.$
 - If the $\hat{\rho} > 0$, then the $C_i > 1$, i = 1,2.
- The design effects in the two samples (C_1, C_2) are used as correction factors to modify the standard test statistic comparing two binomial proportions (Equation 10.3) for clustering effects.

Hypothesis Testing

- To test $H_0: p_1 = p_2$ vs. $H_1: p_1 \neq p_2$
- p_i : the underlying success rate among observations in group i
- The test statistic is

factors

$$z = \left[|\hat{p}_1 - \hat{p}_2| - \left(\frac{c_1}{2M_1} + \frac{c_2}{2M_2} \right) \right] / \sqrt{\hat{p}\hat{q}(C_1)M_1 + C_2/M_2}$$

Remember: Two-Sample Test for Binomial Proportions

$$z = \left[|\hat{p}_1 - \hat{p}_2| - \left(\frac{1}{2M_1} + \frac{1}{2M_2} \right) \right] / \sqrt{\hat{p}\hat{q}(1/M_1 + 1/M_2)}$$

• Only be used if $M_i \hat{p} \hat{q} / C_i \ge 0.5$ for i = 1, 2.

Regression Models for Clustered Binary Data

- We have considered a comparison of two binomial proportions where the units of observation are not independent.
- However, we often would like to consider one or more additional covariates in our modeling.
- For this purpose, we wish to extend logistic regression methods to allow for correlation between subunits within the same cluster.
- A technique called generalized estimating equations (GEE) can perform this type of analysis

What is GEE?

 GEE (Liang and Zeger, 1986) provide a method of inference for a wide variety of models when responses are correlated

- Linear regression (for continuous outcomes)
- Logistic regression (for binary outcomes)
- Poisson regression (for outcomes that are counts)
- Proportional odds (for ordinal categorical outcomes)

Contd.

- GEE are an analysis method, not models in and of themselves
 - You specify a model that you'd like to fit using GEE
 - Model is specified through
 - 1. A link function that relates the mean response to the regression equation
 - "link = logit" for logistic regression
 - "link = log" for Poisson regression
 - 2. An assumed distribution for the response, although distributional assumptions not really strong
 - "binomial" for logistic regression
 - "poisson" for Poisson regression
 - A working correlation matrix (more on this in the next slide)

Working correlation matrix

Exchabgeable

$$\begin{pmatrix}
1 & \rho & \rho & \rho \\
\rho & 1 & \rho & \rho \\
\rho & \rho & 1 & \rho \\
\rho & \rho & \rho & 1
\end{pmatrix}$$

m-dependent 🗻

$$\begin{pmatrix} 1 & \rho & \rho & \rho \\ \rho & 1 & \rho & \rho \\ \rho & \rho & 1 & \rho \\ \rho & \rho & \rho & 1 \end{pmatrix} \qquad \begin{pmatrix} 1 & \rho_1 & \rho_2 & \rho_3 \\ \rho_1 & 1 & \rho_1 & \rho_2 \\ \rho_2 & \rho_1 & 1 & \rho_1 \\ \rho_3 & \rho_2 & \rho_1 & 1 \end{pmatrix}^{\mu}$$

Unstructured

$$egin{pmatrix} 1 &
ho_1 &
ho_2 &
ho_3 \
ho_1 & 1 &
ho_4 &
ho_5 \
ho_2 &
ho_4 & 1 &
ho_6 \
ho_3 &
ho_5 &
ho_6 & 1 \end{pmatrix}$$

Autoregressive.

$$\begin{pmatrix}
1 & \rho_1 & \rho_2 & \rho_3 \\
\rho_1 & 1 & \rho_4 & \rho_5 \\
\rho_2 & \rho_4 & 1 & \rho_6 \\
\rho_3 & \rho_5 & \rho_6 & 1
\end{pmatrix}
\begin{pmatrix}
1 & \rho & \rho^2 & \rho^3 \\
\rho & 1 & \rho & \rho^2 \\
\rho^2 & \rho & 1 & \rho \\
\rho^3 & \rho^2 & \rho & 1
\end{pmatrix}$$

GEE logistic model

• y_{ij} : outcome for the jth subunit in the ith cluster

$$= \begin{cases} 1, & \text{with probability } p_{ij} \\ 0, & \text{with probability } q_{ij} = 1 - p_{ij} \end{cases}$$

- $x_{ij1}, ..., x_{ijk}$ be a set of covariates for the *j*th subunit in the *i*th cluster.
- a model allows for the correlation between outcomes for multiple subunits in the same cluster.

$$\log \operatorname{it}(p_{ij}) = \ln \frac{p_{ij}}{1 - p_{ij}} = \alpha + \beta_1 x_{ij1} + \dots + \beta_k x_{ijk}$$
 where $\operatorname{corr}(p_{ij}, p_{ik}) = \rho$. compound symmetry or

• where $corr(p_{ij}, p_{ik}) = \rho$. compound symmetry or exchangeable correlation structure

Longitudinal Data Analysis

Introduction

- An important application of clustered data methods is in longitudinal data analysis
 - each subject provides repeated measures over time
 - the goal: assess the effect of covariates on the rate of change over time.
- A clinical trial was performed among subjects with retinitis pigmentosa (RP) to compare the rate of decline of ERG (electro-retinogram) amplitude over time among 4 treatment groups.
- How should we compare the rate of decline among the 4 treatment groups?

Example Ophthalmology

- 1. The ERG is an objective measure of the electrical activity in the retina.
 - In normals, the average ERG is about 350 μ V.
 - In RP patients, it declines over time and is often <10 μV and sometimes <1 μV, after which total blindness often occurs.
- 2. Subjects were randomized to either
 - group 1 = 15,000 IU of vitamin A per day,
 - group 2 = 400 IU of vitamin E per day,
 - group 3 = 15,000 IU of vitamin A and 400 IU of vitamin E per day,
 - group 4 = placebo
- 3. were followed annually for 4–6 years.

Longitudinal Data Analysis

$$y_{it} = \alpha + \sum_{j=1}^{3} \beta_j x_{ij} + \gamma t + \sum_{j=1}^{3} \delta_j x_{ij} t + e_{it}$$

- $y_{it} = \ln(ERG \text{ amplitude})$ for the *i*th subject at time t
- $x_{ij} = I$ (the ith subject is in treatment group j)
- ϵ_{it} = error term which is assumed to be normally distributed with mean = 0 and variance = σ^2
 - But over time are not assumed to be independent
 - exchangeable or compound symmetry correlation structure: $corr(e_{it_1}, e_{it_2}) = \rho \neq 0$
 - reasonable for the above relatively short-term clinical trial

Statistical methods

- Statistical methods for longitudinal data
 - Univariate and Multivariate Analysis of Variance
 - 2. generalized estimation equation(GEE)
 - 3. Mixed-effect regression model(MRM)
- See more in
 - 1. http://www.uic.edu/classes/bstt/bstt513/
 - 2. http://tigger.uic.edu/~hedeker/long.html
 - 3. http://www.ats.ucla.edu/stat/r/examples/alda/ch2.htm