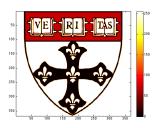
## BIO 226, Spring 2015: Lab 2

### Using the MIXED procedure in SAS

Instructor: Brent Coull TA: Fei Li

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## Background

We will use the MIXED procedure in SAS to model the blood lead levels in the treated group of the 'Treatment of Lead-Exposed Children' (TLC) dataset.

- Exposure to lead is associated with deficits in cognitive ability.
- Children with high lead levels can be treated with injections which generally require hospitalization.



## Background

- In this study, investigators are interested in assessing a new agent, succimer, which can be given orally.
- Blood lead levels were measured at baseline, and after 1, 4 and 6 weeks of follow-up.

In the analysis that follows, we first profile the blood lead levels over time in the treated (succimer) group. And then explore the placebo group before examining the full dataset.

### Read in Dataset

Use the following code to read-in the dataset and print the first few observations:

```
DATA lead:
  INFILE 'D:\BIO226\tlc.txt';
  INPUT id trmt $ v1 v2 v3 v4;
  RUN:
PROC PRINT DATA=lead (obs=5);
  RUN:
                       y1
Obs
       id
              trmt
                      30.8
                              26.9
                                       25.8
                                               23.8
                              14.8
                                      19.5
                                               21.0
                      26.5
                      25.8
                              23.0
                                      19.1
                                               23.2
                      24.7
                              24.5
                                       22.0
                                               22.5
                               2.8
                                        3.2
                      20.4
```

Note that P corresponds to the placebo and A corresponds to 'succimer' treatment.

### Read in Dataset - continued

Since our focus is on the 'succimer' group, we will need to subset these observations from the rest of the data. Use the following code to do the subsetting and then print the first few observations:

```
DATA lead2:
 SET lead;
 IF trmt = 'A';
 RUN:
PROC PRINT DATA=lead2 (obs=5);
 RUN:
Obs
             trmt
                    26.5
                             14.8
                                             21.0
                    25.8
                            23.0
                                  19.1
                                             23.2
                    20.4
                                             9.4
                    20.4
                              5.4
                                              11.9
                    24.8
                             23.1
                                     24 6
```

### SAS Sidenote

- To obtain the subsetted data, we use another DATA step.
- Within any DATA step, the SET statement allows you to access an existing SAS dataset.
- Within any DATA step, the IF statement allows us to keep the observations matching the given criteria.
- Within any DATA step, the DATA statement specifies the name of the new dataset. In the code on the previous slide, we named the new dataset (only subjects with 'succimer' treatment) lead2 rather than overwrite the original dataset. (In case we need to access the original information again.)

## Initial Thoughts on Data

Here the data are in "multivariate" (wide) form and must be transformed to "univariate" (long) form in order to use PROC MIXED.

The "multivariate" form allows us to examine the "profile" of blood lead levels over time. To do this, we calculate the empirical mean lead levels at each of the four time points to get a rough idea of the trend over time.

### Means Over Time

```
PROC MEANS DATA = lead2;
VAR y1-y4;
RUN:
```

Variable	N	Mean	Std Dev	Minimum	Maximum
y1	50	26.5400000	5.0209358	19.7000000	41.1000000
у2	50	13.5220000	7.6724870	2.8000000	39.0000000
у3	50	15.5140000	7.8522065	3.0000000	40.4000000
y4	50	20.7620000	9.2463316	4.1000000	63.9000000

Note that we could also calculate mean lead levels at each timepoint if the data is in "univariate" form using the BY command.

- Are there any apparent differences in the mean blood levels over time?
- Does the variability appear to be constant over time?

## Variance/Covariance Structure

To obtain a covariance or correlation matrix for within subject outcomes, use PROC CORR:

```
PROC CORR cov noprob nosimple data=lead2;
 VAR y1-y4;
 RUN:
Covariance Matrix, DF = 49
        v1
                   y2
                              y3
                                         γ4
     25.20972
                                      22 98542
                15.46542 15.13800
    15.46547
                58.86705 44.02907
                                      35.96595
v3
    15.13800
                44.02907 61.65714
                                      33.02197
     22.98547
                35.96595
                           33.02197
                                      85 49464
```

NOPROB - Suppresses *p*-values NOSIMPLE - Suppresses descriptive statistics

### "Multivariate" to "Univariate" form

We entered the data in "multivariate" form (one line per subject), but in order to use PROC MIXED we need the "univariate" form (one line per observation). The "multivariate" form for the first two subjects looks like:

```
id y1 y2 y3 y4
1 26.5 14.8 19.5 21.0
2 25.8 23.0 19.1 23.2
```

The "univariate" form for the first two subjects becomes:

```
id y
1 26.5
1 14.8
1 19.5
1 21.0
2 25.8
2 23.0
2 19.1
2 23.2
```

### "Multivariate" to "Univariate" form - continued

Note that there is no longer an obvious way to distinguish among the four values of blood lead levels for each subject. To keep track of the time, we generate two new variables:

- 1 t, that indicates the occasion of measurement.
- **2** time, that indicates the number of weeks elapsed since the baseline.

To obtain the "univariate" form, we use another DATA step. Within this new DATA step, we will include statements to create  $\mathbf{y}$ ,  $\mathbf{t}$ , and  $\mathbf{time}$ .

### "Multivariate" to "Univariate" form - continued

To transform from "multivariate" (one line per subject) to "univariate" form (one line per observation) we use:

```
Obs
             trmt
                      v1
                     26.5
                             14.8 19.5
                                               21.0
                     25.8
                             23.0
                                      19.1
DATA lead3:
 SET lead2;
 y=y1; time=0; t=1; OUTPUT;
 v=v2; time=1; t=2; OUTPUT;
 y=y3; time=4; t=3; OUTPUT;
 y=y4; time=6; t=4; OUTPUT;
 DROP y1-y4;
 RUN:
PROC PRINT DATA=lead3 (obs=5);
 RUN:
Obs
             trmt
                     26.5
                    14.8
                    19.5
                     21.0
                     25.8
```

### "Multivariate" Dataset

#### Role of variable t in this dataset:

- Essential for the REPEATED option in PROC MIXED when time is specified as a continuous variable
- Keeps track of the order of repeated measures
- If values are missing, t establishes placement in covariance matrix

Obs	id	trmt	У	time	t
1	2	A	26.5	0	1
2	2	A	14.8	1	2
4	2	A	21.0	6	4
5	3	A	25.8	0	1

#### Role of variable time in this dataset:

- Keeps record of actual time of measurement
- Used as an explanatory variable in the regression model (can be categorical or continuous)

### Visualization of Data

To obtain trajectory plots for each individual, use PROC GPLOT:

```
PROC GPLOT DATA = lead3;

SYMBOL1 interpol=join value=triangle;

SYMBOL2 interpol=join value=triangle;

SYMBOL3 interpol=join value=triangle;

SYMBOL4 interpol=join value=triangle;

SYMBOL5 interpol=join value=triangle;

PLOT y*time=id;

RUN;
```

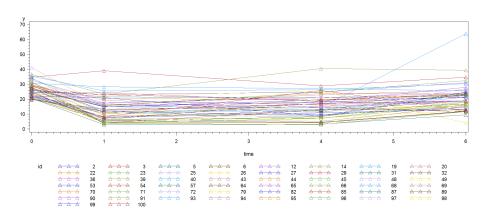
INTERPOL=JOIN connects data points with straight lines.

VALUE a plot symbol for the data points

SYMBOLn will rotate through 5 colors

the "=id" in the PLOT statement tells SAS to rotate through the different colors based on id

### Visualization of Data



### Structure of PROC MIXED

Now the data are in the correct format for PROC MIXED. The following code can be used to model lead level as a function of time. This is also called the "saturated" model because the number of parameters in the model equals the the number of unique means contained in the data (one for each time point).

```
PROC MIXED DATA=lead3;
CLASS id t time;
MODEL y = time / SOLUTION CHISQ;
REPEATED t / TYPE=UN SUBJECT=id R;
RUN;
```

### Additional Notes on PROC MIXED

```
PROC MIXED DATA=lead3;
CLASS id t time;
MODEL y = time / SOLUTION CHISQ;
REPEATED t / TYPE=UN SUBJECT=id R;
RUN:
```

- Parameter estimation SAS uses the REML method by default.
- CLASS statement:
  - 1 Must appear before MODEL statement.
  - Variables specified here will be treated as categorical.
  - 3 Generates appropriate design variables (e.g. dummy variables) when they appear in the model. (similar to the i.variable in STATA).
  - To specify subjects within the REPEATED statement, id must be included in the CLASS statement.
  - 5 To be used in the REPEATED statement, t must be in the CLASS statement.
  - To be included in the model as a categorical variable, time must be in the CLASS statement, otherwise time will be treated as continuous.

### Additional Notes on PROC MIXED - continued

```
PROC MIXED DATA=lead3;
CLASS id t time;
MODEL y = time / SOLUTION CHISQ;
REPEATED t / TYPE=UN SUBJECT=id R;
RUN;
```

- MODEL statement
  - Specifies form of the model
  - 2 SOLUTION displays parameter estimates, standard errors...
- REPEATED statement
  - 1 Specify variable that keeps track of the order of repeated measures
  - 2 TYPE option specifies assumed form of covariance matrix
  - 3 SUBJECT specifies variable that denotes independent units of observation
  - 4 R option displays estimated covariance matrix for individual subject
- SAS Online Documentation
  - 1 http://support.sas.com/onlinedoc/913/docMainpage.jsp
  - 2 SAS/STAT and Base SAS are commonly used sections
  - 3 Google "proc mixed sas" usually the first in the list



## Output from PROC MIXED

## The Mixed Procedure Model Information

Data Set WORK.LEAD3
Dependent Variable y
Covariance Structure Unstructured
Subject Effect id
Estimation Method REML
Residual Variance Method None
Fixed Effects SE Method Model-Based
Degrees of Freedom Method Between-Within

#### Class Level Information

Class	Levels	Values
id	50	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50
t	4	1 2 3 4
time	4	0 1 4 6

mai		

Covariance Param	eters 10
Columns in X	5
Columns in Z	0
Subjects	50
Max Obs Per Sub	ect 4

#### Number of Observations

Number	of	${\tt Observations}$	Read	200
Number	of	Observations	Used	200
Number	οf	Observations	Not Head	0

#### Estimated R Matrix for id 1

Row	Col1	Col2	Col3	Col4
1	25.2098	15.4654	15.1380	22.9854
2	15.4654	58.8671	44.0291	35.9660
3	15.1380	44.0291	61.6571	33.0220
4	22.9854	35.9660	33.0220	85.4946

#### Covariance Parameter Estimates

oo var rance	I di diic cci	LD 0 I m d 0 C D
Cov Parm	Subject	Estimate
UN(1,1)	id	25.2098
UN(2,1)	id	15.4654
UN(2,2)	id	58.8671
UN(3,1)	id	15.1380
UN(3,2)	id	44.0291
UN(3,3)	id	61.6571
UN(4,1)	id	22.9854
UN(4,2)	id	35.9660
UN(4,3)	id	33.0220
UN(4,4)	id	85.4946

```
Fit Statistics
              -2 Res Log Likelihood
                                        1280.3
              AIC (smaller is better)
                                         1300.3
              AICC (smaller is better)
                                        1301.5
              BIC (smaller is better)
                                         1319.5
                 Null Model Likelihood Ratio Test
                        Chi-Square Pr > ChiSq
                            86.73
                                         < .0001
                    Solution for Fixed Effects
                            Standard
Effect time Estimate
                       Error DF t Value Pr > |t|
Intercept
            20.7620 1.3076 49 15.88
                                        <.0001
time
           5.7780 1.1378 49 5.08 <.0001
          -7.2400 1.2036 49 -6.02
                                        <.0001
time
                              49 -4.12
        4 -5.2480 1.2736
                                           0.0001
time
time
                  Type 3 Tests of Fixed Effects
       Nıım
             Den
```

163.72 54.57

DF

49

Effect

time

< .0001

< .0001

Chi-Square F Value Pr > ChiSq Pr > F

## Changing the reference group in an analysis

What if you want to change the model slightly so that the lowest level of time is the reference group (instead of the highest level)? Use the following code:

```
DATA lead4;
SET lead3;
IF time=0 THEN timecat=11;
IF time=1 THEN timecat=1;
IF time=4 THEN timecat=4;
IF time=6 THEN timecat=6;
RUN;

PROC MIXED DATA=lead4;
CLASS id t timecat;
MODEL y = timecat / SOLUTION CHISQ;
REPEATED t / TYPE=um SUBJECT=id R;
RUN:
```

Solution	for Fixed	d Effects				
			Standard			
Effect	timecat	Estimate	Error	DF	t Value	Pr >  t
Intercept		26.5400	0.7101	49	37.38	<.0001
timecat	1	-13.0180	1.0310	49	-12.63	<.0001
timecat	4	-11.0260	1.0639	49	-10.36	<.0001
timecat	6	-5.7780	1.1378	49	-5.08	<.0001
timecat	11	0				

#### Type 3 Tests of Fixed Effects

	Num	Den				
Effect	DF	DF	Chi-Square	F Value	Pr > ChiSq	Pr > F
timecat	3	49	163.72	54.57	<.0001	<.0001

## Changing the reference group in an analysis - continued

Alternatively, you can make use of the ORDER option in the PROC MIXED statement (like we did in Lab 1!).

```
PROC SORT DATA=lead3;
BY id DESCENDING time;
RUN;
PROC MIXED DATA=lead3 ORDER=DATA;
CLASS id time t;
MODEL y = time / SOLUTION CHISQ;
REPEATED t / TYPE=UN SUBJECT=id R;
RUN;
```

## Fitting a model using a linear trend in time (continuous)

What if you believe that lead levels decrease **linearly** with time? By removing time from the CLASS statement, we tell SAS that time is no longer a categorical covariate, but should be considered a continuous covariate. To model time linearly, we fit the model:

```
PROC MIXED DATA=lead3 METHOD = ML;
CLASS id t;
MODEL y = time / SOLUTION CHISQ;
REPEATED t / TYPE=UN SUBJECT=id R;
RUN;
```

Select output from the model is shown below:

Fit Statistics -2 Log Likelihood 1357.4					
Solution for Fixed Effects Standard					
Effect	Estimate	Error	DF	t Value	Pr >  t
Intercept	24.1376	0.6731	49	35.86	<.0001
time	-0.4823	0.1490	49	-3.24	0.0022

## Fitting a model using a linear trend in time (categorical)

Let's compare with the model we previously considered when time was treated as a categorical variable, rather than continuous.

```
PROC MIXED DATA=lead3 METHOD = ML;
CLASS id t time;
MODEL y = time / SOLUTION CHISQ;
REPEATED t / TYPE=UN SUBJECT=id R;
RUN;
```

Select output from the model is shown below:

	Fit Statis	tics			
-2 Log Likelihood			128	6.5	
	Solution for F	ixed Effects			
		Standard			
	Estimate	Error	DF	t Value	Pr >  t
ept	20.7620	1.2945	49	16.04	<.0001
0	5.7780	1.1264	49	5.13	<.0001
1	-7.2400	1.1915	49	-6.08	<.0001
4	-5.2480	1.2608	49	-4.16	0.0001
6	0				
	0 1 4	-2 Log Likeliho  Solution for F  Estimate 20.7620 0 5.7780 1 -7.2400 4 -5.2480	-2 Log Likelihood  Solution for Fixed Effects Standard Estimate Error 20.7620 1.2945 0 5.7780 1.1264 1 -7.2400 1.1915 4 -5.2480 1.2608	-2 Log Likelihood 128  Solution for Fixed Effects Standard Estimate Error DF 20.7620 1.2945 49 0 5.7780 1.1264 49 1 -7.2400 1.1915 49 4 -5.2480 1.2608 49	-2 Log Likelihood 1286.5  Solution for Fixed Effects Standard Estimate Error DF t Value ppt 20.7620 1.2945 49 16.04 0 5.7780 1.1264 49 5.13 1 -7.2400 1.1915 49 -6.08 4 -5.2480 1.2608 49 -4.16

### **Nested Models**

We have two competing models. One is a full model where the outcome at each time point is estimated separately, and the other reduced model is one where we assume that the outcome changes linearly with continuous time.

**1** 
$$E[lead_{ij}] = \beta_0^c + \beta_1^c I(time_{ij} = 0) + \beta_2^c I(time_{ij} = 1) + \beta_3^c I(time_{ij} = 4)$$

$$2 \quad E[lead_{ij}] = \beta_0 + \beta_1 time_{ij}$$

These two models are nested. Why?

### **Nested Models**

**1** 
$$E[lead_{ij}] = \beta_0^c + \beta_1^c I(time_{ij} = 0) + \beta_2^c I(time_{ij} = 1) + \beta_3^c I(time_{ij} = 4)$$

$$2 \quad E[lead_{ij}] = \beta_0 + \beta_1 time_{ij}$$

at time 0 
$$E[lead] = \beta_0^c + \beta_1^c = \beta_0$$
  
at time 1  $E[lead] = \beta_0^c + \beta_2^c = \beta_0 + \beta_1$   
at time 4  $E[lead] = \beta_0^c + \beta_3^c = \beta_0 + 4\beta_1$   
at time 6  $E[lead] = \beta_0^c = \beta_0 + 6\beta_1$ 

Then if we choose

$$\beta_0^c = \beta_0 + 6\beta_1$$
$$\beta_1^c = -6\beta_1$$
$$\beta_2^c = 5\beta_1$$

$$\beta_2^c = -5\beta_1$$

$$\beta_3^c = -2\beta_1$$

we see that model 2 is a special case of model 1. Model 2 is nested in model 1.

## Testing linear effect of time

To test whether the relationship between time and lead levels is linear or not, we can perform a likelihood ratio test with 2 degrees of freedom. For nested models, the likelihood ratio test statistic is:

$$\chi_p^2 = 2(\log \hat{L}_{\textit{full}} - \log \hat{L}_{\textit{reduced}}) = (-2\log \hat{L}_{\textit{reduced}}) - (-2\log \hat{L}_{\textit{full}}).$$

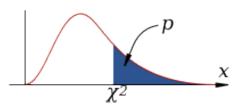
Under the null hypothesis that the reduced model is an adequate fit for the data, this test statistic is asymptotically chi-square distributed with p degrees of freedom. Our test has 2 degrees of freedom since the number of parameters in the reduced (linear) model is two less than the number of parameters in the full (saturated) model.

Our test statistics is  $\chi^2_2=1357.4-1286.5=70.9$ . The corresponding p-value is less than 0.001, and we conclude that the saturated model is a better fit. Since we perform a likelihood ratio test, we must specify METHOD = ML. Why?

## Obtaining chi-square p-values

To get p-values, use the SDF function in a DATA step. The SDF function calculates upper-tail probabilities for a specified distribution.

```
DATA pvalues;
chsq = SDF('chisquare',70.9,2);
RUN;
PROC PRINT DATA=pvalues;
RUN;
Obs chsq
1 4.0203E-16
```

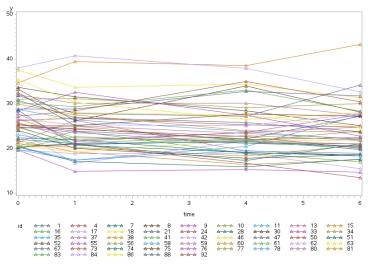


## Placebo Group: Data subset

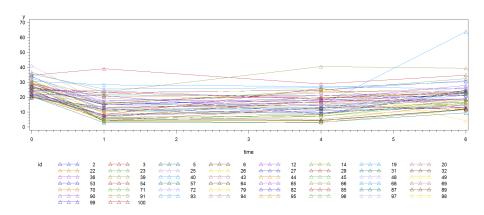
Consider examining only the 'placebo' group now. Let's subset the original data to get only those subjects who received 'placebo.' To conserve our DATA steps, let's also simultaneously get the data in long form.

```
DATA lead4;
 SET lead:
 IF trmt = 'P':
 y=y1; time=0; t=1; OUTPUT;
 y=y2; time=1; t=2; OUTPUT;
 v=v3: time=4: t=3: OUTPUT:
 v=v4: time=6: t=4: OUTPUT:
 DROP v1-v4;
 RUN:
PROC PRINT DATA=lead4 (obs=5);
 RUN;
Obs
       id
             trmt
                              time
                     30.8
                    26.9
 3
                    25.8
                    23.8
                     24.7
```

### Placebo Profiles



### Reminder: Succimer Profiles



## Fitting a model with linear trend in time for Placebo Group

Now let's examine the effect of time (treated linearly) on mean lead levels.

```
PROC MIXED DATA=lead4;
CLASS id t;
MODEL y = time / SOLUTION CHISQ;
REPEATED t / TYPE=UN SUBJECT=id R;
RUN;
```

#### Select output from the model is shown below:

#### Compare to the treatment group:

### Full Dataset

Might be more meaningful to a fit one model instead of two. We can assess the effect of treatment on mean blood level and see if treatment modifies time. Consider the model

$$E[lead_{ij}] = \beta_0 + \beta_1 time_{ij} + \beta_2 treatment_{ij} + \beta_3 time_{ij} \times treatment_{ij}.$$

A note on time: in the treatment group, we rejected the test of linearity for time. This might make us question using time linearly for the full dataset (and for the analysis of the placebo group above). We certainly could and should test for linearity here. However in a moment we will add an interaction in. So for the sake of demonstration, let's keep time linear.

### Reformat Full Dataset

We need to get the original data into the long format. Similar to before, we reshape the data using

```
DATA lead5;
 SET lead;
 y=y1; time=0; t=1; OUTPUT;
 y=y2; time=1; t=2; OUTPUT;
 y=y3; time=4; t=3; OUTPUT;
 v=v4: time=6: t=4: OUTPUT:
 DROP y1-y4;
 RUN;
PROC PRINT DATA=lead3 (obs=5):
 RUN;
          trmt
         P
                 30.8
         P 26.9
                25.8
                 23.8
                 26.5
```

### Interaction Model

Back to our model,

$$\textit{E[lead}_{\textit{ij}}] = \beta_{0} + \beta_{1} \textit{time}_{\textit{ij}} + \beta_{2} \textit{treatment}_{\textit{ij}} + \beta_{3} \textit{time}_{\textit{ij}} \times \textit{treatment}_{\textit{ij}},$$

Recall from lecture that adding this interaction creates, in essence, a different intercept and slope for each group. Observe:

■ Placebo Group Mean Model, treatment<sub>ij</sub> = 0

$$E[lead_{ij}] = \beta_0 + \beta_1 time_{ij}$$

■ Succimer Group Mean Model, *treatment*<sub>ij</sub> = 1

$$E[lead_{ij}] = \beta_0 + \beta_1 time_{ij} + \beta_2 + \beta_3 time_{ij}$$
  
$$E[lead_{ij}] = (\beta_0 + \beta_2) + (\beta_1 + \beta_3) time_{ij}$$

### Fit the Interaction Model

Modifying the code from Slide 34 allows us to run this model. Just include trmt in the class statement and trmt time\*trmt in the model line:

```
PROC MIXED DATA=lead5;
CLASS id t trmt;
MODEL y = time trmt time*trmt / SOLUTION CHISQ;
REPEATED t / TYPE=UN SUBJECT=id R;
RUN;
```

Select output from the model is shown below:

Standard						
Effect	trmt	Estimate	Error	DF	t-Value	Pr >  t
Intercept		26.0395	0.6939	98	37.52	<.0001
time		-0.3687	0.1223	98	-3.01	0.0033
trmt	A	-1.9394	0.9814	98	-1.98	0.0509
trmt	P	0				
time*trmt	A	-0.1695	0.1730	98	-0.98	0.3296
time*trmt	P	0				

The main effect of treatment is no longer significant. What about the interaction?

# Questions?