

Lecture 22

1. Longitudinal models for mean and correlation
2. Correlation matrix and covariance matrix; compound symmetry
3. Proc Mixed: repeated measures
4. Proc Mixed: random effects

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Longitudinal data: example 1

Family income data: total family income, expenditures, debt status for 50 families in two groups (*A* and *B*), annual records from 1990–1995.

Obs	family_ id	income	year	expenses	debt	cohort
1	1	66483	1990	49804	no	A
2	1	69146	1991	65634	no	A
3	1	74643	1992	61820	no	A
4	1	79783	1993	68387	no	A
5	1	81710	1994	85504	yes	A
6	1	86143	1995	75640	no	A
7	2	17510	1990	21609	yes	B
8	2	19484	1992	18180	no	B
9	2	20979	1993	22985	yes	B
10	2	21268	1994	11097	no	B
11	2	22998	1995	21768	no	B

(Example data adapted from UCLA Academic Technology Services, www.ats.ucla.edu/stat/)

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Longitudinal data: example 2

Alzheimer's disease trial. Alzheimer's disease is a progressive incurable deterioration of intellect and memory. A clinical trial compared lecithin (dietary supplement) against placebo, both given as daily for 4 months; 22 patients in lecithin group, 25 in placebo group.

Participant took a memory test at baseline (first visit), and end of each month. Score is number of words recalled from a list, so higher scores are better.

idno	lecithin	score1	score2	score3	score4	score5
1	0	20	15	14	13	13
2	0	14	12	12	10	10
3	0	7	5	5	6	5
4	0	6	10	9	8	7

(Source: Der and Everitt, Ch. 11)

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Longitudinal data model

Model has two parts:

- mean function $y_{ink} = \text{group}_i + \text{time}_j + (\text{group} * \text{time})_{ij} + \varepsilon_{ink}$
- covariance matrix for errors ε_{ij} , containing within-subject correlations

mean function: predicted “average” response at each time = LSmeans

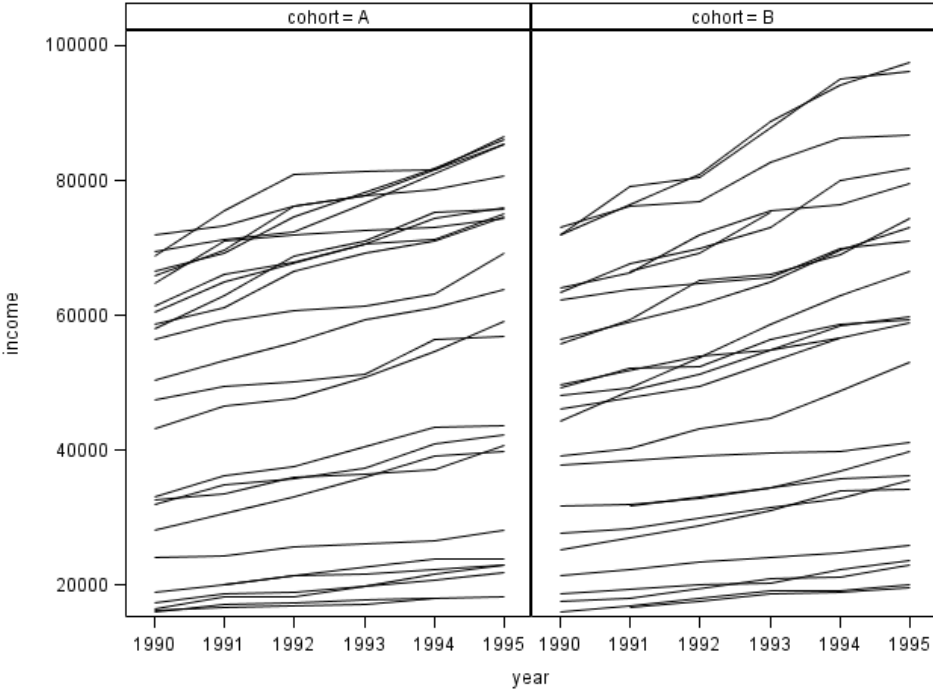
Plot of mean function: interaction plot of LSmeans group * time

This was main interest before, and is still main interest.

LSmeans usually *not* affected by correlation.

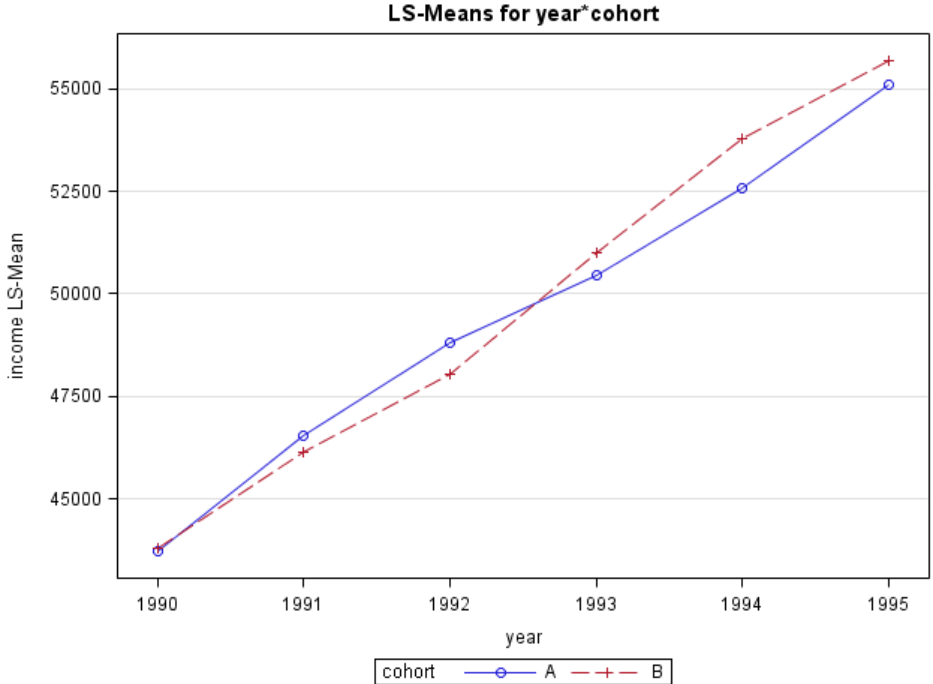
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Family income data: plots of individual families by group.

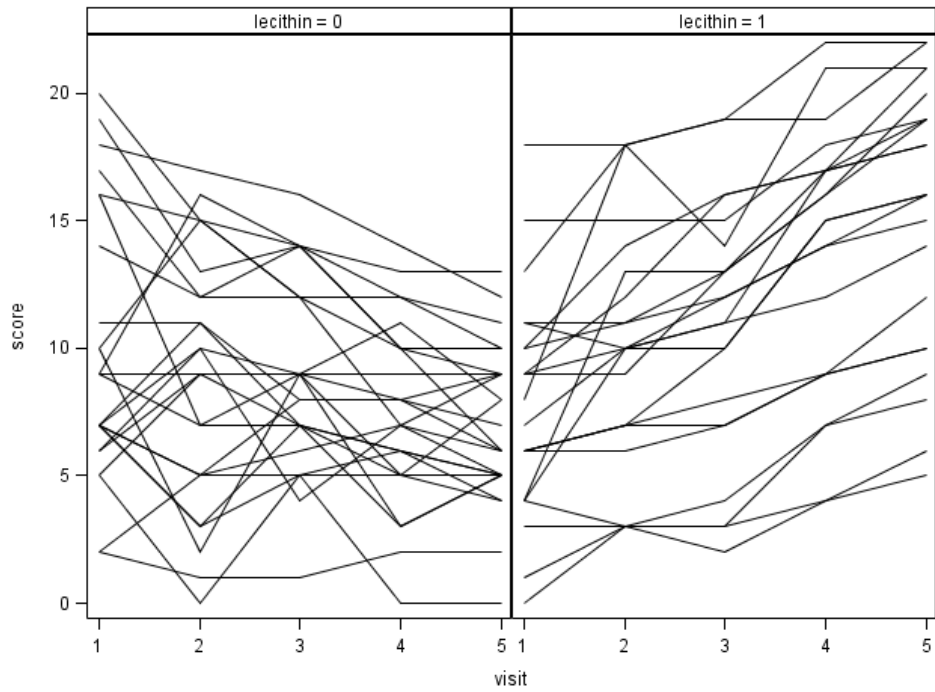


Family income data: mean function by group.

Simplest version is average of all families at each year.

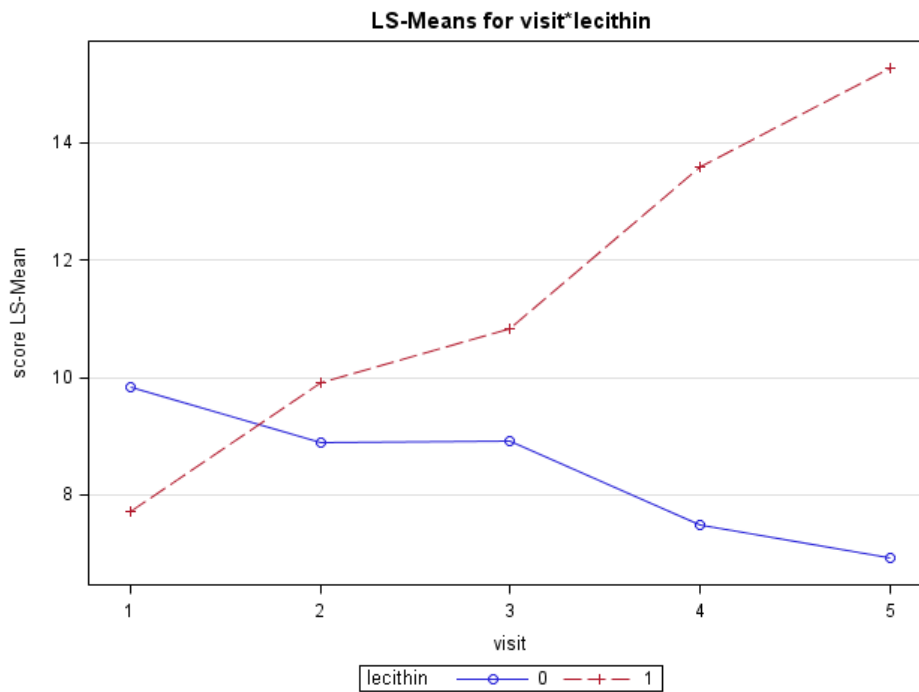


Alzheimer's disease trial: plots of individual profiles by group.



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Alzheimer's disease trial: mean function by group.



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Second part of longitudinal model:

covariance matrix, containing within-subject correlations

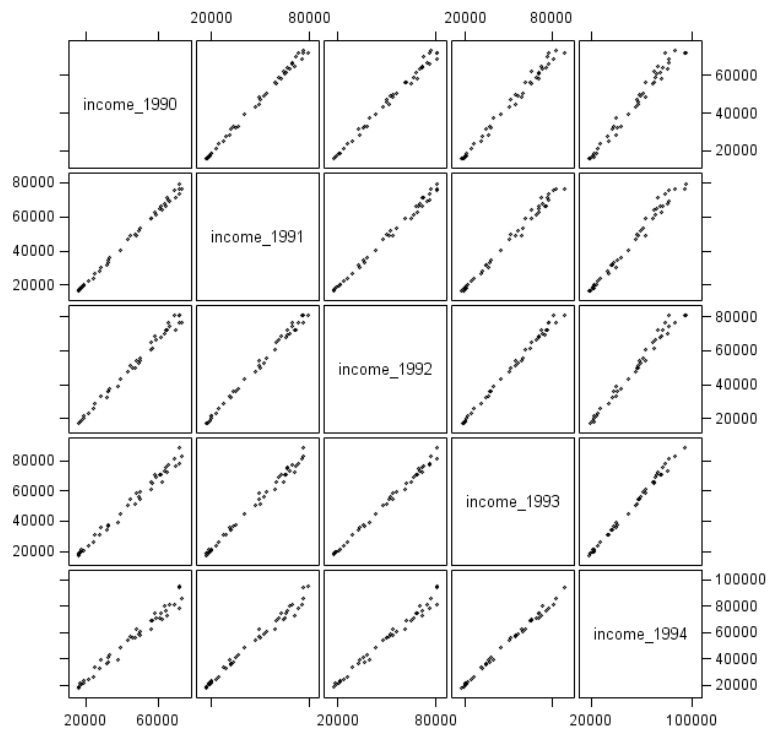
Used to estimate standard errors of LSmeans, regression coefficients.

SEs are affected (usually increased) by including correlation in model.

Correlations are usually *not of interest* = *nuisance parameters*

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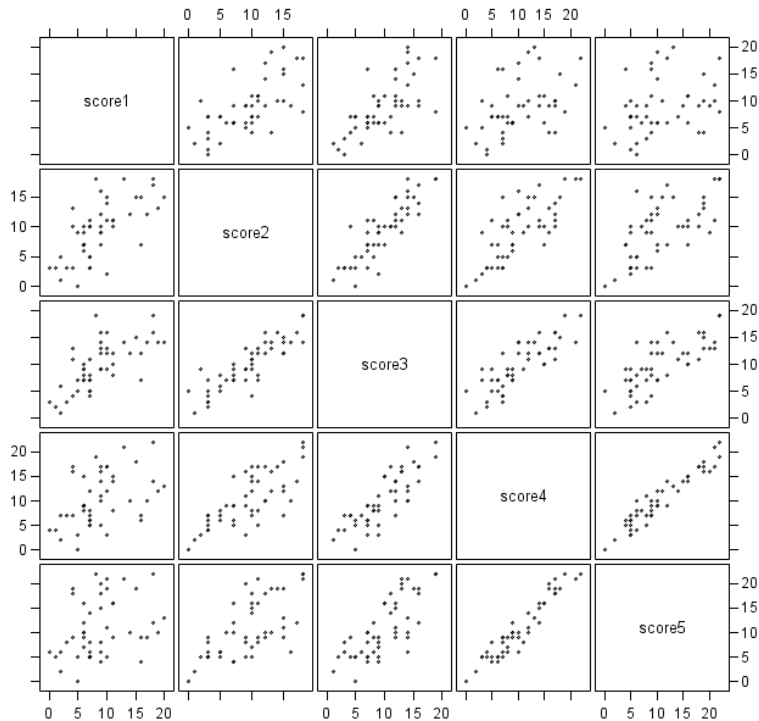
Family income data: within-family correlation plots.



Pearson Correlation Coefficients
 Prob > |r| under H0: Rho=0
 Number of Observations

	income_1990	income_1991	income_1992	income_1993	income_1994	income_1995
income_1990	1.00000 <.0001 46	0.99817 <.0001 42	0.99506 <.0001 40	0.99344 <.0001 41	0.98895 <.0001 43	0.98883 <.0001 44
income_1991	0.99817 <.0001 42	1.00000	0.99735 <.0001 39	0.99604 <.0001 42	0.99282 <.0001 42	0.99194 <.0001 44
income_1992	0.99506 <.0001 40	0.99735 <.0001 39	1.00000	0.99739 <.0001 38	0.99195 <.0001 39	0.99331 <.0001 41
income_1993	0.99344 <.0001 41	0.99604 <.0001 42	0.99739 <.0001 38	1.00000	0.99766 <.0001 41	0.99674 <.0001 43
income_1994	0.98895 <.0001 43	0.99282 <.0001 42	0.99195 <.0001 39	0.99766 <.0001 41	1.00000	0.99817 <.0001 44
income_1995	0.98883 <.0001 44	0.99194 <.0001 44	0.99331 <.0001 41	0.99674 <.0001 43	0.99817 <.0001 44	1.00000

Alzheimer's disease trial: within-patient correlation plots.



Decrease in correlation over longer time intervals:

Pearson Correlation Coefficients, N = 47
Prob > |r| under H0: Rho=0

	score1	score2	score3	score4	score5
score1	1.00000	0.66267 <.0001	0.67951 <.0001	0.42892 0.0026	0.30906 0.0345
score2	0.66267 <.0001	1.00000	0.86712 <.0001	0.75344 <.0001	0.66498 <.0001
score3	0.67951 <.0001	0.86712 <.0001	1.00000	0.82909 <.0001	0.76285 <.0001
score4	0.42892 0.0026	0.75344 <.0001	0.82909 <.0001	1.00000	0.95437 <.0001
score5	0.30906 0.0345	0.66498 <.0001	0.76285 <.0001	0.95437 <.0001	1.00000

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Covariance and correlation matrices

In Alzheimer's trial, each subject's response is a vector of 5 scores:

(score1, score2, score3, score4, score5)

- Population standard deviation of score_k is σ_k
- Population within-subject correlation between score_j and score_k is ρ_{jk}

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Correlation matrix **C**: correlations, with 1s down the diagonal

$$\mathbf{C} = \begin{pmatrix} 1 & \rho_{12} & \rho_{13} & \rho_{14} & \rho_{15} \\ \rho_{21} & 1 & \rho_{23} & \rho_{24} & \rho_{25} \\ \rho_{31} & \rho_{32} & 1 & \rho_{34} & \rho_{35} \\ \rho_{41} & \rho_{42} & \rho_{43} & 1 & \rho_{45} \\ \rho_{51} & \rho_{52} & \rho_{53} & \rho_{54} & 1 \end{pmatrix}$$

Incomplete specification: does not give standard deviations for scores.

C corresponds to scatterplot matrix from Proc Corr

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Alzheimer's disease trial: within-patient correlation.

Pearson Correlation Coefficients, N = 47

	score1	score2	score3	score4	score5
score1	1.00000	0.66267	0.67951	0.42892	0.30906
score2	0.66267	1.00000	0.86712	0.75344	0.66498
score3	0.67951	0.86712	1.00000	0.82909	0.76285
score4	0.42892	0.75344	0.82909	1.00000	0.95437
score5	0.30906	0.66498	0.76285	0.95437	1.00000

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Covariance matrix \mathbf{R} has variances down the diagonal and covariances off the diagonal.

$$\mathbf{R} = \begin{pmatrix} \sigma_1^2 & \sigma_1\sigma_2\rho_{12} & \sigma_1\sigma_3\rho_{13} & \sigma_1\sigma_4\rho_{14} & \sigma_1\sigma_5\rho_{15} \\ \sigma_2\sigma_1\rho_{21} & \sigma_2^2 & \sigma_2\sigma_3\rho_{23} & \sigma_2\sigma_4\rho_{24} & \sigma_2\sigma_5\rho_{25} \\ \sigma_3\sigma_1\rho_{31} & \sigma_3\sigma_2\rho_{32} & \sigma_3^2 & \sigma_3\sigma_4\rho_{34} & \sigma_3\sigma_5\rho_{35} \\ \sigma_4\sigma_1\rho_{41} & \sigma_4\sigma_2\rho_{42} & \sigma_4\sigma_3\rho_{43} & \sigma_4^2 & \sigma_4\sigma_5\rho_{45} \\ \sigma_5\sigma_1\rho_{51} & \sigma_5\sigma_2\rho_{52} & \sigma_5\sigma_3\rho_{53} & \sigma_5\sigma_4\rho_{54} & \sigma_5^2 \end{pmatrix}$$

$\sigma_j\sigma_k\rho_{jk}$ = population **covariance** between score j and score k for $i \neq j$

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As part of longitudinal model, we will estimate covariance matrix

$$\mathbf{R} = \begin{pmatrix} \sigma_1^2 & \sigma_1\sigma_2\rho_{12} & \sigma_1\sigma_3\rho_{13} & \sigma_1\sigma_4\rho_{14} & \sigma_1\sigma_5\rho_{15} \\ \sigma_2\sigma_1\rho_{21} & \sigma_2^2 & \sigma_2\sigma_3\rho_{23} & \sigma_2\sigma_4\rho_{24} & \sigma_2\sigma_5\rho_{25} \\ \sigma_3\sigma_1\rho_{31} & \sigma_3\sigma_2\rho_{32} & \sigma_3^2 & \sigma_3\sigma_4\rho_{34} & \sigma_3\sigma_5\rho_{35} \\ \sigma_4\sigma_1\rho_{41} & \sigma_4\sigma_2\rho_{42} & \sigma_4\sigma_3\rho_{43} & \sigma_4^2 & \sigma_4\sigma_5\rho_{45} \\ \sigma_5\sigma_1\rho_{51} & \sigma_5\sigma_2\rho_{52} & \sigma_5\sigma_3\rho_{53} & \sigma_5\sigma_4\rho_{54} & \sigma_5^2 \end{pmatrix}$$

Without constraints, **15 parameters** : 5 variances σ_j and 10 correlations ρ_{jk} .

Lots parameters to estimate, and we aren't really interested in them.

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Independence: no correlation

Here is the assumed population covariance matrix for ANOVA:

constant variance and independent observations

$$\mathbf{R} = \begin{pmatrix} \sigma^2 & 0 & 0 & 0 & 0 \\ 0 & \sigma^2 & 0 & 0 & 0 \\ 0 & 0 & \sigma^2 & 0 & 0 \\ 0 & 0 & 0 & \sigma^2 & 0 \\ 0 & 0 & 0 & 0 & \sigma^2 \end{pmatrix}$$

Variances equal down diagonal, all correlations = 0

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Simplest correlation matrix: compound symmetry

Most common constraint assumes

- same SD(score) at all visits
- equal correlation between measurements from the same person.

Correlation matrix:

$$\mathbf{C} = \begin{pmatrix} 1 & \rho & \rho & \rho & \rho \\ \rho & 1 & \rho & \rho & \rho \\ \rho & \rho & 1 & \rho & \rho \\ \rho & \rho & \rho & 1 & \rho \\ \rho & \rho & \rho & \rho & 1 \end{pmatrix}$$

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Compound symmetry covariance matrix

$$\mathbf{R} = \begin{pmatrix} \sigma^2 & \sigma^2\rho & \sigma^2\rho & \sigma^2\rho & \sigma^2\rho \\ 0 & \sigma^2 & \sigma^2\rho & \sigma^2\rho & \sigma^2\rho \\ 0 & \sigma^2\rho & \sigma^2 & \sigma^2\rho & \sigma^2\rho \\ 0 & \sigma^2\rho & \sigma^2\rho & \sigma^2 & \sigma^2\rho \\ 0 & \sigma^2\rho & \sigma^2\rho & \sigma^2\rho & \sigma^2 \end{pmatrix}$$

Equal variances at each time,
equal correlation between measurements from same subject.

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Fitting a longitudinal model in Proc Mixed

Part 1. Model for mean function identical to Proc GLM:

$$y_{ijk} = \beta_0 + \beta_i \text{group}_i + \beta_j \text{time}_j + \beta_{ij}(\text{group} * \text{time})_{ij} + \varepsilon_{ijk}$$

```
Proc Mixed data=alz_long ;  
  class lecithin visit idno ;  
  model score = lecithin visit lecithin*visit / solution;  
  LSmeans lecithin*visit / diff ;
```

Measurements are repeated within subjects (idno) but it is not in model.

`diff` requests estimates and tests of all differences between LSmeans

(not available in Proc GLM)

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Part 2. Add the within-subject correlation from repeated measures:

```
Proc Mixed data=alz_long ;
  class lecithin visit idno ;
  model score=lecithin visit lecithin*visit / solution;
  repeated / subject =idno type = CS R Rcorr ;
  LSmeans lecithin*visit / diff;
```

`repeated` specifies the model for the covariance matrix **R**

`subject` variable labeling observations from the same person—usually CLASS variable

`type` structured form for **R**: `CS` means **compound symmetry**

`R Rcorr` print estimate of **R** and the correlation matrix **C**

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The Mixed Procedure

Model Information

Data Set	WORK.ALZ_LONG
Dependent Variable	score
Covariance Structure	Compound Symmetry
Subject Effect	idno
Estimation Method	REML
Residual Variance Method	Profile
Fixed Effects SE Method	Model-Based
Degrees of Freedom Method	Between-Within

Class Level Information

Class	Levels	Values
lecithin	2	0 1
idno	47	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

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Dimensions

Covariance Parameters	2	<i>compound symmetry</i>
Columns in X	18	<i>model terms</i>
Columns in Z	0	
Subjects	47	
Max Obs Per Subject	5	

Number of Observations

Number of Observations Read	235	
Number of Observations Used	235	<i>always check this</i>
Number of Observations Not Used	0	

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Proc Mixed alternates between estimating mean function and estimating correlations, repeating procedure until convergence (or not)

Iteration History

Iteration	Evaluations	-2 Res Log Like	Criterion
0	1	1352.89098164	
1	1	1124.92054066	0.00000000

The Mixed Procedure

Convergence criteria met.

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Regression coefficients for 18 columns in X:

Solution for Fixed Effects

Effect	lecithin	visit	Estimate	Standard Error	DF	t Value	Pr > t
Intercept			15.2727	0.9722	45	15.71	<.0001
lecithin	0		-8.3527	1.3331	45	-6.27	<.0001
lecithin	1		0
visit		1	-7.5455	0.6098	180	-12.37	<.0001
visit		2	-5.3636	0.6098	180	-8.80	<.0001
visit		3	-4.4545	0.6098	180	-7.30	<.0001
visit		4	-1.6818	0.6098	180	-2.76	0.0064
visit		5	0
lecithin*visit	0	1	10.4655	0.8361	180	12.52	<.0001
lecithin*visit	0	2	7.3236	0.8361	180	8.76	<.0001
lecithin*visit	0	3	6.4545	0.8361	180	7.72	<.0001
lecithin*visit	0	4	2.2418	0.8361	180	2.68	0.0080
lecithin*visit	0	5	0
lecithin*visit	1	1	0
lecithin*visit	1	2	0
lecithin*visit	1	3	0
lecithin*visit	1	4	0
lecithin*visit	1	5	0

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ANOVA table:

Type 3 Tests of Fixed Effects

Effect	Num DF	Den DF	F Value	Pr > F
lecithin	1	45	6.24	0.0163
visit	4	180	9.53	<.0001
lecithin*visit	4	180	49.74	<.0001

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Main interest: mean function = LSmeans by treatment for each visit.

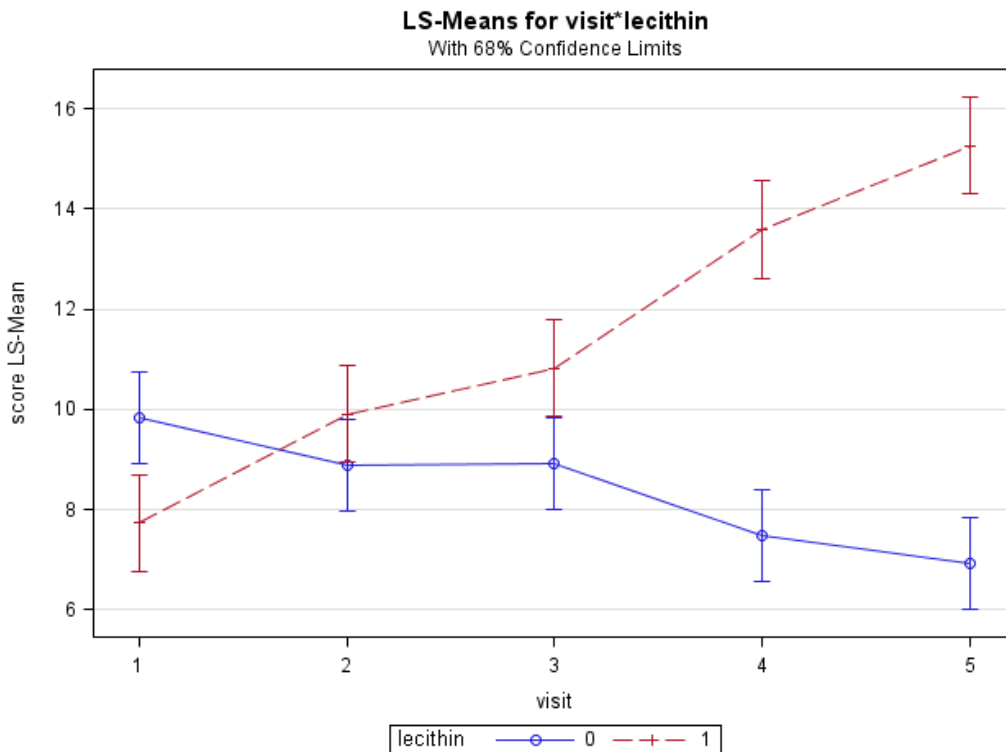
Least Squares Means

Effect	lecithin	visit	Estimate	Standard Error	DF	t Value	Pr > t
lecithin*visit	0	1	9.8400	0.9120	180	10.79	<.0001
lecithin*visit	0	2	8.8800	0.9120	180	9.74	<.0001
lecithin*visit	0	3	8.9200	0.9120	180	9.78	<.0001
lecithin*visit	0	4	7.4800	0.9120	180	8.20	<.0001
lecithin*visit	0	5	6.9200	0.9120	180	7.59	<.0001
lecithin*visit	1	1	7.7273	0.9722	180	7.95	<.0001
lecithin*visit	1	2	9.9091	0.9722	180	10.19	<.0001
lecithin*visit	1	3	10.8182	0.9722	180	11.13	<.0001
lecithin*visit	1	4	13.5909	0.9722	180	13.98	<.0001
lecithin*visit	1	5	15.2727	0.9722	180	15.71	<.0001

Tests of Effect Slices

Effect	visit	Num DF	Den DF	F Value	Pr > F
lecithin*visit	1	1	180	2.51	0.1148
lecithin*visit	2	1	180	0.60	0.4411
lecithin*visit	3	1	180	2.03	0.1562
lecithin*visit	4	1	180	21.01	<.0001
lecithin*visit	5	1	180	39.26	<.0001

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Estimates of covariance and correlation

We assumed the covariance matrix had compound symmetry:

- same SD(score) at all visits
- equal correlation between measurements from the same person.

Correlation matrix:

$$\mathbf{C} = \begin{pmatrix} 1 & \rho & \rho & \rho & \rho \\ \rho & 1 & \rho & \rho & \rho \\ \rho & \rho & 1 & \rho & \rho \\ \rho & \rho & \rho & 1 & \rho \\ \rho & \rho & \rho & \rho & 1 \end{pmatrix}$$

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Estimated R **Correlation Matrix** for idno 1

Row	Col1	Col2	Col3	Col4	Col5
1	1.0000	0.8033	0.8033	0.8033	0.8033
2	0.8033	1.0000	0.8033	0.8033	0.8033
3	0.8033	0.8033	1.0000	0.8033	0.8033
4	0.8033	0.8033	0.8033	1.0000	0.8033
5	0.8033	0.8033	0.8033	0.8033	1.0000

Within-subject correlation estimated as $\hat{\rho} = .8033$

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Estimated R Matrix for idno 1 *Covariance matrix*

Row	Col1	Col2	Col3	Col4	Col5
1	20.7958	16.7052	16.7052	16.7052	16.7052
2	16.7052	20.7958	16.7052	16.7052	16.7052
3	16.7052	16.7052	20.7958	16.7052	16.7052
4	16.7052	16.7052	16.7052	20.7958	16.7052
5	16.7052	16.7052	16.7052	16.7052	20.7958

Common standard deviation of scores estimated as $\sqrt{20.7958} = 4.56$

Proc Mixed fits 2 covariance parameters, but not σ^2 and ρ as you might expect.

Covariance Parameter Estimates		
Cov Parm	Subject	Estimate
CS	idno	16.7052
Residual		4.0906

Covariance matrix **R** has this form:

$$\begin{pmatrix} \text{Res + CS} & \text{CS} & \text{CS} & \text{CS} & \text{CS} \\ \text{CS} & \text{Res + CS} & \text{CS} & \text{CS} & \text{CS} \\ \text{CS} & \text{CS} & \text{Res + CS} & \text{CS} & \text{CS} \\ \text{CS} & \text{CS} & \text{CS} & \text{Res + CS} & \text{CS} \\ \text{CS} & \text{CS} & \text{CS} & \text{CS} & \text{Res + CS} \end{pmatrix}$$

Covariance Parameter Estimates		
Cov Parm	Subject	Estimate
CS	idno	16.7052
Residual		4.0906

Residual = error variance ignoring within-subject correlation

(Residual + CS) = error variance incorporating within-subject correlation

CS = within-subject covariance *can be negative*

if within-subject correlation is negative.

To be sure what estimates are, print correlation and covariance matrices.

```
repeated / subject =idno type = CS R Rcorr ;
```

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Another approach to model correlation: random effects

Predictors in a linear model can be roughly classified into two types:

Fixed effect: we are interested in estimating and comparing specific values of the predictor

Examples: treatment group, or patient characteristics like gender, age, race, disease status.

Random effect: values of the predictor are sample from a population, and we are interested in the mean of the population

Examples: clinics in a multi-clinic study, patients' baseline values, assay plates

A linear model with both fixed and random effects is called a **mixed model**.

Modeling within-subject correlation with a random intercept

To include within-subject correlation in the model:

treat subjects as a random effect, as a sample of subjects from some population.

Each subject has their own *personal intercept*—this is the random effect.

intercept = overall-intercept + subject-effect = $(\beta_0 + b_{0k})$

$$y_{ijk} = (\beta_0 + b_{0k}) + \beta_i \text{group}_i + \beta_j \text{time}_j + \beta_{ij}(\text{group} * \text{time})_{ij} + \varepsilon_{ijk}$$

Assume $\{b_{0k}\}$ are $\text{Normal}(0, \sigma_b^2)$ and independent of the errors $\{\varepsilon_{ijk}\}$.

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Proc Mixed: RANDOM statement

Same model for mean function:

```
Proc Mixed data=alz_long ;  
  class lecithin visit idno ;  
  model score = lecithin visit lecithin*visit / solution;  
  LSmeans lecithin*visit /diff ;
```

Model statement contains *only the fixed effects*.

To fit random intercepts:

```
RANDOM intercept / subject=idno v vcorr ;
```

The **RANDOM** statement lists (and structures) random effects.

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```

Proc Mixed data=alz_long ;
  class lecithin visit idno ;
  model score = lecithin visit lecithin*visit / solution;
  RANDOM intercept / subject =idno v vcorr ;
  LSmeans lecithin*visit /diff ;

```

`subject=` identifies variable that links measurements on same person

`v vcorr` Print estimated covariance matrix and correlation matrix for subject 1;
`v = 5` gives matrices for subject 5. (Used `r rcorr` with REPEATED.)

Equivalent RANDOM statement:

```

RANDOM idno / subject = idno;

```

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The Mixed Procedure

Data Set	WORK.ALZ_LONG
Dependent Variable	score
Covariance Structure	Variance Components <i>not CS</i>
Subject Effect	idno

Dimensions

Covariance Parameters	2	
Columns in <code>X</code>	6	<i>X holds fixed effects</i>
Columns in <code>Z</code> Per Subject	1	<i>Z holds random effects</i>
Subjects	47	
Max Obs Per Subject	5	

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Estimated V Matrix for idno 1

Row	Col1	Col2	Col3	Col4	Col5
1	20.7854	16.7078	16.7078	16.7078	16.7078
2	16.7078	20.7854	16.7078	16.7078	16.7078
3	16.7078	16.7078	20.7854	16.7078	16.7078
4	16.7078	16.7078	16.7078	20.7854	16.7078
5	16.7078	16.7078	16.7078	16.7078	20.7854

Estimated V Correlation Matrix for idno 1

Row	Col1	Col2	Col3	Col4	Col5
1	1.0000	0.8038	0.8038	0.8038	0.8038
2	0.8038	1.0000	0.8038	0.8038	0.8038
3	0.8038	0.8038	1.0000	0.8038	0.8038
4	0.8038	0.8038	0.8038	1.0000	0.8038
5	0.8038	0.8038	0.8038	0.8038	1.0000

Do you recognize this covariance model?

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Random intercepts gives compound symmetry covariance matrix:

Covariance Parameter Estimates

Cov Parm	Subject	Estimate
Intercept	idno	16.7052
Residual		4.0906

Same correlation estimates as repeated measures-compound symmetry model.

Same estimates of LSmeans and regression coefficients.

With random intercept, within-subject correlation cannot be negative.

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Some models in Proc Mixed can be written in more than one way:

```
Proc Mixed; repeated-measures compound symmetry
  class lecithin idno;
  model score=lecithin visit lecithin*visit;
  repeated / subject=idno type=cs r rcorr ;
```

```
Proc Mixed; random intercept
  class lecithin idno;
  model score=lecithin visit lecithin*visit;
  random intercept /subject=idno solution v vcorr;
```

Repeated-measures version allows negative within-subject correlation, random intercept does not.

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To look at the random intercepts, use ODS; get names from SAS Help for Proc Mixed: Details > ODS Table Names

```
Proc Mixed data=one covtest;
  title3 "random intercept";
  class lecithin idno;
  model score=lecithin visit lecithin*visit;
  random int /subject=idno type=un solution v vcorr;
  ODS output SolutionR = random_intercepts;
```

```
Proc Print data = random_intercepts;
```

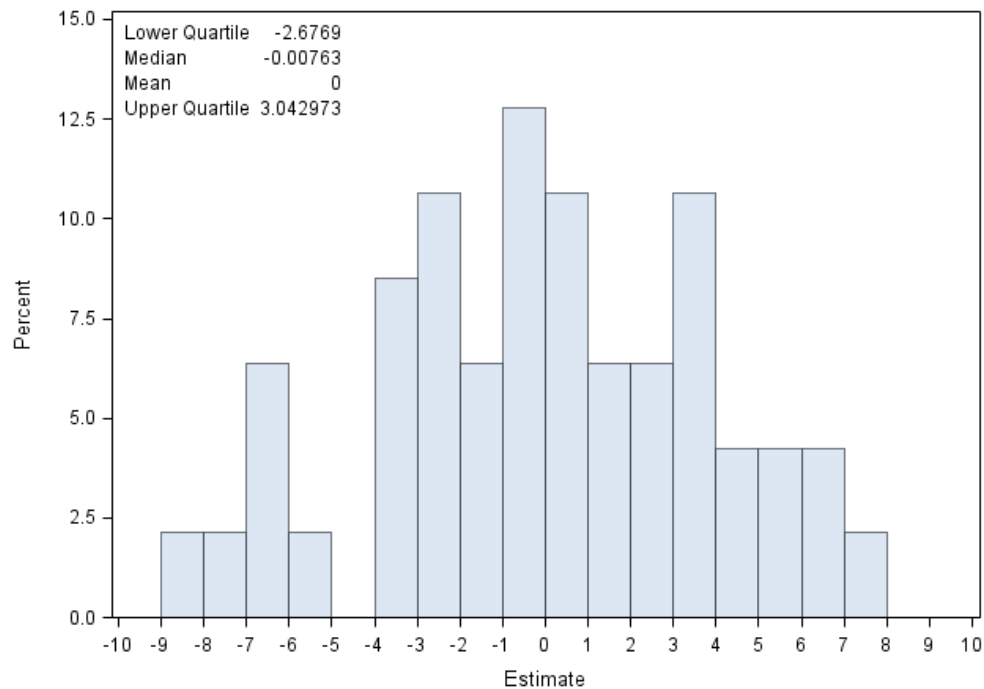
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Overall intercept is 15.3. Estimated random effects \hat{b}_{0k} :

Solution for Random Effects

Effect	idno	Estimate	Std Err	Pred	DF	t Value	Pr > t
Intercept	1	6.2852	1.1911		138	5.28	<.0001
Intercept	2	3.0434	1.1911		138	2.56	0.0117
Intercept	3	-2.6773	1.1911		138	-2.25	0.0262
Intercept	4	-0.3890	1.1911		138	-0.33	0.7445
Intercept	5	-1.5332	1.1911		138	-1.29	0.2002
Intercept	6	0.7551	1.1911		138	0.63	0.5272
Intercept	7	-2.6773	1.1911		138	-2.25	0.0262
Intercept	8	6.6666	1.1911		138	5.60	<.0001
Intercept	9	-0.00763	1.1911		138	-0.01	0.9949
Intercept	10	3.4248	1.1911		138	2.88	0.0047
Intercept	11	-2.4866	1.1911		138	-2.09	0.0387
Intercept	12	0.9458	1.1911		138	0.79	0.4285

We assumed $\{b_{0k}\}$ are Normal with mean zero.



Extensions from here:

- With REPEATED, specify more complex structures for correlation/covariance: different variance at each visit, correlation diminishing with time interval.
- With RANDOM, could assume linear response (visit as continuous predictor) and fit random intercepts and slopes.

Also known as multilevel or hierarchical models.

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Resources on longitudinal data and Proc Mixed

- Verbeke, Molenberghs (2000) *Linear Mixed Models for Longitudinal Data*.
- Gelman and Hill (2007) *Data Analysis Using Regression and Multilevel/Hierarchical Models*.
- Weiss (2005) *Modeling Longitudinal Data*.
- SAS Help > Proc Mixed > Details > Mixed Models Theory
- Littell, *et. al.* (2006) *SAS for Mixed Models, Second Edition*. SAS Press
- PubH 7430 *Statistical Methods for Correlated Data*, offered fall semesters

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