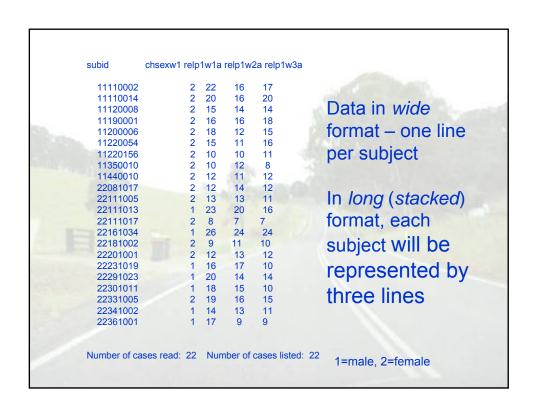
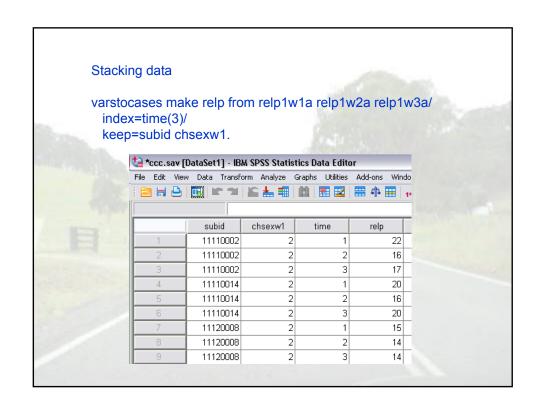
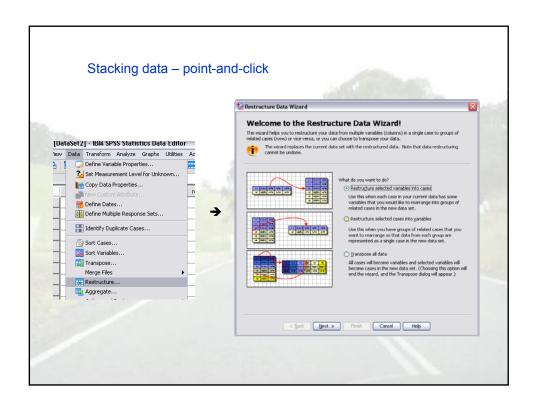


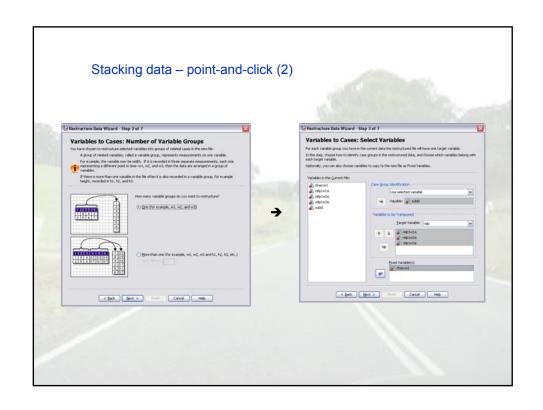
### Outline

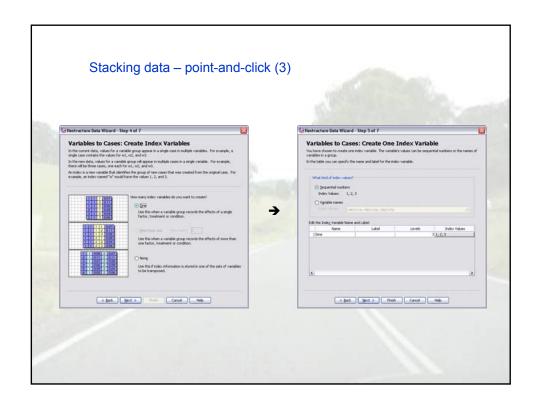
- Distinguish wide and long (stacked) data
- Use restructure data to stack repeated measures data
- Carry out a repeated measures analysis with stacked data using GLM
- Distinguish the fixed, random and nested parts of the model
- Implications of using the stacked form when there are missing data
- Implications of different forms of 'missingness'
- The same analysis using the linear mixed model procedure
- Advantages of the linear mixed model procedure
  - Maximum likelihood estimation
  - Model different correlations between
  - Allow random variation around coefficients as well as the intercept
  - Can be seen as multi-level models
- A between-subject by within-subject analysis
- An individual growth (random coefficient) model











# A GLM analysis with stacked data

Subject will be a random factor. Need to provide numbering for subject factor levels within each group.

sort cases by chsexw1 subid.

compute subwgrp = subwgrp + 1.

if (subid eq lag(subid))subwgrp = lag(subwgrp).

if (chsexw1 ne lag(chsexw1))subwgrp = 1.

leave subwgrp.

execute.

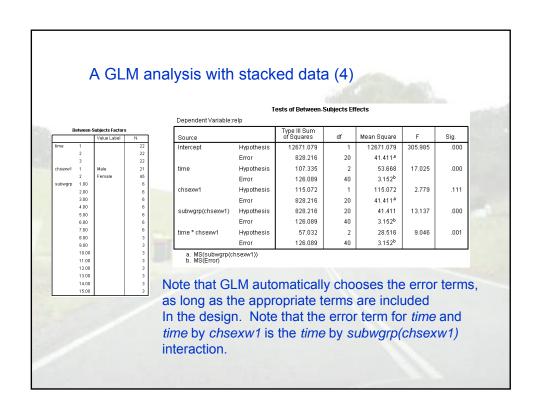
- The *lag* function allows reference to the value of a variable on the previous line of data
- The *leave* command tells SPSS not to initialise the variable to system-missing for the next case

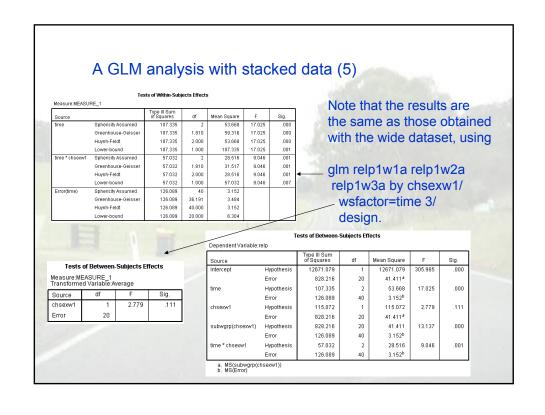
			).O WI	ui ota	oncou c	data (2)
-	subid	chsexw1	time	relp	subwgrp	and the second second
r	22111013	1	1	23	1.00	A CONTRACTOR OF THE PARTY OF TH
+	22111013	1	2	20	1.00	- 🔨
	22111013	1	3	16	1.00	
No.	22161034	1	1	26	2.00	
100	22161034	1	2	24	2.00	
-	22161034	1	3	24	2.00	
	22231019	1	1	16	3.00	The cubicat accordance
-	22231019	1	2	17	3.00	The subject number is
	22231019	1	3	10	3.00	now included, starting at
	22291023	1	1	20	4.00	
	22291023	1	2	14	4.00	1 for each group (sex)
	22291023	1	3	14	4.00	
	22301011	1	1	18	5.00	
-	22301011	1	2	15	5.00	
1	22301011	1	3	10	5.00	
	22341002	1	1	14	6.00	
	22341002	1	2	13	6.00	
	22341002	1	3	11	6.00	
	22361001	1	1	17	7.00	
	22361001	1	2	9	7.00	
	22361001	1	3	9	7.00	✓
	11110002	2	1	22	1.00	
	11110002	2	2	16	1.00	
	11110002	2	3	17	1.00	
	11110014	2	1	20	2.00	

# A GLM analysis with stacked data (3)

glm relp by time chsexw1 subwgrp/ random=subwgrp/ design=time chsexw1 subwgrp(chsexw1) time by chsexw1.

- subwgrp is specified to be a random factor
  - this means that the levels of the factor (subjects in this case) are a random sample of all possible levels
- subwgrp(chsexw1) specifies that subwgrp is nested within chsexw1. Nesting occurs when (for example) the levels of factor A which occur under level 1 of factor B are different from those which occur under level 2 of factor B.





# Missing Data (1)

An important advantage of using stacked data is that we don't lose a whole case when it has missing observations at one or two time points.

But what about bias due to the missing observations?

Here we need to consider formulations regarding missing data, developed by Rubin.

# Missing Data (2)

MCAR – missing completely at random

- 'missingness' unrelated to values of Xi and Y

MAR - missing at random

- 'missingness' unrelated to Y, adjusted for Xi

MNAR – missing not at random

- 'missingness' related to Y
- also referred to as non-ignorable missing

For details, see Schafer, J., & Graham, J. (2002). Missing data: Our view of the state of the art. *Psychological Methods*, 7, 147-177

# Missing Data (3)

An example given by Schafer & Graham (p. 152-153):

All patients have BP measured at Time 1. At Time 2, some patients do not have a BP measurement (i.e., it is missing). The T1 BP is X, the T2 BP is Y.

MCAR: Those with missing Y values are a random sample of patients at T1.

MAR: Those who returned at T2 had BP > 140 at T1

MNAR: Only patients whose BP was > 140 at T2 had their BPs recorded.

## Missing Data (4) and Maximum Likelihood

Rubin showed that we can make valid inferences about the population in the presence of MAR (as well as MCAR) if we use analyses based on <a href="mailto:maximum-likelihood">maximum-likelihood</a> methods.

Keith refers briefly to ML (p. 394) – it is the default method for most SEM programs.

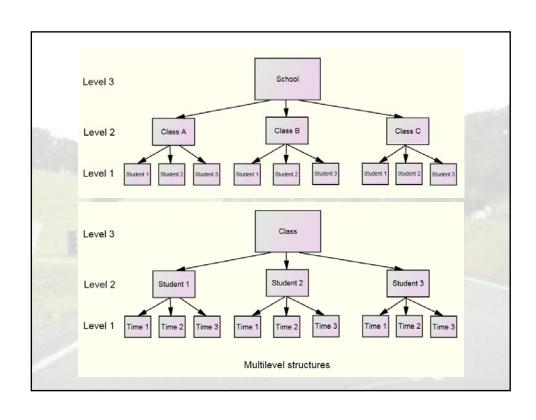
In a nutshell, ML is an iterative method which seeks to find estimates of the population parameters (coefficients, for example) which maximise the likelihood of obtaining the observed sample. (Originated by R. A. Fisher)

GLM does not use ML, the linear mixed model does.

Therefore, for analyses which involve missing data or are unbalanced, we turn to the *linear mixed model*.

## Mixed and multilevel models

- Mixed models are so-called because they contain both *fixed* and *random* factors.
- In repeated measures analyses, subject is a random factor.
- We'll consider mixed models as multi-level models, because this is leads to a framework which is useful for more complex models.
- Judith Singer wrote an article which made the link between mixed and multi-level models. Peugh and Enders based their article on Singer's.



# A two-level model (observations within subjects)

Based on the notation of Peugh & Enders (p. 721)

i = ith observation, j = jth subjects,  $\gamma_{00}$  = grand mean

Level 1 (observation):  $Y_{ij} = B_{0j} + r_{ij}$ 

Level 2 (subject):  $B_{0j} = \gamma_{00} + U_{0j}$ 

Combined:  $Y_{ij} = \gamma_{00} + U_{0j} + r_{ij}$ 

Note:  $\gamma$  = gamma

# A two-level model (observations within subjects)

Based on the notation of Peugh & Enders (p. 721)

i = ith observation, j = jth subject,  $\gamma_{00}$  = grand mean

Level 1 (observations):  $Y_{ij} = B_{0j} + r_{ij}$ 

Score for observation *i* for subject *j* 

Difference between observation *i* and the mean for subject *j* 

Mean (intercept) for subject *j* 

# A two-level model (observations within subjects) Based on the notation of Peugh & Enders (p. 721)

i = ith observation, j = jth subject,  $\gamma_{00}$  = grand mean

Level 2 (subject);  $B_{0j} = \gamma_{00} + U_{0j}$ 

Mean (intercept) for subject j

Grand mean

Difference between mean for subject j and grand mean

A two-level model (observations within subjects) Based on the notation of Peugh & Enders (p. 721)

i = ith observation, j = jth subject,  $\gamma_{00}$  = grand mean

Combined:  $Y_{ij} = [\gamma_{00}] + [U_{0j} + r_{ij}]$ Fixed part Random part

This is an unconditional random intercept model

# A two-level model – introducing two fixed factors

i = ith observation, j = jth subject,  $\gamma_{00}$  = grand mean

Level 1 (observations):  $Y_{ij} = B_{0j} + B_{1j}time2_{ij} + B_{2j}time3_{ij} + r_{ij}$ 

Level 2 (subjects):  $B_{0j} = \gamma_{00} + \gamma_{01} sex_j + U_{0j}$ 

Model:  $Y_{ij} = [\gamma_{00} + \gamma_{01}sex + \gamma_{10}time2_{ij} + \gamma_{20}time3_{ij} +$ 

 $\gamma_{11}(\text{sex * time2}_{ij}) + \gamma_{12}(\text{sex * time3}_{ij})] + [U_{0j} + r_{ij}]$ 

This is still only a random intercept model

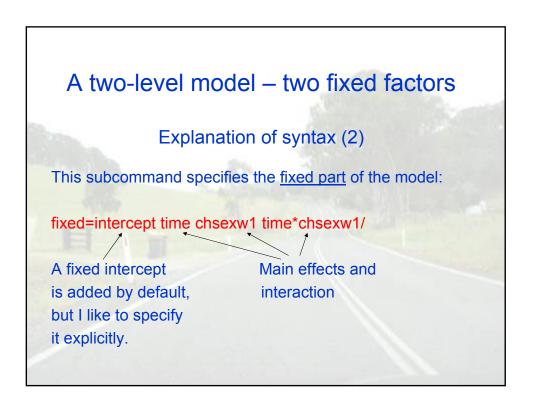
# A two-level model – two fixed factors

It's easier to set up the model in SPSS than to write the equations!

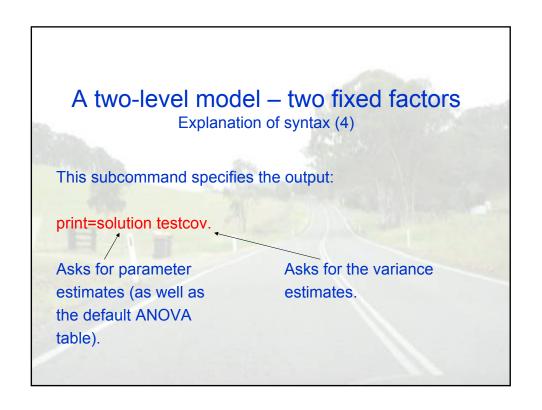
These commands refer to the stacked dataset. We don't need the codes for subjects within groups.

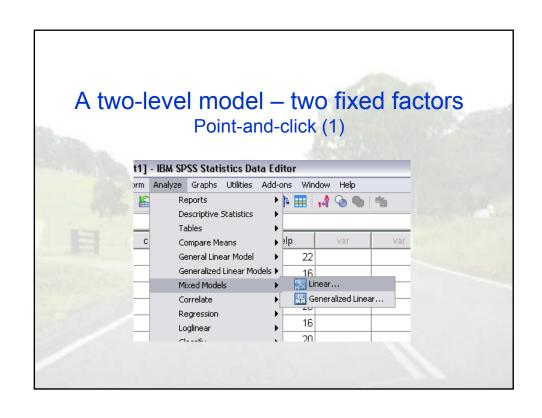
mixed relp by chsexw1 time/ fixed=intercept time chsexw1 time\*chsexw1/ random=intercept | subject(subid)/ print=solution testcov.

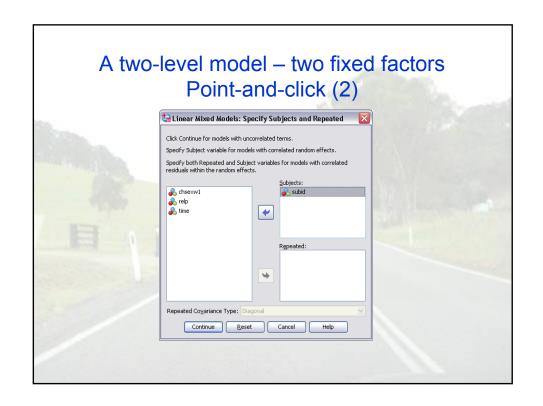
# A two-level model – two fixed factors Explanation of syntax (1) mixed relp by chsexw1 time/ DV categorical variables follow by Time could be treated as a numeric variable, in which case it would be entered after with.

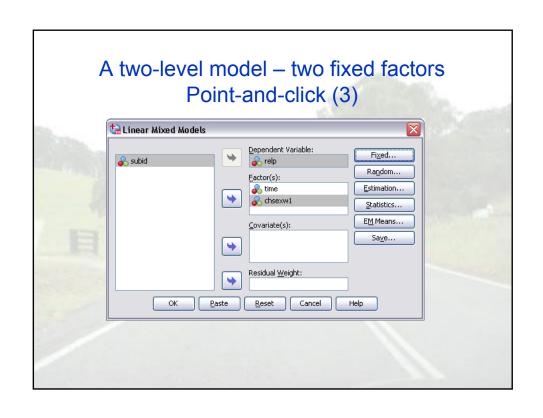


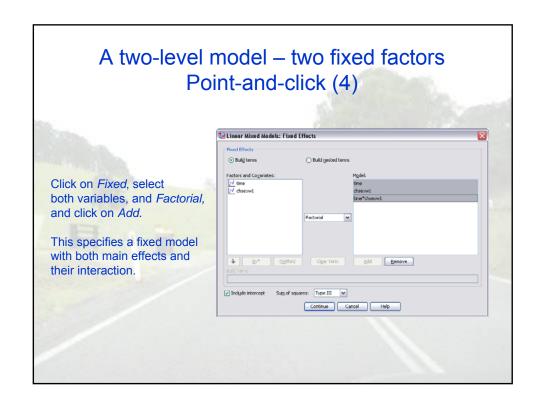
# A two-level model – two fixed factors Explanation of syntax (3) This subcommand specifies the random part of the model: random=intercept | subject(subid)/ Specifies that there Is random variation around the intercept Note use of vertical bar Note use of vertical bar Indicates that observations with the same subid are not independent; those with different values of subid are independent.

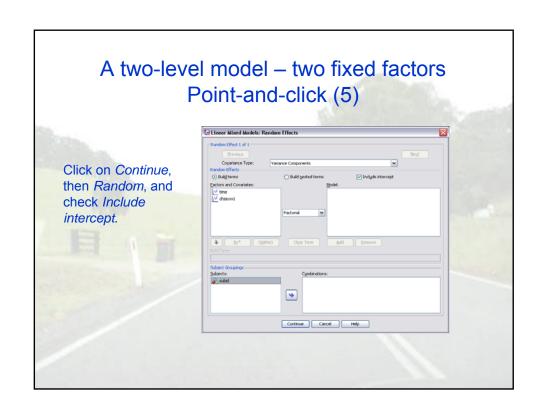


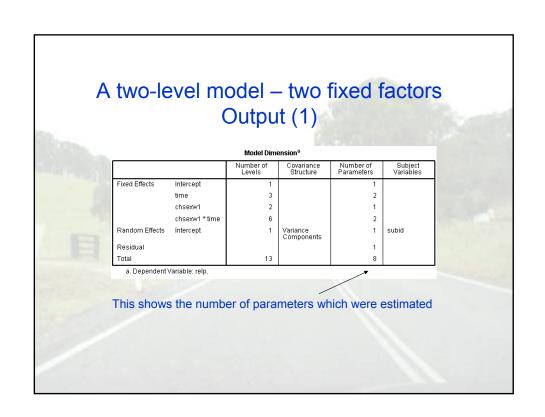












# A two-level model – two fixed factors Output (2)

### Information Criteria<sup>a</sup>

-2 Restricted Log Likelihood	304.630
Akaike's Information Criterion (AIC)	308.630
Hurvich and Tsai's Criterion (AICC)	308.840
Bozdogan's Criterion (CAIC)	314.818
Schwarz's Bayesian Criterion (BIC)	312.818

The information criteria are displayed in smaller-is-better forms.

a. Dependent Variable: relp.

The likelihood referred to here is the probability of obtaining the current sample if the population had the parameter values given in the output.

This likelihood is maximised during the estimation of the parameter values.

The likelihood (probability) is typically small.

For example, the probability represented by -2 Log Likelihood is  $7.09 * 10^{-67}$ .

# A two-level model – two fixed factors Output (3)

### Information Criteria<sup>a</sup>

-2 Restricted Log Likelihood	304.630
Akaike's Information Criterion (AIC)	308.630
Hurvich and Tsai's Criterion (AICC)	308.840
Bozdogan's Criterion (CAIC)	314.818
Schwarz's Bayesian Criterion (BIC)	312.818

The information criteria are displayed in smaller-is-better forms.

a. Dependent Variable: relp.

Under specific conditions, the fit of different models can be compared by referring the difference in the -2LL for the two models to a chi-squared distribution.

If ML is used (as opposed to the default, REML), models differing in fixed or random effects, or both, can be compared.

If REML is used, the models compared must have the same fixed effects but can differ in random effects.

Note: You can switch to maximum-likelihood (ML) from the default restricted or residual ML (REML) by including this sub-command: /method=ml

# A two-level model – two fixed factors Output (4)

# An example of comparing model fit

(1) This shows the fit for the first model:

(2) We then fit a model without the random effect:

### Information Criteria<sup>a</sup>

-2 Restricted Log 304.630 Likelihood

(3) Fit for the second model:

### Information Criteriaª

-2 Restricted Log 350.233 Likelihood

### Note that:

The information criteria are displayed in smaller-is-better forms.

mixed relp by chsexw1 time/ fixed=intercept time chsexw1 time\*chsexw1/ print=solution testcov.

(4) The difference between the -2LL values is 350.233 – 304.63 = 45.6. We can refer this to a chi-squared distribution with one degree of freedom (the models differ only by the random intercept factor, which accounts for 1 df). The p-value is < .0005, which means that the model without the random factor has a worse fit.

# A two-level model – two fixed factors Output (5)

### The ANOVA table

### Type III Tests of Fixed Effects<sup>a</sup>

Source	Numerator df	Denominator df	F	Sig.
Intercept	1	20	301.837	.000
time	2	40.000	17.025	.000
chsexw1	1	20	2.779	.111
chsexw1 * time	2	40.000	9.046	.001

a. Dependent Variable: relp.

By default, Type III tests are performed; Type I (sequential) can be requested.

The coding underlying this table is the same as in GLM (deviation)

# A two-level model – two fixed factors Output (6)

### Parameter estimates

### Estimates of Fixed Effects<sup>b</sup>

						95% Confid	ence Interval
Parameter	Estimate	Std. Error	df	t	Sig.	Lower Bound	Upper Bound
Intercept	13.200000	1.029727	26.249	12.819	.000	11.084342	15.315658
[time=1]	.866667	.648303	40.000	1.337	.189	443602	2.176935
[time=2]	400000	.648303	40.000	617	.541	-1.710268	.910268
[time=3]	Oa	0					
[chsexw1=1]	.228571	1.825512	26.249	.125	.901	-3.522090	3.979233
[chsexw1=2]	Oa	0					
[chsexw1=1] * [time=1]	4.847619	1.149318	40.000	4.218	.000	2.524761	7.170477
[chsexw1=1] * [time=2]	2.971429	1.149318	40.000	2.585	.013	.648571	5.294286
[chsexw1=1] * [time=3]	0ª	0					
[chsexw1=2] * [time=1]	Oa	0					
[chsexw1=2] * [time=2]	Oa	0					
[chsexw1=2] * [time=3]	0 a	0					

This parameter is set to zero because it is redundant.
 Dependent Variable: relp.

The fixed factors are dummy- or indicator-coded and the highestnumbered category is the reference category (as in GLM).

# A two-level model – two fixed factors Output (7)

### Variances

### Estimates of Covariance Parameters

						95% Confidence Interval	
Parameter		Estimate	Std. Error	Wald Z	Sig.	Lower Bound	Upper Bound
Residual		3.152222	.704858	4.472	.000	2.033679	4.885975
Intercept [subject = subid]	Variance	12.752857	4.371400	2.917	.004	6.513798	24.967825

a. Dependent Variable: relp.

- ullet The residual is  $r_{ij}$  the variance of observations within subjects
- ullet The intercept variance is  $U_{0j}$  the between-subject variance
- The <code>intraclass correlation</code>, rho (p) the proportion of the total variance due to individuals is U $_{0j}$  / (U $_{0j}$  + r $_{ij}$ ) = 12.75 / (12.75 + 3.15) = .80

# A two-level model – two fixed factors Further options

mixed relp by chsexw1 time/ fixed=intercept time chsexw1 time\*chsexw1/ random=intercept | subject(subid)/ print=solution testcov/ emmeans=table(time\*chsexw1) compare(time)/

emmeans=table(time\*chsexw1) compare(chsexw1)/
test="test of linear and quadratic time by sex" chsexw1\*time 1 0 -1 -1 0 1;
chsexw1\*time -1 2 -1 1 -2 1.

- The estimated marginal means subcommands test the simple effects of time and sex.
- The *test* command tests the significance of the linear *time* by *sex* and quadratic *time* by *sex* interaction contrasts.

The contrast for linear *time* is -1 0 1, and for quadratic *time* 1 -2 1. These are multiplied by the *sex* contrasts (-1 1) to obtain the interaction contrasts.

# A two-level model – two fixed factors Further options (2)

test="test of linear and quadratic time by sex" chsexw1\*time 1 0 -1 -1 0 1;

L1 is the linear *time by sex* interaction contrast L2 is the quadratic *time by sex* interaction contrast

Contrast Estimates <sup>a</sup> ,b								
95% Confidence Interva							ence Interval	
Contrast	Estimate	Std. Error	df	Test Value	t	Sig.	Lower Bound	Upper Bound
L1	4.847619	1.149318	40.000	0	4.218	.000	2.524761	7.170477
L2	1.095238	1.990677	40.000	0	.550	.585	-2.928070	5.118546

a, test of linear and quadratic time by sex b. Dependent Variable; relp.

chsexw1\*time -1 2 -1 1 -2 1.

# A two-level model – two fixed factors

Further options (3)
Correlations between residuals

The commands specified so far assume *compound symmetry*, which is stronger than *circularity*, in that it assumes that the variances of the DVs are equal (see the footnote on p. 49 of *GLM*).

We can specify different correlations between the residual errors by using the *repeated* subcommand rather than the *random* subcommand:

Subcommand	-2LL*	p for sex*time
repeated=time   subject(subid) covtype(cs)/ repeated=time   subject(subid) covtype(hf)/	313.44 310.08	.00027
repeated=time   subject(subid) covtype(ar1)/	325.88	.012

The fit is slightly better if circularity rather than CS is assumed, but the p-value is unchanged. The assumption of autocorrelation Is not supported. Note the change in the p-value.

## A two-level model – two fixed factors

# A linear growth model

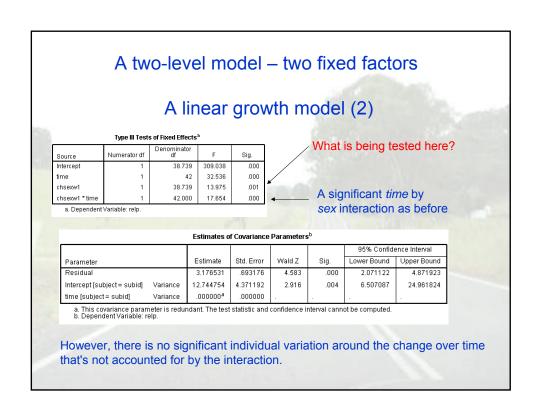
- Treat the effect of time as linear rather than categorical
- Allow individual random variation around the change over time as well as around the intercept.

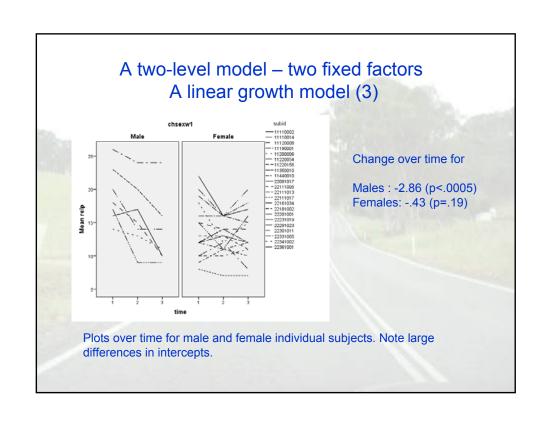
mixed relp by chsexw1 with time/
fixed=intercept time chsexw1 time\*chsexw1/
random=intercept time | subject(subid)/
print=solution testcov.

Time is specified after with and is included in the random statement.

This analysis would give rise to individual growth curves.

<sup>\*</sup> ML rather than REML was used to allowed comparison of models with different random structures.





# Further possibilities: - Models with more than two levels - Other residual structures in repeated measures - Treatment of missing data - Theoretical background – how the correlations between observations affects significance tests in within- and between-subjects models - Correlated observations in entirely between-subjects models