

Two-level models for ordinal outcomes

The data

To illustrate the application of the mixed-effects ordinal probit regression model to longitudinal data, we examined data collected in the NIMH Schizophrenia Collaborative Study on treatment related changes in overall severity. For the present illustration of the ordinal mixed-effects model, we recoded the seven ordered categories of Imps79 into four: 1) normal or borderline mentally ill, 2) mildly or moderately ill, 3) markedly ill, and 4) severely or among the most extremely ill.

For both models discussed in this section and the next example, the repeated ordinal IMPS score (Imps79O) is modeled in terms of a dummy-coded drug effect (TxDrug: placebo = 0 and drug = 1), a time effect (SqrtWeek: square root of week) and a drug by time interaction (Tx*SWeek). In terms of the random effects, this example specifies a random intercepts model, while the next example will show a model that makes allowance for patients to vary in terms of both their intercept and their trend across time (random intercepts and slopes).

The models

To motivate the ordinal regression model, it is often assumed that there is an unobservable latent variable (y) which is related to the actual response through the "threshold concept". For the dichotomous model, one threshold value is assumed, while for the ordinal model, a series of threshold values $\gamma_1, \gamma_2, ..., \gamma_{J-1}$, where J equals the number of ordered categories, $\gamma_0 = -\infty$, and $\gamma_J = \infty$, is assumed. Here, a response occurs in category j (Y = j) if the latent response process y exceeds the threshold value γ_{j-1} , but does not exceed the threshold value γ_j .

Assume that there are i = 1,...N level-2 units and $k = 1,...,n_i$ level-1 units nested within each level-2 unit. The mixed-effects regression model for the latent response variable y_{ik} can be written as follows:

$$y_{ik} = \mathbf{x}_{ik} \mathbf{\beta}_i + \mathbf{w}_{ik} \mathbf{\alpha} + e_{ik}$$

where \mathbf{w}_{ik} is the $p \times 1$ covariate vector and \mathbf{x}_{ik} is the design vector for the r random effects, both vectors being for the k-th level-1 unit nested within level-2 unit i. Also, α is the $p \times 1$ vector of unknown fixed regression parameters, $\boldsymbol{\beta}_i$ is the $r \times 1$ vector of unknown random effects for the level-2 unit i, and e_{ik} are the model residuals. The distribution of the random effects is assumed to be multivariate normal with mean vector $\boldsymbol{\mu}$ and covariance matrix $\boldsymbol{\Sigma}_{\boldsymbol{\beta}}$, and the residuals are assumed to be independently normally distributed with mean 0 and variance σ^2 .

A model with probit link function and random intercept

In the first example of this section we consider the model

$$y_{ik} = \beta_{i0} + \alpha_0 + \alpha_1 \text{TxDrug}_{ik} + \alpha_2 \text{SqrtWeek}_{ik} + \alpha_3 \text{Tx*SWeek}_{ik} + e_{ik}$$

With the above mixed-effects regression model for the underlying and unobservable variable y_{ik} , the probability, for a given level-2 unit i, that $Y_k = j$ (a response occurs in category j), conditional on β and α , is given by the following equation:

$$P(Y_k = j \mid \boldsymbol{\beta}_i, \boldsymbol{\alpha}) = \Phi[(\gamma_j - z_{ik}) / \sigma] - \Phi[(\gamma_{j-1} - z_{ik}) / \sigma]$$

where $z_{ik} = \mathbf{x}_{ik}' \mathbf{\beta}_i + \mathbf{w}_{ik}' \mathbf{\alpha}$ and $\Phi(\cdot)$ represents the cumulative standard normal density function. Without loss of generality, the origin and unit of z may be chosen arbitrarily. For convenience, let $\gamma_1 = 0$ and $\sigma = 1$, then

$$P(\text{Imps79O}_{ik} = j \mid \boldsymbol{\beta}_i, \boldsymbol{\alpha}) = \Phi(\gamma_i - z_{ik}) - \Phi(\gamma_{i-1} - z_{ik}).$$

A model with probit link function with random intercept and slope

In the second example we again consider the model

$$y_{ik} = \beta_{i0} + \beta_{i0} \text{SqrtWeek}_{ik} + \alpha_0 + \alpha_1 \text{TxDrug}_{ik} + \alpha_2 \text{SqrtWeek}_{ik} + \alpha_3 \text{Tx*SWeek}_{ik} + e_{ik}$$

where the vector of unknown parameters β_i in the mixed-effects regression model

$$y_{ik} = \mathbf{x}_{ik}^{'} \mathbf{\beta}_{i} + \mathbf{w}_{ik}^{'} \mathbf{\alpha} + e_{ik}$$

is extended to include both intercept and slope (SqrtWeek) effects.

Example: Probit link function with random intercept

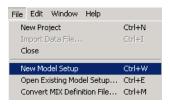
Preparing the data

The model is fitted to the data in **schizx1.ss3**. Use the **File**, **Open** option to activate an **Open** dialog box, and browse for the file **schizx1.xls** in the **Examples** folder.

schizx1.ss3 □ x													
1103	1103 <u>Apply</u>												
	(A) Patient	(B) Imps79	(C) Imps79	(D) Imps79	(E) TxDrug	(F) Week	(G) SgrtWeek	(H) Tx*SWeek					
1	1103	5.50	1	4	1	0	0.00	0.00					
2	1103	3.00	0	2	1	1	1.00	1.00					
3	1103	-9.00	-9	-9	1	2	1.41	1.41					
4	1103	2.50	0	2	1	3	1.73	1.73					
5	1103	-9.00	-9	-9	1	4	2.00	2.00					
6	1103	-9.00	-9	-9	1	5	2.24	2.24					
7	1103	4.00	1	2	1	6	2.45	2.45					
8	1104	6.00	1	4	1	0	0.00	0.00					
9	1104	3.00	0	2	1	1	1.00	1.00					
10	1104	-9.00	-9	-9	1	2	1.41	1.41 ▼					
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Setting up the analysis

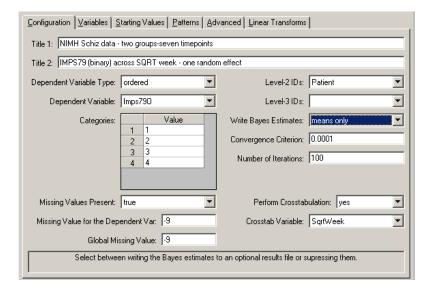
The next step is to describe the model to be fitted. We use the SuperMix interface to provide the model specifications. From the main menu bar, select the **File**, **New Model Setup** option.



The Model Setup window that appears has six tabs. In this example, the Configuration, Variables, and Advanced tabs are used in model specification. By default, the Configuration screen is displayed on top.

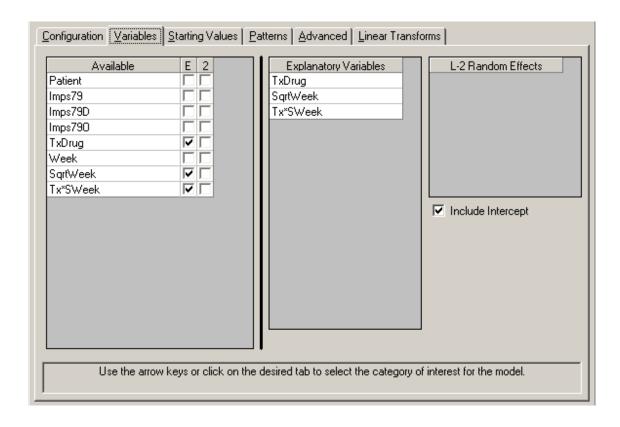
As a first step, enter a title for the analysis in the **Title 1** and **Title 2** text boxes. The patient identification variable (Patient) is used to define the hierarchical structure of the data, and is selected as the Level-2 ID from the **Level-2 IDs** drop-down list box. Select the ordinal outcome variable Imps79O from the **Dependent Variable** drop-down list box. Specify the type of outcome as ordered using the **Dependent Variable Type** drop-down list box. Once this selection is made, the **Categories** grid is displayed, with the distinct values of the categories shown.

The Missing Values Present drop-down list box is used to specify the values of missing data for both outcome and predictors. As a first step, set the value of the Missing Values Present drop-down list box to True. The appearance of the screen will change when this is done, and text boxes for the specification of the missing data codes are displayed. Start by entering the value -9 in the Missing Value for the Dependent Var text box. Do the same for all the predictors included in the model by entering -9 in the Global Missing Value text box. In terms of the missing value specification, notice that even though missing values are coded only for the dependent variable in the input data file, numeric missing value codes must be specified in the model specification file for all model terms (if Missing Values Present = True). In this case, the value -9 was specified for all variables since for the dependent variable this value is the correct missing value code, while for all other model terms (Intcept, TxDrug, SqrtWeek, and Tx*SWeek) this value was never observed. Once -9 is entered in the Missing Value for Dependent Var text box, the categories grid will automatically be updated to display 1, 2, 3, and 4 only.

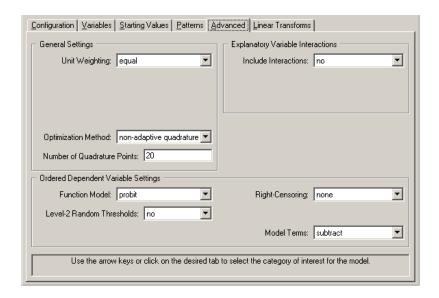


Request a crosstabulation of the variable SqrtWeek by the response variable Imps790 by selecting the **yes** option from the **Perform Crosstabulation** drop-down list box, followed by the selection of SqrtWeek as the **Crosstab Variable**. Finally, request the writing out of Bayes estimates using the **Write Bayes Estimates** drop-down list box. The default setting for the **Number of Iterations** text box is used. Proceed to the **Variables** screen by clicking on this tab.

The **Variables** screen is used to specify the fixed and random effects to be included in the model. Select the explanatory (fixed) variables TxDrug, SqrtWeek, and Tx*SWeek using the check boxes next to the variable names in the **E** column of the **Available** grid. After selecting all the explanatory variables, the random effect(s) at level 2 must be selected. By default, an intercept will be included in the fixed part of the model, as indicated by the check box next to **Include Intercept** in the **Explanatory Variables** grid. Similarly, a random intercept at level 2 is assumed. The intercept is assumed to vary randomly over higher levels of the hierarchy, while the slopes of the predictors TxDrug, SqrtWeek, and Tx*SWeek are assumed to be adequately described by common, fixed coefficients. The completed **Variables** screen is shown below. To change estimation settings such as the number of quadrature points used in estimation, the **Advanced** screen is used. Click **Advanced** to access this screen and complete the model specification process.

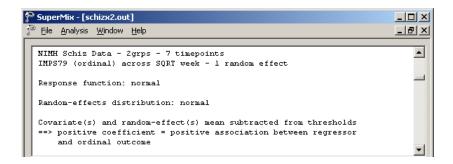


Set the **Function Model** option to probit. All other settings on this screen are left at their previous values, and we can save our model specification to file prior to running the analysis. Select the **File**, **Save** option, provide a name for the model specification file (such as **schizx2.mum**), and run the analysis by selecting the **Run** option from the **Analysis** menu.

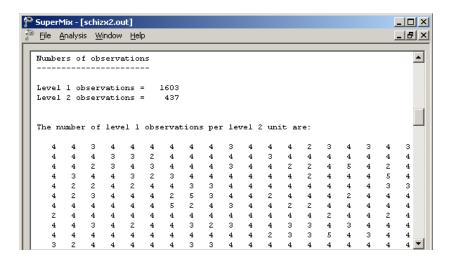


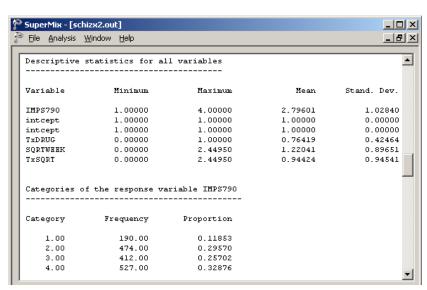
Discussion of results

Portions of the output file **schizx2.out** are shown below.



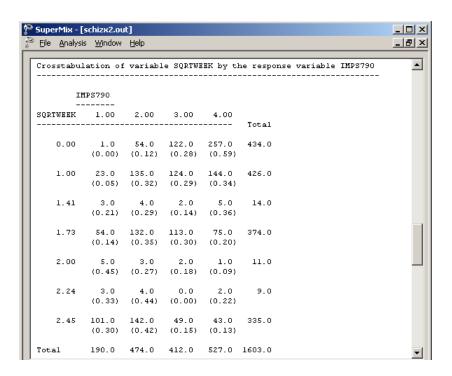
In the first section of the output file, a description of the model specifications is provided. The use of a normal response function (probit link function), and the assumption of a normal distribution of random effects are reported. This is followed by a summary of the number of measurements nested within each subject. Note that for some of the 437 subjects, only 2 measurements are available for analysis.



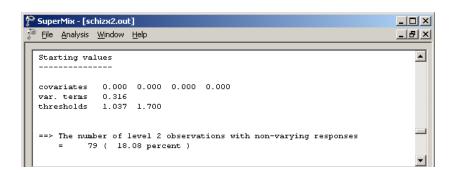


The data summary is followed by descriptive statistics for all the variables included in the model. We note that 33% of the measurements were in the highest category of the outcome variable and correspond to the "severely or among the most extremely ill" group. Only 12% of measurements are in the first category ("normal, not at all ill").

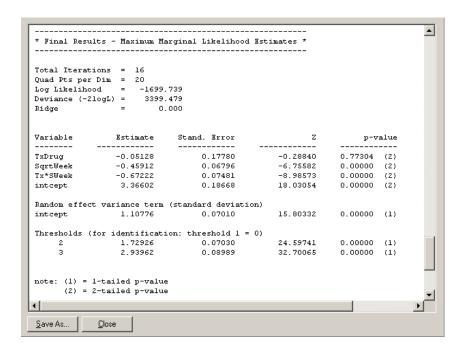
The following portion of the output is a crosstabulation of the seven distinct values of the variable SqrtWeek by the four categories of the outcome variable IMPS790. We note that there are relatively few observations for the third, fifth and sixth weeks. For example, for week 5 (SqrtWeek = 2.24), measurements on only 9 of the 437 patients are available.



The starting values for all parameters are given next. Starting values for the predictors TxDrug, SqrtWeek and TX*SWeek are given in the first line (covariates), while the starting value for the variance component associated with the random level-2 intercept is given in the second line (var. terms). In 18% of the subjects, no change in the category assigned for measurements was observed, as indicated by the last two lines shown below. Since the first threshold is fixed at 0 for identification purposes, starting values for the second and third thresholds only are listed.



The output summarizing the estimated parameters after convergence is shown next. Eighteen iterations were required to obtain convergence. The estimates are shown in the column with heading Estimate, and correspond to the coefficients $\alpha_0, \alpha_1, \alpha_2$, and α_3 in the model specification. The effect of TxDrug was the only nonsignificant effect.



The variation in the intercept over the subjects is estimated as $1.10776^2 = 1.2271$, and from the associated *p*-value we conclude that there is significant variation in the (random) intercept between the patients included in this analysis. In the case of the fixed effects, a 2-tailed *p*-value is used, as the alternative hypothesis considered here is of the form $H_1: \beta \neq 0$. As variances are constrained to be elements of the interval $[0, +\infty)$, the *p*-values used for these effects are 1-tailed. No estimate of the level-1 variance is given, as there is no single level-1 variance for this model.

The results indicate that the treatment groups do not differ significantly at baseline (TxDrug coefficient is not significant). The placebo group seems to improve over time, as the SqrtWeek coefficient is both significant and negative. Note that the interpretation of the main effects depends on the coding of the variable, and significance of, the Tx*SWeek interaction which forms part of the model.

The connection between an ordinal outcome variable y with NCAT categories and an underlying continuous variable y^* is

$$y = j \leftrightarrow \gamma_{j-1} \le y^* \le \gamma_j, \ j = 1, 2, ..., NCAT$$

where it is assumed that $\gamma_0 = -\infty$ and $\gamma_{NCAT} = +\infty$. In addition, γ_1 is usually set to 0 to avoid identification problems. For the present example, NCAT = 4, and from the output we see that $\gamma_2 = 1.72926$ and $\gamma_3 = 2.93962$. These values are used in combination with the coefficients of TxDrug, SqrtWeek, and Tx*SWeek to calculate estimated outcomes for different groups of patients.

Estimated unit-specific probabilities

To evaluate the expected effect of the drug treatment TxDrug and the square of time of treatment, while allowing for the interaction between treatment and the square of time, we use the expression below:

$$\hat{z_{ik}} = 3.36602 - 0.05128 \text{ TxDrug}_{ik} - 0.45912 \text{ SqrtWeek}_{ik} - 0.67222 \text{ Tx} \times \text{SWeek}_{ik}$$

For a typical patient from the control group (TxDrug = 0, SqrtWeek = Tx*SWeek = 0),

$$z_{ik}^{\hat{}} = 3.36602.$$

The probabilities that a typical patient from the control group responded in a specific category at the start of the study are obtained by noting that $\gamma_0 = -\infty$, $\gamma_1 = 0$, $\gamma_2 = 1.72926$, and $\gamma_3 = 2.93962$.

Let $p = \Phi(a) = P(Z \le a)$ where Z has a standard normal distribution. To compute p for a given value of a, use is made of a probability calculator. These calculators can, for example, be found on the internet.

Since $z_{ik} = 3.36602$, it follows that

$$\Phi(\gamma_0 - z_{ik}) = \Phi(-\infty) = 0$$

$$\Phi(\gamma_1 - z_{ik}) = \Phi(-3.36602) = 0.0004$$

$$\Phi(\gamma_2 - z_{ik}) = \Phi(-1.63676) = 0.0508$$

$$\Phi(\gamma_3 - z_{ik}) = \Phi(-0.42640) = 0.3349.$$

Therefore

$$P(\text{Imps79O} = 1) = \Phi(\gamma_1 - z_{ik}) - \Phi(\gamma_0 - z_{ik})$$

$$= 0.0004$$

$$P(\text{Imps79O} = 2) = \Phi(\gamma_2 - z_{ik}) - \Phi(\gamma_1 - z_{ik})$$

$$= 0.0508 - 0.0004$$

$$= 0.0504$$

$$P(\text{Imps79O} = 3) = \Phi(\gamma_3 - z_{ik}) - \Phi(\gamma_2 - z_{ik})$$
$$= 0.3349 - 0.0508$$
$$= 0.2841$$

and

$$P(\text{Imps79O} = 4) = 1 - P(\text{Imps79O} = 3) - P(\text{Imps79O} = 2) - P(\text{Imps79O} = 1)$$

= 1 - 0.2841 - 0.0504 - 0.0004
= 0.6651.

for the four categories of Imps790. We can compare these predicted probabilities with the observed data for the control group as shown in Table 3.3 below. The ratio of responses in the categories of Imps790 when SqrtWeek = 0 are 0.000, 0.102, 0.336 and 0.561 respectively. For example, if Imps790 = 4, the ratio is $\frac{60}{107}$.

Table 3.3: Crosstabulation of Imps79O and SqrtWeek for control group

		SqrtWeek							
		.0000	1.0000	1.4142	1.7321	2.0000	2.2361	2.4495	
Imps79O	1	0	2	0	3	0	0	8	13
	2	11	25	0	24	0	1	24	85
	3	36	26	1	26	1	0	16	106
	4	60	52	4	34	1	1	22	174
Total		107	105	5	87	2	2	70	378

At the end of the study, the corresponding ratios for the observed data were 0.00, 0.10, 0.34, and 0.56 respectively. Here, the variable SqrtWeek = 2.4495 and thus

$$\hat{z}_{ik} = 3.36602 - 0.45912 \text{ SqrtWeek}_{ik}$$

= 3.36602 - (0.45912)(2.4495)
= 2.24141.

The probabilities that a typical patient from the control group responded in a specific category at the conclusion of the study period are obtained as

$$\Phi(\gamma_1 - z_{ik}) = \Phi(-2.24141) = 0.01250$$

$$\Phi(\gamma_2 - z_{ik}) = \Phi(-0.51214) = 0.30428$$

$$\Phi(\gamma_3 - z_{ik}) = \Phi(0.69821) = 0.75748.$$

Therefore

$$P(\text{Imps79O} = 1) = \Phi(\gamma_1 - z_{ik}) - \Phi(\gamma_0 - z_{ik})$$

$$= 0.01250$$

$$P(\text{Imps79O} = 2) = \Phi(\gamma_2 - z_{ik}) - \Phi(\gamma_1 - z_{ik})$$

$$= 0.30428 - 0.01250$$

$$= 0.29178$$

$$P(\text{Imps79O} = 3) = \Phi(\gamma_3 - z_{ik}) - \Phi(\gamma_2 - z_{ik})$$

$$= 0.75748 - 0.30428$$

$$= 0.45320$$

and

$$P(\text{Imps79O} = 4) = 1 - P(\text{Imps79O} = 3) - P(\text{Imps79O} = 2) - P(\text{Imps79O} = 1)$$

= $1 - (0.45320 + 0.29178 + 0.01250)$
= 0.24252 .

The estimated probabilities for a typical patient from the treatment group at the start of the study (TxDrug = 1, SqrtWeek = Tx*SWeek = 0) can be calculated in a similar fashion, using

$$z_{ik}^{\hat{}} = 3.36602 - 0.05128$$

= 3.31474

The probabilities that a typical patient from the treatment group responded in a specific category at the start of the study are obtained as

$$\Phi(\gamma_1 - z_{ik}) = \Phi(-3.31474) = 0.00046$$

$$\Phi(\gamma_2 - z_{ik}) = \Phi(-1.58548) = 0.05643$$

$$\Phi(\gamma_3 - z_{ik}) = \Phi(-0.37512) = 0.35379.$$

Therefore

$$P(\text{Imps79O} = 1) = \Phi(\gamma_1 - z_{ik}) - \Phi(\gamma_0 - z_{ik})$$

= 0.00046

$$\begin{split} P(\text{Imps79O} = 2) &= \Phi(\gamma_2 - z_{ik}) - \Phi(\gamma_1 - z_{ik}) \\ &= 0.05643 - 0.00046 \\ &= 0.05597 \\ P(\text{Imps79O} = 3) &= \Phi(\gamma_3 - z_{ik}) - \Phi(\gamma_2 - z_{ik}) \\ &= 0.35379 - 0.05643 \\ &= 0.29736 \end{split}$$

and

$$P(\text{Imps79O} = 4) = 1 - P(\text{Imps79O} = 3) - P(\text{Imps79O} = 2) - P(\text{Imps79O} = 1)$$

= 1 - 0.29736 - 0.05597 - 0.00046
= 0.64621

for the four groups defined by the categories of Imps790.

At the end of the study, the corresponding ratios for the observed data were 0.35, 0.45, 0.12, and 0.08 respectively. Here, the variable SqrtWeek = 2.4495 and thus

$$\hat{z}_{ik} = 3.36602 - 0.05128 \text{ TxDrug}_{ik} - 0.45912 \text{ SqrtWeek}_{ik} - 0.67222 \text{ Tx*SWeek}_{ik}$$

= $3.36602 - 0.05128 - (0.45912)(2.4495) - (0.67222)(2.4495)$
= 0.54354 .

The probabilities that a typical patient from the treatment group responded in a specific category at the conclusion of the study period are obtained as

$$\Phi(\gamma_1 - z_{ik}) = \Phi(-0.54354) = 0.29338$$

$$\Phi(\gamma_2 - z_{ik}) = \Phi(1.18572) = 0.88213$$

$$\Phi(\gamma_3 - z_{ik}) = \Phi(2.39608) = 0.99171.$$

Therefore

$$P(\text{Imps79O} = 1) = \Phi(\gamma_1 - z_{ik}) - \Phi(\gamma_0 - z_{ik})$$

$$= 0.29338$$

$$P(\text{Imps79O} = 2) = \Phi(\gamma_2 - z_{ik}) - \Phi(\gamma_1 - z_{ik})$$

$$= 0.88213 - 0.29338$$

$$= 0.58875$$

$$P(\text{Imps79O} = 3) = \Phi(\gamma_3 - z_{ik}) - \Phi(\gamma_2 - z_{ik})$$
$$= 0.99171 - 0.88213$$
$$= 0.10957$$

and

$$P(\text{Imps79O} = 4) = 1 - P(\text{Imps79O} = 3) - P(\text{Imps79O} = 2) - P(\text{Imps79O} = 1)$$

= 1 - 0.10957 - 0.58875 - 0.29339
= 0.008.

Estimated population-average probabilities

In this section, we defined the latent response variable model as

$$y_{ik} = \mathbf{x}'_{ik} \mathbf{\beta}_i + \mathbf{w}'_{ik} \mathbf{\alpha} + e_{ik}, \quad k = 1, 2, ..., n_i,$$

where \mathbf{x}_{ik} denotes a design vector for the random effects $\boldsymbol{\beta}_i$ and \mathbf{w}_{ik} the design vector for the predictors in the fixed part of the model with corresponding vector $\boldsymbol{\alpha}$ of regression parameters. Denote the covariance matrix of $\boldsymbol{\beta}_i$ by $\boldsymbol{\Sigma}_{\boldsymbol{\beta}_i}$ and the variance of \boldsymbol{e}_{ik} by $\boldsymbol{\sigma}^2$.

For a probit link function $\sigma^2 = 1$, and for a logistic link function $\sigma^2 = \pi^2/3$. Under the assumption that β_i and e_{ik} are independently distributed, it follows that

$$\sigma_{v_{ik}}^2 = \mathbf{x}_{ik}^{'} \mathbf{\Sigma}_{\beta_i} \mathbf{x}_{ik} + \sigma^2.$$

Let

$$d_{ik} = \frac{\sigma_{y_{ik}}^2}{\sigma^2}.$$

The quantity d_{ik} is called the design effect. The estimated population-average probabilities (Hedeker & Gibbons, 2006) are obtained in a similar fashion as the unit-specific probabilities, but with replacing $\hat{\gamma_j} - \hat{z_{ik}}$ by $\left(\hat{\gamma_j} - \hat{z_{ik}}\right) / \sqrt{d_{ik}}$.

To illustrate, we calculate the estimated population-average probabilities for the control group associated at the end of the study.

From the output, we have $var(\beta_{i1}) = (1.10776)^2$, where β_{i1} denotes the intercept coefficient. In this case, $\mathbf{x}'_{ik} = \mathbf{1}$ and hence, with $\sigma^2 = 1$ for the probit link,

$$\sigma_{y_{ik}}^2 = 1 \times 1.227 \times 1 + 1 = 2.227.$$

Therefore

$$d_{ik} = \frac{2.227}{1} = 2.227.$$

Using the unit-specific values for $\hat{\gamma_j} - \hat{z_{ik}}$ obtained previously, it follows that

$$P(\text{Imps79O} = 1) = \Phi(-2.2414/\sqrt{2.227})$$

$$= 0.06655$$

$$P(\text{Imps79O} = 2) = \Phi(-0.51214/\sqrt{2.227}) - \Phi(-1.50197)$$

$$= 0.36573 - 0.06655$$

$$= 0.29918$$

$$P(\text{Imps79O} = 3) = \Phi(0.69821/\sqrt{2.227}) - \Phi(-0.34319)$$

$$= 0.68006 - 0.36573$$

$$= 0.31433$$

and

$$P(\text{Imps79O} = 4) = 1 - P(0.0665 + 0.29918 + 0.31433)$$

= 0.31994.

The estimated population-average probabilities for the control group are summarized in Table 3.4 below.

Table 3.4: Estimated unit-specific probabilities for control group

		SqrtWeek								
		Sta	art of st	udy	Er	Total				
		Obs. Freq	Ratio	Pred. Prob	Obs. Freq	Ratio	Pred. Prob	Total		
Imps79O	1	0	0	0.01	8	0.11	0.07	8		
	2	11	0.10	0.12	24	0.34	0.30	35		
	3	36	0.34	0.25	16	0.23	0.31	52		
	4	60	0.56	0.61	22	0.31	0.32	82		
Total		107			70			177		

A comparison of these probabilities with the observed ratios given in Table 3.4 for the control group at the end of the study indicate that the population-average results are closer to the observed ratios than is the case for the unit-specific results.

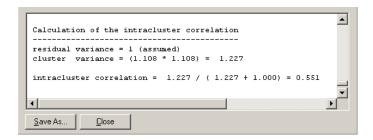
Results for the treatment group are obtained in a similar way and are summarized in Table 3.5 below.

Table 3.5: Estimated population-average probabilities for treatment group

					SqrtWeek					
		Sta	art of st	udy	Er	Total				
		Obs. Freq	Ratio	Pred. Prob	Obs. Freq	Ratio	Pred. Prob	Total		
Imps79O	1	1	0.003	0.01	93	0.35	0.36	94		
	2	43	0.13	0.13	118	0.45	0.43	161		
	3	86	0.26	0.26	33	0.12	0.16	119		
	4	197	0.60	0.60	21	0.08	0.05	218		
Total		327			287			592		

It is interesting to note that the observed frequencies at the start and end of the study are 107 and 70 for the control group, and 327 and 287 for the experimental group. The larger number of observations available in the latter case may partially explain why the predicted probabilities are closer to the observed probabilities for the experimental group when compared to those for the control group. The results clearly demonstrate the effectiveness of a seven week treatment, and the significant drug by time interaction effect: at the end of the study, the estimated population-average proportion of patients in categories 1 or 2 (normal or borderline) are 0.37 for the control group and 0.79 for the treatment group. The corresponding estimated population-average probabilities at the start of the study are 0.13 and 0.14 for the control and experimental groups respectively.

Finally, the estimated intracluster correlation (which in this case is the intra*patient* correlation) for this analysis is given, along with the variation in intercepts over patients.

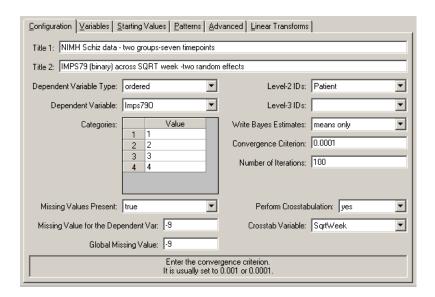


Example: Probit link function with random intercept and slope

To fit a model allowing patients to vary in terms of both their intercept and their trend across time (random intercepts and slopes), the model in the previous example is extended to include both intercept and slope (SqrtWeek) effects.

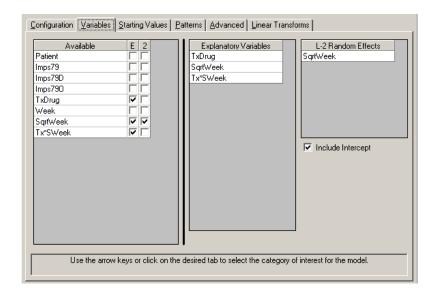
Setting up the analysis

The model is fitted to the data in **schizx1.ss3**, and the model specification file **schizx2.mum** used previously is modified to include a random slope. The first step is to open the **ss3** file, and then the model specification file **schizx3.mum**. This is accomplished by using the **File**, **Open** option to activate the display of an **Open** dialog box, and browsing for the file **schizx1.ss3** in the **Examples** folder. Next, use the **File**, **Open Existing Model Setup** option to activate an **Open** dialog box and browse for the file **schizx2.mum** in the **Examples** folder.



The Model Setup window, with entries corresponding to the contents of the model specification file schizx2.mum is displayed. After adjusting the title in the Title 2 text box of the Configuration screen to reflect the intended changes to the model, proceed to the Variables screen by clicking on this tab.

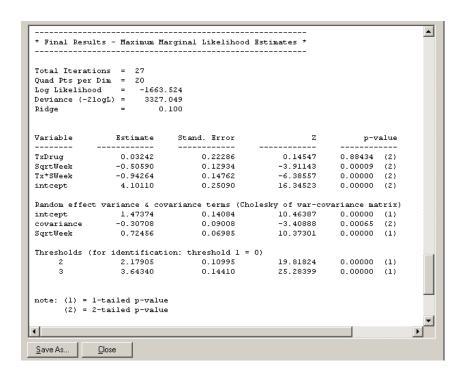
The only change needed on the **Variables** screen is to add the variable SqrtWeek to the **L-2 Random Effects** grid. This is done by checking the check box next to this variable's name under the **2** column of the **Available** grid. Doing so leads to the display of the variable name SqrtWeek in the **L-2 Random Effects** grid as shown below.



Before running the analysis, the model specifications have to be saved. Select the **File**, **Save** option, and provide a new name, for example **schizx3.mum**, for the model specification file. Run the analysis by selecting the **Run** option from the **Analysis** menu.

Discussion of results

Portions of the output file **schizx3.out** are shown below. The estimates are shown in the column with heading Estimate, and correspond to the coefficients α_0 , α_1 , α_2 , and α_3 in the model specification. Results for the fixed effects in this model are similar to those obtained for the random intercepts model. There is significant random variation in the random intercepts and slopes of the patients. For this model, we have $\hat{\gamma}_2 = 2.17905$ and $\hat{\gamma}_3 = 3.64340$, both somewhat higher than those for the previous model ($\hat{\gamma}_2 = 1.72926$ and $\hat{\gamma}_3 = 2.93962$.)



To compare this model to the random intercepts model previously fitted, the likelihood-ratio χ^2 test can be used. Based on this test, there is clear evidence of significant variation in the linear time trends:

$$\chi^2 = -2[-1699.739 - (-1663.354)] = 72.77,$$

(2 degrees of freedom and p < 0.001) over and above the individual intercept variation. Significant negative association between the intercept and linear time terms is indicated, suggesting that those patients with the highest initial severity show the greatest improvement across time (e.g., largest negative time trends).

Note that variances are, by definition, non-negative. It was shown by Miller (1977) and Self & Liang (1987) that, when testing the hypothesis that the variance of a random intercept or slope is zero, the alternative hypothesis is one-sided. This implies that an approximate p-value is obtained as half the p-value obtained from a χ^2 statistic based on the difference in deviances. Snijders & Bosker (1999), compares a random intercept and slope model with a random intercept model. For their example, $\chi^2 = 8.5$ at 2 degrees of freedom with tail probability of p < 0.02, so halving the p-value yields a significant outcome with p < 0.01. Generally speaking, the likelihood-ratio test applied to random coefficients without the adjustment of p-value is conservative.

Finally, the estimated intracluster correlation (which in this case is the intra*patient* correlation) for this analysis is given. The calculation of variance and covariance components is shown, and we note that most of the variation in Imps79O is in intercept, rather than in the slope of SqrtWeek (2.172 vs. 0.619).

