ELECTRONIC APPENDIX: INSTRUCTIONS ON USE OF SOFTWARE AND APPLICATIONS

General. This document is meant to serve as a complement to the printed article by Shah and Madden (2004), abbreviated as SM. Instructions on use of standard procedures and specialized macros in SAS for performing the nonparametric-marginal-effects analyses (12,15,17)[1] are described. Examples include those discussed explicitly in SM and additional ones shown here for elaboration purposes. Additional instructions on the analyses are found in the actual SAS program ("`SM_NPana.sas`") and annotated output ("`SM_NPana.pdf`") files for all of the data sets.

One-way layout. The potato early dying data set (`omer`) consists of the following variables: `sub =` subject (i.e., a unique identifier for each experimental unit; this variable will be needed later on when using a macro); `isol =` isolate (labeled 83, 111, 120, 201, 202, 203), which is the treatment variable; `rating` = disease rating on a 1 to 6 scale. Omer et al. (52) rated disease at six dates, and calculated area under the curves. The data for assessments made during the third week are analyzed. The first step in analyzing these data is to convert the ordinal ratings to ranks, which can be done with `proc rank`.

```
proc rank data=omer out=omer;
var rating; /* requests ranks for the variable rating */
ranks r; /* the ranks are stored under the variable r */
```

The mid-ranks (`r`), determined as the default in the `rank` procedure, are then used by `proc mixed` to calculate the nonparametric test statistics and significance levels (*P*-values).

```
proc mixed data=omer anovaf;
class isol;
model r = isol / chisq;
repeated / type = un(1) group = isol;
lsmeans isol / pdiff;
contrast 'VCG4A vs VCG4B' isol 1 1 –1 –1 –1 1;
```

The `class` statement indicates that `isol` is a factor variable. The model statement specifies that the rank is a function of `isol`. The Wald-type statistic (WTS) is specified by adding the `chisq` option in the `model` statement. The `anovaf` option on the procedure line is an undocumented enhancement that is required for the calculation of the ANOVA-type statistic (ATS), which is used to test the null hypothesis of no treatment differences (equation 5 in SM) (12). The `repeated` statement is used in `proc mixed` to specify properties of the variances (and covariances; see below) within the experimental units (the subjects). Here, the `type=un(1)`and `group=isol` options used together indicate that there is a different variance for each isolate (each factor level), and that the data from the different experimental units are not correlated. The `lsmeans` statement generates the rank means ($\overline{R}_{i\bullet}$). Estimated relative treatment effects ($\hat{p}_i$) can be easily calculated from equation 4 in SM. The `pdiff` option in the `lsmeans` statement requests all pairwise comparisons of mean ranks among treatment levels. These should be considered approximations because they are based on the standard errors estimated by `proc mixed`, which may be inaccurate (17). The `contrast` statement is used to specify linear contrasts of the mean ranks. Here, it is used to test the equality of the 4A and 4B isolates (the first, second, and last isolate are of compatibility group 4A).

[1] Citations and equation numbers refer to the printed version of the article (SM).

Part of the output from use of `mixed` is displayed in Box 1. Note that the ATS and WTS are both significant here, and that the degrees of freedom for the ATS test are not integers.

WTS statistics, etc., in **blue**

Box 1: Partial Output from one-way layout example

Type 3 Tests of Fixed Effects

Effect	Num DF	Den DF	Chi-Square	F Value	Pr > ChiSq	Pr > F	ANOVA Num DF	ANOVA Den DF
isol	5	42	135.35	27.07	<.0001	<.0001	3.86	30.6

Type 3 Tests of Fixed Effects

Effect	ANOVA Chi-Square	ANOVA F Value	ANOVA Pr > ChiSq	ANOVA Pr > F
isol	10.10	10.10	0.0177	<.0001

The ATS df, statistics and *P* values (in **red**) are provided with the ANOVAF option.

Contrasts

Label	Num DF	Den DF	F Value	Pr > F	ANOVA Num DF	ANOVA Den DF	ANOVA F Value	ANOVA Pr > F
VCG4A vs VCG4B	1	42	20.47	<.0001	1	30.6	20.47	<.0001

Contrast of VCG4A and VCG4B.

Least Squares Means

Effect	isol	Estimate	Standard Error	DF	t Value	Pr > |t|
isol	111	27.7500	2.4550	42	11.30	<.0001
isol	120	21.5625	4.6660	42	4.62	<.0001
isol	201	17.6250	4.2022	42	4.19	0.0001
isol	202	11.6250	2.7004	42	4.30	<.0001
isol	203	25.6875	3.5342	42	7.27	<.0001
isol	83	42.7500	1.4423	42	29.64	<.0001

In addition to the desired statistics, the output from `proc mixed` includes several items that are not relevant to this nonparametric analysis. For instance, the standard normal-based linear-model *F* test (`F Value = 27.07`; in black here) for the isolates is calculated, which should just be ignored. Moreover, `mixed` does not directly calculate the standard errors, variances, and confidence intervals for the $\hat{p}_i$ values. To obtain these, one must use the `LD_CI` macro. Note that for the LD_CI macro to work properly, the data set must not contain any missing values (but equal sample sizes are not required). For a one-way layout, the macro is invoked with five arguments. The argument `alpha` specifies the type I error probability α. For this example, the SAS code is

```
%LD_CI(data=omer, var=rating, group=isol, alpha=0.05,
subject=sub);
```

Note that the actual disease variable (not the ranking) is specified. Results are shown in Box 2. The Variance (*Var*) in the output actually is the variance of $\sqrt{N}(\hat{p}_i - p_i)$, where N is number of observations (here), p_i is the true relative effect (a constant), and $\hat{p}_i$ is the estimate of the relative effect. For short, this can be written as: $\sqrt{N} \cdot \hat{p}_i$. The standard error (se) of $\hat{p}_i$ is given by: $(Var/N)^{1/2}$.

Box 2: Partial output (potato early dying)

```
Bias-Estimation and Confidence-Intervals for Relative Effects


SAS-Data-Filename: omer
Response-Variable: dis3          Observations:        48
Group-Variable:    isol          Groups:               6
Time-Variable:     _none_        Timepoints:           1
Subject-Variable   sub           Subjects:            48


Relative Effects, Biases, Variances and Confidence-Limits (alpha=0.05)


Group    RE       Bias     Variance lower    upper

111        .56771   .00000   .12565   .46539   .66227
120        .43880   .00000   .33708   .29119   .60398
201        .35677   .00000   .27509   .23236   .51894
202        .23177   .00000   .12193   .15663   .35627
203        .52474   .00000   .20817   .39739   .64761
83         .88021   .00000   .01711   .81933   .90368
```

Relative effects (p_i) for each isolate.

RE: estimated relative effect (*p_hat* = $\hat{p}$)

Variance (*Var*): Variance of $(\sqrt{N})\cdot(p\_hat - p)$, not variance of *p_hat*. The standard error of *p_hat* can be determined by: $\sqrt{(Var/N)}$.

Note that one can obtain the estimates of the relative effects by subtracting ½ from the mean ranks in Box 1 and dividing by 48 (*N*). Results for this analysis are presented and discussed in more detail in the printed version of the article (SM).

Many programs could be used to perform a classic Kruskal-Wallis (KW) test for this one-way layout (such as `npar1way` in SAS). One can actually use `proc mixed` to perform this traditional test by overriding the residual error variance with the theoretical value. For a general case, with one factor labeled `trt`, with six levels (six different treatments), eight replication of each treatment, with data ranks labeled `r`, and the data in a file labeled `a`, one can use:

```
proc mixed data=a noprofile;
class trt;
model r = trt / chisq; * the WTS (chisquare) is KW statistic here;
parms (196) / eqcons=1; *forces error variance to be fixed ;
```

A KW test is based on a single theoretical variance (see pages 17-18 of Brunner and Puri [17]) under the null hypothesis of no treatment effect, $N\cdot(N+1)/12$. For this example, $N = 6\cdot 8 = 48$. Thus, the variance is $48\cdot 49/12 = 196.0$ here. The `parms` statement indicates a starting value for the residual variance. To force `mixed` to not update or modify this value, one must use `eqcons=1` as an option on the `parms` statement (indicating that the first [and only] variance term is *eq*ual to the specified *cons*tant) and `noprofile` as an option on the procedure statement. The WTS (obtained with the `chisq` option) *is* the KW test statistic for the case with no ties. More details for this hypothetical example are found in the SAS program file and annotated output accompanying this article. The use of another macro, OWL, is also demonstrated in these files for this one-way layout.

Two-way crossed factorial. The biocontrol data set (`krause`) consists of variables for:

potting mix type (`potting = 1,…,9;` actual descriptions are given in the Krause et al. [35]), fortification status (mix had been either fortified or not [`bioadd = 1` (i.e., natural) or `2` (i.e. fortified)] with a combination of biocontrol organisms; subject (`sub`; unique identifier for each observation), and disease rating (`dismd`). The median rating across the five sub-samples (pots) for each replication of each mix-fortification combination was determined before the data file was created and used in the analysis. There were 32 plants per pot, and the ratings of these were first averaged to obtain the pot values. It would have been more consistent with the nonparametric approach to use median ratings per pot, but the raw data for the plants were not available. `Proc mixed` can be used to calculate the nonparametric statistics for this data set. The analysis begins with obtaining the midranks (`r`) of the ratings, as described above, and then the invocation of `mixed`:

```
proc rank data=krause out=krause;
var dismd; /* requests ranks for the variable dismd */
ranks r; /* the ranks are stored under the variable r */

proc mixed data=krause anovaf;
class bioadd potting;
model r = bioadd | potting / chisq;
repeated / type=un(1) group=bioadd*potting;
lsmeans bioadd | potting;
```

It is important to re-emphasize the need for the `anovaf` undocumented option to obtain the ATS for the ranks. The "`bioadd | potting`" term in the `model` statement is a shorthand way of writing the two main effects and the interaction terms (= `bioadd potting bioadd*potting`). The "`group=bioadd*potting`" option on the `repeated` statement indicates that a separate variance is specified for each combination of fortification and potting mix. For factorial crossed designs in general, one uses this statement to select the proper options for conducting the nonparametric analysis of ranks. If there were three crossed factors (`A, B`, and `C`), one would use the following pair of statements to perform the analysis:

```
model r = A|B|C / chisq;
repeated / type=un(1) group=A*B*C;
```

Model fitting with `proc mixed` involves so-called restricted (or residual) maximum likelihood, which is an iterative procedure. If the method fails to converge (which might happen when all the rating values of one treatment are identical), then one can add the option `method=mivque0` to the `mixed` statement to perform a so-called minimum variance quadratic unbiased estimation procedure. This option can be used at all times with the nonparametric methods discussed in SM.

The `lsmeans` statement in `proc mixed` gives the mean ranks, which can be used to obtain the estimated relative treatment effects (equation 10 in SM), but the variances and confidence limits of the estimated p_{ij} should be obtained using the `LD_CI` macro. Partial output for the biocontrol example is given in Box 3.

The WTS results are shown in **blue**.

Box 3. Partial output (biocontrol factorial).

Type 3 Tests of Fixed Effects

Effect	Num DF	Den DF	Chi-Square	F Value	Pr > ChiSq	Pr > F
bioadd	1	126	3.54	3.54	0.0598	0.0621
potting	8	126	529.28	66.16	<.0001	<.0001
bioadd*potting	8	126	18.84	2.36	0.0157	0.0214

The ATS df, statistics, and *P* values (in **red**) are provided with the ANOVAF option..

Type 3 Tests of Fixed Effects

Effect	ANOVA Num DF	ANOVA Den DF	ANOVA Chi-Square	ANOVA F Value	ANOVA Pr > ChiSq	ANOVA Pr > F
bioadd	1	89.1	3.54	3.54	<.0001	0.0631
potting	6.83	89.1	49.26	49.26	<.0001	<.0001
bioadd*potting	6.83	89.1	2.49	2.49	0.8697	0.0231

The $\overline{R}_{ij}$ are the LS Means estimates.

Least Squares Means

Effect	bioadd	potting	Estimate	Standard Error	DF	t Value
bioadd	1		75.8542	2.5610	126	29.62
bioadd	2		69.1458	2.4789	126	27.89
potting		1	21.2500	3.0981	126	6.86
potting		2	88.8750	5.1375	126	17.30
potting		3	73.8125	5.9121	126	12.49
potting		4	26.6250	3.6479	126	7.30
potting		5	111.91	7.1471	126	15.66
potting		6	104.34	6.0780	126	17.17
potting		7	26.0625	4.0926	126	6.37
potting		8	104.72	6.1633	126	16.99
potting		9	94.9063	5.4986	126	17.26
bioadd*potting	1	1	21.9375	4.6266	126	4.74
bioadd*potting	1	2	95.1250	7.1712	126	13.26
bioadd*potting	1	3	93.2500	11.6051	126	8.04
bioadd*potting	1	4	23.3750	5.0194	126	4.66
bioadd*potting	1	5	107.94	11.0951	126	9.73
bioadd*potting	1	6	105.56	7.9105	126	13.34
bioadd*potting	1	7	25.3125	5.4959	126	4.61
bioadd*potting	1	8	100.81	6.3210	126	15.95
bioadd*potting	1	9	109.38	6.5341	126	16.74
bioadd*potting	2	1	20.5625	4.1214	126	4.99
bioadd*potting	2	2	82.6250	7.3586	126	11.23
bioadd*potting	2	3	54.3750	2.2653	126	24.00
bioadd*potting	2	4	29.8750	5.2947	126	5.64
bioadd*potting	2	5	115.88	9.0123	126	12.86
bioadd*potting	2	6	103.13	9.2301	126	11.17
bioadd*potting	2	7	26.8125	6.0658	126	4.42
bioadd*potting	2	8	108.63	10.5825	126	10.26
bioadd*potting	2	9	80.4375	8.8456	126	9.09

Note that the significance level for the WTS and ATS are different, with the former being preferred because of the moderate sample sizes here. The test of main effects and interactions for a 2-way layout such at this one could also have been done using the SAS macro `npar`, available at E. Brunner's web site (http://www.ams.med.uni-goettingen.de/Projekte/LD/Makros_LD.html).

The `LD_CI` macro for estimating relative effects, their standard errors, and confidence intervals, is designed to be used for just one crossed factor (and also up to one time or sub-plot

factor; see below). Therefore, one must use a variable label for the combination of potting mix and fortification in this example (`trt`). If the data file did not already have such a variable, one could easily be created in the `data` step if `bioadd` was coded as 1 ("natural") and 2 ("fortified") with the statement: "`trt = 10*bioadd + potting;`". This creates a two-digit label, ranging from 11 for the first level of `bioadd` and `potting`, to 29 for the second level of `bioadd` and highest level ("9") of `potting`. A subject identifier is also needed (`sub`), which corresponds to a unique number for each observation with crossed factorials. The macro is invoked with:

```
%LD_CI(data=krause, var=dismd, group=trt, alpha=0.05,
subject=sub);
```

Results for this analysis are given in Box 4.

Box 4. Partial output (biocontrol factorial)

Relative Effects, Biases, Variances and Confidence-Limits (alpha=0.05)

Group	RE	Bias	Variance	lower	upper
11	.14887	.00000	.12874	.10130	.22041
12	.65712	.00000	.35004	.55443	.74544
13	.64410	.00000	.83086	.48468	.77400
14	.15885	.00000	.15076	.10726	.23589
15	.74609	.00000	.76487	.57613	.85828
16	.72960	.00000	.40830	.61195	.81892
17	.17231	.00000	.17167	.11671	.25350
18	.69661	.00000	.28554	.60211	.77526
19	.75608	.00000	.30466	.65335	.83307
21	.13932	.00000	.10906	.09562	.20546
22	.57031	.00000	.34064	.47338	.66154
23	.37413	.00000	.02241	.35006	.39893
24	.20399	.00000	.15760	.14804	.27808
25	.80122	.00000	.50093	.65542	.88883
26	.71267	.00000	.53805	.57809	.81447
27	.18273	.00000	.20874	.12161	.27220
28	.75087	.00000	.69084	.58928	.85813
29	.55512	.00000	.48176	.44076	.66329

RE: estimated relative effect (*p_hat* = $\hat{p}$)

Coding for combination of `bioadd` (fortification; 1 or 2) and `potting` mix (1 to 9)

Variance (*Var*): Variance of $(\sqrt{N})\cdot(p\_hat - p)$, not variance of *p_hat*. The standard error of *p_hat* can be obtained from: $\sqrt{(Var/N)}$. $N = 144$ in this example.

A full discussion of the results is given in the printed version of this article (SM).

Repeated measures – powdery mildew of wheat example. P. E. Lipps and L. V. Madden (unpublished data) evaluated the severity of powdery mildew (caused by *Blumeria graminis* (DC.) E. O. Speer f. sp. *tritici* Ém. Marchal) on three wheat cultivars (Becker, Cardinal, Dynasty), as part of a multi-year variety evaluation. They assessed 10 tillers per plot and used a 0 to 10 rating scale (39) in assessing the severity of powdery mildew on each rated tiller. The scale involves both the highest leaf where symptoms are observed and the area visibly diseased on this leaf. The data set

analyzed in this example consists of the median ratings over the 10 tillers assessed in each plot. Disease assessments were done at Feekes growth stages 8, 9, 10, 10.3, and 10.5.1. There were four replicate plots for each cultivar.

The `F1_LD_F1` macro is used to determine the effects of cultivar and time, and whether there was a significant cultivar×time interaction:

```
%F1_LD_F1(data=wheat, factor=cultivar, var=dis, time=time,
subject=sub);
```

This SAS macro is invoked with five arguments. The `data` argument is the name of the data set containing the observations. `Factor` is the name of the whole-plot factor (or class) variable, `var` is the name of response variable (not the ranking), `time` is the name of the time factor variable, and `subject` is a name of the subject variable in the data set. Here there are 12 subjects (three cultivars replicated four times). In general, A is used for the whole-plot factor and B for time.

Test statistics indicated a significant effect of cultivar in the overall development of powdery mildew, and a strong effect of time, but no significant interaction (see Box 5). The latter indicates that the disease progress curves were not different in profile. One can also test whether time has an effect for *each* of the levels of cultivar (factor A). This null hypothesis [$H_0^F(B_i)$] can be written as: $H_0^F(B_i): \overline{F}_{i1} = \overline{F}_{i2} = ... = \overline{F}_{ib}$, which can be called the 'no simple time effect' hypothesis. Rejecting this hypothesis for some of the levels of cultivar (i.e., for some *i* values) and not others is one (but not the only) indication of an interaction. The simple time effects were significant ($P < 0.01$) for each cultivar, indicating that disease rating changed over time for all tested cultivars. This is not surprising, given the nonsignificant interaction. The major part of the computer output can, in this example, be reduced to a simple table (Table A1).

TABLE A1. Test statistics for the effects of cultivar and time on the severity of powdery mildew of wheat

	ANOVA-type statistic (ATS)			
Effect	df_N	df_D	ATS	*P* value
Cultivar (C)	1.87	7.90	4.57	0.050
Time (T)	2.53	∞	52.47	<0.001
C×T	3.52	∞	1.76	0.142

[a] df_N = numerator degrees of freedom; df_D = denominator degrees of freedom.

The estimates of the relative effects and their confidence intervals are obtained with the `LD_CI` macro:

```
%LD_CI(data=wheat, var=dis, group=cultivar, time=time,
subject=sub);
```

The macro here is invoked with five arguments. The `data, var, time`, and `subject` arguments have the same definitions as in the `F1_LD_F1` macro. The argument `group` has the same meaning as the argument `factor` in the `F1_LD_F1` macro. Box 6 shows some of the output from this macro. Note that with repeated measures, the estimated relative marginal effects may be (slightly) biased. Figure A1 shows median disease severity plotted over time, as well as the estimated relative treatment effects ($\hat{p}_{ij}$).

Box 5. Partial Output (wheat powdery mildew).

```
Wald-type-statistic
Approximation for   large sample sizes with Chi-Square_DF

                W     DF P_VALUE

A  8.3295 2.0000  .01553
T  323.44 4.0000  .00000
AT 205.16 8.0000  .00000

Anova-type-statistic
Box-Approximation for small sample sizes with Chi-square_DF

                B     DF P_VALUE

A  4.5686 1.8701  .01204
T  52.465 2.5291  .00000
AT 1.7620 3.5211  .14206

Anova-type-statistic
modified Box-Approximation for the whole-plot factor A
        for small sample sizes with F(DF1,DF2)

                B    DF1    DF2 P_VALUE

A 4.5686 1.8701 7.9022  .04970

Tests for the simple >> time << effect (T)
  Wald-type (Chi-square_DF1, asymptotic)
ANOVA-Type (Chi-square_DF1/DF1, asymptotic)

Statistic cultivar T       DF1     P_VALUE

Wald      1         160.53  3.0000  .00000
ANOVA     1         31.733  1.4967  .00000
Wald      6         55.552  3.0000  .00000
ANOVA     6         27.977  2.0435  .00000
Wald      7         636.91  3.0000  .00000
ANOVA     7         7.4391  1.4627  .00211
```

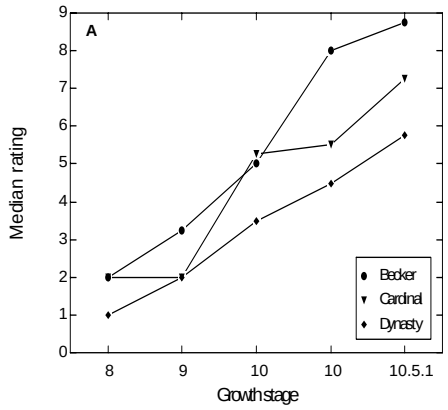
Do not use the Wald type statistics (WTS). The ANOVA-type statistics (ATS) are preferable for sample size situations

B is the value of the test statistic (as in "Box-type statistic). DF is the numerator degrees of freedom. The denominator df is ∞ here. A is the whole plot factor. T is the time factor. AT is the whole plot factor-time interaction.

Chi-square test is used here with ATS, equivalent to F test with ∞ for denominator df. Test appropriate for T and AT.

Use the degrees of freedom and *P* value given by the Box approximation for the F test of the whole plot factor. Note: DF1 and DF2 correspond to df_N and df_D in article.

Tests of simple time effects (see text). Use ANOVA (i.e., ATS) results.



Box 6. Partial Output

Relative Effects, Biases, Variances and Confidence-Limits(alpha=0.05)

Group	Time	RE	Bias	Variance	ower	upper
1	1	.21250	-.0021	.05344	.11529	.37831
1	2	.43542	.00069	.03635	.33278	.54485
1	3	.53333	.00139	.13847	.32996	.72473
1	4	.88958	-.0021	.00118	.86778	.90692
1	5	.95833	.00208	.00052	.92817	.96491
6	1	.16667	-.0007	.02524	.09918	.28339
6	2	.26875	-.0007	.04781	.16692	.41150
6	3	.60208	-.0063	.03365	.49476	.69915
6	4	.67083	.00278	.01722	.59218	.73968
6	5	.79583	.00486	.04399	.64562	.88512
7	1	.15833	.00000	.04847	.07687	.33972
7	2	.26042	-.0028	.13226	.11593	.51465
7	3	.36667	.00486	.14434	.19130	.59554
7	4	.48958	-.0035	.04038	.37868	.60168
7	5	.69167	.00139	.03931	.56826	.78951

Cultivar

Estimates of relative effects (RE: *p_hat* = $\hat{p}$) can be biased with repeated measures.

Variance (*Var*): Variance of $(\sqrt{S})\cdot(p\_hat - p)$, where *S* is number of subjects, not variance of *p_hat*. The standard error of *p_hat* is given by $\sqrt{(Var/S)}\cdot$

Shah and Madden, Fig 1

Figure A1. Median disease ratings (**A**) and estimated relative marginal effects ($\hat{p}_{ij}$) (**B**) for powdery mildew on three wheat cultivars assessed over five growth stages. Vertical bars in **B** represent 95% confidence intervals of $\hat{p}_{ij}$.

Repeated measures – potato early dying example, *revisited*. The data set of Omer et al. (52) is analyzed here. Disease ratings were made on each plant (the subject) at six times, and the effects of `isol`, time (`week`), and their interaction on rating was assessed. The analysis can be done with the `F1_LD_F1` macro:

```
%F1_LD_F1(data = potato, factor=isol, var=rating, time=week,
subject=sub);
```

In this instance there are 48 subjects (six isolates replicated eight times). The data file, `potato`, is of the same format as `omer`, except that there is a variable indicating the time (`week`). Output for

the tests of main effects and interactions are shown in Box 7. As indicated in SM, all effects were significant, including the 'simple time effects' for each level of fungal isolate.

Box 7. Partial output for potato early dying (repeated measures)

```
Analysis using the F1_LD_F1 macro

                Wald-type statistic
Approximation for  large sample sizes with Chi-Square_DF

                     W     DF P_VALUE

A  194.49 5.0000  .00000
T  7282.8 5.0000  .00000
AT 1962.3 23.000  .00000

                ANOVA-type statistic
Box-approximation for small sample sizes with Chi-square_DF

                     B     DF P_VALUE

A  35.276 4.2218  .00000
T  457.78 3.1255  .00000
AT 7.7821 10.898  .00000

                ANOVA-type statistic
modified Box-approximation for the whole-plot factor A
        for small sample sizes with F(DF1,DF2)

     B    DF1    DF2 P_VALUE

A 35.276 4.2218 34.134  .00000

Tests for the simple >> week << effect (T)
  Wald-type (Chi-square_DF1, asymptotic)
ANOVA-type (Chi-square_DF1/DF1, asymptotic)

Statistic isol  T       DF1     P_VALUE

Wald      111   93.140  4.0000  .00000
ANOVA     111   93.095  1.8224  .00000
Wald      120   453.99  4.0000  .00000
ANOVA     120   114.41  2.2890  .00000
Wald      201   2803.5  5.0000  .00000
ANOVA     201   72.047  2.1526  .00000
Wald      202   158.84  5.0000  .00000
ANOVA     202   17.265  2.5853  .00000
Wald      203   3674.1  5.0000  .00000
ANOVA     203   70.833  2.0437  .00000
Wald      83    97.502  2.0000  .00000
ANOVA     83    210.04  1.5874  .00000
```

Do not use the Wald-type statistics. The ANOVA-type statistics (ATS) are appropriate and in **red**.

DF: df_N; $df_D = \infty$ for F tests of T and A*T

Use the Box-approximation for the typically small sample sizes in most investigations.

DF1: df_N; DF2 = df_D for F tests of A (=isolate)

B is the label for the F value (as in Box-type).

Is there a significant effect of time for each isolate? Use **ANOVA** (ATS), not Wald (WTS)

Patterned alternatives can be tested using options in the F1_LD_F1 macro. First, a data set must be created containing the hypothesized alternative for the pairwise interactions:

```
data interaction_pattern;
input week weight;
cards;
1 1
```

```
2 2
3 3
4 4
5 5
6 6;
run;
```

The first variable in the `interaction_pattern` data set represents the time variable label, and the second (`weight`) gives the specific alternative hypothesis being tested. These names are arbitrary. Here the hypothesized pattern (w_j = 1, 2, 3, 4, 5, 6) represents disease progress curves which are diverging over the 6-wk period [i.e., H_0: $p_{ij} - p_{i'j}$ increases linearly with time for any two isolates (i and i')]. The `F1_LD_F1` macro is then called as follows:

```
%F1_LD_F1(data=potato, var=rating, group=isol, time=week,
subject=sub, data_pit=interaction_pattern, var_pit=weight,
time_pit=week);
```

where `data_pit` gives the name of the data set containing the pairwise interaction pattern, `var_pit` specifies the name of the variable describing the relative differences between the disease progress curves at each assessment time (the weight), and `time_pit` gives the name of the time variable in the `data_pit` data set. Box 8 shows the output of test results for some pairwise interactions ("global alternative"; equation 12 in SM) and the patterned pairwise interactions presented here. As discussed in SM, in cases where curves were diverging, significance level was lower for the patterned alternative than the global alternative (e.g., isolates 111 and 201). However, the significance level was very high with the patterned-alternative test, and higher than the significance level for the global-alternative test, if the curves were not diverging (e.g., 111 and 120), whether or not they were significantly different.

The confidence intervals for the relative effects are obtained with the LD_CI macro:

```
%LD_CI(data=potato, var=dis, group=isol, time=week, subject=sub);
```

Box 9 shows the output for the estimated relative effects and confidence intervals.

Full discussion of the results for hypothesis tests and estimates of the relative effects are given in SM.

The analysis of repeated measures can be done with `proc mixed`, but currently this requires a two-step process after the data are ranked and sorted by isolate (the treatment factor), subject, and time (in that order), in order to obtain the correct denominator degrees of freedom (df_D) for tests of time and the interaction with time. The procedure is used as follows:

```
proc mixed data=potato anovaf method=mivque0;
class isol week;
model r = isol|week / chisq;
repeated week / sub=sub group=isol type=un;
```

The major difference between this situation and the (crossed) factorial situation is in the `repeated` statement. Unlike the simpler (crossed) factorial case, one allows for covariance (or correlation) of the ranks within the experimental units (subjects). This is specified with `type=un`, where the `un` stands for 'unstructured' variance-covariance. One specifies a separate variance-covariance matrix for each treatment with `group=isol`, because it is expected that variability will depend on level of the ranks. The other difference is that `method=mivque0` *must* be specified as an option on the mixed statement (where it was generally optional for crossed factorials).

Box 8. Partial output for repeated measures (potato)

Test for pairwise comparisons

PAIRS	TEST	F	DF	P_VALUE
111*120	isol	2.0331	1.0000	.15391
111*120	week	205.17	2.8508	.00000
111*120	isol*week	1.1716	2.8508	.31810
111*201	isol	23.123	1.0000	.00000
111*201	week	163.37	2.7945	.00000
111*201	isol*week	3.4020	2.7945	.01941

. . . {continued} . . .

The tests for pairwise interactions are here. The lines to look at are the ones labelled isol*week in the 'TEST' column. Others are not relevant.

Pattern-Test for pairwise isol * week interaction

Approximation for large sample sizes with normal-distribution
Approximation for small sample sizes with t_DF
SAS-Datafile: interaction_pattern, Pattern-variable: weight1

	T	P_VALUE_NV	DF	P_VALUE_T_DF
111*120	-.7374	.76956	9.6337	.76077
111*201	3.5510	.00019	13.516	.00168

. . . {continued} . . .

This section of the output contains the statistics for tests of specific 'patterned' alternatives.

Use *P* for t-test (with DF for *df*)

Box 9. Partial output for repeated measures (potato)

Relative Effects, Biases, Variances and Confidence-Limits (alpha=0.05)

Group	Time	RE	Bias	Variance	lower	upper
111	1	.17535	.00000	.00415	.15793	.19441
111	2	.30035	-.0001	.09897	.21992	.39649
111	3	.45833	.00006	.02061	.41810	.49915
111	4	.67491	-.0004	.08133	.58940	.74957
111	5	.86719	.00047	.08542	.75732	.92839
111	6	.91146	.00000	.00048	.90505	.91740
120	1	.17535	.00000	.00415	.15793	.19441
120	2	.20660	.00006	.04391	.15404	.27273
120	3	.36458	-.0002	.15092	.26359	.48007
120	4	.67556	-.0004	.05690	.60459	.73886
120	5	.81076	.00059	.06276	.72860	.87094
120	6	.91146	.00000	.00048	.90505	.91740
201	1	.17535	.00000	.00415	.15793	.19441

p_hat

Variance (*Var*): Variance of $(\sqrt{S})\cdot p\_hat$, where *S* is number of subjects, not variance of *p_hat*. The standard error of *p_hat* is given by $\sqrt{(Var/S)}$.

As explained on page 116 of Brunner et al. (12), corrections to the calculated df_D must be made after running mixed, in order to obtain $df_D = \infty$ for the F tests of time and time*treatment (`isol`, in this case). Moreover, corrections for the treatment factor denominator degrees of freedom *may* also be needed for small sample sizes (Madden, *unpublished*). This case is easy to identify because SAS prints $df_D = 1$ for the treatment F test. The SAS program file for this example shows how both adjustments (when necessary) can be automatically made or identified when running `mixed`. Currently, it is more direct to use the `F1_LD_F1` macro for performing a repeated measures analysis. If there are two crossed factors in addition to time, one would use the `F2_LD_F1` macro.

Split plot example. Harveson and Rush (30) examined the effects of eight cultivar mixtures and two irrigation frequencies on sugar beet root rot caused by a complex of fungal pathogens. We examine here one of the data sets (`beet`) from the first planting of the 1994 study. The experimental design was a split plot with irrigation frequency as the whole-plot factor (`irr`) and cultivar mixture as the sub-plot factor (`cult`). The two irrigation frequency levels were: dry (two applications of water after emergence), and wet (five applications of water after emergence). The cultivar mixtures were Rhizosen, HH67, Ranger, MH9155, Rhizosen + Ranger mixture, HH67 + Ranger mixture, MH9155 + Ranger mixture, and a blend of all four cultivars. There were six replicates in the experiment, giving 12 unique subjects (two levels of whole plot times six replications) for the whole-plot factor. Beet root rot was rated on a 0 to 4 ordinal scale at harvest. Because there were multiple plants rated per plot (per *ijk* combination), median disease rating per plot (`rating`) was first determined before setting up the SAS data file.

The analysis can be performed with the `F1_LD_F1` macro.

```
%F1_LD_F1(data=beet, factor=irr, var=rating, time=cult,
subject=subject);
```

The macro is invoked with five arguments. `Factor` is the name of the whole-plot factor variable, `var` is the name of response variable, `time` is the name of the sub-plot factor, and `subject` is a name of the subject variable in the data set. The confidence intervals for the relative treatment effects are obtained with the `LD_CI` macro:

```
%LD_CI(data=beet, var=rating, group=irr, time=cult,
subject=subject);
```

The sub-plot factor is called `time` in these macros because of the analogy (discussed in SM) between the repeated measures factor and the sub-plot factor. Box 10 shows the output for hypothesis tests and estimates of the relative effects. Results are assembled in convenient form in Tables A2 and A3.

Perusal of the median ratings and estimated relative effects indicates that irrigation frequency had a large effect on disease, as expected, and that the effect of cultivar was not as clear cut. The estimated relative marginal effects ranged from 0.33 up to 0.76, with most of the values with wet conditions being higher than for the dry conditions. There was a highly significant effect of irrigation frequency on the level of root decay, but the effect of beet cultivar was marginal, and there was no evidence of an interaction. As often found with ordinal data (see pages 64 and 65 in Brunner et al. [12]), even in cases where the medians were numerically identical, the estimated relative effects revealed numerical (if not necessarily significant) differences in some of the cultivars.

Box 10. Partial output for split plot (sugarbeet)

```
ANOVA-type statistic
Box-approximation for small sample sizes with Chi-square_DF

          B     DF P_VALUE
A  40.265 1.0000  .00000
T  2.2066 3.9261  .06686
AT .86950 3.9261  .47961
```

DF: df_N; df_D=∞ for F tests of T and A*T

The ATS (in **red**) are preferable for the typically small sample sizes encountered. A: irrigation; T: cultivar

```
ANOVA-type statistic
modified Box-approximation for the whole-plot factor A
        for small sample sizes with F(DF1,DF2)

          B    DF1    DF2 P_VALUE
A 40.265 1.0000 7.7121  .00026
```

DF1: df_N; DF2=df_D ; for F test of A (=irrigation) (or any whole plot).

```
Relative Effects, Biases, Variances and Confidence-Limits (alpha=0.05)

Group    Time      RE       Bias     Variance lower    upper

dry      4waymix    .33160   .00139   .04737   .22344   .46519
dry      HH67       .40538   -.0024   .10734   .24267   .59593
dry      HH67Rang   .46441   .00035   .05597   .33682   .59753
dry      MH9155     .33160   -.0007   .02376   .25173   .42452
dry      Rang9155   .37847   -.0031   .21498   .17236   .65127
dry      Ranger     .46441   .00035   .05597   .33682   .59753
dry      RhizRang   .34635   .00417   .17482   .16293   .60376
dry      Rhizosen   .39063   .00000   .00553   .34957   .43354
wet      4waymix    .53819   .00104   .11991   .34687   .71751
wet      HH67       .68576   .00000   .10135   .48285   .82998
wet      HH67Rang   .75955   -.0005   .05606   .59771   .86387
wet      MH9155     .39063   .00000   .00553   .34957   .43354
wet      Rang9155   .40538   .00156   .12388   .23281   .60960
wet      Ranger     .75955   -.0005   .06713   .58016   .87089
wet      RhizRang   .71094   -.0021   .12141   .48001   .85935
wet      Rhizosen   .63715   .00052   .14572   .40635   .81265
```

Estimated relative treatment effects (p_hat), variances of , and 95% upper and lower confidence limits for p_{ij}.

Macros for analysis are available from Dr. Edgar Brunner of the University of Gottingen, Germany. Websites:
http://www.ams.med.uni-goettingen.de/Projekte/LD/Makros_LD.html
or
http://www.ams.med.uni-goettingen.de/de/sof/ld/makros.html

All output from PROC MIXED is for version 8.1 of SAS. It is expected that the ATS and WTS output will have a different (clearer) appearance in version 9.1.

TABLE A2. Median, rank and estimated relative marginal effects for beet root decay in relation to cultivar and irrigation (dry or wet) (data from planting 2 of Harveson & Rush (30))

	Median disease rating		Mean rank ($\overline{R}_{ij\bullet}$)		Relative marginal effect ($\hat{p}_{ij}$)[a]	
Cultivar (or mixture)	Dry	Wet	Dry	Wet	Dry	Wet
HH67	2.0	3.0	39.4	66.3	0.41 (0.095)	0.69 (0.092)
MH9155	2.0	2.0	32.3	38.0	0.33 (0.044)	0.39 (0.021)
Ranger	2.0	3.0	45.1	73.4	0.46 (0.068)	0.76 (0.075)
Rhizosen	2.0	2.5	38.0	61.7	0.39 (0.021)	0.64 (0.110)
HH67 + Ranger	2.0	3.0	45.1	73.4	0.46 (0.068)	0.76 (0.068)
MH9155 + Ranger	2.0	2.0	36.8	39.4	0.38 (0.134)	0.41 (0.102)
Rhizosen + Ranger	2.0	3.0	33.8	68.8	0.35 (0.121)	0.71 (0.101)
4-way	2.0	2.0	32.3	52.2	0.33 (0.063)	0.54 (0.100)

[a] Standard errors (*se*) are given in the brackets after the $\hat{p}_{ij}$ estimates. $se = \sqrt{Var / S}$, where *Var* is equals the variance of $S^{1/2} \cdot (\hat{p}_{ij} - p_{ij})$, which is displayed by the LD_CI macro. *S* is the total number of subjects (12 in this case), *not* the total number of observations.

TABLE A3. Test statistics for the effects of irrigation frequency and cultivar on the decay of beet roots by soilborne pathogens (data from Harveson & Rush (26))

	ANOVA-type statistic (ATS)			
Effect	df_N [a]	df_D	ATS	*P* value
Irrigation (I)	1	7.71	40.27	<0.001
Cultivar (C)	3.93	∞	2.21	0.067
I×C	3.93	∞	0.86	0.480

[a] df_N = numerator degrees of freedom; df_D = denominator degrees of freedom.

SAS Program Files:

```
/* SM_NPana.sas */

/* ONE WAY LAYOUT */
/*
Nonparametric (relative marginal effects) analysis for data
from Test 1 of Omer et al. (2000). Am. J. Pot. Res. 77: 325-333.
Assumes Version 8 or higher of SAS/STAT.
Assumes that the macros F1_LD_F1 and LD_CI are in the designated path.
NOTE: Change the pathway to these macros for your computer!
The macros are available for download at:
http://www.ams.med.uni-goettingen.de/Projekte/LD/Makros_LD.hmtl
or
http://www.ams.med.uni-goettingen.de/de/sof/ld/makros.html

*/

/* Identify pathway to macros.*/

%INCLUDE 'c:\Documents and Settings\madden.1\My Documents\My SAS Files\ld_ci.sas';
%INCLUDE 'c:\Documents and Settings\madden.1\My Documents\My SAS Files\f1_ld_f1.sas';

options ls =100 ps= 1000 nodate nocenter nonumber;

/*
isol = isolate of Verticillium dahliae
vcg = vegetative compatibility group
rep = replicate
disi = disease rating in week i (i= 1 to 6)
auc = area under disease progress curve.  Original paper analyzed this
      variable. Not used here.
sub = subject (a unique identifier for each experimental unit)
*/

data omer;
       input isol $ vcg $ rep dis1 dis2 dis3 dis4 dis5 dis6
          auc sub;
       datalines;
83      4A      1       1       2       5       6       6       6       157.5   49
83      4A      2       1       1       4       6       6       6       143.5   50
83      4A      3       1       1       3       6       6       6       136.5   51
83      4A      4       1       1       3       6       6       6       136.5   52
83      4A      5       1       2       5       6       6       6       157.5   53
83      4A      6       1       1       3       6       6       6       136.5   54
83      4A      7       1       2       4       6       6       6       150.5   55
83      4A      8       1       2       3       6       6       6       143.5   56
111     4A      1       1       2       3       5       6       6       136.5   57
111     4A      2       1       1       2       3       6       6       108.5   58
111     4A      3       1       2       3       5       6       6       136.5   59
111     4A      4       1       1       2       4       6       6       115.5   60
111     4A      5       1       1       2       4       6       6       115.5   61
111     4A      6       1       2       2       4       6       6       122.5   62
111     4A      7       1       2       2       2       3       6       87.5    63
111     4A      8       1       1       2       5       6       6       122.5   64
120     4A      1       1       2       2       5       6       6       129.5   65
120     4A      2       1       1       1       3       4       6       87.5    66
120     4A      3       1       1       3       4       6       6       122.5   67
120     4A      4       1       1       3       5       6       6       129.5   68
120     4A      5       1       1       1       4       4       6       94.5    69
120     4A      6       1       1       2       5       6       6       122.5   70
120     4A      7       1       1       1       3       5       6       94.5    71
120     4A      8       1       1       2       3       4       6       94.5    72
201     4B      1       1       1       2       3       3       4       80.5    185
201     4B      2       1       1       1       4       4       4       87.5    186
201     4B      3       1       1       1       3       5       5       91.0    187
201     4B      4       1       2       3       4       4       4       108.5   188
201     4B      5       1       1       2       4       4       5       98.0    189
201     4B      6       1       1       1       3       3       4       73.5    190
201     4B      7       1       1       1       4       4       4       87.5    191
```

```
201     4B      8       1       1       2       3       4       5       91.0    192
202     4B      1       1       1       1       1       2       3       49.0    193
202     4B      2       1       1       1       1       1       2       38.5    194
202     4B      3       1       1       1       2       2       2       52.5    195
202     4B      4       1       1       2       2       3       3       70.0    196
202     4B      5       1       2       2       2       2       2       66.5    197
202     4B      6       1       1       1       2       3       4       66.5    198
202     4B      7       1       1       1       1       3       3       56.0    199
202     4B      8       1       1       1       3       4       4       80.5    200
203     4B      1       1       1       3       4       5       5       112.0   201
203     4B      2       1       1       1       3       4       4       80.5    202
203     4B      3       1       1       3       4       4       4       101.5   203
203     4B      4       1       1       2       4       4       5       98.0    204
203     4B      5       1       1       2       4       5       5       105.0   205
203     4B      6       1       1       2       4       5       5       105.0   206
203     4B      7       1       2       2       3       4       4       94.5    207
203     4B      8       1       2       2       3       3       4       87.5    208
;
run;

/*Check the dataset*/
proc print data=omer;
run;

/* A 1-way analysis for ratings made during week 3. */
/*Before using Proc Mixed, one needs the ranks of the observations*/
proc rank data=omer out=omer;
  var dis3; *requests ranks for the ratings made during the third week;
  ranks r; *ranks are stored under the variable r;
run;

/*One-way analysis with Proc Mixed. Output may look different in version 9.1*/
proc mixed data=omer anovaf;
        title1 '1-way analysis using MIXED, with contrasts of 4A & 4B';
        class isol;
        model r = isol / chisq ;
        repeated / type=un(1) group=isol;
        lsmeans isol /pdiff;
        contrast 'VCG4A vs VCG4B' isol 1 1 -1 -1 -1 1;
        run;

title1 '1-way analysis using macro; each observation is a subject';
%ld_ci(data=omer,var=dis3,group=isol,alpha=0.05,subject=sub);
run;

/*-------------------------------------------------------------*/

/* REPEATED MEASURES (one whole plot, one time factor) */

/* Repeated measures analysis (disease rating over time).
For this analysis, one must first create a SAS dataset with
a separate record for each time. */
data potato;
  set omer;
  array dis{6} dis1-dis6; *store the weekly ratings in an array;
        do i=1 to 6;
          week = i;
          rating=dis{i};
          output;
        end;
        drop i dis1-dis6 auc r;
run;

/*Create a data set for testing specific time profile interactions*/
data interaction_pattern;
  input week weight1 weight2;
  datalines;
  1 1 1
  2 2 1
  3 3 2
  4 4 3
  5 5 2
```

```
  6 6 1
;
run;

title1'Potato early decay. Repeated measures analysis';
title2'Analysis using the F1_LD_F1 macro';
%F1_LD_F1(data=potato, factor=isol, var=rating, time=week, subject=sub,
          data_pit=interaction_pattern, var_pit=weight1, time_pit=week);
run;

/*Calculate the confidence intervals*/
%LD_CI(data=potato, var=rating, group=isol, time=week, subject=sub);


/*Here is the repeated measures analysis using Proc Mixed*/
/*There is sometimes an error in the ATS Den df (and hence P value)
given by Proc Mixed for the test of the whole plot factor
when there is a small number of reps, so one should check
the output carefully.  There is however a workaround for this error
(contact the authors for the SAS code).
Nevertheless, this error should be fixed in later SAS versions.
Below is the Proc Mixed code (results are correct for the
number of reps in this case)*/
/*First, obtain the ranks of the disease ratings.*/
proc rank data=potato out=potato;
  var rating;
  ranks r;
run;
/*Note that for Proc Mixed the data must be sorted by the whole-plot factor,
then by subjects, then by the sub-plot factor*/
proc sort data=potato out=potato;
  by isol sub week;
run;

/*Now the ranks are analyzed*/
title2 'Analysis with Proc Mixed, disease ratings over time';
proc mixed data=potato anovaf method=mivque0;
  class isol week;
  model r = isol|week / chisq;
  repeated week / sub=sub group=isol type=un;
  ods output tests3=s3; /* makes output file s3 with test results */
run;


/*
Note that there are two possible corrections needed
in doing the analysis with Proc Mixed (for versions 9.0 and earlier).
First, the P values
for the tests of the time factor and the interaction
with time need to be corrected (the denominator df should be infinity;
we use a very large denominator df as an approximation in the code below.

The second issue is that sometimes, if the number of replications
is small, Proc Mixed will give a wrong denomiator df for the main
effect factor.  One needs to check the output carefully for this error.
Generally, denominator df = 1 when there is a problem.
Below, we provide the code for automatically flagging this error
should it occur.

Note: in version 9.1, corrections may not be needed. Plus, the
WTS and ATS results may be displayed differently.

*/

/*
The test results are put in a file; then the correct P values are
obtained by using chi-square probabilities (=F with DDF=infinity).
Print out WTS and ATS (with flag).
*/
title3 'Corrections to Proc Mixed tests';
data s3;
       set s3;
```

```
       if (Effect ne "isol") then do;

              pval= 1 - probchi(ANOVAnumDF*ANOVAFValue,ANOVAnumDF);
              ANOVAdenDF=10000; /* ~infinity */
              end;
       if (Effect eq "isol") then do;
              pval=ANOVAProbF;
              if(ANOVADenDF <= 1 or ANOVADenDF > DenDF) then pval=-1;
              end;
       /* flag incorrect with a minus one for P */

       if (pval >= 0) then flag = 'Results OK';
       if (pval < 0) then flag = 're-run whole-plot with type=CS';
/* re-run with type=CS to get correct whole-plot result
       if df=1; otherwise, all is OK for this factor.   */

proc print data=s3;
       var Effect NumDf ChiSq ProbChiSq ANOVANumDF ANOVADenDF ANOVAFValue  pval flag;
run;

/*-----------------------------------------------------------*/

/* TWO-WAY LAYOUT (2 crossed factors) */

/*
Nonparametric (relative marginal effects) analysis for data
from Krause et al.(2001). Phytopathology 91: 1116-1123.
Assumes Version 8 or higher of SAS/STAT.
Assumes that the macro LD_CI is in the designated path.
NOTE: Change the pathway to these macros for your computer!
The macros are available for download at:
http://www.ams.med.uni-goettingen.de/Projekte/LD/Makros_LD.html
or
http://www.ams.med.uni-goettingen.de/de/sof/ld/makros.html

*/

/* Identify pathway to macros.*/

%INCLUDE 'c:\Documents and Settings\madden.1\My Documents\My SAS Files\ld_ci.sas';
%INCLUDE 'c:\Documents and Settings\madden.1\My Documents\My SAS Files\f1_ld_f1.sas';


/* batch = rep
                              */
/* bioadd = biocontrol added (1=natural 2=fortified) (Factor)
                                 */
/* potting = potting mix (or soil media), and how it was handled (Factor)  */
/* dismd = disease rating based on medians of subsamples                                */
/* treatment = interaction of potting and biocontrol                                    */
/* subject = unique code for each record
       */

data krause;
       input batch bioadd potting dismd @@;
       treatment=10*bioadd + potting;
    subject=100*batch + treatment;
datalines;
 1 1 1 1.00  1 2 1 1.00
 2 1 1 1.06  2 2 1 1.06
 3 1 1 1.06  3 2 1 1.19
 4 1 1 1.38  4 2 1 1.06
 5 1 1 1.19  5 2 1 1.19
 6 1 1 1.31  6 2 1 1.13
 7 1 1 1.25  7 2 1 1.31
 8 1 1 1.13  8 2 1 1.25
 1 1 2 3.88  1 2 2 2.84
 2 1 2 4.30  2 2 2 3.52
 3 1 2 3.20  3 2 2 2.64
 4 1 2 3.78  4 2 2 2.94
 5 1 2 3.34  5 2 2 2.48
 6 1 2 3.80  6 2 2 3.73
```

```
 7 1 2 3.30  7 2 2 4.06
 8 1 2 2.83  8 2 2 3.41
 1 1 3 3.14  1 2 3 1.63
 2 1 3 2.69  2 2 3 2.23
 3 1 3 4.39  3 2 3 2.81
 4 1 3 3.89  4 2 3 2.44
 5 1 3 4.17  5 2 3 1.86
 6 1 3 2.50  6 2 3 2.44
 7 1 3 4.00  7 2 3 2.36
 8 1 3 2.42  8 2 3 1.98
 1 1 4 1.13  1 2 4 1.13
 2 1 4 1.13  2 2 4 1.44
 3 1 4 1.50  3 2 4 1.06
 4 1 4 1.06  4 2 4 1.06
 5 1 4 1.06  5 2 4 1.19
 6 1 4 1.06  6 2 4 1.81
 7 1 4 1.44  7 2 4 1.44
 8 1 4 1.19  8 2 4 1.38
 1 1 5 4.06  1 2 5 3.34
 2 1 5 3.23  2 2 5 2.98
 3 1 5 4.38  3 2 5 4.27
 4 1 5 2.20  4 2 5 4.09
 5 1 5 4.02  5 2 5 4.56
 6 1 5 3.42  6 2 5 4.25
 7 1 5 4.14  7 2 5 3.78
 8 1 5 4.61  8 2 5 4.50
 1 1 6 3.86  1 2 6 3.91
 2 1 6 4.11  2 2 6 4.56
 3 1 6 4.27  3 2 6 2.52
 4 1 6 3.58  4 2 6 3.08
 5 1 6 3.44  5 2 6 4.14
 6 1 6 3.14  6 2 6 3.67
 7 1 6 3.33  7 2 6 3.80
 8 1 6 4.33  8 2 6 3.92
 1 1 7 1.44  1 2 7 1.06
 2 1 7 1.44  2 2 7 1.13
 3 1 7 1.31  3 2 7 1.44
 4 1 7 1.06  4 2 7 1.19
 5 1 7 1.19  5 2 7 1.00
 6 1 7 1.06  6 2 7 2.31
 7 1 7 1.00  7 2 7 1.38
 8 1 7 1.25  8 2 7 1.13
 1 1 8 3.72  1 2 8 3.23
 2 1 8 3.88  2 2 8 3.25
 3 1 8 3.28  3 2 8 4.53
 4 1 8 3.97  4 2 8 4.63
 5 1 8 3.55  5 2 8 2.95
 6 1 8 2.98  6 2 8 4.50
 7 1 8 3.91  7 2 8 4.05
 8 1 8 4.17  8 2 8 3.56
 1 1 9 2.94  1 2 9 2.75
 2 1 9 3.94  2 2 9 2.53
 3 1 9 4.17  3 2 9 2.77
 4 1 9 3.92  4 2 9 3.19
 5 1 9 4.09  5 2 9 2.27
 6 1 9 3.72  6 2 9 4.11
 7 1 9 3.89  7 2 9 3.31
 8 1 9 4.09  8 2 9 3.91
;
run;

title 'Analysis of Krause et al. data set';
title2 'Marginal effects model by Proc Mixed';

proc print data=krause;
run;

/*First, obtain the ranks*/
proc rank data=krause out=krause;
  var dismd;
  ranks r;
run;
```

```
/* For repeated measures using Proc Mixed, one must sort data by:
   CROSSED FACTORS, SUBJECT, REPEATED */
/* For NON-repeated measures, sorting is not needed */
proc sort data=krause out=krause;
  by bioadd potting;
run;

/* Note that the analysis is done on the RANKS (obtained from Proc Rank).
The ANOVAF gives the Anova-Type Statistic (ATS), but is not yet a
documented SAS option (i.e.not in manuals)
For repeated measures, must use MIVQUE0 method; for factorials, not required.
Must use CHISQ option for Wald-Type Statistics (WTSs)
Must use REPEATED, with GROUP = A*B*C (or whatever), and unstructured/diagonal
residual variances [type=UN(1)]
Note: p_i,j = (1/N)*(Rbar_i,j - 0.5) ; Rbar_i,j is given as LSMEANS   */

proc mixed data=krause anovaf /* method=mivque0 */;
       class bioadd potting;
       model r = bioadd|potting / chisq;
       repeated / type=un(1) group=bioadd*potting;
       lsmeans bioadd|potting;
run;


/* Now get confidence intervals and variances for p_i,j values (marginal effects)  */
/* There can be only one factor for this CI macro. So, use Treatment (interaction) */

title2 'confidence intervals';
%LD_CI(data=krause,var=dismd,group=treatment,alpha=0.05,subject=subject);

run;

/*-------------------------------------------------------------*/

/* REPEATED MEASURES (one whole plot, one time factor) */

/*
Nonparametric (relative marginal effects) analysis of
wheat powdery mildew in a variety  trial, 1995.
Lipps & Madden (unpublished data).
Assumes Version 8 or higher of SAS/STAT.
Assumes that the macros F1_LD_F1 and LD_CI are in the designated path.
NOTE: Change the pathway to these macros for your computer!
The macros are available for download at:
http://www.ams.med.uni-goettingen.de/Projekte/LD/Makros_LD.hmtl
or
http://www.ams.med.uni-goettingen.de/de/sof/ld/makros.html

*/

/* Identify pathway to macros.*/

%INCLUDE 'c:\Documents and Settings\madden.1\My Documents\My SAS Files\ld_ci.sas';
%INCLUDE 'c:\Documents and Settings\madden.1\My Documents\My SAS Files\f1_ld_f1.sas';


/*
Three varieties: 1) Becker; 6) Cardinal; 7) Dynasty.
Five assessment times:        1) day 130 (GS 8)
                                      2) day 139 (GS 9)
                                      3) day 143 (GS 10)
                                      4) day 150 (GS 10.3)
                                      5) day 156 (GS 10.5.1).
Four replications, giving 3*4 = 12 unique subjects.

Response (y): 0-10 rating score (based on % severity
and highest leaf with symptoms).

 cultivar = wheat cultivar
 time = assessment time (growth stage)
 dis = rating score
```

```
 sub = subject*/


data wheat;
        input cultivar time dis sub;
datalines;
1       1       2.0     11
1       1       0.0     21
1       1       3.0     31
1       1       2.0     41
1       2       3.5     11
1       2       2.5     21
1       2       5.0     31
1       2       3.0     41
1       3       2.0     11
1       3       5.0     21
1       3       6.0     31
1       3       5.0     41
1       4       8.0     11
1       4       7.0     21
1       4       8.0     31
1       4       8.0     41
1       5       8.5     11
1       5       8.0     21
1       5       10.0 31
1       5       9.0     41
6       1       2.0     16
6       1       2.0     26
6       1       2.0     36
6       1       0.0     46
6       2       2.0     16
6       2       2.0     26
6       2       4.0     36
6       2       2.0     46
6       3       3.0     16
6       3       5.0     26
6       3       5.5     36
6       3       5.5     46
6       4       5.0     16
6       4       5.0     26
6       4       6.0     36
6       4       6.0     46
6       5       5.0     16
6       5       8.0     26
6       5       7.5     36
6       5       7.0     46
7       1       0.0     17
7       1       2.0     27
7       1       2.5     37
7       1       0.0     47
7       2       0.0     17
7       2       2.0     27
7       2       2.0     37
7       2       5.0     47
7       3       1.0     17
7       3       2.0     27
7       3       5.0     37
7       3       5.0     47
7       4       2.5     17
7       4       5.0     27
7       4       5.0     37
7       4       4.0     47
7       5       5.0     17
7       5       6.5     27
7       5       6.5     37
7       5       5.0     47
;
run;

title1 'wheat powdery mildew, 1995; 3 cultivars, 5 times';
/* see annotated output (lipps.doc) for explanations */
%f1_ld_f1(data=wheat,var=dis,factor=cultivar,time=time,subject=sub);
```

```
run;
%ld_ci(data=wheat,var=dis,group=cultivar,time=time,alpha=0.05,subject=sub);
run;

/*-----------------------------------------------------------*/

/* SPLIT PLOT */

/*
Nonparametric (relative marginal effects) analysis of
beet root decay. Data are from Harveson & Rush 2002 Pl. Dis. 86:901-908.
Assumes Version 8 or higher of SAS/STAT.
Assumes that the macros F1_LD_F1 and LD_CI are in the designated path.
NOTE: Change the pathway to these macros for your computer!
The macros are available for download at:
http://www.ams.med.uni-goettingen.de/Projekte/LD/Makros_LD.hmtl
or
http://www.ams.med.uni-goettingen.de/de/sof/ld/makros.html

*/

/* Identify pathway to macros.*/

%INCLUDE 'c:\Documents and Settings\madden.1\My Documents\My SAS Files\ld_ci.sas';
%INCLUDE 'c:\Documents and Settings\madden.1\My Documents\My SAS Files\f1_ld_f1.sas';

/*Effect of irrigation and beet variety on beet root rot*/
/*Disease ratings done on a 0-4 scale*/
/*Data here are for planting 2*/

/*plot = plot number*/
/*irr = irrigation treatment (wet or dry)*/
/*var = variety (8 trt levels)*/
/*rep = replicate (they did 6 reps)*/
/*rating = median rating on the 0-5 scale for the plot.
  Ratings done on each beet root, but variable number of roots
  were harvested per plot*/
/*subject = subject code.  Each irr by rep combination is a unique
  subject (12 subjects altogether)*/

options ls =100 ps= 1000 nodate nocenter nonumber;
data beet;
input plot irr $ var $ subject rep rating;
cards;
1       wet     Rhizosen        1       1       2
2       wet     HH67    1       1       3
3       wet     Ranger  1       1       3
4       wet     MH9155  1       1       2
5       wet     RhizRang        1       1       3
6       wet     HH67Rang        1       1       3
7       wet     Rang9155        1       1       3
8       wet     4waymix 1       1       2
9       dry     4waymix 2       1       1
10      dry     Rang9155        2       1       4
11      dry     HH67Rang        2       1       2
12      dry     RhizRang        2       1       1
13      dry     MH9155  2       1       2
14      dry     Ranger  2       1       2
15      dry     HH67    2       1       3
16      dry     Rhizosen        2       1       2
17      dry     Rang9155        3       2       2
18      dry     HH67    3       2       2
19      dry     4waymix 3       2       2
20      dry     Rhizosen        3       2       2
21      dry     MH9155  3       2       2
22      dry     HH67Rang        3       2       2
23      dry     Ranger  3       2       2
24      dry     RhizRang        3       2       2
25      wet     RhizRang        4       2       2
26      wet     Ranger  4       2       2
27      wet     HH67Rang        4       2       3
28      wet     MH9155  4       2       2
```

```
29      wet     Rhizosen        4       2       3
30      wet     4waymix 4       2       3
31      wet     HH67    4       2       3
32      wet     Rang9155        4       2       2
33      wet     MH9155  5       3       2
34      wet     Ranger  5       3       3
35      wet     HH67Rang        5       3       2
36      wet     RhizRang        5       3       2
37      wet     Rang9155        5       3       2
38      wet     4waymix 5       3       3
39      wet     HH67    5       3       3
40      wet     Rhizosen        5       3       2
41      dry     Rhizosen        6       3       2
42      dry     HH67    6       3       2
43      dry     4waymix 6       3       2
44      dry     Rang9155        6       3       2
45      dry     RhizRang        6       3       1
46      dry     HH67Rang        6       3       3
47      dry     Ranger  6       3       3
48      dry     MH9155  6       3       2
49      dry     Ranger  7       4       2
50      dry     Rhizosen        7       4       2
51      dry     4waymix 7       4       2
52      dry     HH67Rang        7       4       2
53      dry     MH9155  7       4       1
54      dry     RhizRang        7       4       2
55      dry     Rang9155        7       4       1
56      dry     HH67    7       4       1
57      wet     HH67    8       4       2
58      wet     Rang9155        8       4       2
59      wet     RhizRang        8       4       4
60      wet     MH9155  8       4       2
61      wet     HH67Rang        8       4       3
62      wet     4waymix 8       4       2
63      wet     Rhizosen        8       4       2
64      wet     Ranger  8       4       3
65      wet     HH67    9       5       2
66      wet     MH9155  9       5       2
67      wet     Rang9155        9       5       2
68      wet     RhizRang        9       5       3
69      wet     Rhizosen        9       5       3
70      wet     Ranger  9       5       3
71      wet     HH67Rang        9       5       3
72      wet     4waymix 9       5       2
73      dry     4waymix 10      5       2
74      dry     HH67Rang        10      5       2
75      dry     Ranger  10      5       2
76      dry     Rhizosen        10      5       2
77      dry     RhizRang        10      5       3
78      dry     Rang9155        10      5       2
79      dry     MH9155  10      5       2
80      dry     HH67    10      5       2
81      dry     Rhizosen        11      6       2
82      dry     Ranger  11      6       2
83      dry     HH67    11      6       2
84      dry     MH9155  11      6       2
85      dry     RhizRang        11      6       2
86      dry     HH67Rang        11      6       2
87      dry     4waymix 11      6       2
88      dry     Rang9155        11      6       1.5
89      wet     Rang9155        12      6       1
90      wet     4waymix 12      6       2
91      wet     HH67Rang        12      6       3
92      wet     RhizRang        12      6       3
93      wet     MH9155  12      6       2
94      wet     HH67    12      6       3
95      wet     Ranger  12      6       3
96      wet     Rhizosen        12      6       4
;
run;

/*Analysis using the F1_LD_F1 macro*/
```

```
title1'Effect of irrigation and variety on beet root decay';
title2'Analysis using the F1_LD_F1 macro';
%F1_LD_F1(data=beet, factor=irr, var=rating, time=var, subject=subject);
run;

/*Calculate the confidence intervals*/
title2'Confidence intervals using the LD_CI macro';
%LD_CI(data=beet, var=rating, group=irr, time=var, subject=subject);

run;
```

Annotated Output:

Annotated output from analysis of data sets in SM_NPana.sas. These correspond partly to examples in Shah & Madden (Phytopathology, volume 94 [2004]).

Omer et al. data set

1-way analysis using MIXED, with contrasts of 4A & 4B

```
The Mixed Procedure

                  Model Information

Data Set                      WORK.OMER
Dependent Variable            r
Covariance Structure          Unstructured
Group Effect                  isol
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

isol          6    111 120 201 202 203 83


            Dimensions

Covariance Parameters             6
Columns in X                      7
Columns in Z                      0
Subjects                         48
Max Obs Per Subject               1
Observations Used                48
Observations Not Used             0
Total Observations               48


                    Iteration History

Iteration    Evaluations    -2 Res Log Like       Criterion

        0              1       320.54753756
        1              1       309.95074066      0.00000000


                  Convergence criteria met.


 Covariance Parameter Estimates

Cov Parm    Group       Estimate

UN(1,1)     isol 111     48.2143
UN(1,1)     isol 120      174.17
UN(1,1)     isol 201      141.27
UN(1,1)     isol 202     58.3393
UN(1,1)     isol 203     99.9241
```

DISCLAIMER:
All comments are shown for the benefit of the reader. We make no attempt to completely explain the output, and our explanations may be inadequate or incomplete for some purposes.

Output from PROC MIXED (regarding WTS and ATS results) may look different in SAS version 9.1. Current output is for Version 8.1.

Separate variance estimates for each level of the factor (i.e. each isolate in this example).

```
UN(1,1)      isol 83      16.6429


           Fit Statistics

-2 Res Log Likelihood            310.0
AIC (smaller is better)          322.0
AICC (smaller is better)         324.4
BIC (smaller is better)          333.2


  Null Model Likelihood Ratio Test

    DF    Chi-Square      Pr > ChiSq

     5         10.60          0.0600


                      Type 3 Tests of Fixed Effects

                                                                    ANOVA  ANOVA
            Num   Den                                               Num    Den
Effect       DF    DF  Chi-Square  F Value    Pr > ChiSq  Pr > F     DF     DF

isol          5    42      135.35    27.07        <.0001  <.0001   3.86   30.6


              Type 3 Tests of Fixed Effects

               ANOVA     ANOVA F           ANOVA     ANOVA
Effect     Chi-Square      Value      Pr > ChiSq    Pr > F

isol            10.10      10.10          0.0177    <.0001


                           Contrasts

                                                ANOVA  ANOVA
                Num   Den                       Num    Den   ANOVA F   ANOVA
Label            DF    DF  F Value  Pr > F      DF     DF    Value  Pr > F

VCG4A vs VCG4B    1    42    20.47  <.0001       1   30.6    20.47  <.0001


                        Least Squares Means

                                 Standard
Effect    isol    Estimate          Error      DF    t Value    Pr > |t|

isol      111      27.7500         2.4550      42      11.30      <.0001
isol      120      21.5625         4.6660      42       4.62      <.0001
isol      201      17.6250         4.2022      42       4.19      0.0001
isol      202      11.6250         2.7004      42       4.30      <.0001
isol      203      25.6875         3.5342      42       7.27      <.0001
isol      83       42.7500         1.4423      42      29.64      <.0001


                   Differences of Least Squares Means

                                       Standard
Effect    isol    _isol    Estimate          Error      DF    t Value    Pr > |t|

isol      111      120       6.1875         5.2724      42       1.17      0.2472
isol      111      201      10.1250         4.8668      42       2.08      0.0436
isol      111      202      16.1250         3.6495      42       4.42      <.0001
```

Ignore the standard F statistics in the output.
WTS statistics are in **blue**.

The ATS df, statistics and *P* values (in **red**) are provided with the ANOVAF option..

Contrast of VCG4A and VCG4B.

The $\overline{R}_{ij}$ are the LS Means estimates.

isol	111	203	2.0625	4.3032	42	0.48	0.6342
isol	111	83	-15.0000	2.8473	42	-5.27	<.0001
isol	120	201	3.9375	6.2794	42	0.63	0.5340
isol	120	202	9.9375	5.3911	42	1.84	0.0723
isol	120	203	-4.1250	5.8534	42	-0.70	0.4849
isol	120	83	-21.1875	4.8839	42	-4.34	<.0001
isol	201	202	6.0000	4.9951	42	1.20	0.2364
isol	201	203	-8.0625	5.4908	42	-1.47	0.1495
isol	201	83	-25.1250	4.4428	42	-5.66	<.0001
isol	202	203	-14.0625	4.4478	42	-3.16	0.0029
isol	202	83	-31.1250	3.0615	42	-10.17	<.0001
isol	203	83	-17.0625	3.8172	42	-4.47	<.0001

1-way analysis using macro; each observation is a subject

LD_CI
Bias-Estimation and Confidence-Intervals for Relative Effects

SAS-Data-Filename:	omer		
Response-Variable:	dis3	Observations:	48
Group-Variable:	isol	Groups:	6
Time-Variable:	_none_	Timepoints:	1
Subject-Variable	sub	Subjects:	48

Relative effects (p_i) for each isolate.

Relative Effects, Biases, Variances and Confidence-Limits (alpha=0.05)

Group	RE	Bias	Variance	lower	upper
111	.56771	.00000	.12565	.46539	.66227
120	.43880	.00000	.33708	.29119	.60398
201	.35677	.00000	.27509	.23236	.51894
202	.23177	.00000	.12193	.15663	.35627
203	.52474	.00000	.20817	.39739	.64761
83	.88021	.00000	.01711	.81933	.90368

RE: estimated relative effect (*p_hat*).

Variance (*Var*): Variance of $(\sqrt{N})\cdot(p\_hat-p)$, not variance of *p_hat*. The standard error of *p_hat* is given by: $\sqrt{(Var/N)}$.

Omer et al. data set.
Potato early decay. Repeated measures analysis.
Analysis using the F1_LD_F1 macro

F1_LD_F1 --- subjects(A) x T
A(=FACTOR), T(=TIME): fixed, subjects: random

SAS-datafile-name: potato
Response variable: rating

Class Level Information

Output from the F1_LD_F1 macro.

CLASS		LEVELS
A	ISOL	6
T	WEEK	6

Total number of observations 288
Number of missing values 0

RTE = Relative Treatment Effects
Nobs = Number of observations (do not count the repeated measurements within the cells)

SOURCE		Rank mean	Nobs	RTE
isol	111	163.10	48	0.5645978
isol	120	151.43	48	0.5240524
isol	201	130.48	48	0.4513166
isol	202	95.698	48	0.3305483
isol	203	140.67	48	0.4866898
isol	83	185.63	48	0.6427951
week	1	51.000	48	0.1753472
week	2	70.500	48	0.2430556
week	3	118.17	48	0.4085648
week	4	186.13	48	0.6445313
week	5	213.52	48	0.7396557
week	6	227.69	48	0.7888455
isol*week	111*1	51.000	8	0.1753472
isol*week	111*2	87.000	8	0.3003472
isol*week	111*3	132.50	8	0.4583333
isol*week	111*4	194.88	8	0.6749132
isol*week	111*5	250.25	8	0.8671875
isol*week	111*6	263.00	8	0.9114583
isol*week	120*1	51.000	8	0.1753472
isol*week	120*2	60.000	8	0.2065972
isol*week	120*3	105.50	8	0.3645833
isol*week	120*4	195.06	8	0.6755642
isol*week	120*5	234.00	8	0.8107639
isol*week	120*6	263.00	8	0.9114583
isol*week	201*1	51.000	8	0.1753472
isol*week	201*2	60.000	8	0.2065972
isol*week	201*3	91.750	8	0.3168403
isol*week	201*4	179.25	8	0.6206597
isol*week	201*5	192.13	8	0.6653646
isol*week	201*6	208.75	8	0.7230903
isol*week	202*1	51.000	8	0.1753472
isol*week	202*2	60.000	8	0.2065972

Relative marginal effects for each isolate at each assessment week.

```
isol*week 202*3    69.000         8 0.2378472
isol*week 202*4    100.75         8 0.3480903
isol*week 202*5    137.56         8 0.4759115
isol*week 202*6    155.88         8 0.5394965
isol*week 203*1    51.000         8 0.1753472
isol*week 203*2    69.000         8 0.2378472
isol*week 203*3    123.50         8 0.4270833
isol*week 203*4    183.81         8 0.6365017
isol*week 203*5    204.19         8 0.7072483
isol*week 203*6    212.50         8 0.7361111
isol*week 83 *1    51.000         8 0.1753472
isol*week 83 *2    87.000         8 0.3003472
isol*week 83 *3    186.75         8 0.6467014
isol*week 83 *4    263.00         8 0.9114583
isol*week 83 *5    263.00         8 0.9114583
isol*week 83 *6    263.00         8 0.9114583


Warning:
Do not use the Wald-type-statistic, because the covariance matrix is singular.

                    Analysis using the F1_LD_F1 macro

                           Wald-type statistic
         Approximation for   large sample sizes with Chi-Square_DF

                                  W     DF P_VALUE

                            A  194.49 5.0000  .00000
                            T  7282.8 5.0000  .00000
                            AT 1962.3 23.000  .00000

                           ANOVA-type statistic
          Box-approximation for small sample sizes with Chi-square_DF

                                  B     DF P_VALUE

                            A  35.276 4.2218  .00000
                            T  457.78 3.1255  .00000
                            AT 7.7821 10.898  .00000

                           ANOVA-type statistic
            modified Box-approximation for the whole-plot factor A
                    for small sample sizes with F(DF1,DF2)

                              B    DF1    DF2 P_VALUE

                          A 35.276 4.2218 34.134  .00000


                 Tests for the simple >> week << effect (T)
                   Wald-type (Chi-square_DF1, asymptotic)
                ANOVA-type (Chi-square_DF1/DF1, asymptotic)

                   Statistic isol T       DF1     P_VALUE

                   Wald      111   93.140  4.0000  .00000
                   ANOVA     111   93.095  1.8224  .00000
```

Do not use the Wald-type statistics. The ANOVA-type statistics (ATS) are appropriate and in red.

Use the Box-approximation for the typically small sample sizes in most investigations.

B is the label for the F value.

Wald	120	453.99	4.0000	.00000
ANOVA	120	114.41	2.2890	.00000
Wald	201	2803.5	5.0000	.00000
ANOVA	201	72.047	2.1526	.00000
Wald	202	158.84	5.0000	.00000
ANOVA	202	17.265	2.5853	.00000
Wald	203	3674.1	5.0000	.00000
ANOVA	203	70.833	2.0437	.00000
Wald	83	97.502	2.0000	.00000
ANOVA	83	210.04	1.5874	.00000

Test for pairwise comparisons

PAIRS	TEST	F	DF	P_VALUE
111*120	isol	2.0331	1.0000	.15391
111*120	week	205.17	2.8508	.00000
111*120	isol*week	1.1716	2.8508	.31810
111*201	isol	23.123	1.0000	.00000
111*201	week	163.37	2.7945	.00000
111*201	isol*week	3.4020	2.7945	.01941
111*202	isol	65.120	1.0000	.00000
111*202	week	88.372	2.5875	.00000
111*202	isol*week	11.083	2.5875	.00000
111*203	isol	13.208	1.0000	.00028
111*203	week	162.83	2.1719	.00000
111*203	isol*week	2.8928	2.1719	.05092
111*83	isol	13.379	1.0000	.00025
111*83	week	260.29	2.0672	.00000
111*83	isol*week	7.5256	2.0672	.00046
120*201	isol	6.9406	1.0000	.00843
120*201	week	183.93	2.8245	.00000
120*201	isol*week	3.5106	2.8245	.01649
120*202	isol	35.713	1.0000	.00000
120*202	week	98.926	3.3568	.00000
120*202	isol*week	13.618	3.3568	.00000
120*203	isol	2.0935	1.0000	.14792
120*203	week	181.77	2.7428	.00000
120*203	isol*week	4.6077	2.7428	.00424
120*83	isol	21.225	1.0000	.00000
120*83	week	290.50	2.7735	.00000
120*83	isol*week	9.9006	2.7735	.00000
201*202	isol	18.349	1.0000	.00002
201*202	week	71.488	2.7323	.00000
201*202	isol*week	5.8244	2.7323	.00088
201*203	isol	3.0284	1.0000	.08182
201*203	week	141.95	2.6582	.00000
201*203	isol*week	.93121	2.6582	.41577
201*83	isol	89.274	1.0000	.00000
201*83	week	238.93	2.2364	.00000
201*83	isol*week	11.456	2.2364	.00000
202*203	isol	34.859	1.0000	.00000
202*203	week	70.082	2.7847	.00000
202*203	isol*week	6.1391	2.7847	.00053
202*83	isol	139.90	1.0000	.00000
202*83	week	119.19	2.6641	.00000
202*83	isol*week	25.743	2.6641	.00000
203*83	isol	77.304	1.0000	.00000
203*83	week	241.33	2.0152	.00000
203*83	isol*week	7.9323	2.0152	.00035

The tests for pairwise interactions are here. The lines to look at are the ones labelled isol*week in the 'TEST' column.

```
        Pattern-Test for pairwise isol * week interaction


    Approximation for large sample sizes with normal-distribution
            Approximation for small sample sizes with t_DF
     SAS-Datafile: interaction_pattern, Pattern-variable: weight1

                    T        P_VALUE_NV       DF     P_VALUE_T_DF

     111*120      -.7374        .76956       9.6337        .76077
     111*201      3.5510        .00019       13.516        .00168
     111*202      5.9510        .00000       11.798        .00004
     111*203      3.0863        .00101       13.868        .00406
     111*83       -.5930        .72342       12.009        .71792
     120*201      5.7781        .00000       10.707        .00007
     120*202      7.2644        .00000       8.0779        .00004
     120*203      4.5458        .00000       9.1914        .00066
     120*83        .12631       .44974       12.342        .45076
     201*202      3.6667        .00012       10.527        .00199
     201*203      -.0074        .50295       12.971        .50289
     201*83       -5.058        1.0000       13.261        .99990
     202*203      -3.400        .99966       12.479        .99750
     202*83       -6.922        1.0000       9.2758        .99997
     203*83       -4.143        .99998       11.330        .99923


                                  LEVELS
                    1         2         3         4         5         6

    PATTERN         1         2         3         4         5         6
```

This section of the output contains the statistics for tests of specific 'patterned' alternatives.

The specified patterned alternative is given here.

```
                                  LD_CI
        Bias-Estimation and Confidence-Intervals for Relative Effects


                       SAS-Data-Filename: potato
          Response-Variable: rating       Observations:       288
          Group-Variable:    isol         Groups:               6
          Time-Variable:     week         Timepoints:           6
          Subject-Variable   sub          Subjects:            48


    Relative Effects, Biases, Variances and Confidence-Limits (alpha=0.05)


       Group         Time RE       Bias     Variance lower    upper

       111              1   .17535   .00000   .00415   .15793   .19441
       111              2   .30035   -.0001   .09897   .21992   .39649
       111              3   .45833   .00006   .02061   .41810   .49915
       111              4   .67491   -.0004   .08133   .58940   .74957
       111              5   .86719   .00047   .08542   .75732   .92839
       111              6   .91146   .00000   .00048   .90505   .91740
       120              1   .17535   .00000   .00415   .15793   .19441
       120              2   .20660   .00006   .04391   .15404   .27273
       120              3   .36458   -.0002   .15092   .26359   .48007
       120              4   .67556   -.0004   .05690   .60459   .73886
       120              5   .81076   .00059   .06276   .72860   .87094
       120              6   .91146   .00000   .00048   .90505   .91740
       201              1   .17535   .00000   .00415   .15793   .19441
       201              2   .20660   -.0002   .04233   .15488   .27141
```

Output from the LD_CI macro giving the relative treatment effects, variances etc.

201	3	.31684	.00003	.13300	.22419	.42812
201	4	.62066	.00037	.02763	.57257	.66636
201	5	.66536	-.0002	.03126	.61353	.71327
201	6	.72309	.00006	.01858	.68281	.75983
202	1	.17535	.00000	.00415	.15793	.19441
202	2	.20660	.00031	.03945	.15646	.26894
202	3	.23785	.00012	.06627	.17333	.31869
202	4	.34809	-.0006	.11278	.26039	.44832
202	5	.47591	-.0001	.11209	.38327	.57034
202	6	.53950	.00025	.05555	.47250	.60502
203	1	.17535	.00000	.00415	.15793	.19441
203	2	.23785	.00012	.07520	.16969	.32448
203	3	.42708	-.0004	.07788	.35074	.50729
203	4	.63650	-.0005	.02107	.59447	.67642
203	5	.70725	.00022	.03003	.65578	.75360
203	6	.73611	.00050	.01454	.70051	.76868
83	1	.17535	.00000	.00415	.15793	.19441
83	2	.30035	.00000	.10046	.21939	.39726
83	3	.64670	.00000	.06096	.57399	.71284
83	4	.91146	.00000	.00048	.90505	.91740
83	5	.91146	.00000	.00048	.90505	.91740
83	6	.91146	.00000	.00048	.90505	.91740

Potato early decay. Repeated measures analysis.

Analysis with Proc Mixed, disease ratings over time

The Mixed Procedure

Model Information

Data Set	WORK.POTATO
Dependent Variable	r
Covariance Structure	Unstructured
Subject Effect	sub
Group Effect	isol
Estimation Method	MIVQUE0
Residual Variance Method	None
Fixed Effects SE Method	Model-Based
Degrees of Freedom Method	Between-Within

This next section presents the output from Proc Mixed.

Class Level Information

Class	Levels	Values
isol	6	111 120 201 202 203 83
week	6	1 2 3 4 5 6

Dimensions

Covariance Parameters	126
Columns in X	49
Columns in Z	0
Subjects	48
Max Obs Per Subject	6
Observations Used	288
Observations Not Used	0
Total Observations	288

Covariance Parameter Estimates

Cov Parm	Subject	Group	Estimate
UN(1,1)	sub	isol 111	5.25E-8
UN(2,1)	sub	isol 111	-209E-29
UN(2,2)	sub	isol 111	1481.14
UN(3,1)	sub	isol 111	-167E-29
UN(3,2)	sub	isol 111	390.86
UN(3,3)	sub	isol 111	309.43
UN(4,1)	sub	isol 111	-244E-29
UN(4,2)	sub	isol 111	-41.1429
UN(4,3)	sub	isol 111	354.21
UN(4,4)	sub	isol 111	1361.05
UN(5,1)	sub	isol 111	-214E-29
UN(5,2)	sub	isol 111	-524.57
UN(5,3)	sub	isol 111	138.43
UN(5,4)	sub	isol 111	1047.32
UN(5,5)	sub	isol 111	1300.50
UN(6,1)	sub	isol 111	-183E-29
UN(6,2)	sub	isol 111	-282E-29
UN(6,3)	sub	isol 111	-212E-29
UN(6,4)	sub	isol 111	-282E-29
UN(6,5)	sub	isol 111	-229E-29
UN(6,6)	sub	isol 111	5.25E-8
UN(1,1)	sub	isol 120	5.25E-8
UN(2,1)	sub	isol 120	-226E-29
UN(2,2)	sub	isol 120	648.00
UN(3,1)	sub	isol 120	-327E-29
UN(3,2)	sub	isol 120	180.00
UN(3,3)	sub	isol 120	2284.29
UN(4,1)	sub	isol 120	-257E-29
UN(4,2)	sub	isol 120	333.64
UN(4,3)	sub	isol 120	864.96
UN(4,4)	sub	isol 120	949.89
UN(5,1)	sub	isol 120	-111E-29
UN(5,2)	sub	isol 120	298.29
UN(5,3)	sub	isol 120	1132.57
UN(5,4)	sub	isol 120	787.39
UN(5,5)	sub	isol 120	1057.57
UN(6,1)	sub	isol 120	-217E-29
UN(6,2)	sub	isol 120	-242E-29
UN(6,3)	sub	isol 120	-387E-29
UN(6,4)	sub	isol 120	-268E-29
UN(6,5)	sub	isol 120	-203E-29
UN(6,6)	sub	isol 120	5.25E-8
UN(1,1)	sub	isol 201	5.25E-8
UN(2,1)	sub	isol 201	-743E-30
UN(2,2)	sub	isol 201	648.00
UN(3,1)	sub	isol 201	-211E-29
UN(3,2)	sub	isol 201	712.29
UN(3,3)	sub	isol 201	2052.50
UN(4,1)	sub	isol 201	-128E-29
UN(4,2)	sub	isol 201	187.71
UN(4,3)	sub	isol 201	99.0714
UN(4,4)	sub	isol 201	380.64
UN(5,1)	sub	isol 201	-193E-29
UN(5,2)	sub	isol 201	55.2857
UN(5,3)	sub	isol 201	-125.11
UN(5,4)	sub	isol 201	112.11
UN(5,5)	sub	isol 201	476.20
UN(6,1)	sub	isol 201	-18E-28
UN(6,2)	sub	isol 201	-115.71
UN(6,3)	sub	isol 201	93.2143
UN(6,4)	sub	isol 201	-78.2143
UN(6,5)	sub	isol 201	197.68

A separate variance for each treatment and time, separate covariance for each pair of times, for each treatment

UN(6,6)	sub	isol 201	241.07
UN(1,1)	sub	isol 202	5.25E-8
UN(2,1)	sub	isol 202	-203E-29
UN(2,2)	sub	isol 202	648.00
UN(3,1)	sub	isol 202	-146E-29
UN(3,2)	sub	isol 202	555.43
UN(3,3)	sub	isol 202	1110.86
UN(4,1)	sub	isol 202	-235E-29
UN(4,2)	sub	isol 202	228.86
UN(4,3)	sub	isol 202	457.71
UN(4,4)	sub	isol 202	1862.21
UN(5,1)	sub	isol 202	-932E-30
UN(5,2)	sub	isol 202	-149.79
UN(5,3)	sub	isol 202	91.2857
UN(5,4)	sub	isol 202	1124.45
UN(5,5)	sub	isol 202	1909.96
UN(6,1)	sub	isol 202	-205E-29
UN(6,2)	sub	isol 202	-338.14
UN(6,3)	sub	isol 202	-285.43
UN(6,4)	sub	isol 202	458.68
UN(6,5)	sub	isol 202	1062.76
UN(6,6)	sub	isol 202	969.48
UN(1,1)	sub	isol 203	5.25E-8
UN(2,1)	sub	isol 203	-815E-30
UN(2,2)	sub	isol 203	1110.86
UN(3,1)	sub	isol 203	-203E-29
UN(3,2)	sub	isol 203	-10.2857
UN(3,3)	sub	isol 203	1152.86
UN(4,1)	sub	isol 203	-168E-29
UN(4,2)	sub	isol 203	-469.29
UN(4,3)	sub	isol 203	383.25
UN(4,4)	sub	isol 203	356.85
UN(5,1)	sub	isol 203	-17E-28
UN(5,2)	sub	isol 203	-513.00
UN(5,3)	sub	isol 203	159.04
UN(5,4)	sub	isol 203	294.93
UN(5,5)	sub	isol 203	524.92
UN(6,1)	sub	isol 203	-143E-29
UN(6,2)	sub	isol 203	-308.57
UN(6,3)	sub	isol 203	154.29
UN(6,4)	sub	isol 203	234.64
UN(6,5)	sub	isol 203	271.07
UN(6,6)	sub	isol 203	257.14
UN(1,1)	sub	isol 83	5.25E-8
UN(2,1)	sub	isol 83	9.72E-27
UN(2,2)	sub	isol 83	1481.14
UN(3,1)	sub	isol 83	-202E-29
UN(3,2)	sub	isol 83	684.00
UN(3,3)	sub	isol 83	886.36
UN(4,1)	sub	isol 83	-186E-29
UN(4,2)	sub	isol 83	-121E-29
UN(4,3)	sub	isol 83	-133E-29
UN(4,4)	sub	isol 83	5.25E-8
UN(5,1)	sub	isol 83	-861E-29
UN(5,2)	sub	isol 83	-641E-29
UN(5,3)	sub	isol 83	-92E-29
UN(5,4)	sub	isol 83	-14E-28
UN(5,5)	sub	isol 83	5.25E-8
UN(6,1)	sub	isol 83	-602E-30
UN(6,2)	sub	isol 83	-13E-29
UN(6,3)	sub	isol 83	-586E-30
UN(6,4)	sub	isol 83	-235E-30
UN(6,5)	sub	isol 83	-706E-31
UN(6,6)	sub	isol 83	5.25E-8

Fit Statistics

-2 Res Log Likelihood	477.6
AIC (smaller is better)	729.6
AICC (smaller is better)	987.7
BIC (smaller is better)	965.4

Null Model Likelihood Ratio Test

DF	Chi-Square	Pr > ChiSq
125	1965.84	<.0001

Use the ATS statistics, which are in **red.** Ignore the standard F statistics. The WTS statistics are in blue.

Type 3 Tests of Fixed Effects

Effect	Num DF	Den DF	Chi-Square	F Value	Pr > ChiSq	Pr > F	ANOVA Num DF	ANOVA Den DF
isol	5	42	194.49	38.90	<.0001	<.0001	4.22	34.1
week	5	210	7282.80	1456.56	<.0001	<.0001	3.13	85.1
isol*week	25	210	1962.31	78.49	<.0001	<.0001	10.9	85.1

Type 3 Tests of Fixed Effects

Effect	ANOVA Chi-Square	ANOVA F Value	ANOVA Pr > ChiSq	ANOVA Pr > F
isol	35.28	35.28	<.0001	<.0001
week	457.78	457.78	<.0001	<.0001
isol*week	7.78	7.78	0.6501	<.0001

Proc Mixed may not give the correct denominator df for the main effect factor. Additionally, the *P* values for the time factor and the interaction term must be corrected. We have written SAS code to do these checks and calculate the correct *P* values. Below is the output from that code. Starting in Version 9.1 (not 9.0) of SAS, output may have a somewhat different appearance, and correct df should be displayed

Potato early decay. Repeated measures analysis.
Analysis with Proc Mixed, disease ratings over time
Corrections to Proc Mixed tests

Obs	Effect	NumDF	ChiSq	Prob ChiSq	ANOVA DenDF	ANOVA F Value	ANOVA p val	flag
1	isol	5	194.49	<.0001	4.22	34.1	35.28	6.8119E-12	Results OK
2	week	5	7282.80	<.0001	3.13	1E4	457.78	0	Results OK
3	isol*week	25	1962.31	<.0001	10.9	1E4	7.78	1.541E-13	Results OK

Krause et al. data set

```
                    Analysis of Krause et al. data set                    11
                  Marginal effects model by Proc Mixed
                                10:59 Wednesday, March 26, 2003

                        The Mixed Procedure

                        Model Information

  Data Set                        WORK.KRAUSE
  Dependent Variable              r
  Covariance Structure            Unstructured
  Group Effect                    bioadd*potting
  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

    bioadd          2    1 2
    potting         9    1 2 3 4 5 6 7 8 9

                         Dimensions

                Covariance Parameters            18
                Columns in X                     30

                        The Mixed Procedure

                         Dimensions

                Columns in Z                      0
                Subjects                        144
                Max Obs Per Subject               1
                Observations Used               144
                Observations Not Used             0
                Total Observations              144

                          Iteration History

  Iteration    Evaluations    -2 Res Log Like       Criterion

          0              1      1166.80197565
          1              1      1134.77032379      0.00000000

                    Convergence criteria met.

                  Covariance Parameter Estimates

            Cov Parm    Group                 Estimate
```

Header information from Proc Mixed.

UN(1,1)	bioadd*potting	1	1	171.25
UN(1,1)	bioadd*potting	1	2	411.41
UN(1,1)	bioadd*potting	1	3	1077.43
UN(1,1)	bioadd*potting	1	4	201.55
UN(1,1)	bioadd*potting	1	5	984.82
UN(1,1)	bioadd*potting	1	6	500.60
UN(1,1)	bioadd*potting	1	7	241.64
UN(1,1)	bioadd*potting	1	8	319.64
UN(1,1)	bioadd*potting	1	9	341.55
UN(1,1)	bioadd*potting	2	1	135.89
UN(1,1)	bioadd*potting	2	2	433.20
UN(1,1)	bioadd*potting	2	3	41.0536
UN(1,1)	bioadd*potting	2	4	224.27
UN(1,1)	bioadd*potting	2	5	649.77
UN(1,1)	bioadd*potting	2	6	681.55
UN(1,1)	bioadd*potting	2	7	294.35
UN(1,1)	bioadd*potting	2	8	895.91
UN(1,1)	bioadd*potting	2	9	625.96

Separate variance estimates for each combination of the levels of the two factors.

Fit Statistics

-2 Res Log Likelihood	1134.8
AIC (smaller is better)	1170.8
AICC (smaller is better)	1177.2
BIC (smaller is better)	1224.2

Null Model Likelihood Ratio Test

DF	Chi-Square	Pr > ChiSq
17	32.03	0.0149

Type 3 Tests of Fixed Effects

Effect	Num DF	Den DF	Chi-Square	F Value	Pr > ChiSq	Pr > F
bioadd	1	126	3.54	3.54	0.0598	0.0621
potting	8	126	529.28	66.16	<.0001	<.0001
bioadd*potting	8	126	18.84	2.36	0.0157	0.0214

Ignore the standard F statistics in the output.
WTS statistics are in **blue**.

Type 3 Tests of Fixed Effects

Effect	ANOVA Num DF	ANOVA Den DF	ANOVA Chi-Square	ANOVA F Value	ANOVA Pr > ChiSq	ANOVA Pr > F
bioadd	1	89.1	3.54	3.54	<.0001	0.0631
potting	6.83	89.1	49.26	49.26	<.0001	<.0001
bioadd*potting	6.83	89.1	2.49	2.49	0.8697	0.0231

The ATS df, statistics and *P* values (in **red**) are provided with the ANOVAF option..

Least Squares Means

The $\overline{R}_{ii}$ are the LS Means estimates.

Effect	bioadd	potting	Estimate	Standard Error	DF	t Value
bioadd	1		75.8542	2.5610	126	29.62
bioadd	2		69.1458	2.4789	126	27.89
potting		1	21.2500	3.0981	126	6.86
potting		2	88.8750	5.1375	126	17.30
potting		3	73.8125	5.9121	126	12.49
potting		4	26.6250	3.6479	126	7.30
potting		5	111.91	7.1471	126	15.66
potting		6	104.34	6.0780	126	17.17
potting		7	26.0625	4.0926	126	6.37
potting		8	104.72	6.1633	126	16.99
potting		9	94.9063	5.4986	126	17.26
bioadd*potting	1	1	21.9375	4.6266	126	4.74
bioadd*potting	1	2	95.1250	7.1712	126	13.26
bioadd*potting	1	3	93.2500	11.6051	126	8.04
bioadd*potting	1	4	23.3750	5.0194	126	4.66
bioadd*potting	1	5	107.94	11.0951	126	9.73
bioadd*potting	1	6	105.56	7.9105	126	13.34
bioadd*potting	1	7	25.3125	5.4959	126	4.61
bioadd*potting	1	8	100.81	6.3210	126	15.95
bioadd*potting	1	9	109.38	6.5341	126	16.74
bioadd*potting	2	1	20.5625	4.1214	126	4.99
bioadd*potting	2	2	82.6250	7.3586	126	11.23
bioadd*potting	2	3	54.3750	2.2653	126	24.00
bioadd*potting	2	4	29.8750	5.2947	126	5.64
bioadd*potting	2	5	115.88	9.0123	126	12.86
bioadd*potting	2	6	103.13	9.2301	126	11.17
bioadd*potting	2	7	26.8125	6.0658	126	4.42
bioadd*potting	2	8	108.63	10.5825	126	10.26
bioadd*potting	2	9	80.4375	8.8456	126	9.09

LD_CI
Bias-Estimation and Confidence-Intervals for Relative Effects

LD_CI macro output.

SAS-Data-Filename: krause

Response-Variable:	dismd	Observations:	144
Group-Variable:	treatment	Groups:	18
Time-Variable:	_none_	Timepoints:	1
Subject-Variable	subject	Subjects:	144

Relative Effects, Biases, Variances and Confidence-Limits (alpha=0.05)

RE: estimated relative effect *(p_hat)*

Group	RE	Bias	Variance	lower	upper
11	.14887	.00000	.12874	.10130	.22041
12	.65712	.00000	.35004	.55443	.74544
13	.64410	.00000	.83086	.48468	.77400
14	.15885	.00000	.15076	.10726	.23589
15	.74609	.00000	.76487	.57613	.85828
16	.72960	.00000	.40830	.61195	.81892

17	.17231	.00000	.17167	.11671	.25350
18	.69661	.00000	.28554	.60211	.77526
19	.75608	.00000	.30466	.65335	.83307
21	.13932	.00000	.10906	.09562	.20546
22	.57031	.00000	.34064	.47338	.66154
23	.37413	.00000	.02241	.35006	.39893
24	.20399	.00000	.15760	.14804	.27808
25	.80122	.00000	.50093	.65542	.88883
26	.71267	.00000	.53805	.57809	.81447
27	.18273	.00000	.20874	.12161	.27220
28	.75087	.00000	.69084	.58928	.85813
29	.55512	.00000	.48176	.44076	.66329

Coding for combination of `bioadd` (fortification; 1 or 2) and `potting` mix (1 to 9)

Variance (*Var*): Variance of $(\sqrt{N})\cdot(p\_hat-p)$, not variance of *p_hat*. The standard error of *p_hat* is given by: $\sqrt{(Var/N)}$.

Lipps & Madden data set

wheat powdery mildew, 1995; 3 cultivars, 5 times

F1_LD_F1 --- subjects(A) x T
A(=FACTOR), T(=TIME): fixed, subjects: random

F1_LD_F1 macro prints some general header information.

SAS-datafile-name: wheat
Response variable: dis

Class Level Information

CLASS		LEVELS
A	CULTIVAR	3
T	TIME	5

Total number of observations 60
Number of missing values 0

RTE = Relative Treatment Effects
Nobs = Number of observations (do not count the repeated measurements within the cells)

SOURCE		Rank mean	Nobs	RTE
cultivar	1	36.850	20	0.6058333
cultivar	6	30.550	20	0.5008333
cultivar	7	24.100	20	0.3933333
time	1	11.250	12	0.1791667
time	2	19.792	12	0.3215278
time	3	30.542	12	0.5006944
time	4	41.500	12	0.6833333
time	5	49.417	12	0.8152778
cultivar*time	1*1	13.250	4	0.2125
cultivar*time	1*2	26.625	4	0.4354167
cultivar*time	1*3	32.500	4	0.5333333
cultivar*time	1*4	53.875	4	0.8895833
cultivar*time	1*5	58.000	4	0.9583333
cultivar*time	6*1	10.500	4	0.1666667
cultivar*time	6*2	16.625	4	0.26875
cultivar*time	6*3	36.625	4	0.6020833
cultivar*time	6*4	40.750	4	0.6708333
cultivar*time	6*5	48.250	4	0.7958333
cultivar*time	7*1	10.000	4	0.1583333
cultivar*time	7*2	16.125	4	0.2604167
cultivar*time	7*3	22.500	4	0.3666667
cultivar*time	7*4	29.875	4	0.4895833
cultivar*time	7*5	42.000	4	0.6916667

Relative treatment effects for each cultivar at each assessment time.

Warning:

```
Do not use the Wald-type-statistic, because the covariance matrix is singular.

Warning:

The estimated covariance matrix is not positive semidefinite due to missing
values.
```

It is common (and acceptable) for the covariance matrix to be singular.

```
                        Wald-type-statistic
Approximation for   large sample sizes with Chi-Square_DF

                          W     DF P_VALUE

A  8.3295 2.0000  .01553
T  323.44 4.0000  .00000
AT 205.16 8.0000  .00000
```

Do not use the Wald type statistics (WTS). The ANOVA-type statistics (ATS) are preferable for sample size situations

```
                      Anova-type-statistic
Box-Approximation for small sample sizes with Chi-square_DF

                          B     DF P_VALUE

A  4.5686 1.8701  .01204
T  52.465 2.5291  .00000
AT 1.7620 3.5211  .14206
```

B is the value of the test statistic (as in "Box-type statistic). DF is the numerator degrees of freedom. The denominator df is ∞ here. A is the whole plot factor. T is the time factor. AT is the whole plot factor-time interaction.

Chi-square test is used here, equivalent to F test with ∞ for denominator df. Test appropriate for T and AT.

```
                      Anova-type-statistic
modified Box-Approximation for the whole-plot factor A
        for small sample sizes with F(DF1,DF2)

                          B    DF1    DF2 P_VALUE

A 4.5686 1.8701 7.9022  .04970
```

Use the degrees of freedom and *P* value given by the Box approximation for the test of the whole plot factor. Note: DF1 and DF2 correspond to df_N and df_D in article.

```
Tests for the simple >> time << effect (T)
  Wald-type (Chi-square_DF1, asymptotic)
ANOVA-Type (Chi-square_DF1/DF1, asymptotic)

Statistic cultivar T       DF1     P_VALUE

Wald      1         160.53  3.0000  .00000
ANOVA     1         31.733  1.4967  .00000
Wald      6         55.552  3.0000  .00000
ANOVA     6         27.977  2.0435  .00000
Wald      7         636.91  3.0000  .00000
ANOVA     7         7.4391  1.4627  .00211

      Test for pairwise comparisons
```

Tests of simple time effects (see eq. 12 in S&M). Use ANOVA (i.e., ATS) results.

Tests of the cultivar*time term for each pair of cultivars are used to determine if the disease profiles over time are the

PAIRS	TEST	F	DF	P_VALUE
1*6	cultivar	3.0259	1.0000	.08194
1*6	time	57.683	2.4133	.00000
1*6	cultivar*time	2.3532	2.4133	.08384
1*7	cultivar	7.9535	1.0000	.00480
1*7	time	29.979	1.9359	.00000
1*7	cultivar*time	1.8773	1.9359	.15443
6*7	cultivar	2.0989	1.0000	.14740
6*7	time	26.414	2.3043	.00000
6*7	cultivar*time	1.2371	2.3043	.29254

LD_CI

Bias-Estimation and Confidence-Intervals for Relative Effects

Output from the LD_CI macro

SAS-Data-Filename: wheat

Response-Variable:	dis	Observations:	60
Group-Variable:	cultivar	Groups:	3
Time-Variable:	time	Timepoints:	5
Subject-Variable	sub	Subjects:	12

Relative Effects, Biases, Variances and Confidence-Limits (alpha=0.05)

Group	Time	RE	Bias	Variance	lower	upper
1	1	.21250	-.0021	.05344	.11529	.37831
1	2	.43542	.00069	.03635	.33278	.54485
1	3	.53333	.00139	.13847	.32996	.72473
1	4	.88958	-.0021	.00118	.86778	.90692
1	5	.95833	.00208	.00052	.92817	.96491
6	1	.16667	-.0007	.02524	.09918	.28339
6	2	.26875	-.0007	.04781	.16692	.41150
6	3	.60208	-.0063	.03365	.49476	.69915
6	4	.67083	.00278	.01722	.59218	.73968
6	5	.79583	.00486	.04399	.64562	.88512
7	1	.15833	.00000	.04847	.07687	.33972
7	2	.26042	-.0028	.13226	.11593	.51465
7	3	.36667	.00486	.14434	.19130	.59554
7	4	.48958	-.0035	.04038	.37868	.60168
7	5	.69167	.00139	.03931	.56826	.78951

Estimates may be biased for repeated measures. Note: Variance (*Var*) is really variance of $(\sqrt{S})\cdot(p\_hat-p)$, where *S* is number of subjects, not variance of *p_hat*. To get standard error of *p_hat*, calculate $\sqrt{(Var/S)}$

Harveson et al. data set

Effect of irrigation and variety on beet root decay
Analysis using the F1_LD_F1 macro

F1_LD_F1 --- subjects(A) x T
A(=FACTOR), T(=TIME): fixed, subjects: random

SAS-datafile-name: beet
Response variable: rating

F1_LD_F1 macro output

Class Level Information

CLASS		LEVELS
A	IRR	2
T	VAR	8

Total number of observations 96
Number of missing values 0

RTE = Relative Treatment Effects
Nobs = Number of observations (do not count the repeated measurements within the cells)

SOURCE		Rank mean	Nobs	RTE
irr	dry	37.854	48	0.3891059
irr	wet	59.146	48	0.6108941
var	4waymix	42.250	12	0.4348958
var	HH67	52.875	12	0.5455729
var	HH67Rang	59.250	12	0.6119792
var	MH9155	35.167	12	0.3611111
var	Rang9155	38.125	12	0.3919271
var	Ranger	59.250	12	0.6119792
var	RhizRang	51.250	12	0.5286458
var	Rhizosen	49.833	12	0.5138889
irr*var	dry*4waymix	32.333	6	0.3315972
irr*var	dry*HH67	39.417	6	0.4053819
irr*var	dry*HH67Rang	45.083	6	0.4644097
irr*var	dry*MH9155	32.333	6	0.3315972
irr*var	dry*Rang9155	36.833	6	0.3784722
irr*var	dry*Ranger	45.083	6	0.4644097
irr*var	dry*RhizRang	33.750	6	0.3463542
irr*var	dry*Rhizosen	38.000	6	0.390625
irr*var	wet*4waymix	52.167	6	0.5381944
irr*var	wet*HH67	66.333	6	0.6857639
irr*var	wet*HH67Rang	73.417	6	0.7595486
irr*var	wet*MH9155	38.000	6	0.390625
irr*var	wet*Rang9155	39.417	6	0.4053819
irr*var	wet*Ranger	73.417	6	0.7595486
irr*var	wet*RhizRang	68.750	6	0.7109375
irr*var	wet*Rhizosen	61.667	6	0.6371528

Relative treatment effects for each irrigation*variety combination.

Effect of irrigation and variety on beet root decay
Analysis using the F1_LD_F1 macro

```
Warning:
Do not use the Wald-type-statistic, because the covariance matrix is singular.

                        Analysis using the F1_LD_F1 macro

                                  Wald-type statistic
          Approximation for   large sample sizes with Chi-Square_DF


                                       W     DF P_VALUE

                                  A  40.265 1.0000  .00000
                                  T  82.447 7.0000  .00000
                                  AT 30.970 7.0000  .00006


                                  ANOVA-type statistic
                    Box-approximation for small sample sizes with Chi-square_DF

                                       B     DF P_VALUE

                                  A  40.265 1.0000  .00000
                                  T  2.2066 3.9261  .06686
                                  AT .86950 3.9261  .47961


                                  ANOVA-type statistic
                       modified Box-approximation for the whole-plot factor A
                               for small sample sizes with F(DF1,DF2)

                                       B    DF1    DF2 P_VALUE

                                  A 40.265 1.0000 7.7121  .00026

                        Analysis using the F1_LD_F1 macro

                     Tests for the simple >> var << effect (T)
                       Wald-type (Chi-square_DF1, asymptotic)
                    ANOVA-type (Chi-square_DF1/DF1, asymptotic)


                       Statistic irr T       DF1     P_VALUE

                       Wald      dry  25.000  5.0000  .00014
                       ANOVA     dry  .36903  2.0653  .69821
                       Wald      wet  14.338  5.0000  .01360
                       ANOVA     wet  2.5982  3.0108  .05024


                    Effect of irrigation and variety on beet root decay
                     Confidence intervals using the LD_CI macro

                                       LD_CI
          Bias-Estimation and Confidence-Intervals for Relative Effects


                                SAS-Data-Filename: beet
             Response-Variable: rating        Observations:        96
             Group-Variable:    irr           Groups:               2
             Time-Variable:     var           Timepoints:           8
             Subject-Variable   subject       Subjects:            12
```

The ATS (in red) are preferable for the typically small sample sizes encountered.

Use the Box-approximation for the test of the whole plot factor.

Output from the LD_CI macro.

Relative Effects, Biases, Variances and Confidence-Limits (alpha=0.05)

Group	Time	RE	Bias	Variance	lower	upper
dry	4waymix	.33160	.00139	.04737	.22344	.46519
dry	HH67	.40538	-.0024	.10734	.24267	.59593
dry	HH67Rang	.46441	.00035	.05597	.33682	.59753
dry	MH9155	.33160	-.0007	.02376	.25173	.42452
dry	Rang9155	.37847	-.0031	.21498	.17236	.65127
dry	Ranger	.46441	.00035	.05597	.33682	.59753
dry	RhizRang	.34635	.00417	.17482	.16293	.60376
dry	Rhizosen	.39063	.00000	.00553	.34957	.43354
wet	4waymix	.53819	.00104	.11991	.34687	.71751
wet	HH67	.68576	.00000	.10135	.48285	.82998
wet	HH67Rang	.75955	-.0005	.05606	.59771	.86387
wet	MH9155	.39063	.00000	.00553	.34957	.43354
wet	Rang9155	.40538	.00156	.12388	.23281	.60960
wet	Ranger	.75955	-.0005	.06713	.58016	.87089
wet	RhizRang	.71094	-.0021	.12141	.48001	.85935
wet	Rhizosen	.63715	.00052	.14572	.40635	.81265

Relative treatment effects (p_{ij}), variances, and 95% upper and lower confidence limits for p_{ij}.

The following is annotated output from SAS, using both standard procedures (RANK and MIXED, NPAR1WAY), and macros from Brunner et al. (LD_CI and OWL). All for a 1-way layout here (with generated data). Purpose is to show:

1) the relationship between the general approach of Brunner based on relative treatment effects and the classic Kruskal Wallis test for 1-way designs; and
2) how to interpret output, and compare the output from several different programs (procedures or macros); and
3) how to obtain marginal effects analyses with MIXED and also obtain classic Kruskal Wallis (KW) results with MIXED.

Disclaimer: Comments to help the reader. No attempt is made to thoroughly explain all of the output. We make no guarantee that the annotation is correct in all cases

```
                    1-way analysis using MIXED, with contrasts of two groups
21
                      Full marginal-treatment-effects analysis of Brunner
                                                              15:24 Tuesday, May 20,
2003

                                  The Mixed Procedure

                                   Model Information

 Data Set                     WORK.A
 Dependent Variable           r
 Covariance Structure         Unstructured
 Group Effect                 trt
 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

   trt           6    1 2 3 4 5 6

                                   Dimensions

                         Covariance Parameters            6
                         Columns in X                     7
                         Columns in Z                     0
                         Subjects                        48
                         Max Obs Per Subject              1
                         Observations Used               48
                         Observations Not Used            0
                         Total Observations              48

                                 Iteration History

 Iteration    Evaluations    -2 Res Log Like       Criterion

         0              1       334.33448547
         1              1       316.60486686      0.00000000

                              Convergence criteria met.
```

Use of MIXED to do general analysis; can ignore much of output

1-way analysis using MIXED, with contrasts of two groups
22
Full marginal-treatment-effects analysis of Brunner
15:24 Tuesday, May 20,
2003

The Mixed Procedure

Covariance Parameter
Estimates

Cov Parm	Group	Estimate
UN(1,1)	trt 1	50.6964
UN(1,1)	trt 2	181.14
UN(1,1)	trt 3	44.5000
UN(1,1)	trt 4	272.70
UN(1,1)	trt 5	14.5000
UN(1,1)	trt 6	184.29

Variances for each treatment. With standard Kruskal Wallis, these are considered all the same, 48*(49)/12 = 196 (under **null** hypothesis).

Fit Statistics

-2 Res Log Likelihood	316.6
AIC (smaller is better)	328.6
AICC (smaller is better)	331.0
BIC (smaller is better)	339.8

Null Model Likelihood Ratio Test

DF	Chi-Square	Pr > ChiSq
5	17.73	0.0033

WTS statistic in ***blue***

ATS in ***red***

Type 3 Tests of Fixed Effects

Effect	Num DF	Den DF	Chi-Square	F Value	Pr > ChiSq	Pr > F	ANOVA Num DF	ANOVA Den DF	ANOVA Chi-Square	ANOVA F Value
trt	5	42	129.37	25.87	<.0001	<.0001	3.44	26.8	6.38	6.38

Type 3 Tests of Fixed Effects

Effect	ANOVA Pr > ChiSq	ANOVA Pr > F
trt	0.0944	0.0015

ATS and WTS results may be displayed somewhat differently (more clearly) in version 9.1 of SAS.

1-way analysis using MIXED, with contrasts of two groups 23
Full marginal-treatment-effects analysis of Brunner
15:24 Tuesday, May 20, 2003

Example contrast of two groups. This is an ATS. Could have obtained WTS by adding chisq option to contrast statement.

The Mixed Procedure

Contrasts

Label	Num DF	Den DF	F Value	Pr > F	ANOVA Num DF	ANOVA Den DF	ANOVA F Value	ANOVA Pr > F
A vs B	1	42	0.24	0.6258	1	26.8	0.24	0.6272

Least Squares Means

Effect	trt	Estimate	Standard Error	DF	t Value	Pr > |t|
trt	1	**24.8750**	2.5174	42	9.88	<.0001
trt	2	24.0000	4.7585	42	5.04	<.0001
trt	3	14.2500	2.3585	42	6.04	<.0001
trt	4	15.1250	5.8384	42	2.59	0.0131
trt	5	41.7500	1.3463	42	31.01	<.0001
trt	6	27.0000	4.7996	42	5.63	<.0001

Note: p1^ = (Rbar1-0.5)/N = (24.875-0.5)/48 = 0.508.

Mean ranks and their estimated standard errors. One can get p^ (estimated relative treatment effects) from these means, and *rough* estimates of se(p^) from the standard errors of the rank means. Based on actual variability.

Differences of Least Squares Means

Effect	trt	_trt	Estimate	Standard Error	DF	t Value	Pr > |t|
trt	1	2	**0.8750**	**5.3833**	42	**0.16**	0.8717
trt	1	3	10.6250	3.4496	42	3.08	0.0036
trt	1	4	9.7500	6.3580	42	1.53	0.1327
trt	1	5	-16.8750	2.8547	42	-5.91	<.0001
trt	1	6	-2.1250	5.4197	42	-0.39	0.6970
trt	2	3	9.7500	5.3109	42	1.84	0.0735
trt	2	4	8.8750	7.5319	42	1.18	0.2453
trt	2	5	-17.7500	4.9452	42	-3.59	0.0009
trt	2	6	-3.0000	6.7586	42	-0.44	0.6594
trt	3	4	-0.8750	6.2968	42	-0.14	0.8901
trt	3	5	-27.5000	2.7157	42	-10.13	<.0001
trt	3	6	-12.7500	5.3477	42	-2.38	0.0217
trt	4	5	-26.6250	5.9916	42	-4.44	<.0001
trt	4	6	-11.8750	7.5580	42	-1.57	0.1236
trt	5	6	14.7500	4.9848	42	2.96	0.0051

Df do not correspond to ATS. One could override the default

Above are the differences of the mean ranks ("Estimate") and the standard error of the difference (SED). This SED is based on *actual* variability (not that assumed by Kruskal Wallis). The "t" value is Estimate/SED. Two rank means are different if Estimate (of difference) is more than ~2*SED. Thus, this part of the output gives *multiple comparisons.*

<u>Treatments 1 vs 2:</u>
Estimate = 24.875-24.0 = 0.875
SED = $\sqrt{\{(2.517^2)+(4.758^2)\}}$ = 5.383.
t = 0.875/5.383 = 0.16.
Thus, 1 and 2 are not different.

```
          Estimated marginal treatment effects using macro; each observation is a subject
24
                                                '                        15:24 Tuesday, May 20,
2003

                                        LD_CI
                  Bias-Estimation and Confidence-Intervals for Relative Effects


                                SAS-Data-Filename: a
                Response-Variable: x            Observations:        48
                Group-Variable:    trt          Groups:               6
                Time-Variable:     _none_       Timepoints:           1
                Subject-Variable   sub          Subjects:            48


Relative Effects, Biases, Variances and Confidence-Limits (alpha=0.05)


                  Group    RE       Bias     Variance lower    upper

                    1    .50781   .00000   .15206   .39948   .61510
                    2    .48958   .00000   .37156   .32795   .65441
                    3    .28646   .00000   .13802   .19989   .40819
                    4    .30469   .00000   .55162   .15862   .55706
                    5    .85938   .00000   .04585   .76096   .89736
                    6    .55208   .00000   .36951   .38106   .70696
```

Note: p^ = (Rbar-0.5)/N, where N is number of observations (also, number of subjects *here*, because this is not a repeated measures). For group 1, p^ = 0.5078 = (24.875-0.5)/48.

LD_CI macro: Non-parametric approach to confidence interval (CI) for estimated relative effect (RE), also known as p^. Uses *actual* variability, not simple value of KW. Ideally, one should use this macro to get se(p^) = √{Variance/N}, and conf. int. for p.

The printed variance here is not the square of the standard error of estimated p [se(p^)]. For technical reasons, one divides the printed variance by number of subjects, and then takes the square root to get se(p^). For the first group shown (p1^=.508), se(.508) = √{.1521/48} = 0.056. This is because the printed variance is of [√*N*]*[*p_hat – p*], where p is the theoretical (constant) value.

If one goes back to the MIXED output (above), the se for the first mean rank was 2.517. The se for p1^ is *roughly* se(Rbar1)/N = 2.517/48 = 0.052, pretty close to the more sophisticated 0.056 calculated here.

Note: one does *not* divide the se(Rbar) by the

This macro uses a sophisticated algorithm to get the limits of the confidence interval, by "linearizing" the interval, avoiding p values (or Rbars) that are out of the possible range. Mostly affects p limits near 0 and 1.

One can estimated the SED for groups 1 and 2; SED = √{[se(p1^)^2]+[se(p2^)]^2} = √{.056^2 + .088^2} = √{0.011} = 0.104.

To get this from the MIXED output (which gives rough values of the se's, one can use: 5.383/48 = 0.112 (slightly different from the value here).

Macro OWL for 1-way layouts. Does standard Krukal Wallis (KW) chi-squre test, plus other things. Variances and confidence intervals more general than simple KW versions.

```
Direct 1-way Kruskal-Wallis analysis with macro                25
But, variances of relative treatment effects direct from data (not assumed)
                                                 15:24 Tuesday, May 20, 2003

                              NONPARAMETRIC
                              ONE-WAY LAYOUT


     Data Information, Estimation, Confidence Intervals (alpha = 0.05)


                                Data Set: a


                          Total Sample Size:        48


                                                                Confidence Intervals
      Nr. Class Levels       n_i Rank Means       p_i       p_L       p_U

        1            1         8     24.875 0.5078125 0.3974957 0.6181293
        2            2         8         24 0.4895833 0.3171421 0.6620246
        3            3         8      14.25 0.2864583  0.181359 0.3915576
        4            4         8     15.125 0.3046875 0.0945775 0.5147975
        5            5         8      41.75  0.859375 0.7987982 0.9199518
        6            6         8         27 0.5520833 0.3801175 0.7240492


                    Hypothesis Testing: F_1 = ... = F_a


                                  p-Values
                     Statistic     Chi-Sq. Appr.   F-Appr.     Exact

     Kruskal-Wallis 20.292092         0.0011014         .         0
     F-Test Rank    31.910693         6.1882E-6 0.0001809         .

          Number of Simulations for the Exact p-Value: 1000
```

Single factor tests *only*. Note: confidence intervals are based on *actual* variability (not assumed value of KW).

Limits are simpler than done with LD macro.
Standard errors (or variances) not shown. This approach and the one done by LD macro are *both* valid, but this macro can only be used for pure 1-way layout.

F test uses same data (ranks), but is more valid for *small* sample sizes. It can be obtained from the general relative effects analysis (done above with MIXED on ranks). Note: 31.9107/5 = **6.38**, which was the ATS in MIXED output above. Here, however, no corrections in df (that's why we used 5 here, instead of 3.44; correction not necessary for 1-way case, but acceptable).

Note: OWL macro also does randomization testing (see below).

This is the classic (standard) chi-square test of KW, with adjustment for ties. There are *a*-1 df (where a is #groups [*a*=6 here]). One can also get this from MIXED (see below), if you *force* MIXED to use *N*(N+1)*/12 for the error (residual) variance.

More from OWL macro

```
            Direct 1-way Kruskal-Wallis analysis with macro              26
But, variances of relative treatment effects direct from data (not assumed)
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                  Pairwise Comparisons (alpha = 0.05)
```

Samples		Statistic	p-Values			Decision (Holm-Proc.)		
			Normal	t-Appr.	Exact	Normal	t-Appr.	Exact
1	2	0.1625397	0.8708808	0.8733802	0.8890443	0	0	0
1	3	3.0800914	0.0020694	0.0087767	0.0104118	1	0	0
1	4	1.5335022	0.1251522	0.1491222	0.1522922	0	0	0
1	5	-5.911217	3.3959E-9	0.0000514	0.0001554	1	1	1
1	6	-0.392091	0.6949912	0.7013436	0.7185703	0	0	0
2	3	1.8358568	0.0663788	0.0893499	0.0933955	0	0	0
2	4	1.1783175	0.2386701	0.2597894	0.2604507	0	0	0
2	5	-3.589313	0.0003316	0.0032986	0.0037296	1	1	1
2	6	-0.443879	0.6571298	0.6644283	0.6702409	0	0	0
3	4	-0.13896	0.889482	0.8916116	0.9142191	0	0	0
3	5	-10.12632	0	1.5551E-7	0.0001554	1	1	1
3	6	-2.384189	0.0171168	0.0330481	0.0354312	0	0	0
4	5	-4.443704	8.8423E-6	0.0006622	0.001554	1	1	1
4	6	-1.571191	0.1161383	0.1401505	0.1418803	0	0	0
5	6	2.9589963	0.0030864	0.0110787	0.0052836	1	0	0

All possible *pairwise comparisons*, done a few different ways with OWL. Note: although a standard Kruskal-Wallis test is done first (above), the treatment comparisons are based on actual variances, not simple assumed values of Kruskal Wallis (under null hypothesis)

Statistic is difference of p^'s for treatment pair divided by SED of treatment pair. Note: the "Statistic" here is about the same as the t-value found with MIXED (*above*, for relative effects analysis) for pairwise differences of mean ranks. This shows that the standard errors in MIXED (for mean rank differences) are the same ones calculated with OWL (for differences of p^s), but the latter is only used for 1-way layouts. Significance values for *statistic* here are similar to those found for MIXED (but MIXED used different dfs [but this could be modified]). Even though MIXED deals with ranks, and OWL with p^, the statistic and t values are ratios, and no other conversions are needed.

OWL macro also does pairwise comparisons with a randomization procedure (1000 randomizations by default)

<u>Treatments 1 vs 2:</u>
(p1^-p2^)/SED(p1^-p2^) = 0.018/0.112 = 0.16.
Note: used SED = 0.112 (obtained from MIXED, above).

```
Direct 1-way Kruskal-Wallis analysis with SAS nonparametric PROCedure    27
                                  '            15:24 Tuesday, May 20, 2003

                        The NPAR1WAY Procedure

              Wilcoxon Scores (Rank Sums) for Variable x
                      Classified by Variable trt

                    Sum of      Expected       Std Dev          Mean
 trt       N        Scores      Under H0      Under H0         Score

 1         8         199.0         196.0     36.147845       24.8750
 2         8         192.0         196.0     36.147845       24.0000
 3         8         114.0         196.0     36.147845       14.2500
 4         8         121.0         196.0     36.147845       15.1250
 5         8         334.0         196.0     36.147845       41.7500
 6         8         216.0         196.0     36.147845       27.0000


                    Kruskal-Wallis Test

                Chi-Square         20.2921
                DF                       5
                Pr > Chi-Square     0.0011
```

This is standard (classic) Kruskal Wallis analysis, done with **NPAR1way** in SAS

Although not commonly mentioned in books, KW method assumes that the residual variance (V) of a rank (not mean rank) under the null hypothesis is N*(N+1)/12 = 48*49/12 = 196 (here).

Classic KW chi-square test.

=Mean rank.

Standard error (se) of mean rank is: $\sqrt{\{V/n\}}$, or $\sqrt{\{N*(N+1)/(12*n)\}}$, in which n is number of reps for the treatment. Here, se(Rbar1)= $\sqrt{\{196/8\}}$ = 4.95.
This is for the null hypothesis.

Standard error of a difference (of two mean ranks) is:
SED = $\sqrt{\{V*(1/n1 + 1/n2)\}}$ = $\sqrt{\{[N*(N+1)/12]*[1/n1 + 1/n2]\}}$ = $\sqrt{\{196*(1/8 + 1/8)\}}$ = 7.0 (here).
This is for the null hypothesis.

Compare SE and SED here with the values from MIXED above (more general relative treatment effects analysis). The KW values could be larger or smaller than the values obtained directly from the data.

```
    Kruskal Wallis approach with MIXED; Chi-square = WTS = KW statistic here  28
Need NOPROFILE and fixed error variance, N*(N+1)/12, with PARMS (196)/eqcons=1
    No tie correction. St.errors of R_bar and differences are KW type (here)
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                          The Mixed Procedure

                           Model Information

            Data Set                      WORK.A
            Dependent Variable            r
            Covariance Structure          Variance Components
            Estimation Method             REML
            Residual Variance Method      Parameter
            Fixed Effects SE Method       Model-Based
            Degrees of Freedom Method     Between-Within


                       Class Level Information

         Class    Levels    Values

         trt           6    1 2 3 4 5 6


                           Dimensions

               Covariance Parameters             1
               Columns in X                      7
               Columns in Z                      0
               Subjects                         48
               Max Obs Per Subject               1
               Observations Used                48
               Observations Not Used             0
               Total Observations               48


                        Parameter Search

          CovP1            Res Log Like    -2 Res Log Like

          196.00              -169.0281          338.0562


                        Iteration History

      Iteration    Evaluations    -2 Res Log Like       Criterion

              1              1       338.05620989      0.00000000

                    Convergence criteria met.
```

Options were chosen so that there is a single (residual) variance, *forced* to equal N*(N+1)/12 = 196 (here). (See above for NPAR1WAY output. Called "CovP1" (covariance parameter 1) here.

This is how you get a standard (*classic*) Kruskal Wallis test using PROC MIXED. One uses the assumed residual variance under the null hypothesis of no treatment effect.

```
    Kruskal Wallis approach with MIXED; Chi-square = WTS = KW statistic here  29
Need NOPROFILE and fixed error variance, N*(N+1)/12, with PARMS (196)/eqcons=1
    No tie correction. St.errors of R_bar and differences are KW type (here)
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                          The Mixed Procedure

                      Covariance Parameter
                            Estimates

                      Cov Parm     Estimate

                      Residual       196.00


                            Fit Statistics

                    -2 Res Log Likelihood           338.1
                    AIC (smaller is better)         338.1
                    AICC (smaller is better)        338.1
                    BIC (smaller is better)         338.1


                       PARMS Model Likelihood Ratio Test

                         DF    Chi-Square      Pr > ChiSq

                          0          0.00          1.0000


                        Type 3 Tests of Fixed Effects

                    Num     Den
      Effect         DF      DF    Chi-Square    F Value      Pr > ChiSq    Pr > F

      trt             5      42         20.29       4.06          0.0011    0.0043


                             Least Squares Means

                                        Standard
          Effect    trt    Estimate       Error      DF    t Value    Pr > |t|

          trt       1       24.8750      4.9497    1000       5.03      <.0001
          trt       2       24.0000      4.9497    1000       4.85      <.0001
          trt       3       14.2500      4.9497    1000       2.88      0.0041
          trt       4       15.1250      4.9497    1000       3.06      0.0023
          trt       5       41.7500      4.9497    1000       8.43      <.0001
          trt       6       27.0000      4.9497    1000       5.45      <.0001
```

Residual variance as N*(N+1)/12; do not estimate this. 48*49/12 = 196.

The Chi-square test in red is the Kruskal Wallis statistic here (see NPAR1WAY above). Ignore F value.

These are the rank means and the standard Kruskal Wallis standard errors = $\sqrt{\{N(N+1)/[n*12]\}}$, N=total points, n=#reps in treatment.

Se(Rbar) = $\sqrt{\{(48*49)/(8*12)}$ = 4.95 for all treatments (compare with first MIXED output).

Forced df=1000 (BIG number) so that the t tests are really z (st. normal) tests (which is usually done with KW).

```
    Kruskal Wallis approach with MIXED; Chi-square = WTS = KW statistic here  30
Need NOPROFILE and fixed error variance, N*(N+1)/12, with PARMS (196)/eqcons=1
    No tie correction. St.errors of R_bar and differences are KW type (here)
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                              The Mixed Procedure

                      Differences of Least Squares Means

                                                Standard
  Effect    trt    _trt    Estimate             Error      DF    t Value    Pr > |t|

  trt       1      2         0.8750            7.0000    1000       0.13      0.9005
  trt       1      3        10.6250            7.0000    1000       1.52      0.1294
  trt       1      4         9.7500            7.0000    1000       1.39      0.1640
  trt       1      5       -16.8750            7.0000    1000      -2.41      0.0161
  trt       1      6        -2.1250            7.0000    1000      -0.30      0.7615
  trt       2      3         9.7500            7.0000    1000       1.39      0.1640
  trt       2      4         8.8750            7.0000    1000       1.27      0.2051
  trt       2      5       -17.7500            7.0000    1000      -2.54      0.0114
  trt       2      6        -3.0000            7.0000    1000      -0.43      0.6683
  trt       3      4        -0.8750            7.0000    1000      -0.13      0.9005
  trt       3      5       -27.5000            7.0000    1000      -3.93      <.0001
  trt       3      6       -12.7500            7.0000    1000      -1.82      0.0688
  trt       4      5       -26.6250            7.0000    1000      -3.80      0.0002
  trt       4      6       -11.8750            7.0000    1000      -1.70      0.0901
  trt       5      6        14.7500            7.0000    1000       2.11      0.0354
```

These are differences of rank means and the st. errors of the differences (SED), calculated according to the Kruskal Wallis method. DF=1000 was chosen so that the t value (difference/SED) is really a z (standard normal) value.

Standard error of a difference (SED) = $\sqrt{\{[N*(N+1)/12]*[(1/n1) + (1/n2)]\}}$ which simplifies to $\sqrt{\{a*(N+1)/6\}}$ when all treatments have same # reps. Here, SED = $\sqrt{\{6*49/6\}} = 7.0$ (compare with first MIXED output).

The classic KW results here (for comparison of mean ranks) are not necessarily the same as for the more general analysis done above (either with the relative treatment effects or with OWL (because those methods used actual variability, not that assumed for 1-way layouts). Results do agree with NPAR1WAY (by definition).