**Technical documentation Amiga Power Analysis Tool**

**Comparisons, interaction factors and modifiers**

The default comparison is between the GMO and the comparator (CMP) averaged over all levels of all other factors. This implies that the other factors provide effective replications.

The default comparison can be changed in the Design tab (for all endpoints), in the Interactions tab (making the comparison endpoint specific) and finally in the Comparisons tab to make it specific for comparisons. Suppose we have two additional factors F and G with 3 and 2 levels respectively. Further suppose that we would like to make the following comparison which is averaged over all levels of G:

|  |  |  |
| --- | --- | --- |
|  | GMO | CMP |
| F1 | 1 | 0 |
| F2 | 0 | 1 |
| F3 | 0 | 1 |

F is called an interaction factor. It is then assumed that the mean count of the CMP for F2 and F3 are both equal to the general mean (as given in the Endpoints data tab), and the mean count of the GMO for F1 equals in which is some factor which is defined by the limits of concern in the Endpoints tab. The dummies which are used in fitting the associated model for F are given below.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Variety | F | G | Comparison | Constant | Dum[1] | Dum[2] | Dum[3] | Dum[4] |
| GMO | F1 | G1 | 1 | 1 | 1 | 0 | 0 | 0 |
| GMO | F1 | G2 | 1 | 1 | 1 | 0 | 1 | 0 |
| GMO | F2 | G1 | 0 | 1 | 0 | 1 | 0 | 0 |
| GMO | F2 | G2 | 0 | 1 | 0 | 1 | 0 | 0 |
| GMO | F3 | G1 | 0 | 1 | 0 | 0 | 1 | 0 |
| GMO | F3 | G2 | 0 | 1 | 0 | 0 | 1 | 0 |
| CMP | F1 | G1 | 0 | 1 | 0 | 0 | 0 | 1 |
| CMP | F1 | G2 | 0 | 1 | 0 | 0 | 0 | 1 |
| CMP | F2 | G1 | -1 | 1 | 0 | 0 | 0 | 0 |
| CMP | F2 | G2 | -1 | 1 | 0 | 0 | 0 | 0 |
| CMP | F3 | G1 | -1 | 1 | 0 | 0 | 0 | 0 |
| CMP | F3 | G2 | -1 | 1 | 0 | 0 | 0 | 0 |

Note that although the full interaction table Variety\*F contains 6 cells, there are only 5 parameters associated with the table (including the constant parameter). This is because it is assumed that F2 and F3 for CMP have equal means. The vector Dum[1] in the model Constant + Dum[1,2,3,4] is associated with the statistical test of the comparison. More specifically a statistical test can be constructed by comparing the fit of the full model “Constant + Dum[1,2,3,4]” with the fit of the restricted model “Constant + Dum[2,3,4]”.

The remaining factor G in this example can be specified as a modifier. This will modify the mean count of G1 and G2 in the same way for all levels of the factors Variety and F. This implies that a modifier is an additive term in the model, similarly to (random) block effects. Also a modifier provides extra levels of replication for the comparison.

As an example suppose the general mean for CMP equals =10. Further suppose that the other means in the Variety\*F table are specified as below. Note that in the Comparions tab the user will not be able to modify the mean count for cells that are part of the comparison, and also that is set to 1 to specify the mean counts for the levels which are associated with the GMO comparison (in this case cell GMO-F1).

|  |  |  |
| --- | --- | --- |
|  | GMO | CMP |
| F1 | 10 | 8 |
| F2 | 6 | 10 |
| F3 | 4 | 10 |

Further suppose that factor G is a modifier with multiplicative values 0.5 for G1 and 1 for G2. The basic means which are used in the simulation are then given by

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Variety | F | G | Comparison | Mean |
| GMO | F1 | G1 | 1 | 5 |
| GMO | F1 | G2 | 1 | 10 |
| GMO | F2 | G1 | 0 | 3 |
| GMO | F2 | G2 | 0 | 6 |
| GMO | F3 | G1 | 0 | 2 |
| GMO | F3 | G2 | 0 | 4 |
| CMP | F1 | G1 | 0 | 4 |
| CMP | F1 | G2 | 0 | 8 |
| CMP | F2 | G1 | -1 | 5 |
| CMP | F2 | G2 | -1 | 10 |
| CMP | F3 | G1 | -1 | 5 |
| CMP | F3 | G2 | -1 | 10 |

In case there are extra varieties, in addition to GMO and CMP, the mean counts for these are set to the general mean , irrespective of any interaction factors, and modified according to the modifiers. However in fitting the model it is assumed that these extra varieties do interact with the interaction factors. In the example above, with F as interaction factor, this results in three extra dummies for every extra variety.

**Simulation distributions**

The mean count for CMP and its associated coefficient variation , as specified in the Endpoints data tab, define the dispersion parameter of the associated distribution. This dispersion parameter is then used for **all** other mean counts. For the power model, with variance function , the parameter is first derived as . This value of is the used for all mean counts levels. However since there is no true distribution associated with the power model, for every mean count level separately, a corresponding value of the negative binomial dispersion parameter is calculated by equating the variance functions of the power model and the negative binomial distribution. The negative binomial distribution, with a unit specific dispersion parameter, is then used to simulate data.

In the Modifiers tab the user can specify a coefficient of variation for block effects. In that case the basic model for the mean counts is in which represents all the factors in the model and is a random normally distributed block effect. For a lognormal distribution the coefficient of variation is given by . and this equation is used to calculate the variance of the random block effect. Then for every simulated dataset random block effects are generated and applied to the mean counts. Note that block effects are always part of the fitted model, even in case blocks are not considered to be modifiers.

**LN and SQ models for analysis**

The LN and SQ models simply transform the simulated data and then perform a linear regression on the transformed scale. The two-sided difference test for the comparison is obtained by fitting the full model and then calculating the squared t-value for dummy Dum[1]. This is then compared with a critical F‑value with appropriate degrees of freedom.

The equivalence test uses the generalized confidence interval (GCI) approach as described in one of the AMIGA reports. This requires estimated means for the CMP and the GMO. In case there are no modifiers these are given simply by the estimate for the Constant in the model (for CMP) and by the sum of the estimates for the Constant and Dum[1] (for GMO). However when there are modifiers it is necessary to average over the modifiers. In GenStat this can be done by using the PREDICT directive with dum[1] set to 0 (for CMP) and 1 (for GMO) and all other dummies to 0. GCI also requires the effective level of replication of both estimates. This is calculated as where equals the standard errors of the two predicted means.

**OP model for analysis**

A deviance based difference test is obtained by fitting the full model and the restricted model. The deviance difference is scaled by Pearsons statistic and the test statistic is compared to an F distribution.

The equivalence test is based on comparing the deviance of the model in which the ratio of the GMO and CMP is set to the limit of concern, employing an offset in the model, with the deviance of the full model. This is only necessary when the estimate of Dum[1] is inside the interval set by the limits of concern, since when it is outside this interval the equivalence hypothesis will not be rejected. In case the estimate of Dum[1] is smaller than zero the relevant null-hypothesis concerns the lower limit of concern, while when the estimate is larger than zero the upper limit of concern is of interest. Again Pearsons statistic is used to scale the deviance difference and the test statistic is compared with the F statistic. This approach is checked by means of the GenStat program EquivalencePoisson.gen.

**NB model for analysis**

The approach is largely the same as for the OP model. The only difference is that the deviance difference is not scaled and that the test statistics are compared with a critical value based on the Chi-squared distribution.

**Timing in GenStat**

Fitting the NB model is notably slow since this uses a robust bisection algorithm to estimate the dispersion parameter. On the other hand fitting the LN and SQ models is fast although the GCI approach can be time consuming when the number of samples is large.

The following settings were used for timing of the example with factors F and G in the example above

1. Using a grid of 5 values for the difference between limits of concern 0.5 and 2.0
2. 6 difference replications 2,3,4,5 , 6 and 7
3. Blocking with a 10% coefficient of variation
4. 10000 samples for the GCI approach for LN and SQ
5. simulation by means of the negative binomial distribution
6. 10 datasets were simulated for each 5x6 = 30 settings

|  |  |
| --- | --- |
| Fitted models | Seconds |
| LN SQ | 24 |
| LN SQ OP | 28 |
| LN SQ OP NB | 191 |

Hopefully multiple instances of Rdotnet are possible so that multiple processors can be used simultaneously for different parts of the simulation.