

The GENMOD Procedure

The GENMOD procedure fits generalized linear models with a number of built-in link functions and probability distributions. The available link functions are the identity, log, logit, probit, power, cumulative complementary log-log, cumulative logit, cumulative probit, and complementary log-log. PROC GENMOD also allows user-defined link functions. The available probability distributions are binomial, gamma, inverse Gaussian, multinomial, negative binomial, normal, and Poisson. You can also specify a user-defined probability distribution.

Selected PROC GENMOD statement options:

PLOTS (*global-plot-options*) = (*plot-request (options)*)... *plot-request (options)*

Examples:

- PLOTS=ALL
- PLOTS=PREDICTED
- PLOTS=(PREDICTED RESCHI)
- PLOTS(UNPACK)=DFBETA

The default plots with the *plots=all* option in the PROC GENMOD statement include diagnostic plots, DFBETA plots, standardized DFBETA plots, and plots of the residuals versus the observation number.

Selected GENMOD procedure statements:

- CLASS specifies the classification variables to be used in the analysis. If the CLASS statement is used, it must appear before the MODEL statement.
- MODEL specifies the response variable and the predictor variables.
- ESTIMATE provides a means for obtaining a test for a specified hypothesis concerning the model parameters. It can be used to produce the ratio of the expected number of events for subjects in one category compared to another category along with the 95% confidence limits.

Close