In order to apply the generalized linear model, we need to make a few modifications of the generic recipe for applying the general linear model.

Table 16.1 Generic Recipe for Statistical Inference with the Generalized Linear Model.

    Introduction. Data set with context and goals of analysis.
1.   Construct model. Begin with verbal and graphical model.
      Distinguish response from explanatory variables
      Assign symbols, state units and type of measurement scale for each.
      Make preliminary choice of error model.
      Write out statistical model.
2.   Execute model   Place data in model format, code model statement.
                   Compute fitted values from parameter estimates.
                   Compute residuals and plot against fitted values.
3.   Evaluate the model, using residuals.
      If fitted line inappropriate, revise the model (back to step 1).
      If errors not homogeneous, revise error model (step 1).
      If heterogeneity due to influential outliers, revise error model or link function.
      Residuals independent ? (plot residuals versus residuals at lag 1)
        If not add term to capture non-independence (often spatial or temporal).
      If using chisquare, t, or F distribution to estimate Type I error, check normality.
        Evaluate residuals with histogram and quantile or normal score plot.
      If not met, check p-value with empirical distribution (by randomization).
4.   Report evidence. Calculate omnibus likelihood ratio from ANOVA or ANODEV table.
      If negligible, then skip to step 10.
5.   Choose mode of inference: evidentialist, frequentist, priorist.
      Priorist: Give probable cause for prior distribution.
      Frequentist: What is the target of inference?
        Hypothesis testing? If so, state test statistic, its distribution (t or F).
        Fixed Type I error required? If so, state α.
6.   Statistical analysis.
    If evidentialist, report *LR* for fixed terms, then Step 7.
    If frequentist Table Source, *df, SS*. Calculate t or F from *MS*.
      If normal error, *p* from probability model. Otherwise, *p* by randomization.
      If fixed α (Type I error) calculate confidence limits as appropriate, then Step 7.
      If α not fixed, report *p* by category, then Step7.
    If priorist, state and justify prior probability. Compute posterior probability, then to Step7.
7.   Report science conclusions. Interpret parameters of biological interest (means, slopes, odds ratios) along with one measure of uncertainty (R^2, st. error, st. dev., or confidence intervals) or posterior probability.