Table 8.3 Generic Recipe for Statistical Inference with the General Linear Model.

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.
   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 straight line inappropriate, revise the model (back to step 1).
   If errors not homogeneous, consider using generalized linear model (step 1)
   If n small, evaluate assumptions for using chisquare, t, or F distribution.
   residuals homogeneous ? (residual versus fit plot)
   residuals independent ? (plot residuals versus residuals at lag 1)
   residuals normal ? (histogram of residuals, quantile or normal score plot)
   If not met, empirical distribution (by randomization) may be necessary
4. Partition df and SS according to model. Write SS and df for each term in model.
   State the full (null) and reduced (alternative) model
   Calculate likelihood ratio for omnibus model.
   If sufficient evidence for omnibus model Step 5, otherwise step 10.
5. Define target of inference. Choose mode of inference: evidentialist, frequentist, priorist.
   If priorist, see recipe. If evidentialist, step 9.
6. State test statistic, and sampling distribution (t, F. χ^2, or Monte Carlo).
   Fixed Type I error or Fisher sorting?
7. ANOVA: Table Source, SS, and df. Calculate MS, F-ratio.
   Obtain Type I error (p-value) from distribution (F or t).
8. Recompute Type I error if necessary.
   If assumptions not met compute Type I error by randomization if:
   sample small ($n < 30$) and if Type I error near fixed α.
9. Report statistical conclusion about fixed terms and factor contrasts in the model.
   For frequentist inference report either the ANOVA table, or F-ratio (df1,df2),
   or t-statistics (df=1) and Type I error (not α) for fixed terms and factor contrasts.
10. Report science conclusions. Interpret parameters of biological interest (means, slopes)
    along with one measure of uncertainty (st. error, st. dev., or conf. intervals).
    Use t or Monte Carlo distribution to compute confidence limits as needed.

The next chapters work through the generic recipe step by step for commonly used analyses in biology