

reflect different evolutionary models (Paradis, 2012). PLogR is conceptually based on logistic regression, which uses the logit link function to transform a binary response variable into an odds ratio suitable for describing as a linear model;

$$\ln\left(\frac{p}{(1-p)}\right) = \beta_0 + \beta_1 x \quad (5.1)$$

The odds ratio can be readily converted back into a probability that an observation with a given value of the predictor variable is of state 1;

$$p = \frac{e^{(\beta_0 + \beta_1 x)}}{1 + e^{(\beta_0 + \beta_1 x)}} \quad (5.2)$$

PLogR differs from standard logistic regression ~~by accounting~~ for the degree of phylogenetic signal by estimating the parameter  $\alpha$  (Ives & Garland, 2010). The implementation of PLogR as provided by PHYLOLM (Ho & Ane, 2014) was used here.

Single character evolution was analysed using discrete category Markov models, as implemented in the DIVERSITREE package for R. These Markov models allow alternative hypotheses of character transition to be evaluated. The following models of evolution were evaluated (Table 5.9): a) full model, with all rates different; b) equal rates model, with only a single rate; c) two rate model with separate forward and reverse rates; d) progression model with  $n \rightarrow n+1$  and  $n \rightarrow n-1$  expected to be greater than other transitions, e) jump model with  $0 \rightarrow n$  and  $n \rightarrow 0$  expected to be greater than other transitions, f) correlated evolution model with large  $n \rightarrow n+2$  and  $n \rightarrow n-2$  transitions.



Determining correlated evolution between discrete traits is a subject that has yet to reach maturity (Maddison & FitzJohn, 2015). In this study, the correlation of female secondary sexual characters and the environment

