Models to describe the evolution of biological sequences abound. With the increased number of models statistical procedure have been suggested to select the "best" model from a large class of typically nested models. While these procedures are widely used, the Litmus test, if the best model really describes the observed data, is typically not carried out. We will prevent a method to do exactly that. Moreover, we will suggest an algorithms that gives a biologically interpretation to explain the difference between observed data and predicted data by the model. Several examples will illustrate the strategy.