



## Exploring character conflict in molecular data\*

ROBERT H. CRUICKSHANK

*Department of Ecology, Faculty of Agriculture and Life Sciences, PO Box 84, Lincoln University, Lincoln 7647, Christchurch, New Zealand. E-mail: Rob.Cruickshank@lincoln.ac.nz*

\**In: Carvalho, M.R. de & Craig, M.T. (Eds) (2011) Morphological and Molecular Approaches to the Phylogeny of Fishes: Integration or Conflict?. Zootaxa, 2946, 1–142.*

### Abstract

Mooi & Gill (2010) have made a number of criticisms of statistical approaches to the phylogenetic analysis of molecular data as it is currently practiced. There are many different uses for molecular phylogenies, and for most of them statistical methods are entirely appropriate, but for taxonomic purposes the way that these methods have been used is questionable. In these cases it is necessary to introduce an extra step into the analysis – exploration of character conflict. Existing methods for exploring character conflict in molecular data such as spectral analysis, phylogenetic networks, likelihood mapping and sliding window analyses are briefly reviewed, but there is also a need for development of new tools to facilitate the analysis of large data sets. Incorporation of previous phylogenies as priors in Bayesian analyses could help to provide taxonomic stability, while still leaving room for new data to alter these conclusions if they contain sufficiently strong phylogenetic signal. Molecular phylogeneticists should make a clearer distinction between the different uses to which their phylogenies are put; methods suitable in one context may not be appropriate in others.

**Key words:** molecular systematics, character conflict, spectral analysis, phylogenetic networks, likelihood mapping, sliding window analyses, Bayesian priors, taxonomic stability

### Introduction

In a recent issue of *Zootaxa*, Mooi and Gill (2010) criticise the way that molecular data are typically used in taxonomy. They raise a number of interesting and important points and make four recommendations that they believe would bring molecular systematics “back to its fundamental principles” (p.26). The first of these is that molecular taxonomists should “examine data quality, character distribution, and evidence; plot characters to identify and examine character conflict, and weigh evidence for homology” (p.26). Identification and exploration of character conflict does indeed appear to be a missing step in many, if not most, molecular phylogenetic studies. There are a number of possible reasons for this, some of which are discussed below. The purpose of this brief review is to draw attention to several tools for exploring character conflict in molecular data that are freely available but not widely used, in the hope that more widespread adoption of these techniques may begin to satisfy at least some of the criticisms of Mooi & Gill.

### Background

There are many different uses for molecular phylogenies and reasons for constructing them. For most of these purposes a statistical approach is entirely appropriate. For example, evolutionary biologists interested reconstructing ancestral character states, or ecologists wanting to examine the phylogenetic structure of ecological communities, can use Bayesian approaches to incorporate phylogenetic uncertainty into their analyses (Huelsenbeck et al 2001).