**Acknowledgements**

We would like to thank Liam Revell who maintains an active weblog ([www.blog.phytools.org](http://www.blog.phytools.org)) that provided insights into many of the functions in his package Phytools that our approach uses. HB would like to thank the instructors of the Bodega Bay Applied Phylogenetics Workshop. The exercises and introduction that they provided to R and comparative approaches were integral to the development of this package.