How does including fossils into phylogenetic trees changes our interpretation of phylogenetic comparative methods?

by

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ABSTRACT

Here is the abstract of my thesis. It's pretty amazing as you can see. It features fieldwork and experiments and stuff!

PREFACE

Several chapters from my thesis have been published elsewhere:

?? has been previously published as:

> FitzJohn R.G., Maddison W.P., and Otto S.P. 2009. Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. Systematic Biology 58:595–611.

Here I explain what I did for this paper, and what the other coauthors did. Can just repeat this for each chapter if all are published already or in prep. Basically for anything you do with other people.

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ACKNOWLEDGEMENTS

I would like to acknowledge Dr Rich FitzJohn for letting me use his thesis template!

0.1 HOW DOES INCLUDING FOSSILS INTO PHYLOGENETIC TREES CHANGES OUR INTERPRETATION OF PHYLOGENETIC COMPARATIVE METHODS?

1. Phylogenetic inference and missing data with fossils

2. Spatio-temporal disparity with fossil

3. Interpreting trait evolution from trees including fossil taxa

CHAPTER 1

INTRODUCTION

> "Really grandiose sounding quotes from Darwin always make a thesis feel more professional" Natalie Cooper, p. 15

Here is the introduction to the thesis.

1.1 SUBSECTION OF MY INTRO

Here I introduce some concepts.

1.2 ANOTHER SUBSECTION OF MY INTRO

Here I introduce other concepts and provide a figure.

1.3 STRUCTURE & CONTENTS OF THIS THESIS

In this thesis, I do some really cool stuff. In chapter 2, I do some lab work. In **??**, I train a velociraptor to ride a hoverboard. Finally, in chapter 3, I close with a discussion of the limitations of the methods used in the thesis, and suggest some future directions.

FIGURE 1.1: A nice happy face for you to enjoy.

CHAPTER 2

EXTENSIVE LAB STUDY REVEALS EXCITING RESULTS IN MY STUDY SYSTEM

2.1 SUMMARY

Here is the chapter abstract.

2.2 INTRODUCTION

Here is the introduction.

2.3 WE ALL LOVE A FEW EQUATIONS

We like to put in some equations for a bit of fun. where λ_i is the speciation rate in state i, μ_i is the extinction rate in state i, and q_{ij} is the rate of transition from state i to j forward in time.

2.4 RESULTS

We briefly present the results of our lab work and equations

2.5 DISCUSSION

Here is the discussion

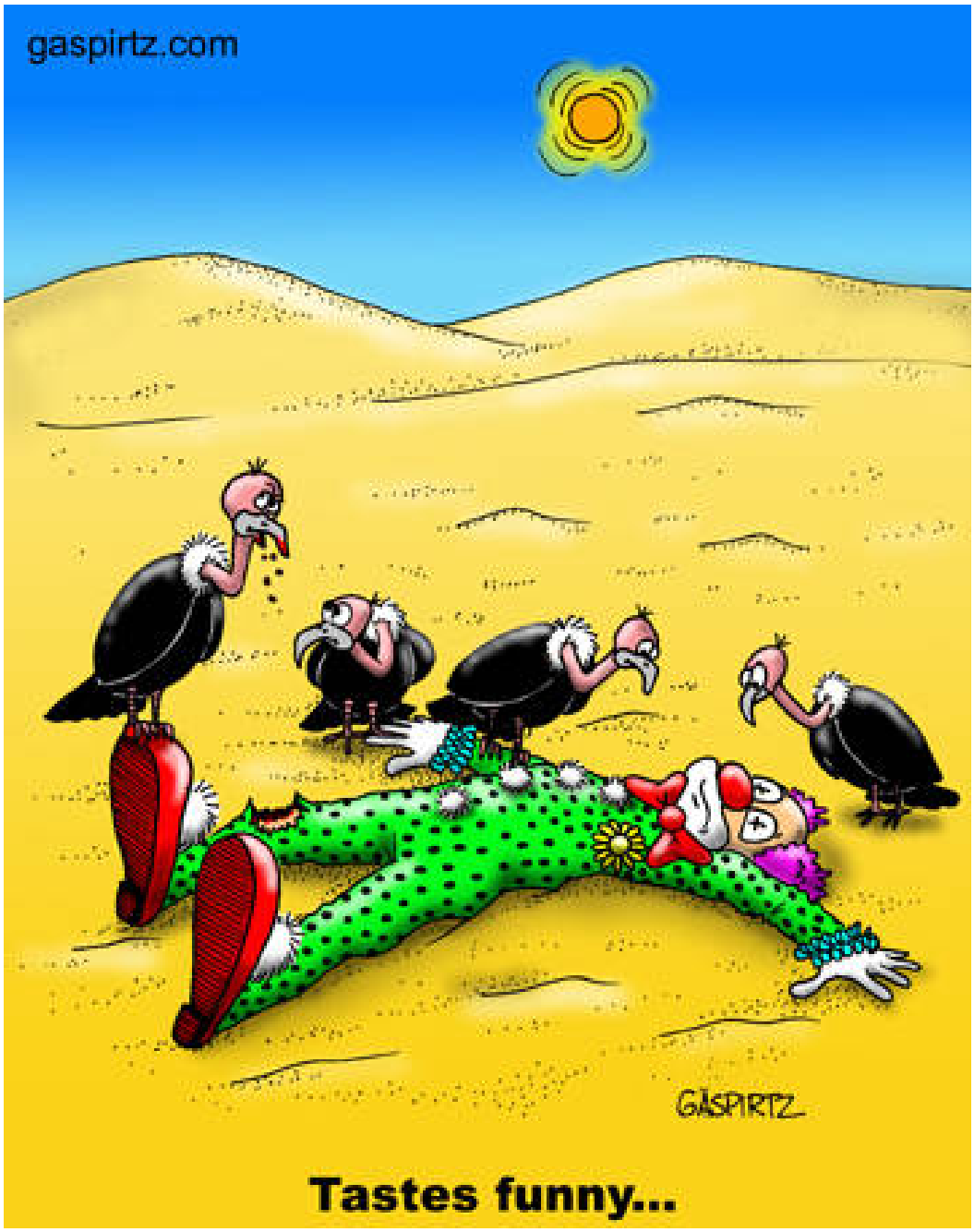

FIGURE 2.1: Long explanation of the figure

CHAPTER 3

CONCLUSION

So here are my conclusions...

3.1 FUTURE DIRECTIONS

There's so much more to do!

3.1.1 *Improving my models*

I'd like to write better analytical models! And try my methods on T rex too.

APPENDIX A

SUPPLEMENTARY INFORMATION TO CHAPTER 2

A.1 ADDITIONAL COOL EQUATIONS

This probability is given by the likelihood given that the root is in state i divided by the sum of the likelihoods over both root states, $D_{Ri}/(D_{R0} + D_{R1})$. The overall likelihood is then:

$$D_R = D_{R0}\frac{D_{R0}}{D_{R0} + D_{R1}} + D_{R1}\frac{D_{R1}}{D_{R0} + D_{R1}} \tag{A.1}$$