My paper written in latex.

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Abstract

Some short abstract here

Key words: Total Evidence method, data structure, phylogenetic, fossil, topology.

1 Introduction

Let's start with a first sentence. And then get some cites to support it (e.g Cooper et al., 2008; Brazeau, 2011; Harrison and Larsson, 2015).

2 Material and Methods

2.1 Material

I got my data from Kembel et al. (2010).

2.2 Methods

R is awesome for doing some analysis (R Core Team, 2015). And it can use pretty sophisticate equations like the Mind Blowing Metric Quotient (MBMQ):

$$MBMQ = \frac{\sum observations}{n} \tag{1}$$

where *n* is the total number of *observations*.

3 Results

Check this out: I made a table and a figure!

Table 1: This table doesn't make much sense but some values are highlighted so that's cool.

	A	В	C
exp1	0.1	0.2	0.3
exp2	0.4	0.5	0.05
ехрз	bla ¹	bli	blo

¹ And we can even add footnotes! How awesome!

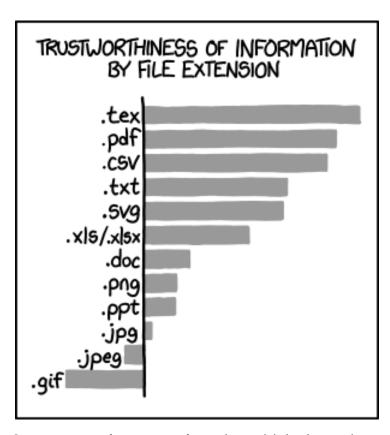


Figure 1: Some nice information from http://xkcd.com/1301/ (CC-BY NC 2.5)

4 Discussion

We can now link to Table 1 or Figure 1.1 But it is also possible to refer to equation 1 or the section 2.2. Try adding more elements or shuffle them around to see that the links will automatically update! Of course, real manuscripts are more complex (more authors, more odd things and more journal requirements) but LaTeX friendly journals often propose easy-to-use templates.

5 Acknowledgements

Thanks folks

References

- Brazeau, M. D. 2011. Problematic character coding methods in morphology and their effects. Biol. J. Linn. Soc. 104:489–498.
- Cooper, N., J. Rodríguez, and A. Purvis. 2008. A common tendency for phylogenetic overdispersion in mammalian assemblages. P. Roy. Soc. B-Biol. Sci. 275:2031–2037.
- Harrison, L. B. and H. C. E. Larsson. 2015. Among-character rate variation distributions in phylogenetic analysis of discrete morphological characters. Syst. Biol. 64:307–324.
- Kembel, S., P. Cowan, M. Helmus, W. Cornwell, H. Morlon, D. Ackerly, S. Blomberg, and C. Webb. 2010. Picante: R tools for integrating phylogenies and ecology. Bioinformatics 26:1463–1464.
- R Core Team. 2015. R: a language and environment for statistical computing. R Foundation for Statistical Computing Vienna, Austria.