

TECE progress meeting

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<http://github.com/richelbilderbeek/Science>

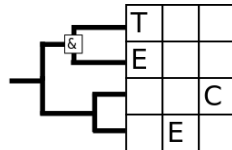
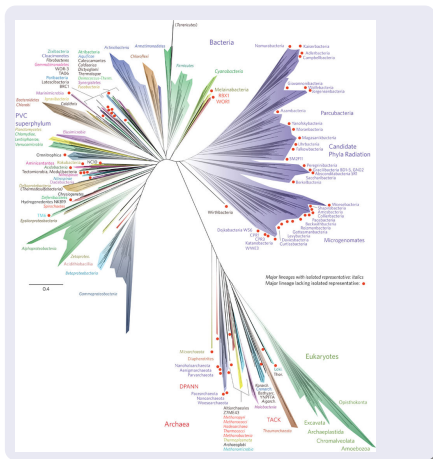


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- 3 Introduction
- 4 Preliminary results
- 5 Work in progress

Tree of life²



Uses RAxML¹

¹Stamatakis, Alexandros. 2014. Bioinformatics 30.9 (2014).

²Hug, Laura A., et al. 2016. Nature Microbiology 1 (2016).

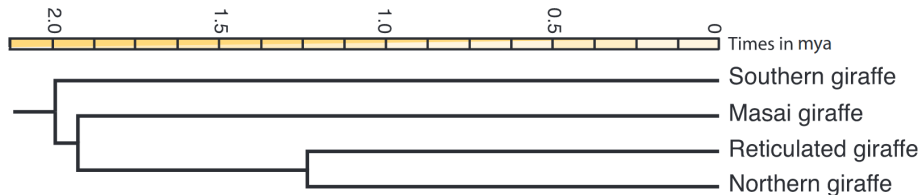
New giraffe species ... ³⁴



³Fennessy, Julian, et al. 2016. Current Biology 26.18.

⁴Picture by Julian Fennessy

... for quite some time⁵



⁵Fennessy, Julian, et al. 2016. *Current Biology* 26.18.

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Research question

What is the error we make today ...

- in inferring phylogenies
- caused by ignoring that speciation takes time to complete?

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From DNA to phylogeny

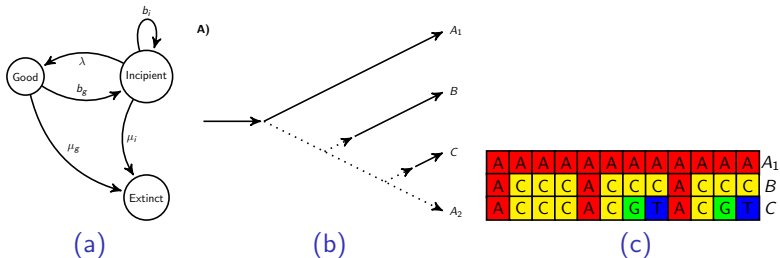
Using BEAST2⁶ Using constant-rate birth-death model⁷

⁶⁶⁶Bouckaert, Remco, et al. 2014. PLoS computational biology 10.4.

⁶⁶⁶Nee, Sean, et al. 1994. Philos Trans R Soc Lond B Biol Sci 344.1309.

Simulating DNA

From PBD phylogeny⁸ to DNA alignment⁹.



⁶⁶⁶Etienne, Rampal S., and James Rosindell. 2012. Systematic Biology 61.2.

⁶⁶⁶Schliep, Klaus Peter. 2010. Bioinformatics btq706.

Measuring error

Using nLTT statistic¹⁰

⁶⁶⁶Janzen, Thijs et al. 2015. Methods in Ecology and Evolution 6.5.

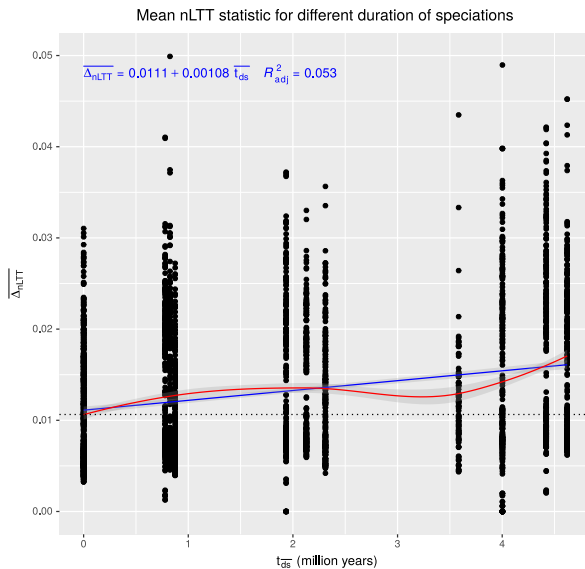
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Longer duration of speciation

Expectation: a longer duration of speciation give more error, as the BD model assumes this equals zero IS THAT REALLY SO?.

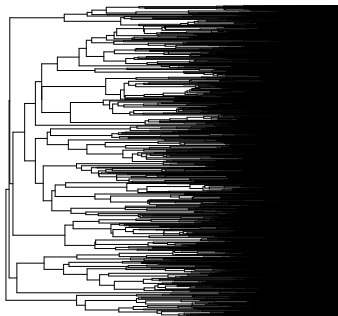
Longer duration of speciation



figure_error_expected_mean_dur_spec_mean

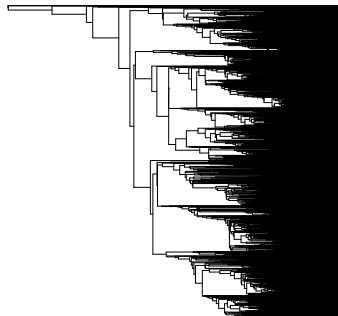
Effect of bad estimation

original species tree



(d)

posterior tree



(e)

Longer DNA alignments

Expectation: a longer DNA alignments give less error, as there is more information available

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