TECE progress meeting

Richèl JC Bilderbeek

University of Groningen

2017-09-13
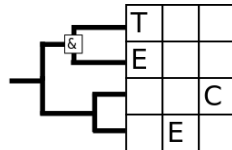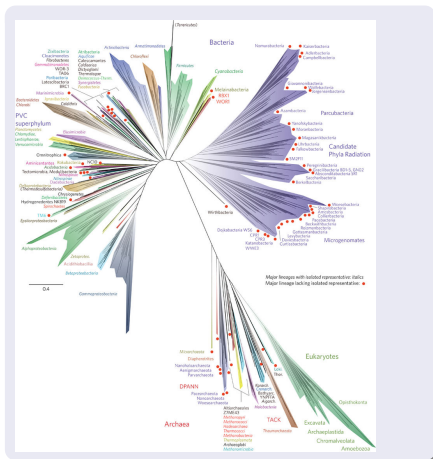
http://github.com/richelbilderbeek/Science

Table of Contents

Tree of life[2]

Uses RAxML[1]

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[1]Stamatakis, Alexandros. 2014. Bioinformatics 30.9 (2014).
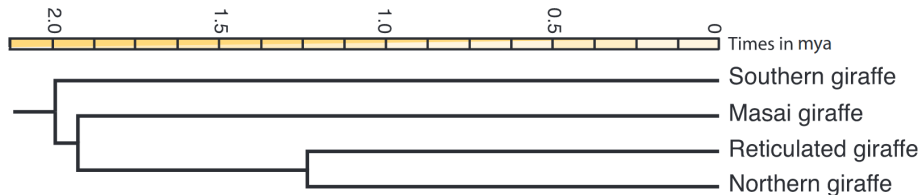[2]Hug, Laura A., et al. 2016. Nature Microbiology 1 (2016).

New giraffe species ... [34]

[3]Fennessy, Julian, et al. 2016. Current Biology 26.18.
[4]Picture by Julian Fennessy

... for quite some time[5]

[5]Fennessy, Julian, et al. 2016. Current Biology 26.18.

Table of Contents

Research question

What is the error we make today ...

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

Table of Contents

From DNA to phylogeny

Using BEAST2[6]Using constant-rate birth-death model[7]

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[6]Bouckaert, Remco, et al. 2014. PLoS computational biology 10.4.

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

Simulating DNA

From PBD phylogeny[8]to DNA alignment[9].

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[666]Etienne, Rampal S., and James Rosindell. 2012. Systematic Biology 61.2.
[666]Schliep, Klaus Peter. 2010. Bioinformatics btq706.

Measuring error

Using nLTT statistic[10]

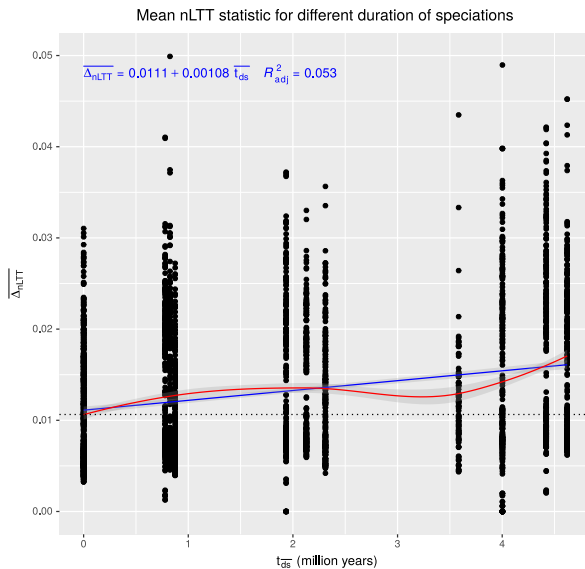666 Janzen, Thijs et al. 2015. Methods in Ecology and Evolution 6.5.

Table of Contents

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?.
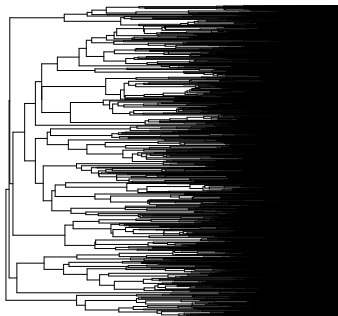
Longer duration of speciation

Mean nLTT statistic for different duration of speciations

$\overline{\Delta_{nLTT}} = 0.0111 + 0.00108\ \overline{t_{ds}}\quad R^2_{adj} = 0.053$

$\overline{\Delta_{nLTT}}$

$t_{\overline{ds}}$ (million years)

figure_error_expected_mean_dur_spec_mean

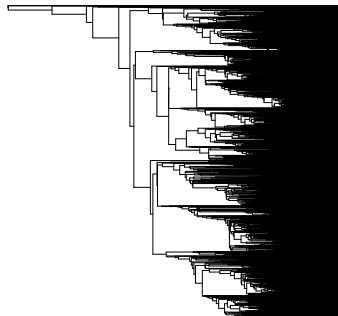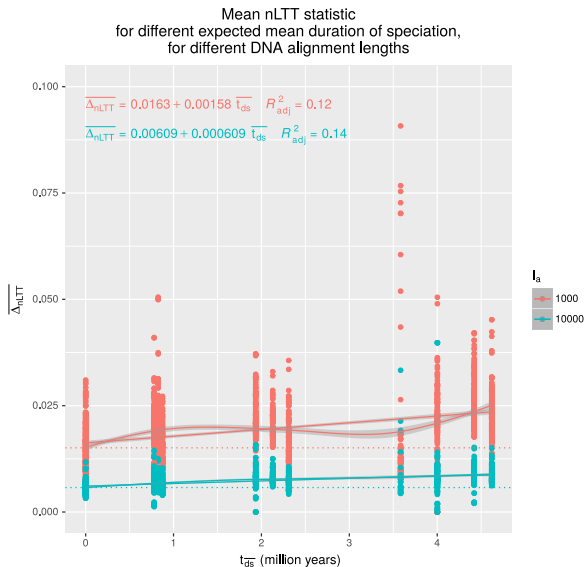# Effect of bad estimation

(a)

(b)

Longer DNA alignments

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

Longer duration of speciation

Mean nLTT statistic
for different expected mean duration of speciation,
for different DNA alignment lengths

figure_error_expected_mean_dur_spec_mean_alignment_length

Table of Contents