TECE progress meeting

Richèl JC Bilderbeek

University of Groningen

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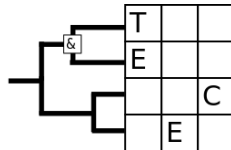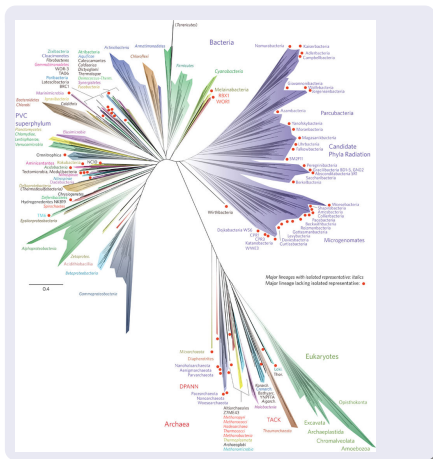
http://github.com/richelbilderbeek/Science

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Tree of life[2]

Uses RAxML[1]

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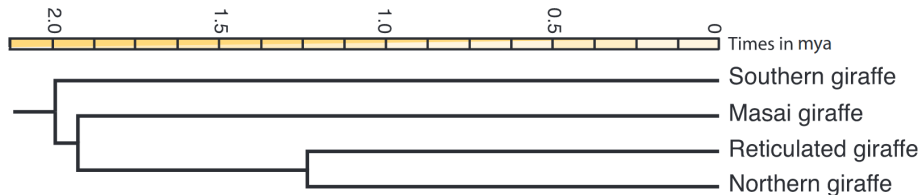[2]Hug, Laura A., et al. 2016. Nature Microbiology 1 (2016).

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.

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Research question

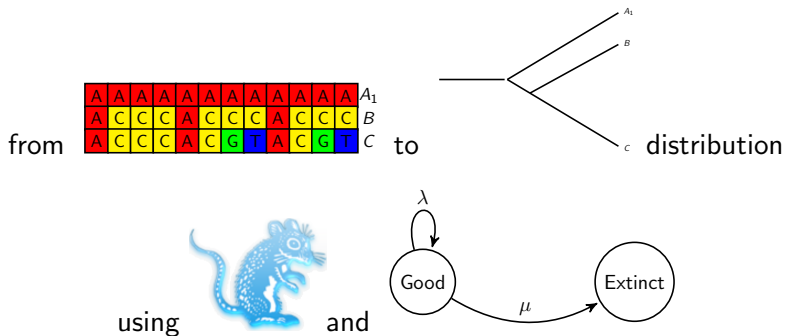What is the error we make today ...

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

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Common: from DNA to phylogeny[67]

from ... to ... distribution

using ... and ...

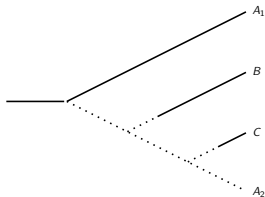[666] Bouckaert, Remco, et al. 2014. PLoS computational biology 10.4.
[666] Nee, Sean, et al. 1994. Philos Trans R Soc Lond B Biol Sci 344.1309.

Novel: simulating DNA[89]
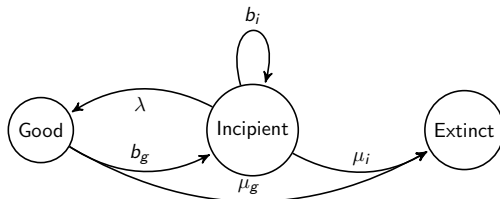
using

simulate and

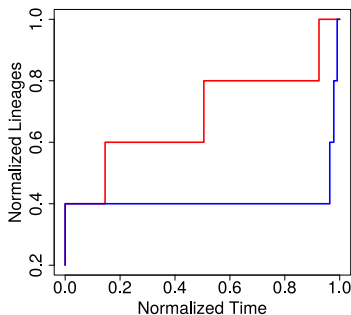[666] Etienne, Rampal S., and James Rosindell. 2012. Systematic Biology 61.2.
[666] Schliep, Klaus Peter. 2010. Bioinformatics btq706.

Measuring error using nLTT statistic[10]

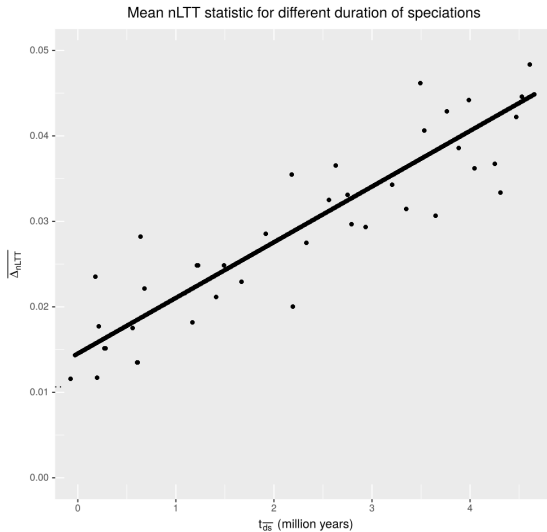compare 'true' tree   with inferred tree

using

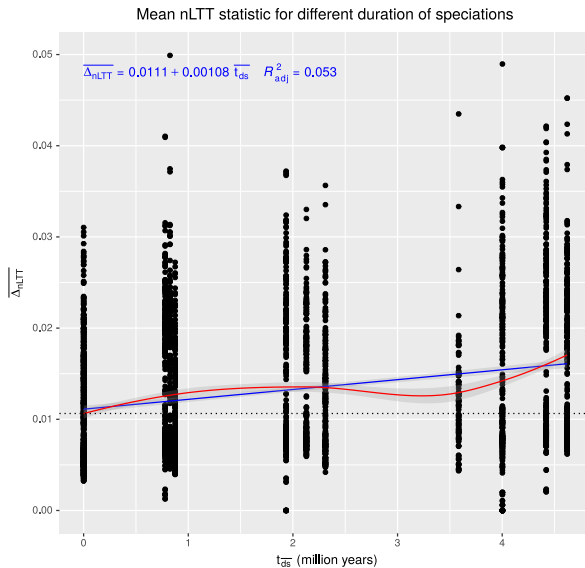[666] Janzen, Thijs et al. 2015. Methods in Ecology and Evolution 6.5.

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Longer duration of speciation

Mean nLTT statistic for different duration of speciations
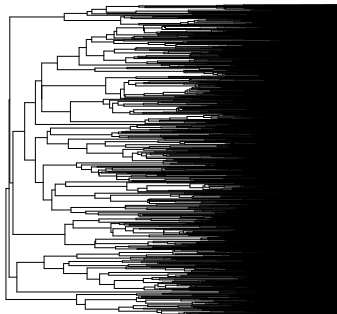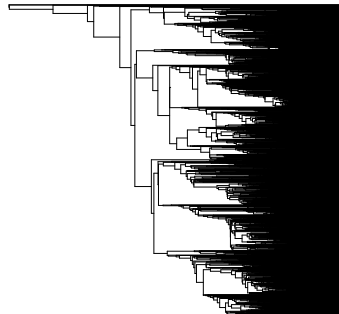
Longer duration of speciation

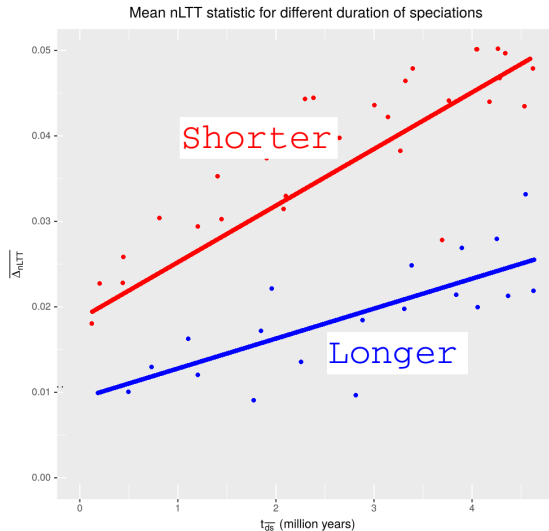figure_error_expected_mean_dur_spec_mean

Effect of bad estimation

original species tree

posterior tree

Longer DNA alignments

Mean nLTT statistic for different duration of speciations

Longer duration of speciation

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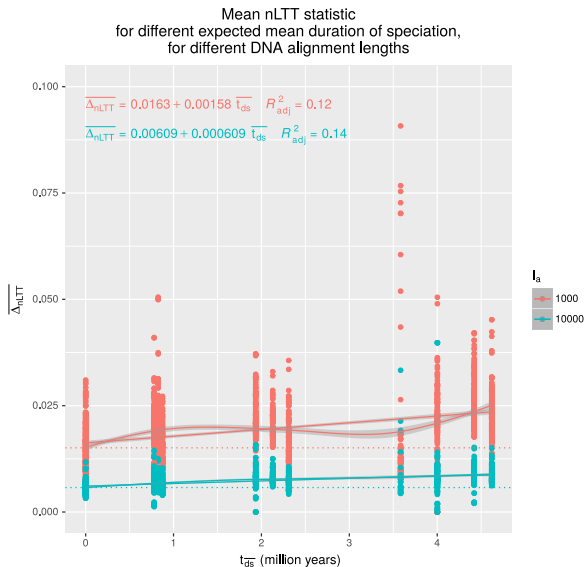
figure_error_expected_mean_dur_spec_mean_alignment_length

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Preliminary conclusions

It is shown that:

1. ↑ protractedness leads to ↑ error
2. ↓ DNA sequence leads to ↑ error
3. (not shown) sampling subspecies has no effect
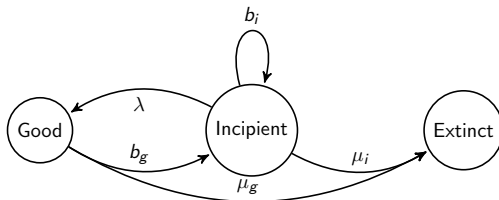4. (not shown) number of taxa has no effect
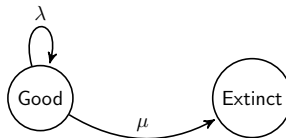
if $t \geq 16 : 00$, then done

☺THANKS! ☺

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Parameter estimation

given   ,

then for $\lambda \to \infty$, becomes

- λ: speciation rate
- μ: extinction rate

Parameter estimation

takes a $\begin{array}{l} A_1 \\ B \\ C \end{array}$ and creates

a distribution of $\left\{ \mathcal{T}, \hat{\lambda}, \hat{\mu} \right\}$

- $\mathcal{T}$: a phylogeny
- $\hat{\lambda}$: estimated speciation rate
- $\hat{\mu}$: estimated extinction rate