TECE progress meeting

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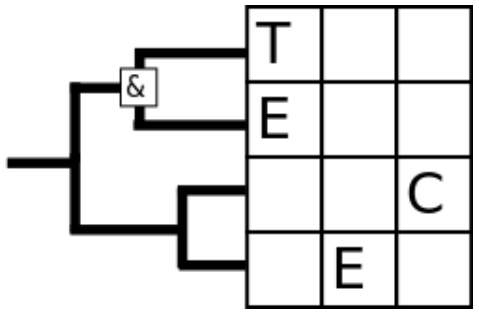
http://github.com/richelbilderbeek/Science



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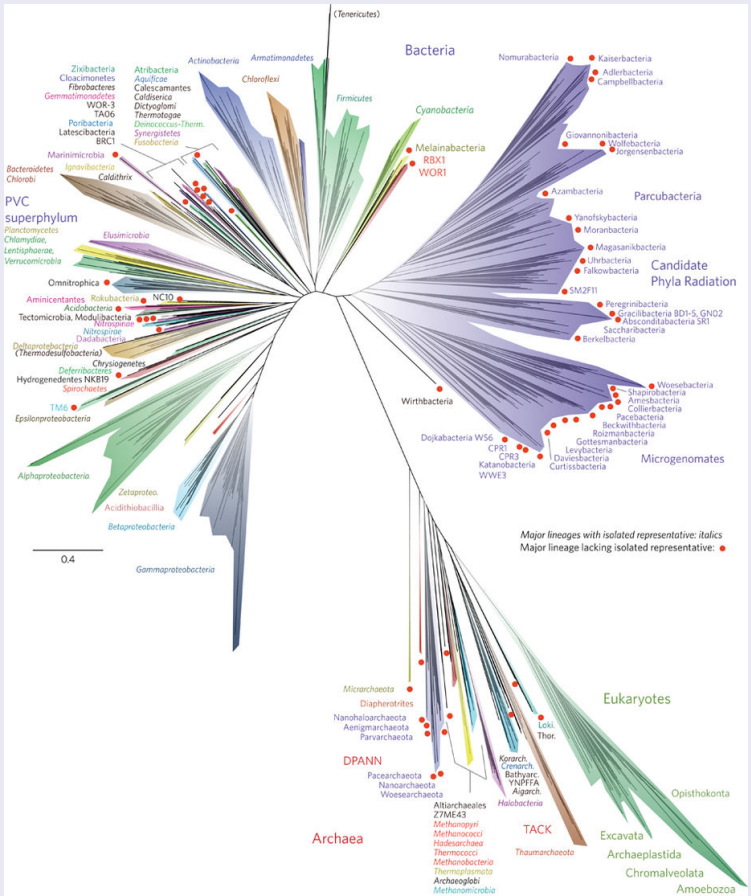
Tree of life[2]



Uses RAxML[1]

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

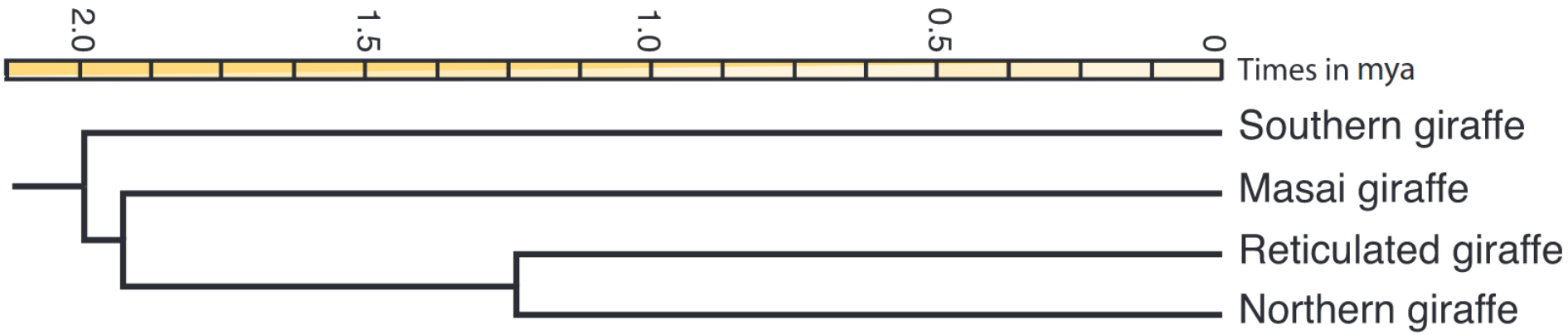
[2] Hug, Laura A., et al. 2016. Nature Microbiology 1 (2016).

New giraffe species ... [3][4]

[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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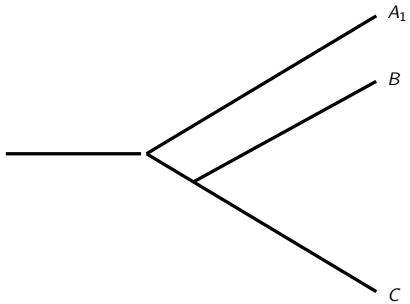
Common: from DNA to phylogeny[67]

from

A	A	A	A	A	A	A	A	A	A	A	A	A_1
A	C	C	C	A	C	C	C	A	C	C	C	B
A	C	C	C	A	C	G	T	A	C	G	T	C

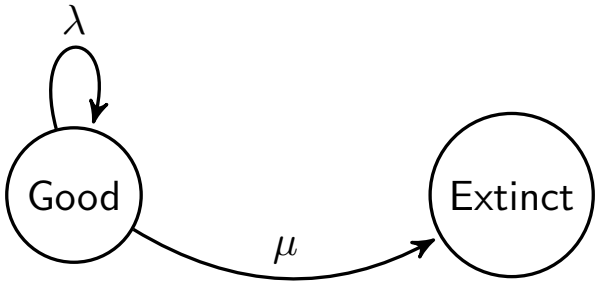
to



distribution

using

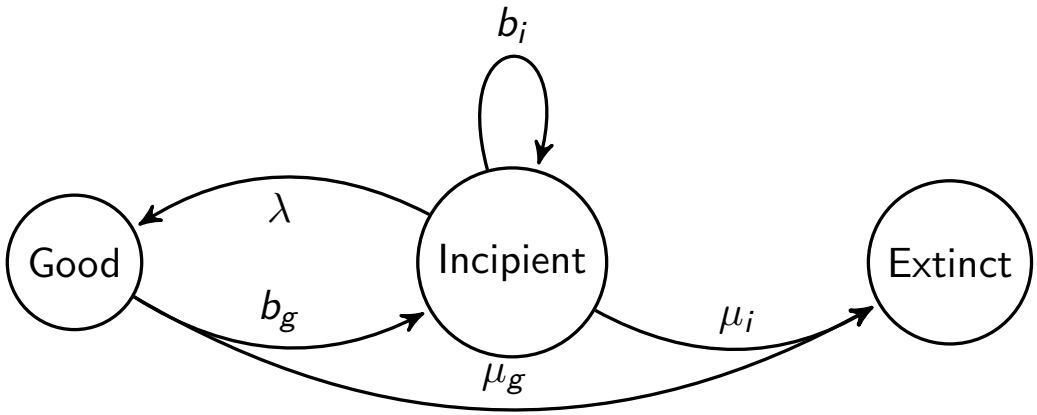
and



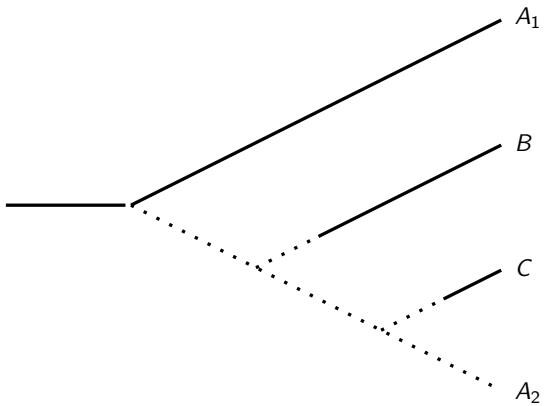
[666] Bouckaert, Remco, et al. 2014. PLoS computational biology 10.4.

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

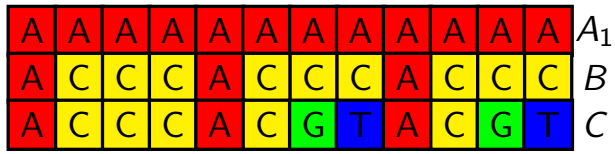
Novel: simulating DNA[89]



using

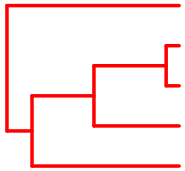
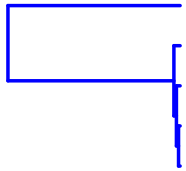


simulate and

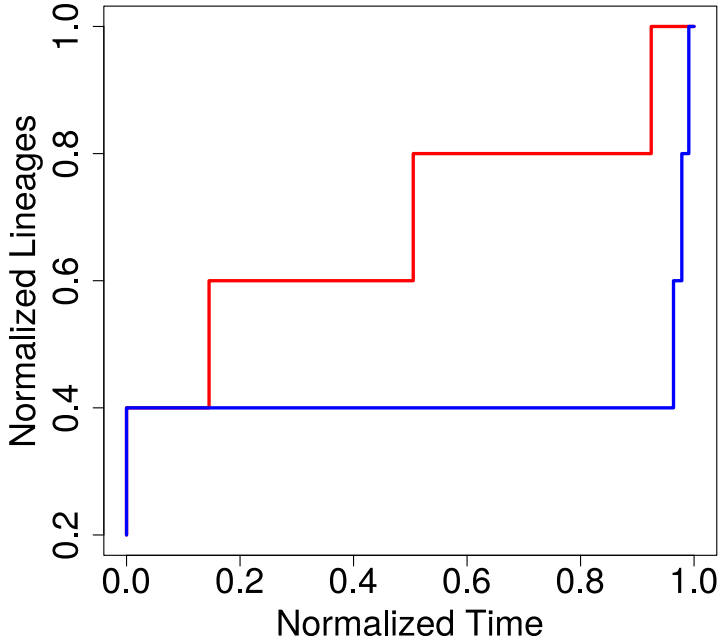


[666] Etienne, Rampal S., and James Rosindell. 2012. Systematic Biology 61.2.
[666] Schliep, Klaus Peter. 2010. Bioinformatics btq706.

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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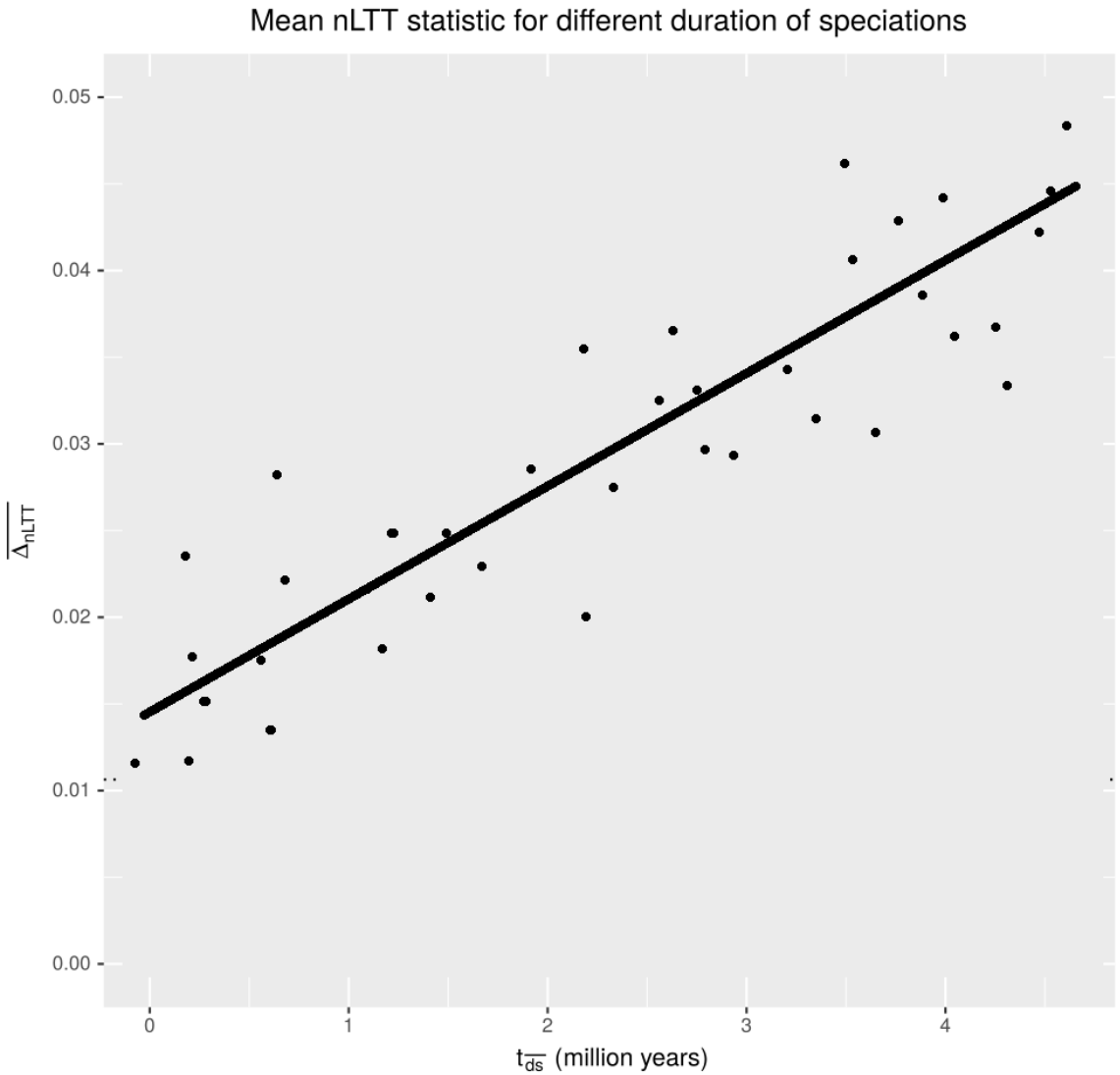
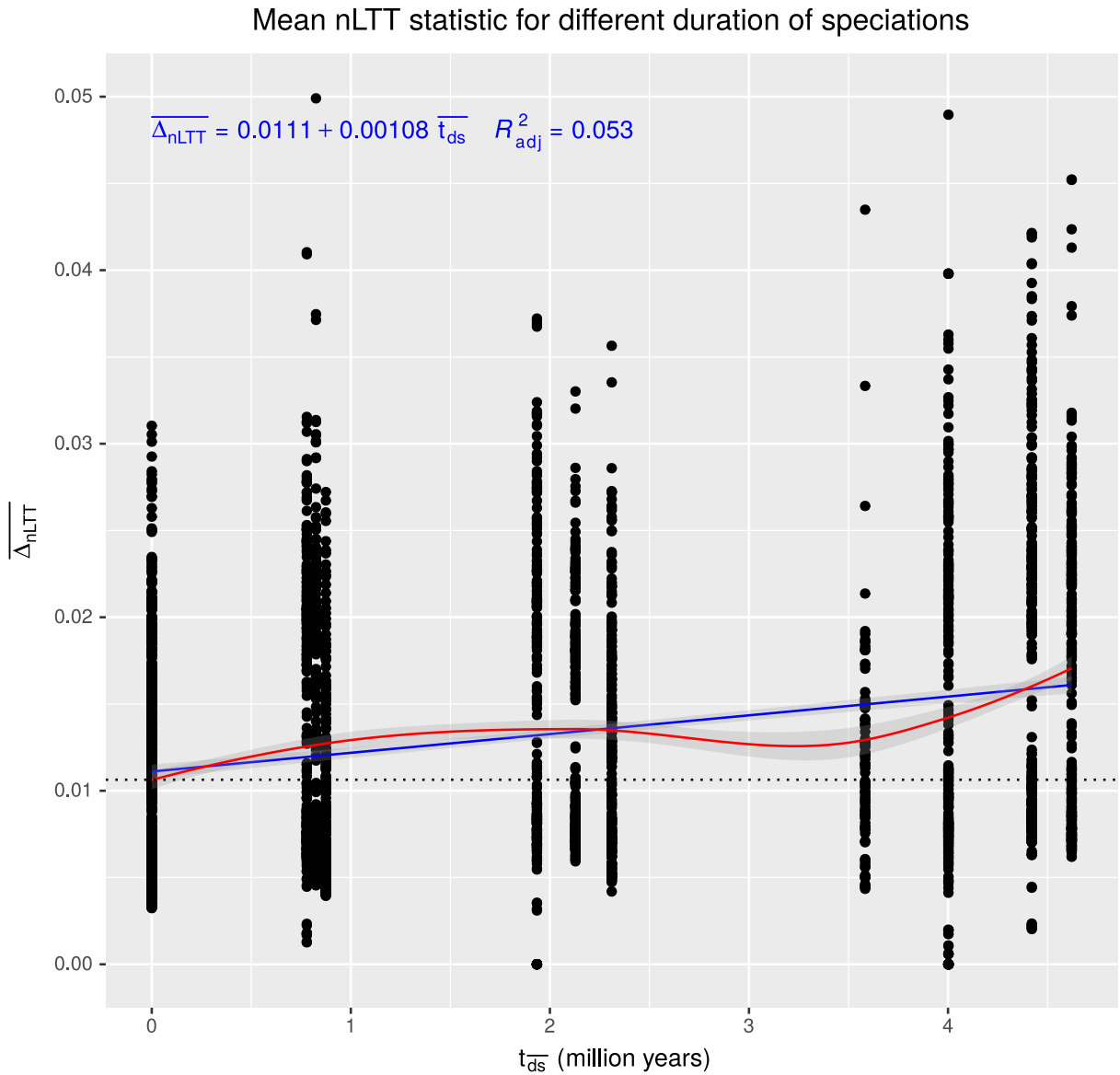
Longer duration of speciation

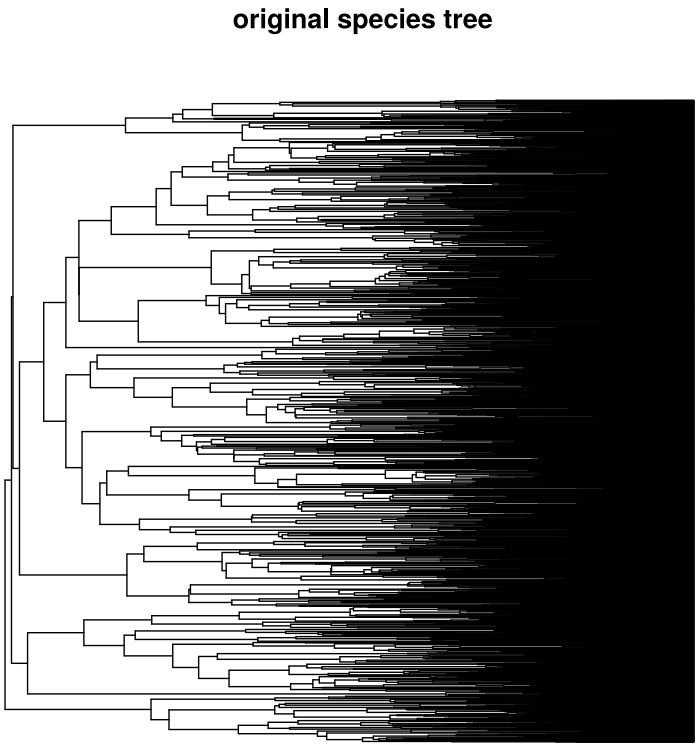


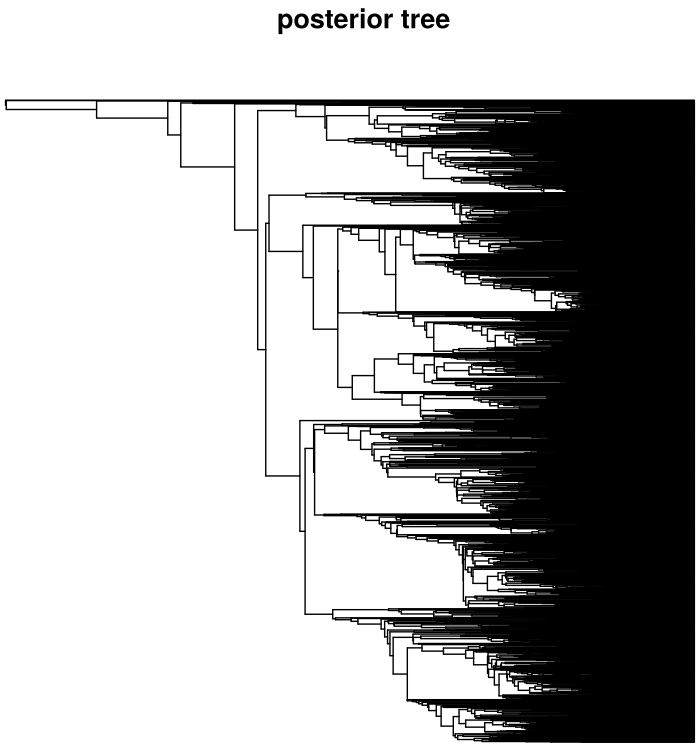
Longer duration of speciation



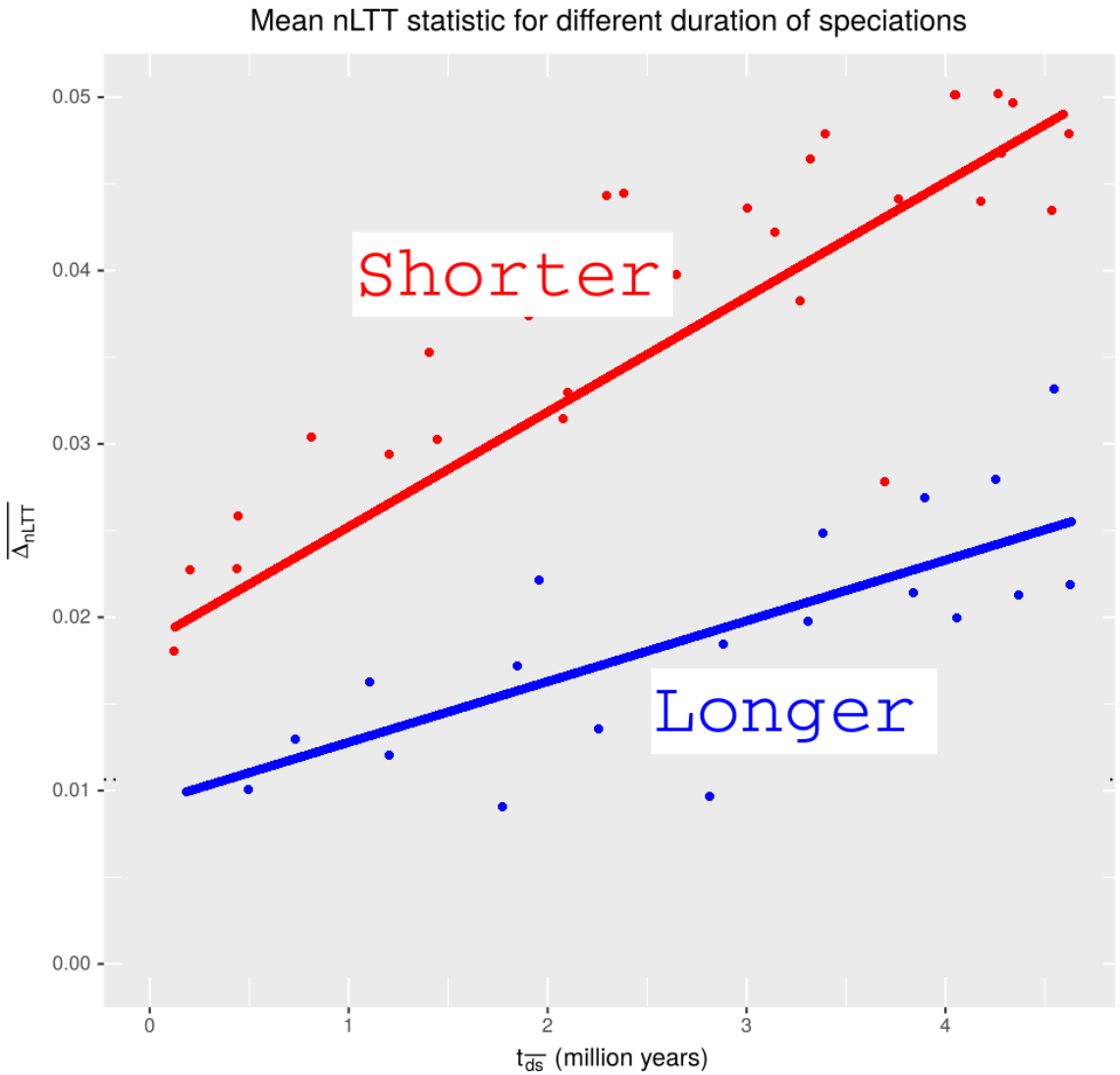
figure_error_expected_mean_dur_spec_mean

Effect of bad estimation

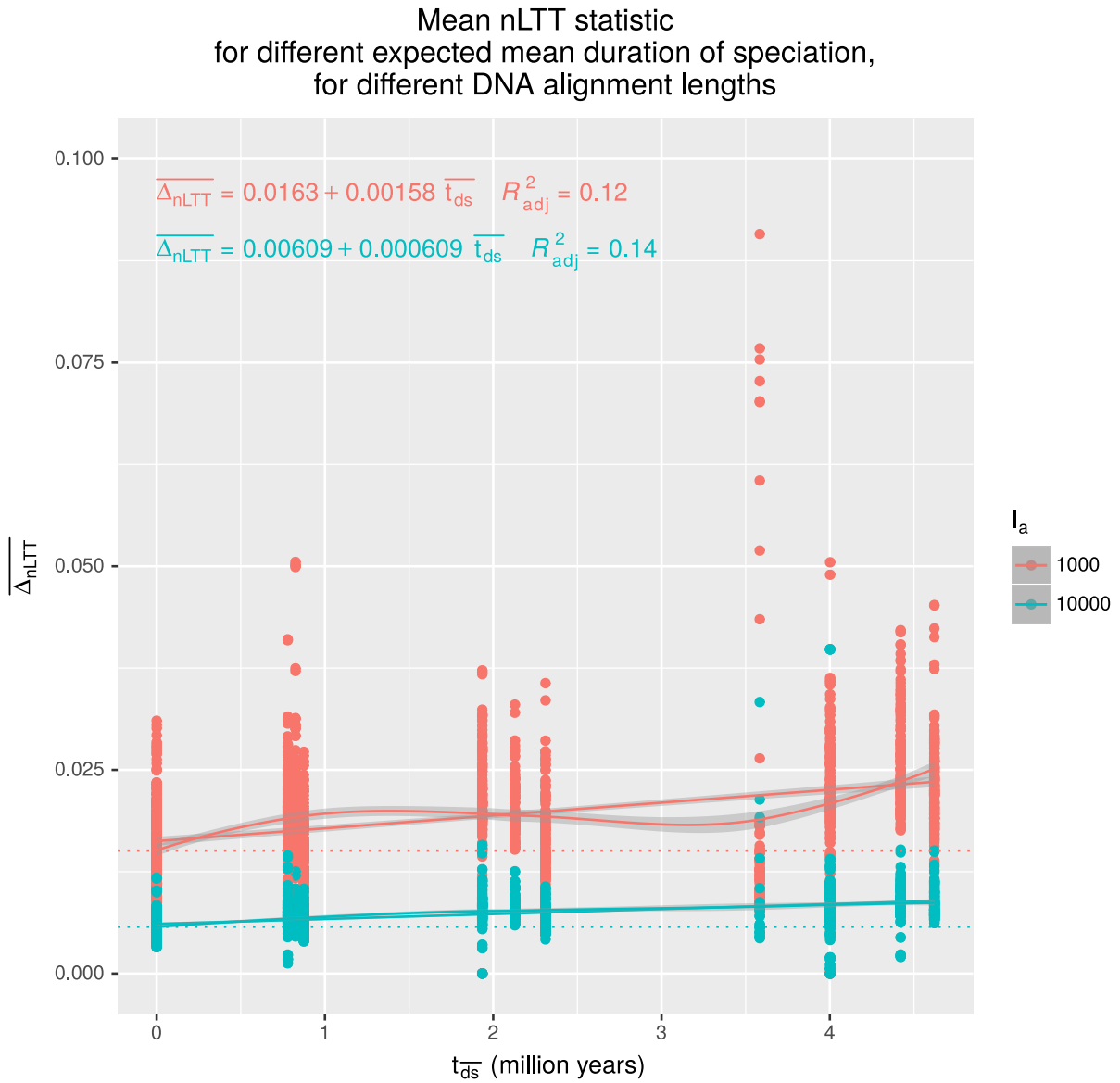




Longer DNA alignments



Longer duration of speciation



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 $t \leq 16:00$, then done

☺THANKS! ☺

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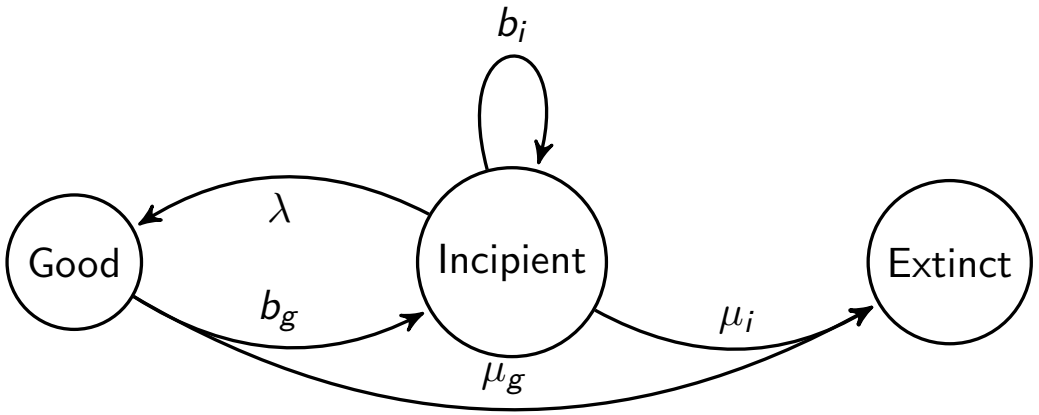
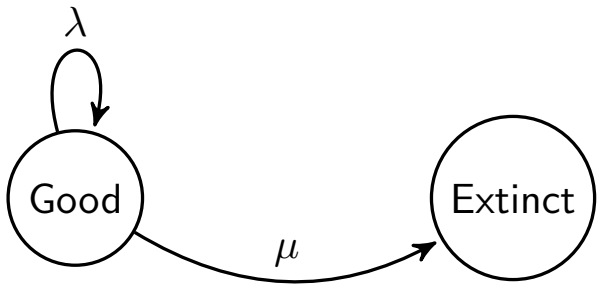
Parameter estimation



given ,



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