

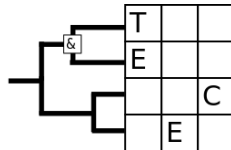
# TECE progress meeting

Richèl JC Bilderbeek

University of Groningen

2017-09-13

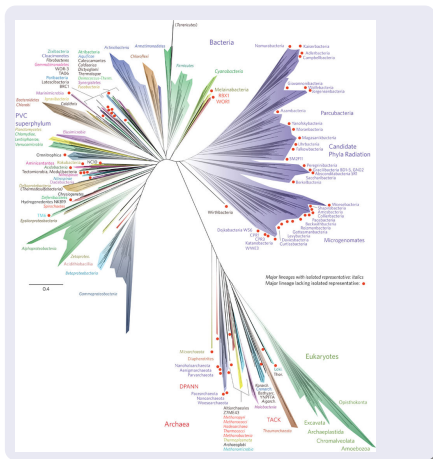
<http://github.com/richelbilderbeek/Science>



# Table of Contents

- 1 Problem
- 2 Research question
- 3 Introduction
- 4 Preliminary results
- 5 Work in progress

# Tree of life<sup>2</sup>



Uses RAxML<sup>1</sup>

<sup>1</sup>Stamatakis, Alexandros. 2014. Bioinformatics 30.9 (2014).

<sup>2</sup>Hug, Laura A., et al. 2016. Nature Microbiology 1 (2016).

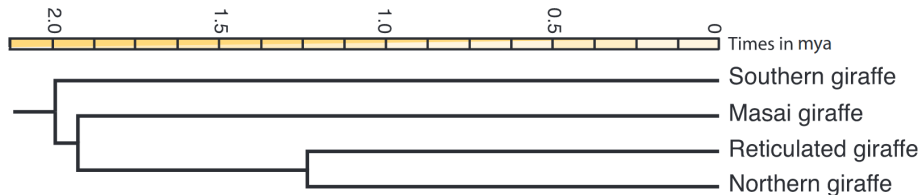
# New giraffe species ... <sup>34</sup>



<sup>3</sup>Fennessy, Julian, et al. 2016. Current Biology 26.18.

<sup>4</sup>Picture by Julian Fennessy

... for quite some time<sup>5</sup>



<sup>5</sup>Fennessy, Julian, et al. 2016. *Current Biology* 26.18.

# Table of Contents

- 1 Problem
- 2 Research question
- 3 Introduction
- 4 Preliminary results
- 5 Work in progress

# Research question

What is the error we make today ...

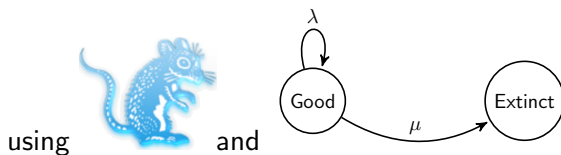
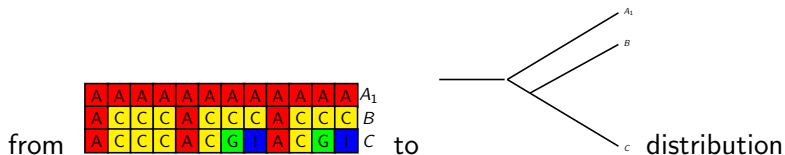
- in inferring phylogenies
- caused by ignoring that speciation takes time to complete?

# Table of Contents

- 1 Problem
- 2 Research question
- 3 Introduction**
- 4 Preliminary results
- 5 Work in progress



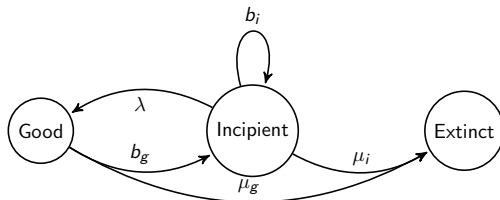
# Common: from DNA to phylogeny<sup>67</sup>



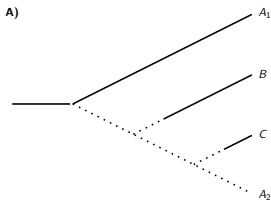
<sup>666</sup>Bouckaert, Remco, et al. 2014. PLoS computational biology 10.4.

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

# Novel: simulating DNA<sup>89</sup>



using



simulate

and

A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A <sub>1</sub>
A	C	C	C	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	A	C	G	T	C

<sup>666</sup>Etienne, Rampal S., and James Rosindell. 2012. Systematic Biology 61.2.

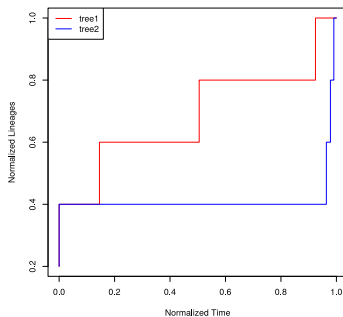
<sup>666</sup>Schliep, Klaus Peter. 2010. Bioinformatics btq706.

# Measuring error using nLTT statistic<sup>10</sup>

compare 'true' tree



with inferred tree



using

<sup>666</sup> Janzen, Thijs et al. 2015. Methods in Ecology and Evolution 6.5.

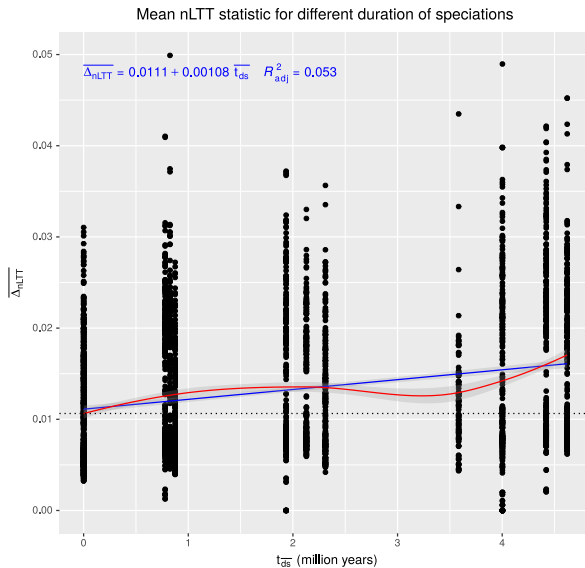
# Table of Contents

- 1 Problem
- 2 Research question
- 3 Introduction
- 4 Preliminary results**
- 5 Work in progress

# 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?.

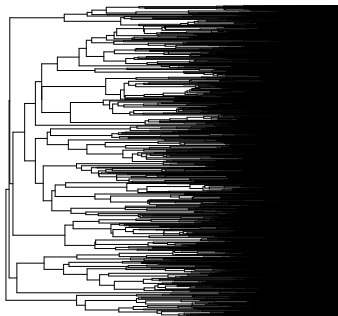
# Longer duration of speciation



figure\_error\_expected\_mean\_dur\_spec\_mean

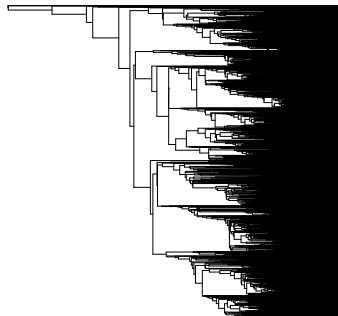
# Effect of bad estimation

original species tree



(h)

posterior tree



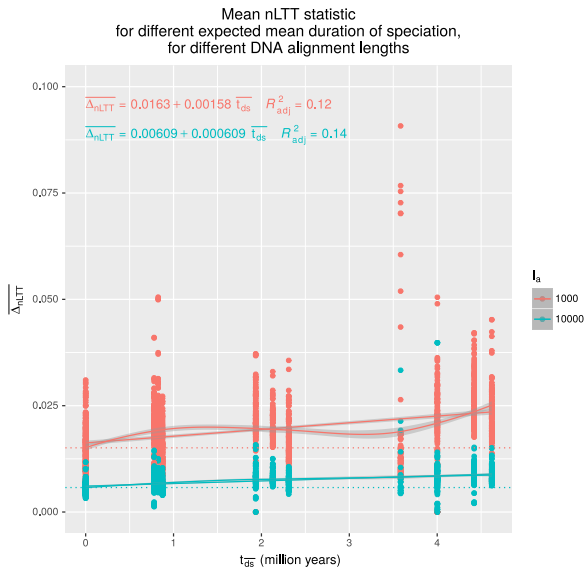
(i)

# Longer DNA alignments

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



# Longer duration of speciation



figure\_error\_expected\_mean\_dur\_spec\_mean\_alignment\_length

# Table of Contents

- 1 Problem
- 2 Research question
- 3 Introduction
- 4 Preliminary results
- 5 Work in progress**