TECE progress meeting

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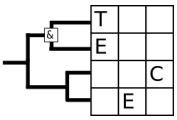
http://github.com/richelbilderbeek/Science



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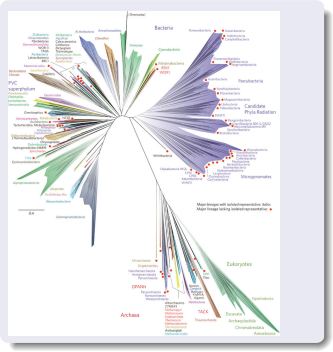
Tree of life[2]



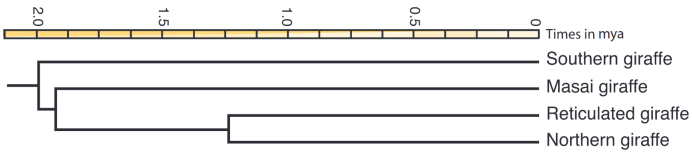
Uses RAxML[1]

[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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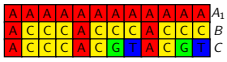
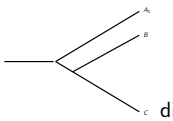
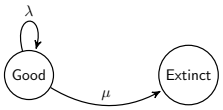
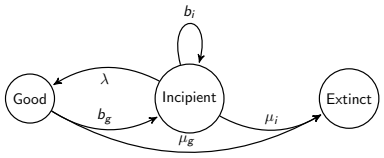
Common: from DNA to phylogeny[6][7]

from  to  distribution

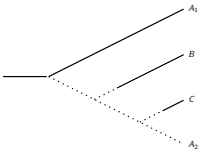
using and 

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

Novel: simulating DNA[8][9]



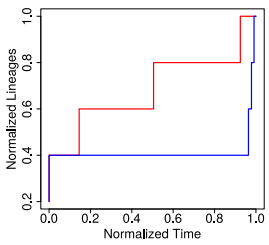
using

simulate  and

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

Measuring error using nLTT statistic[10]

compare 'true' tree with inferred tree



using

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

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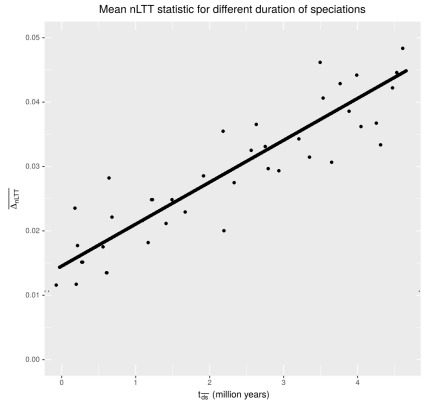
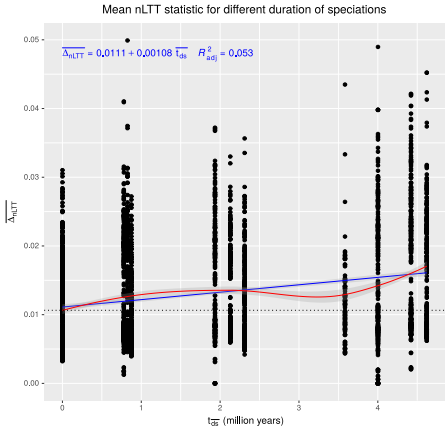
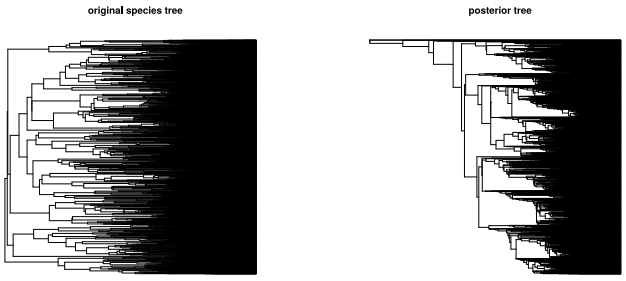
Longer duration of speciation



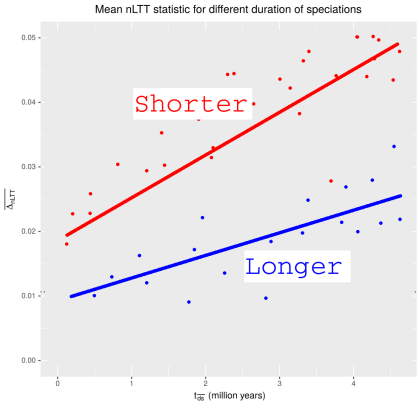
Longer duration of speciation



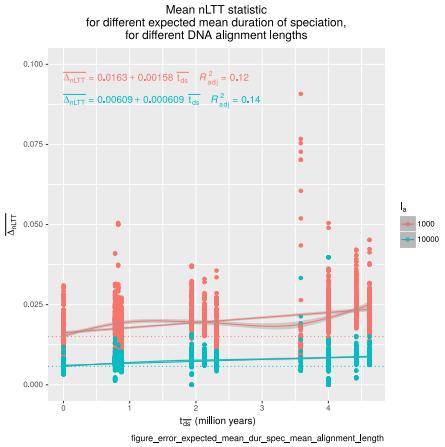
Effect of bad estimation



Longer DNA alignments



Longer duration of speciation



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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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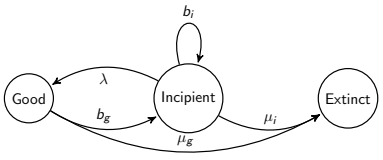
Current problem

Incomplete documentation

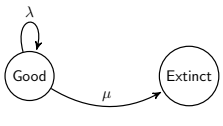
Parameter estimation

given



,

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



- λ: speciation rate
- μ: extinction rate

Parameter estimation

takes a

and creates

a distribution of $\left\{\mathcal{T}, \hat{\lambda}, \hat{\mu}, \hat{t_0}, \right\}$

- $\mathcal{T}$: a phylogeny
- $\hat{\lambda}$: estimated speciation rate
- $\hat{\mu}$: estimated extinction rate
- $\hat{t_0}$: estimated crown age

Naive expectation

Parameters to create phylogenies:

λ	speciation rate	0.3
μ	extinction rate	0.2
t_0	crown age	15

Expected parameter estimates:

$\hat{\lambda}$	estimated speciation rate	0.31	0.29	0.28
$\hat{\mu}$	estimated extinction rate	0.19	0.21	0.2
$\hat{t_0}$	estimated crown age	14.9	15.1	15.2

Real results

Parameters to create phylogenies:

λ	speciation rate	0.3
μ	extinction rate	0.2
t_0	crown age	15

Parameter estimates:

birthRate2	18.591	23.7402	16.1756	22.7706	24.0203
relativeDeathRate2	0.69492	0.3817	0.60621	0.49113	0.29777
TreeHeight	0.1515	0.14719	0.14579	0.15033	0.1514

relativeDeathRate2

Parameters to create phylogenies:

λ	speciation rate	0.3
μ	extinction rate	0.2
t_0	crown age	15

Parameter estimates:

b	birthRate2	18.59	23.740	16.176	22.771	24.020
d	relativeDeathRate2	0.6949	0.382	0.6062	0.4911	0.2978
z_0	TreeHeight	0.152	0.1472	0.1458	0.1503	0.151

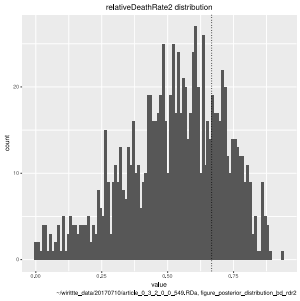
Hypothesis:

$$d = \frac{\mu}{\lambda} \approx 0.67$$

relativeDeathRate2

```
@Description("Birth Death model based on Gernhard 2008. <br/>" +
        "This derivation conditions directly on fixed N taxa. <br/>" +
        "The inference is directly on b-d (strictly positive) and d/b (constrained in [0,1)) <br/>" +
        "Verified using simulated trees generated by Klass tree sample. (http://www.klaashartmann.com/treesa
```

```
final public Input<RealParameter> relativeDeathRateParameterInput =
        new Input<>("relativeDeathRate", "relative death rate parameter, mu/lambda in birth death model"
```



birthRate2 and TreeHeight

Parameters to create phylogenies:

λ	speciation rate	0.3
μ	extinction rate	0.2
t_0	crown age	15

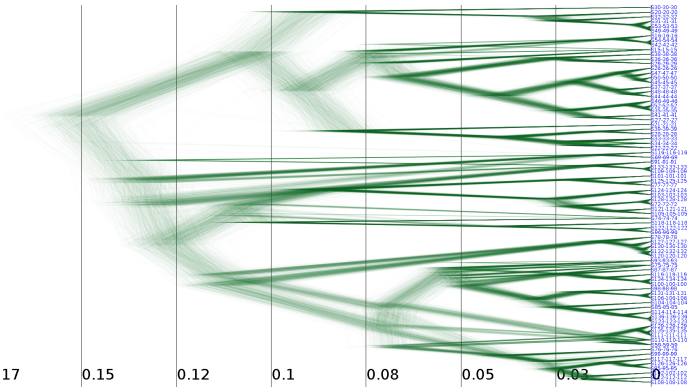
Parameter estimates:

b	birthRate2	18.59	23.740	16.176	22.771	24.020
d	relativeDeathRate2	0.6949	0.382	0.6062	0.4911	0.2978
z_0	TreeHeight	0.152	0.1472	0.1458	0.1503	0.151

Hypothesis ☹:

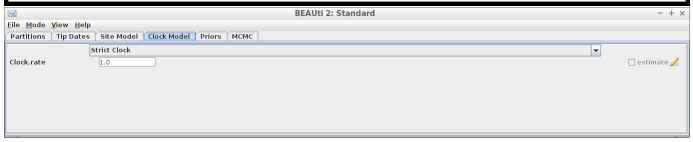
$$b = \lambda - \mu = 0.1$$

TreeHeight



birthRate2 and TreeHeight

```
@Description("Pure birth model (i.e. no deaths)")
public class YuleModel extends SpeciesTreeDistribution {
    final public Input<RealParameter> birthDiffRateParameterInput =
            new Input<>("birthDiffRate", "birth difference rate parameter, lambda - mu in birth/death model", V
    final public Input<RealParameter> originHeightParameterInput =
            new Input<>("originHeight", "the height of the point of origin of the process");
```

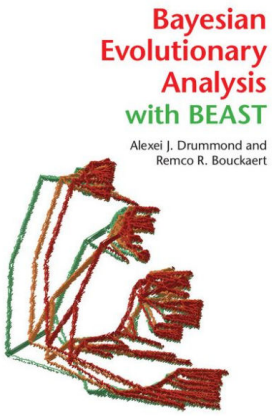


The three parameters λ, μ, ρ are non-identifyable, meaning that the probability density of a time tree is determined by two parameters $\lambda - mu$ and $\lambda \cdot \rho$ [11].

[11] Stadler, Tanja. 2009. Journal of theoretical biology 261.1

Discussion

- Two out of three estimated parameters are unknown ...
- ... even with access to the BEAST book, online documentation and source code



Thanks

☺THANKS! ☺