

The space of sampled ancestor trees

@GSA2016

Alex Gavryushkin

ETH Zürich

Joint work with
Alexei Drummond, the University of Auckland, NZ,
Erick Matsen and Chris Whidden,
Fred Hutch Cancer Research Center, Seattle, WA, USA

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Motivation

- General statistics is at least 5 years ahead of phylostatistics.

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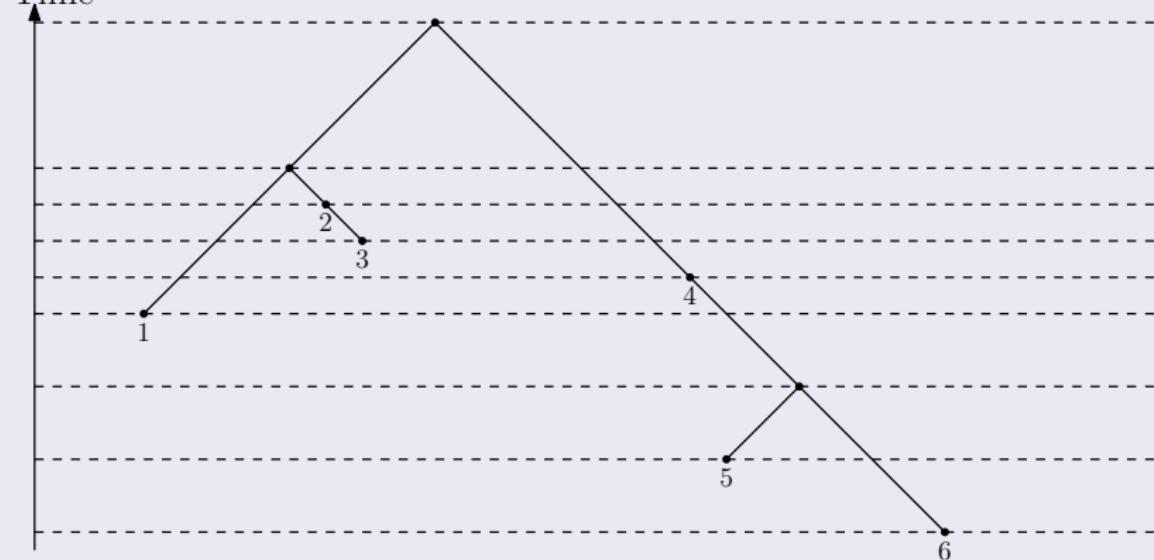
- General statistics is at least 5 years ahead of phylostatistics.
- The discrete component of tree space is *the bottleneck* for tree search algorithms.
- What's wrong with trees?

Same as above but with a mortarboard on

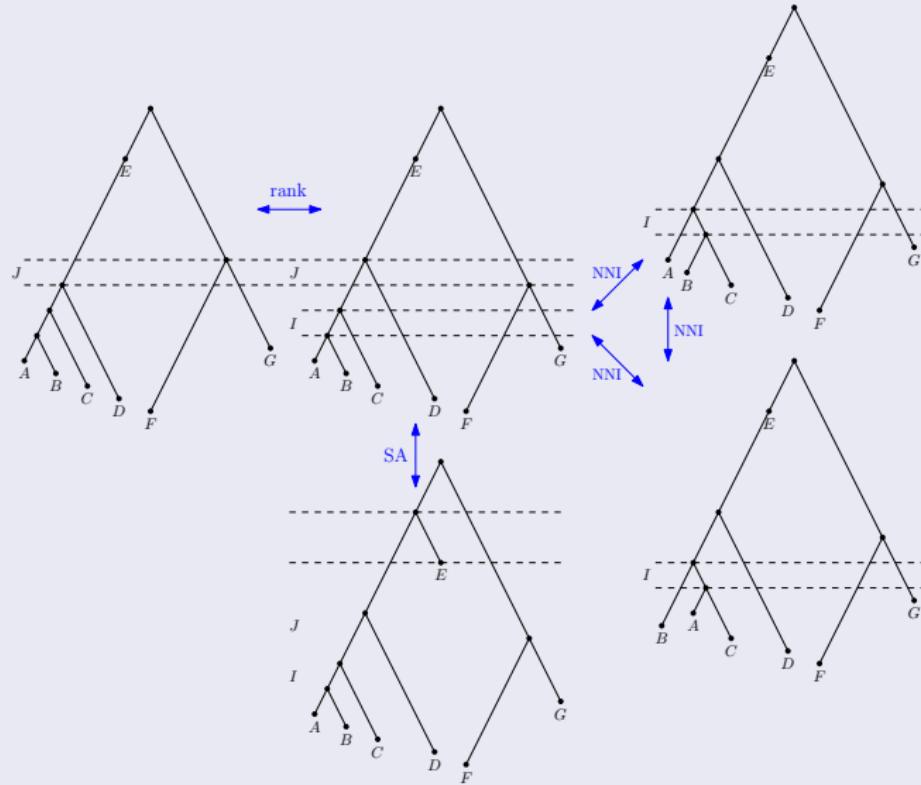
- MCMC algorithms
 - Improving efficiency = smart proposals
 - Point estimates AKA posterior summary
- Tree search methods in general
 - Semi-convergence
 - Valleys
 - Terraces

Sampled ancestor tree

Time

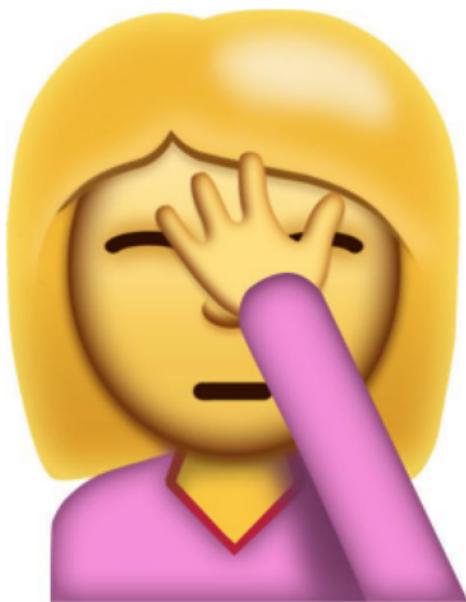


Sampled ancestor tree graph



Graph = Metric space

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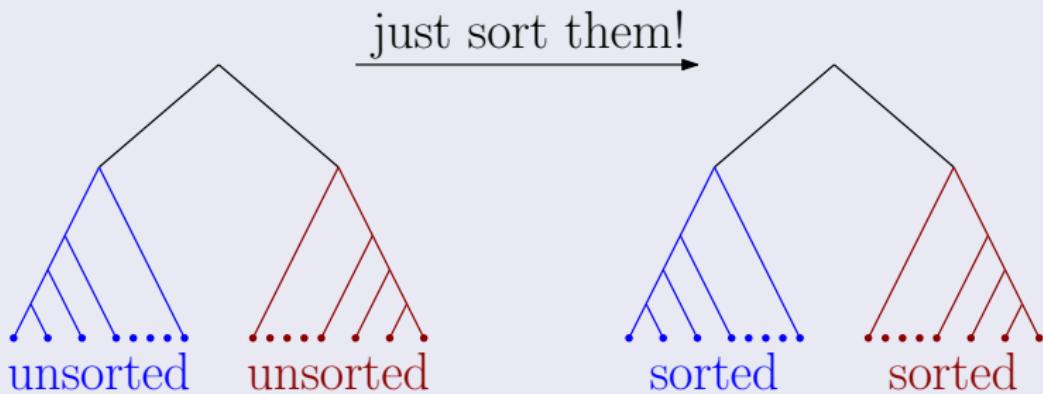
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I'm talking about the NNI graph here.

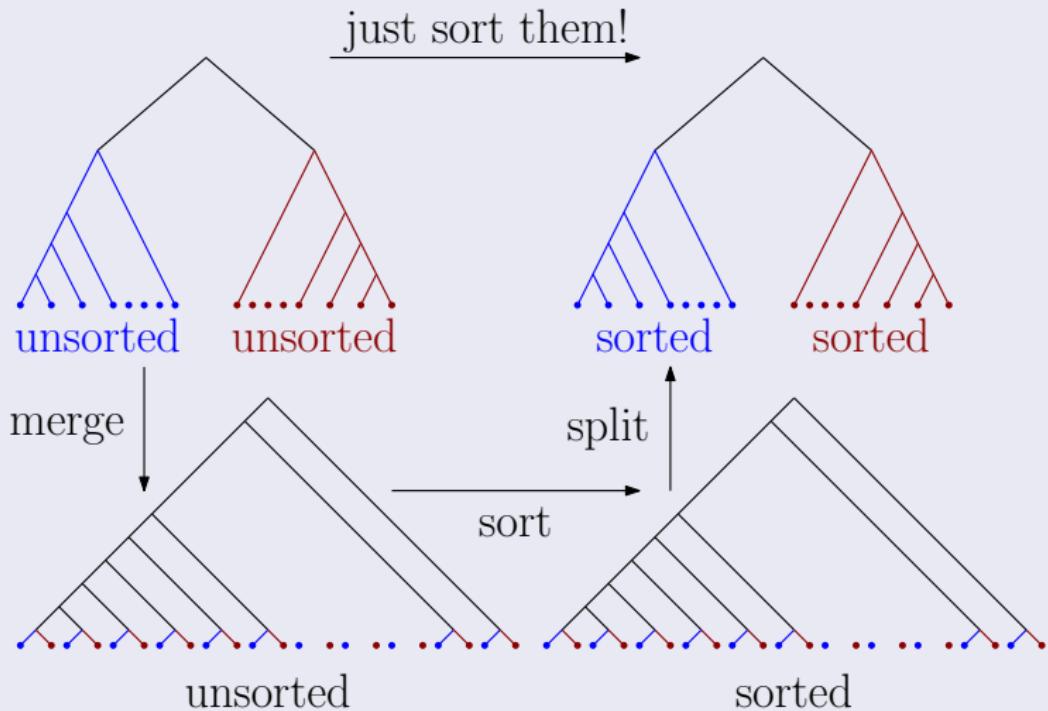
What is actually “wrong”

The Split Theorem



What is actually “wrong”

Merge and sort trick



Sampled ancestor trees (the SANNI graph) free from all these
(G, Whidden, Matsen. *bioRxiv*, 2016)

- Split Theorem. Tick.
- Merge and sort trick. Tick.

Good news!

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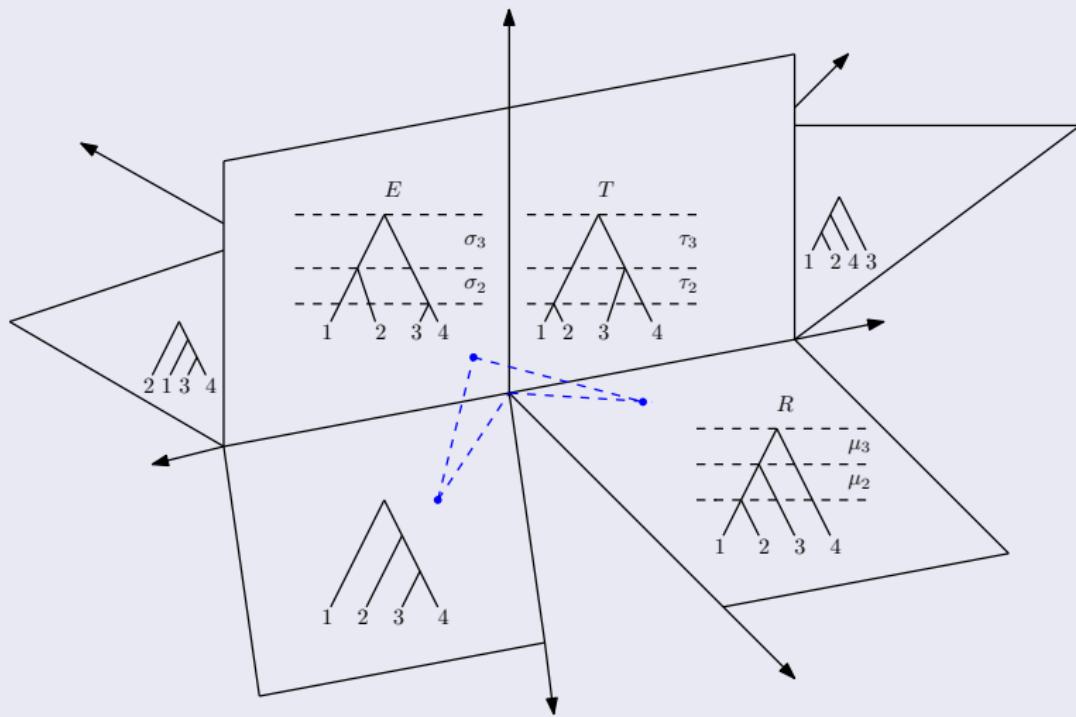
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Even more good news

Efficient approximate algorithm for computing shortest
SANNI-paths.

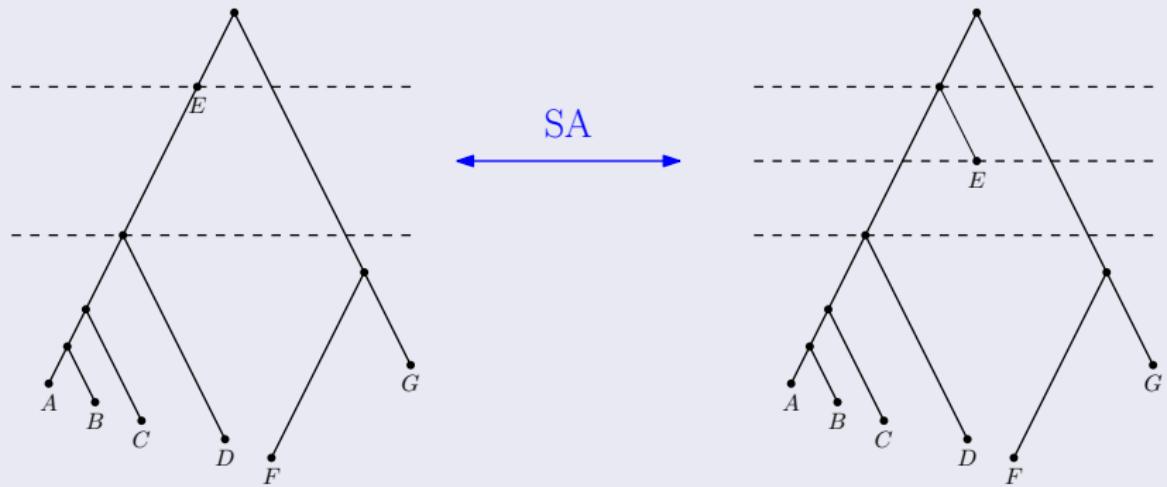
What about branch lengths?

G and Drummond. *JTB*, 2016



Looks like a problem

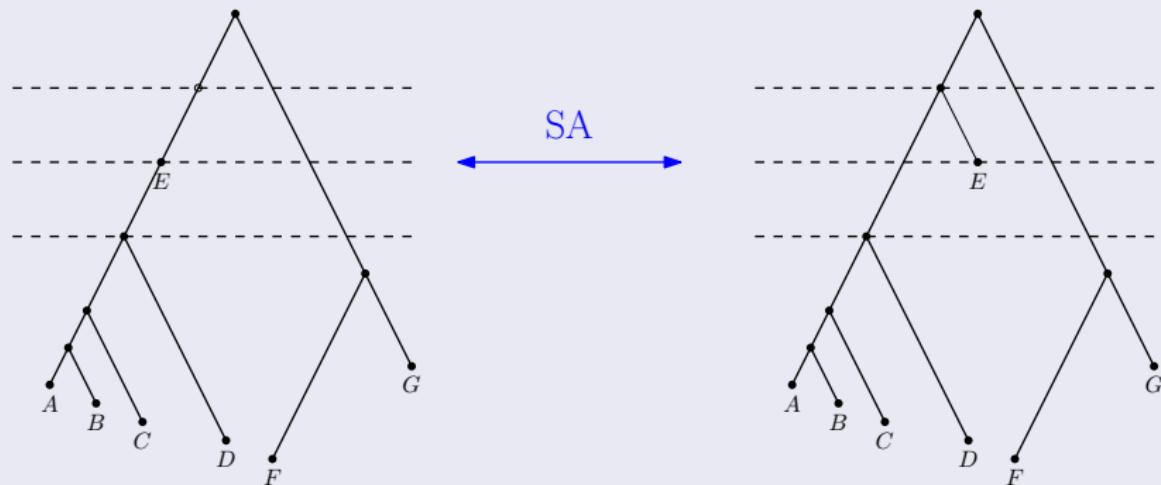
Trees have different dimensions



Branch lengths are fine too!

Stadler (*JTB*, 2010) is cheating* anyway...

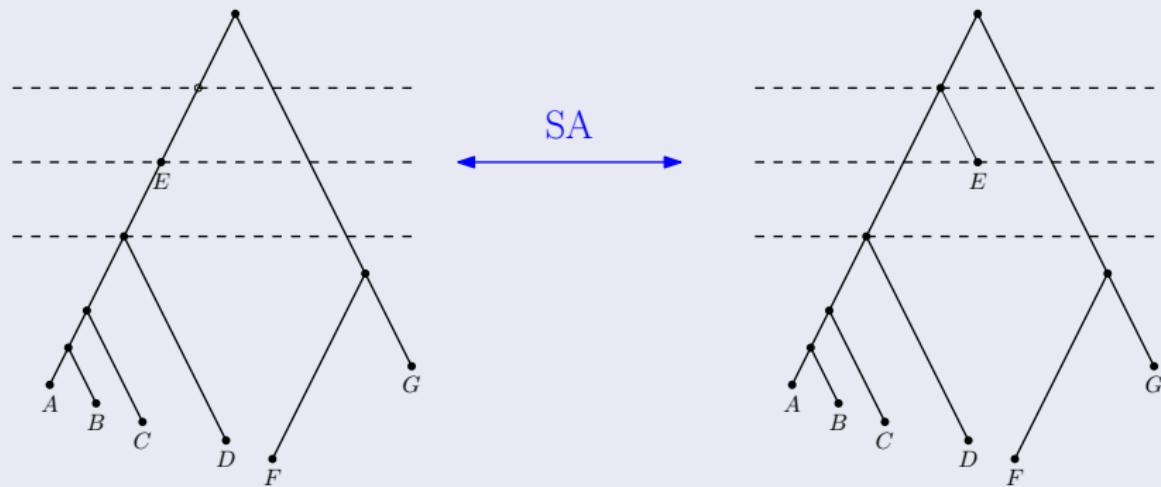
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... so we can too: introduce “imaginary” nodes:



*by putting non-zero probability mass onto facets of the space

What we've done

- Introduced the SANNI graph on ranked sampled ancestor trees (to the best of our knowledge)
- Sampled ancestor trees and classical phylogenetic trees have different geometric and algorithmic properties
- Often, geometric and algorithmic results for classical trees do not scale to sampled ancestor trees
- Natural and efficient data structures
- Connections to other areas of math

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- Connections to other areas of math
- Failed to prove that SANNI is NP-hard

References

-  **Li, Tromp, and Zhang**
Some Notes on the Nearest Neighbour Interchange Distance.
Computing and Combinatorics, 343–351, 1996.
-  **Dasgupta, He, Jiang, Li, Tromp, and Zhang**
On Computing the Nearest Neighbor Interchange Distance
Discrete Mathematical Problems with Medical Applications, Vol. 55, 2000.
-  **Alex Gavryushkin and Alexei Drummond**
The space of ultrametric phylogenetic trees
Journal of Theoretical Biology, Vol. 402, 197–208, 2016
-  **Alex Gavryushkin, Chris Whidden, and Frederick A. Matsen IV**
Combinatorics of discrete time-trees: algorithmic insights and open problems
bioRxiv, 2016 ← available as a blog post by Matsen
-  <https://github.com/gavruskin/tauGeodesic>
-  <https://github.com/gavruskin/tTauCurvature>

Thank you for your attention!

Funding

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