

Support Metrics

Phylogenetic trees are just ...

Phylogenetic trees are just ... hypotheses!

It is important to know how much we can be **confident** in our findings...

These are the metrics we are going to explore:

- nonparametric & parametric bootstrap (**BPs**)
- Transfer Bootstrap Expectation (**TBE**)
- parametric & nonparametric jackknife
- SH-like approximate Likelihood Ratio Test (**SHaLRT**)
- genes & sites Concordance Factors (**gCFs & sCFs**)
- Posterior Probabilities (**PP**)
- Quartet Support (**QS**) ... will see that in **lesson 13!**

non-parametric bootstrapping

Is a general statistical method for estimating the parameters of an unknown probability distribution by resampling from a sample that was drawn from this distribution.

Transferred to phylogenetics by **Felsenstein** in [this paper](#) from 1985.

This is the process step-by-step:

- start with an alignment of length **n**
- generate a bootstrapped alignment:
 - randomly sample **n** columns with replacement
 - arrange the new columns into a bootstrapped alignment of length **n**
- build a tree from the bootstrapped alignment with the same method as for the original alignment
- repeat the process many times and store all resulting bootstrap trees
- the **bootstrap proportion (BPs)** is the percentage of trees containing a given bipartition

It reflects the consistency with the sequence data support that branch.

BPs are typically shown on the “best tree” or the majority-rule consensus of bootstrap trees.

species 1 AGAATCTGCAATTGCTCAGCTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTGCTCGCTCAAAGCTGGCTCAG
species 2 AGGATCTAAAGTTGCTCTCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTCAAAGCTGGCTCAG
species 3 AGGAATCTGCAGCCGCTCCTCCGATCTGTCTGATGATGTCTGCCTGGCTCTTGCTCTGCTGGCTCAAACCTGGCCAG
species 4 CGGAAATGCAGTTGCTCTGCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTGTTGCTCGCTCAAACCTGGCTCAG
species 5 AGGAATCTGCAGTTGCTCATCCGATCTGTGTGATGATCTGAGTCTGGATCGTCTTGCTGGCTCAAACCTGACCCCG
species 6 AGGAAATGCAGCCGCTCCCCCGATCTGTGTGATGATCTGTCTGAGTCTGGATCTTGCTGCTCGCTCAAACCGGACTCAG
species 7 AGGAATCTGCAGTTGCTCTCCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTGCTCGCTCAAACCGGGCTCAG

species 1
species 2
species 3
species 4
species 5
species 6
species 7

species 1	AGAATCTGCAATTGCTCAGCTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTTGCTCGCTCAAAGCTGGCTCAG
species 2	AGGATCTAAAGTTGCTCTCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTCAAAGCTGGCTCAG
species 3	AGGAATCTGCAGCCGCTCCTCCGATCTGTCTGATGATGTCTGCCTGGCTCTTGCTCTGCTGGCTCAAACCTGGCCCAG
species 4	CGGAAATGCAGTTGCTCTGCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTGTTGCTCGCTCAAACCTGGCTCAG
species 5	AGGAATCTGCAGTTGCTCATCCGATCTGTGTGATGATCTGAGTCTGGATCGTCTTGCTGGCTCAAACCTGACCCCCG
species 6	AGGAAATGCAGCCGCTCCCCCGATCTGTGTGATGATCTGTCTGAGTCTGGATCTTGCTGCTCGCTCAAACCGGACTCAG
species 7	AGGAATCTGCAGTTGCTCTCCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTGGCTCGCTCAAACCGGGCTCAG

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species 1	G
species 2	G
species 3	G
species 4	G
species 5	G
species 6	G
species 7	G

species 1 AGAATCTGCAATTGCTCAGCTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTGCTCGCTCAAAGCTGGCTCAG
species 2 AGGATCTAAAGTTGCTCTCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTCAAAGCTGGCTCAG
species 3 AGGAATCTGCAGCCGCTCCTCCGATCTGTCTGATGATGTCTGCCTGGCTCTTGCTCTGCTGGCTCAAACCTGGCCAG
species 4 CGGAAATGCAGTTGCTCTGCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTGTTGCTCGCTCAAACCTGGCTCAG
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species 6 AGGAAATGCAGCCGCTCCCCCGATCTGTGTGATGATCTGTCTGAGTCTGGATCTTGCTGCTCGCTCAAACCGGACTCAG
species 7 AGGAATCTGCAGTTGCTCTCCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTGCTCGCTCAAACCGGGCTCAG

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species 1 GA
species 2 GT
species 3 GC
species 4 GT
species 5 GA
species 6 GC
species 7 GT

species 1 AGAATCTGCAATTGCTCAGCTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTGCTCGCTCAAAGCTGGCTCAG
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species 3 AGGAATCTGCAGCCGCTCCTCCGATCTGTCTGATGATGTCTGCCTGGCTCTTGCTCTGCTGGCTCAAACCTGGCCAG
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species 1 GAA
species 2 GTA
species 3 GCA
species 4 GTA
species 5 GAA
species 6 GCA
species 7 GTA

species 1 AGAATCTGCAATTGCTCAGCTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTGCTCGCTCAAAGCTGGCTCAG
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species 3 AGGAATCTGCAGCCGCTCCTCCGATCTGTCTGATGATGTCTGCCTGGCTCTTGCTCTGCTGGCTCAAACCTGGCCAG
species 4 CGGAAATGCAGTTGCTCTGCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTGTTTGCTCGCTCAAACCTGGCTCAG
species 5 AGGAATCTGCAGTTGCTCATCCGATCTGTGTGATGATCTGAGTCTGGATCGTCTTGCTGGCTCAAACCTGACCCCG
species 6 AGGAAATGCAGCCGCTCCCCCGATCTGTGTGATGATCTGTCTGAGTCTGGATCTTGCTGCTCGCTCAAACCGGACTCAG
species 7 AGGAATCTGCAGTTGCTCTCCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTGCTCGCTCAAACCGGGCTCAG

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species 1 GAAC
species 2 GTAC
species 3 GCAC
species 4 GTAC
species 5 GAAG
species 6 GCAG
species 7 GTAC

species 1 AGAATCTGCAATTGCTCAGCTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTGCTCGCTCAAAGCTGGCTCAG
species 2 AGGATCTAAAGTTGCTCTCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTCAAAGCTGGCTCAG
species 3 AGGAATCTGCAGCCGCTCCTCCGATCTGTCTGATGATGTCTGCCTGGCTCTTGCTCTGCTGGCTCAAACCTGGCCAG
species 4 CGGAAATGCAGTTGCTCTGCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTGTTGCTCGCTCAAACCTGGCTCAG
species 5 AGGAATCTGCAGTTGCTCATCCGATCTGTGTGATGATCTGAGTCTGGATCGTCTTGCTGGCTCAAACCTGACCCCG
species 6 AGGAAATGCAGCCGCTCCCCCGATCTGTGTGATGATCTGTCTGAGTCTGGATCTTGCTGCTCGCTCAAACCGGACTCAG
species 7 AGGAATCTGCAGTTGCTCTCCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTGCTCGCTCAAACCGGGCTCAG

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species 1 GAACA
species 2 GTACT
species 3 GCACC
species 4 GTACT
species 5 GAAGA
species 6 GCAGC
species 7 GTACT

species 1 AGAATCTGCAATTGCTCAGCTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTGCTCGCTCAAAGCTGGCTCAG
species 2 AGGATCTAAAGTTGCTCTCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTCAAAGCTGGCTCAG
species 3 AGGAATCTGCAGCCGCTCCTCCGATCTGTCTGATGATGTCTGCCTGGCTCTTGCTCTGCTGGCTCAAACCTGGCCAG
species 4 CGGAAATGCAGTTGCTCTGCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTGTTGCTCGCTCAAACCTGGCTCAG
species 5 AGGAATCTGCAGTTGCTCATCCGATCTGTGTGATGATCTGAGTCTGGATCGTCTTGCTGGCTCAAACCTGACCCG
species 6 AGGAAATGCAGCCGCTCCCCCGATCTGTGTGATGATCTGTCTGAGTCTGGATCTTGCTGCTCGCTCAAACCGGACTCAG
species 7 AGGAATCTGCAGTTGCTCTCCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTGCTCGCTCAAACCGGGCTCAG

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species 1 GAACAA
species 2 GTACTA
species 3 GCACCC
species 4 GTACTA
species 5 GAAGAC
species 6 GCAGCA
species 7 GTACTA

species 1 AGAATCTGCAATTGCTCAGCTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTGCTCGCTCAAAGCTGGCTCAG
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species 7 AGGAATCTGCAGTTGCTCTCCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTGCTCGCTCAAACCGGGCTCAG

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species 1 GAACAAT
species 2 GTACTAT
species 3 GCACCCT
species 4 GTACTAT
species 5 GAAGACT
species 6 GCAGCAG
species 7 GTACTAG

species 1 AGAATCTGCAATTGCTCAGCTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTGCTCGCTCAAAGCTGGCTCAG
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species 3 AGGAATCTGCAGCCGCTCCTCCGATCTGTCTGATGATGTCTGCCTGGCTCTTGCTCTGCTGGCTCAAACCTGGCCAG
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species 6 AGGAAATGCAGCCGCTCCCCCGATCTGTGTGATGATCTGTCTGAGTCTGGATCTTGCTGCTCGCTCAAACCGGACTCAG
species 7 AGGAATCTGCAGTTGCTCTCCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTGCTCGCTCAAACCGGGCTCAG

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species 1 GAACAATG
species 2 GTACTATG
species 3 GCACCCTG
species 4 GTACTATG
species 5 GAAGACTG
species 6 GCAGCAGG
species 7 GTACTAGG

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species 6 AGGAAATGCAGCCGCTCCCCCGATCTGTGTGATGATCTGTCTGAGTCTGGATCTTGCTGCTCGCTCAAACCGGACTCAG
species 7 AGGAATCTGCAGTTGCTCTCCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTGCTCGCTCAAACCGGGCTCAG

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species 1 GAACAATGGT
species 2 GTACTATGTT
species 3 GCACCCTGTT
species 4 GTACTATGGT
species 5 GAAGACTGTG
species 6 GCAGCAGGCT
species 7 GTACTAGGTT

species 1 AGAATCTGCAATTGCTCAGCTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTGCTCGCTCAAAGCTGGCTCAG
species 2 AGGATCTAAAGTTGCTCTCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTCAAAGCTGGCTCAG
species 3 AGGAATCTGCAGCCGCTCCTCCGATCTGTCTGATGATGTCTGCCTGGCTCTTGCTCTGCTGGCTCAAACCTGGCCAG
species 4 CGGAAATGCAGTTGCTCTGCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTGTTTGCTCGCTCAAACCTGGCTCAG
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species 6 AGGAAATGCAGCCGCTCCCCCGATCTGTGTGATGATCTGTCTGAGTCTGGATCTTGCTGCTCGCTCAAACCGGACTCAG
species 7 AGGAATCTGCAGTTGCTCTCCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTGCTCGCTCAAACCGGGCTCAG

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species 1 GAACAATGGTA
species 2 GTACTATGTTT
species 3 GCACCCTGTT
species 4 GTACTATGGTT
species 5 GAAGACTGTGA
species 6 GCAGCAGGCTC
species 7 GTACTAGGTTT

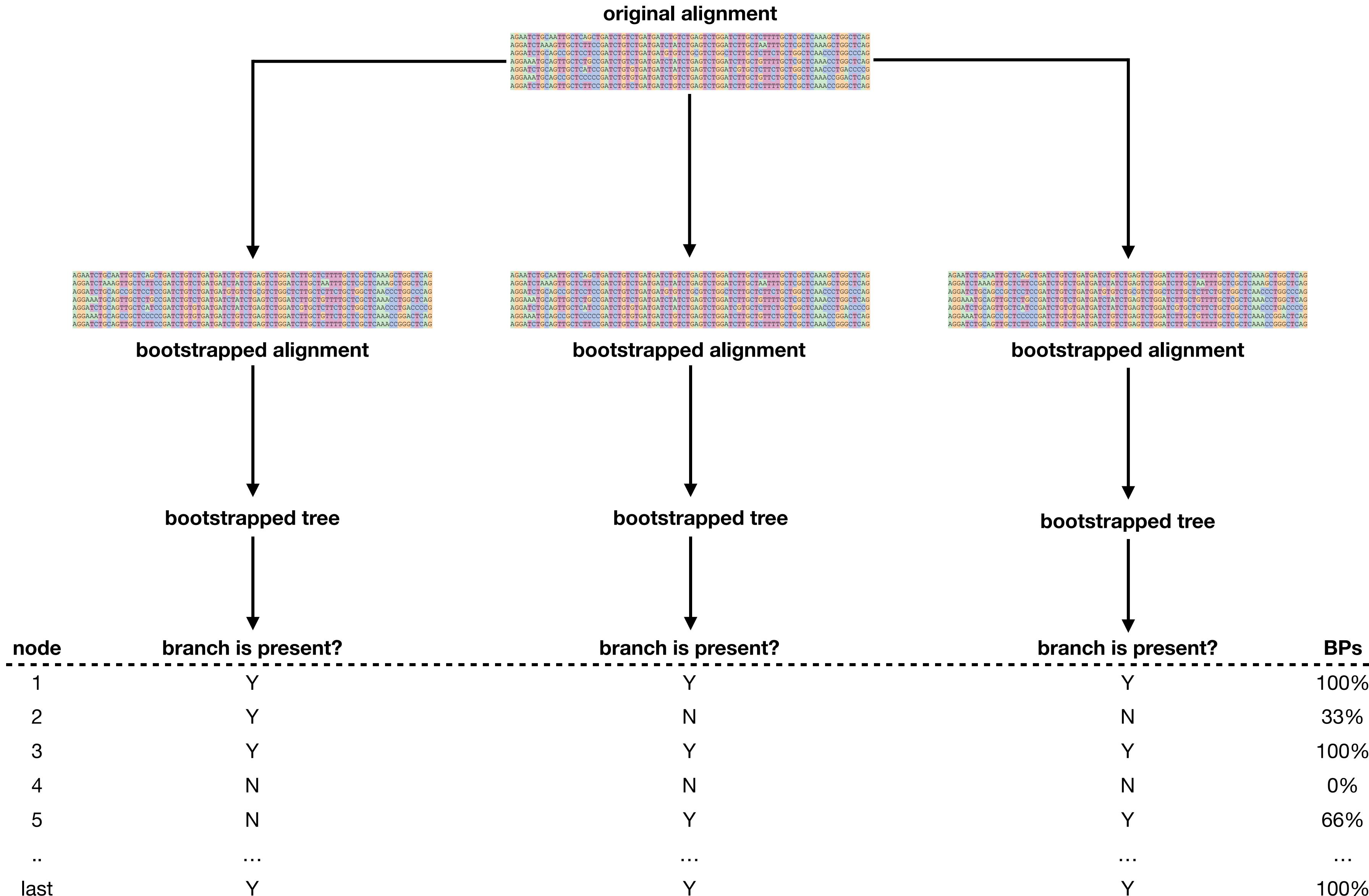
species 1 AGAATCTGCAATTGCTCAGCTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTGCTCGCTCAAAGCTGGCTCAG
species 2 AGGATCTAAAGTTGCTCTCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTCAAAGCTGGCTCAG
species 3 AGGAATCTGCAGCCGCTCCTCCGATCTGTCTGATGATGTCTGCCTGGCTCTTGCTCTGCTGGCTCAAACCTGGCCAG
species 4 CGGAAATGCAGTTGCTCTGCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTGTTTGCTCGCTCAAACCTGGCTCAG
species 5 AGGAATCTGCAGTTGCTCATCCGATCTGTGTGATGATCTGAGTCTGGATCGTCTTGCTGGCTCAAACCTGACCCCG
species 6 AGGAAATGCAGCCGCTCCCCCGATCTGTGTGATGATCTGTCTGAGTCTGGATCTTGCTGCTCGCTCAAACCGGACTCAG
species 7 AGGAATCTGCAGTTGCTCTCCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTGGCTCAAACCGGGCTCAG

species 1 GAACAATGGTA...
species 2 GTACTATGTTT...
species 3 GCACCCTGTTC...
species 4 GTACTATGGTT...
species 5 GAAGACTGTGA...
species 6 GCAGCAGGCTC...
species 7 GTACTAGGTTT...

...AGTAAA
...TGTAT
...CGTCAC
...TGTAT
...AGTAAA
...CGGCAC
...TGGTAT

Sampling with replacement!

Is the same information present in this bootstrapped alignment?



parametric bootstrapping

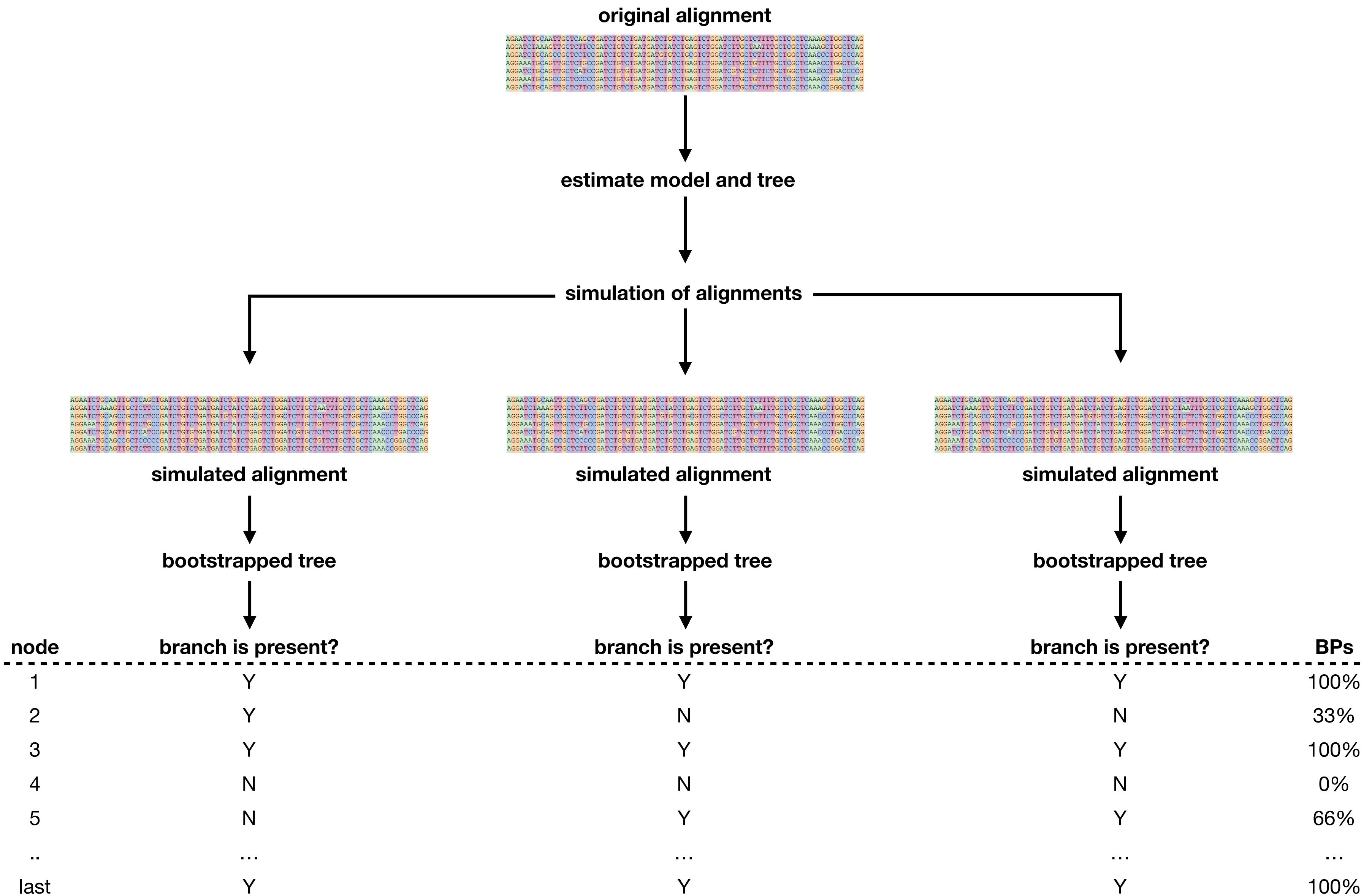
A **model-based approach** to estimate support using simulated data.

This is the process step-by-step:

- estimate from the original alignment X :
 - model of substitution
 - a phylogenetic tree T
- use the model and tree T to simulate replicate alignments X_i
- phylogenetic trees T_i are inferred for each of the alignments X_i
- branch support values are derived - as in non-parametric bootstrapping - by computing the percentage with which a certain branch occurs in the set of generated trees T_i

⚠ Important:

- parametric bootstrap values **depend heavily on the model** estimated from the original data
- if the model is misspecified, support values may be biased or misleading



transfer bootstrap expectation (TBE)

The bootstrap is used extensively 😊 but scaling to thousands of tips introduces new challenges 🤯. Felsenstein BPs yield **low support on deep branches** and is **not robust to taxon sampling** noise.

This is due to its **binary scoring** system: a branch is either **present** or **absent** in a replicate tree.

Lemoine et al. 2018 introduced TBE which uses a **transfer index based on gradual distances** of a branch in the replicate tree to the reference branch, capturing partial support in bootstrap trees.

In detail:

- for a reference clade **R**, split the tips into two complementary groups.
- for each bipartition **B** in the bootstrap tree, compute the transfer distance: that is the minimum number of tips that need to be moved from one side to the other so that **B** matches **R**
- select the branch with the smallest transfer distance - i.e. the best-matching clade
- compute the transfer index from this match: $\text{Transfer Index} = 1 - \frac{\text{Transfer Distance}}{\min(|R|, |\neg R|)}$
- averaging the transfer indices across all replicates gives the TBE value for the clade **R**

jacknife

A resampling method related to BPs but uses **deletion rather than resampling** with replacement.

This is the process step-by-step:

- generate a jackknifed alignment from the starting alignment
 - randomly delete a fixed proportion of alignment columns
 - typically, 50% of sites are removed per replicate as in Felsenstein 1985
 - equivalent to drawing $n/2$ sites without replacement from an alignment of length n
- build a tree from the jackknifed alignment with the same method as for the original alignment
- repeat the process many times and store all resulting jackknife trees
- the **jacknife** is the percentage of trees containing a given bipartition.

It reflects the consistency with the sequence data support that branch.

Jacknife is typically shown on the “best tree” or the majority-rule consensus of bootstrap trees.

... an parametric version of the jacknife is also possible, but not shown!

species 1 AGAATCTGCAATTGCTCAGCTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTTGCTCGCTCAAAGCTGGCTCAG
species 2 AGGATCTAAAGTTGCTCTTCCGATCTGTCTGATGATCTATCTGAGTCTGGATCTTGCTCTAATTGCTCGCTCAAAGCTGGCTCAG
species 3 AGGATCTGCAGCCGCTCCTCCGATCTGTCTGATGATGTCTGCGTCTGGCTCTTGCTCTGCTGGCTCAAACCTGGCCAG
species 4 CGGAAATGCAGTTGCTCTGCCGATCTGTCTGATGATCTATCTGAGTCTGGATCTTGCTGTTTGCTCGCTCAAACCTGGCTCAG
species 5 AGGATCTGCAGTTGCTCATCCGATCTGTGTGATGATCTATCTGAGTCTGGATCGTCTTGCTCTGCTGGCTCAAACCTGACCCG
species 6 AGGAAATGCAGCCGCTCCCCCGATCTGTGTGATGATCTGTCTGAGTCTGGATCTTGCTGTTCTGCTCGCTCAAACCGGACTCAG
species 7 AGGATCTGCAGTTGCTCTCCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTTGCTCGCTCAAACCGGGCTCAG

species 1 AGAATCTGCAATTGCTCAGCTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTTGCTCGCTCAAAGCTGGCTCAG
species 2 AGGATCTAAAGTTGCTCTTCCGATCTGTCTGATGATCTATCTGAGTCTGGATCTTGCTCTAATTGCTCGCTCAAAGCTGGCTCAG
species 3 AGGATCTGCAGCCGCTCCTCCGATCTGTCTGATGATGTCTGCGTCTGGCTCTTGCTCTGCTGGCTCAAACCTGGCCAG
species 4 AGGAAATGCAGTTGCTCTGCCGATCTGTCTGATGATCTATCTGAGTCTGGATCTTGCTGTTTGCTCGCTCAAACCTGGCTCAG
species 5 AGGATCTGCAGTTGCTCATCCGATCTGTGTGATGATCTATCTGAGTCTGGATCGTCTTGCTCTGCTGGCTCAAACCTGACCCG
species 6 AGGAAATGCAGCCGCTCCCCCGATCTGTGTGATGATCTGTCTGAGTCTGGATCTTGCTGTTCTGCTCGCTCAAACCGGACTCAG
species 7 AGGATCTGCAGTTGCTCTCCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTTGCTCGCTCAAACCGGGCTCAG

species 1 AGAATCTGCAATTGCTCAGCTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTTGCTCGCTCAAAGCTGGCTCAG
species 2 AGGATCTAAAGTTGCTCTCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTCTGCTAAAGCTGGCTCAG
species 3 AGGATCTGCAGCCGCTCCTCCGATCTGTCTGATGATGTCTGCCTGGCTCTTGCTCTGCTGGCTCAAACCTGGCCAG
species 4 CGGAAATGCAGTTGCTCTGCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTGTTTGCTCGCTCAAACCTGGCTCAG
species 5 AGGATCTGCAGTTGCTCATCCGATCTGTGTGATGATCTGAGTCTGGATCGTCTTGCTCTGCTGGCTCAAACCTGACCCCG
species 6 AGGAAATGCAGCCGCTCCCCCGATCTGTGTGATGATCTGTCTGAGTCTGGATCTTGCTGTTCTGCTCGCTCAAACCGGACTCAG
species 7 AGGATCTGCAGTTGCTCTCCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTTGCTCGCTCAAACCGGGCTCAG

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species 1 AGAATCTGCAATTGCTCA CTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTTGCTCGCTCAAAGCTGGCTCAG
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species 3 AGGATCTGCAGCCGCTCC CCGATCTGTCTGATGATGTCTGCCTGGCTCTTGCTCTGCTGGCTCAAACCTGGCCAG
species 4 AGGAAATGCAGTTGCTCT CCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTGTTTGCTCGCTCAAACCTGGCTCAG
species 5 AGGATCTGCAGTTGCTCA CCGATCTGTGTGATGATCTGAGTCTGGATCGTCTTGCTCTGCTGGCTCAAACCTGACCCCG
species 6 AGGAAATGCAGCCGCTCC CCGATCTGTGTGATGATCTGTCTGAGTCTGGATCTTGCTGTTCTGCTCGCTCAAACCGGACTCAG
species 7 AGGATCTGCAGTTGCTCT CCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTTGCTCGCTCAAACCGGGCTCAG

species 1 AGAATCTGCAATTGCTCAGCTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTTGCTCGCTCAAAGCTGGCTCAG
species 2 AGGATCTAAAGTTGCTCTCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTCTGCTAAAGCTGGCTCAG
species 3 AGGAATCTGCAGCCGCTCCTCCGATCTGTCTGATGATGTCTGCCTGGCTCTTGCTCTGCTGGCTCAAACCTGGCCAG
species 4 CGGAAATGCAGTTGCTCTGCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTGTTTGCTCGCTCAAACCTGGCTCAG
species 5 AGGAATCTGCAGTTGCTCATCCGATCTGTGTGATGATCTGAGTCTGGATCGTCTTGCTGGCTCAAACCTGACCCCG
species 6 AGGAAATGCAGCCGCTCCCCCGATCTGTGTGATGATCTGTCTGAGTCTGGATCTTGCTGCTCGCTCAAACCGGACTCAG
species 7 AGGAATCTGCAGTTGCTCTCCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTGCTCGCTCAAACCGGGCTCAG

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species 1 AGAATCTGCAATTGCTCA CTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTT CTCTTTGCTCGCTCAAAGCTGGCTCAG
species 2 AGGATCTAAAGTTGCTCT CCGATCTGTCTGATGATCTGAGTCTGGATCTT CTAATTGCTCGCTCAAAGCTGGCTCAG
species 3 AGGAATCTGCAGCCGCTCC CCGATCTGTCTGATGATGTCTGCCTGGCTCTT CTCTTCTGCTGGCTCAAACCTGGCCAG
species 4 AGGAAATGCAGTTGCTCT CCGATCTGTCTGATGATCTGAGTCTGGATCTT CTGTTTGCTCGCTCAAACCTGGCTCAG
species 5 AGGAATCTGCAGTTGCTCA CCGATCTGTGTGATGATCTGAGTCTGGATCGT CTCTTCTGCTGGCTCAAACCTGACCCCG
species 6 AGGAAATGCAGCCGCTCC CCGATCTGTGTGATGATCTGTCTGAGTCTGGATCTT CTGTTCTGCTCGCTCAAACCGGACTCAG
species 7 AGGAATCTGCAGTTGCTCT CCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTT CTCTTTGCTCGCTCAAACCGGGCTCAG

species 1 AGAATCTGCAATTGCTCAGCTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTTGCTCGCTCAAAGCTGGCTCAG
species 2 AGGATCTAAAGTTGCTCTCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTCTGCTAAAGCTGGCTCAG
species 3 AGGAATCTGCAGCCGCTCCTCCGATCTGTCTGATGATGTCTGCCTGGCTCTTGCTCTGCTGGCTCAAACCTGGCCAG
species 4 CGGAAATGCAGTTGCTCTGCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTGTTTGCTCGCTCAAACCTGGCTCAG
species 5 AGGAATCTGCAGTTGCTCATCCGATCTGTGTGATGATCTGAGTCTGGATCTGCTGGCTCAAACCTGACCCCG
species 6 AGGAAATGCAGCCGCTCCCCCGATCTGTGTGATGATCTGTCTGAGTCTGGATCTTGCTGCTCGCTCAAACCGGACTCAG
species 7 AGGAATCTGCAGTTGCTCTCCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTGGCTCGCTCAAACCGGGCTCAG

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species 1 AGAATCTGCAATTGCTCA CTGATCTGTCTGATGATCTGTCTGAGTCTGG TCTT CTCTTTGCTCGCTCAAAGCTGGCTCAG
species 2 AGGATCTAAAGTTGCTCT CCGATCTGTCTGATGATCTGAGTCTGG TCTT CTAATTGCTCGCTCAAAGCTGGCTCAG
species 3 AGGAATCTGCAGCCGCTCC CCGATCTGTCTGATGATGTCTGCCTGG TCTT CTCTTCTGCTGGCTCAAACCTGGCCAG
species 4 AGGAAATGCAGTTGCTCT CCGATCTGTCTGATGATCTGAGTCTGG TCTT CTGTTTGCTCGCTCAAACCTGGCTCAG
species 5 AGGAATCTGCAGTTGCTCA CCGATCTGTGTGATGATCTGAGTCTGG TCGT CTCTTCTGCTGGCTCAAACCTGACCCCG
species 6 AGGAAATGCAGCCGCTCC CCGATCTGTGTGATGATCTGTCTGAGTCTGG TCTT CTGTTCTGCTCGCTCAAACCGGACTCAG
species 7 AGGAATCTGCAGTTGCTCT CCGATCTGTCTGATGATCTGTCTGAGTCTGG TCTT CTCTTTGCTCGCTCAAACCGGGCTCAG

species 1 AGAATCTGCAATTGCTCAGCTGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTTGCTCGCTCAAAGCTGGCTCAG
species 2 AGGATCTAAAGTTGCTCTCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTCTGCTAAAGCTGGCTCAG
species 3 AGGATCTGCAGCCGCTCCTCCGATCTGTCTGATGATGTCTGCCTGGCTCTTGCTCTGCTGGCTCAAACCTGGCCAG
species 4 CGGAAATGCAGTTGCTCTGCCGATCTGTCTGATGATCTGAGTCTGGATCTTGCTGTTTGCTCGCTCAAACCTGGCTCAG
species 5 AGGATCTGCAGTTGCTCATCCGATCTGTGTGATGATCTGAGTCTGGATCTGCTGGCTCTGCTGGCTCAAACCTGACCCCG
species 6 AGGAAATGCAGCCGCTCCCCCGATCTGTGTGATGATCTGTCTGAGTCTGGATCTTGCTGCTCGCTCAAACCGGACTCAG
species 7 AGGATCTGCAGTTGCTCTCCGATCTGTCTGATGATCTGTCTGAGTCTGGATCTTGCTCTTGGCTCGCTCAAACCGGGCTCAG

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species 1 AGAATCTGCAATTGCTCA CTGATCTGTC GATGATCTGTCTGAGTCTGG TCTT CTCTTTGCTCGCTCAAAGCTGGCTCAG
species 2 AGGATCTAAAGTTGCTCT CCGATCTGTC GATGATCTATCTGAGTCTGG TCTT CTAATTGCTCGCTCAAAGCTGGCTCAG
species 3 AGGATCTGCAGCCGCTCC CCGATCTGTC GATGATGTCTGCCTGG TCTT CTCTTCTGCTGGCTCAAACCTGGCCAG
species 4 AGGAAATGCAGTTGCTCT CCGATCTGTC GATGATCTATCTGAGTCTGG TCTT CTGTTTGCTCGCTCAAACCTGGCTCAG
species 5 AGGATCTGCAGTTGCTCA CCGATCTGTG GATGATCTATCTGAGTCTGG TCGT CTCTTCTGCTGGCTCAAACCTGACCCCG
species 6 AGGAAATGCAGCCGCTCC CCGATCTGTG GATGATCTGTCTGAGTCTGG TCTT CTGTTCTGCTCGCTCAAACCGGACTCAG
species 7 AGGATCTGCAGTTGCTCT CCGATCTGTC GATGATCTGTCTGAGTCTGG TCTT CTCTTTGCTCGCTCAAACCGGGCTCAG

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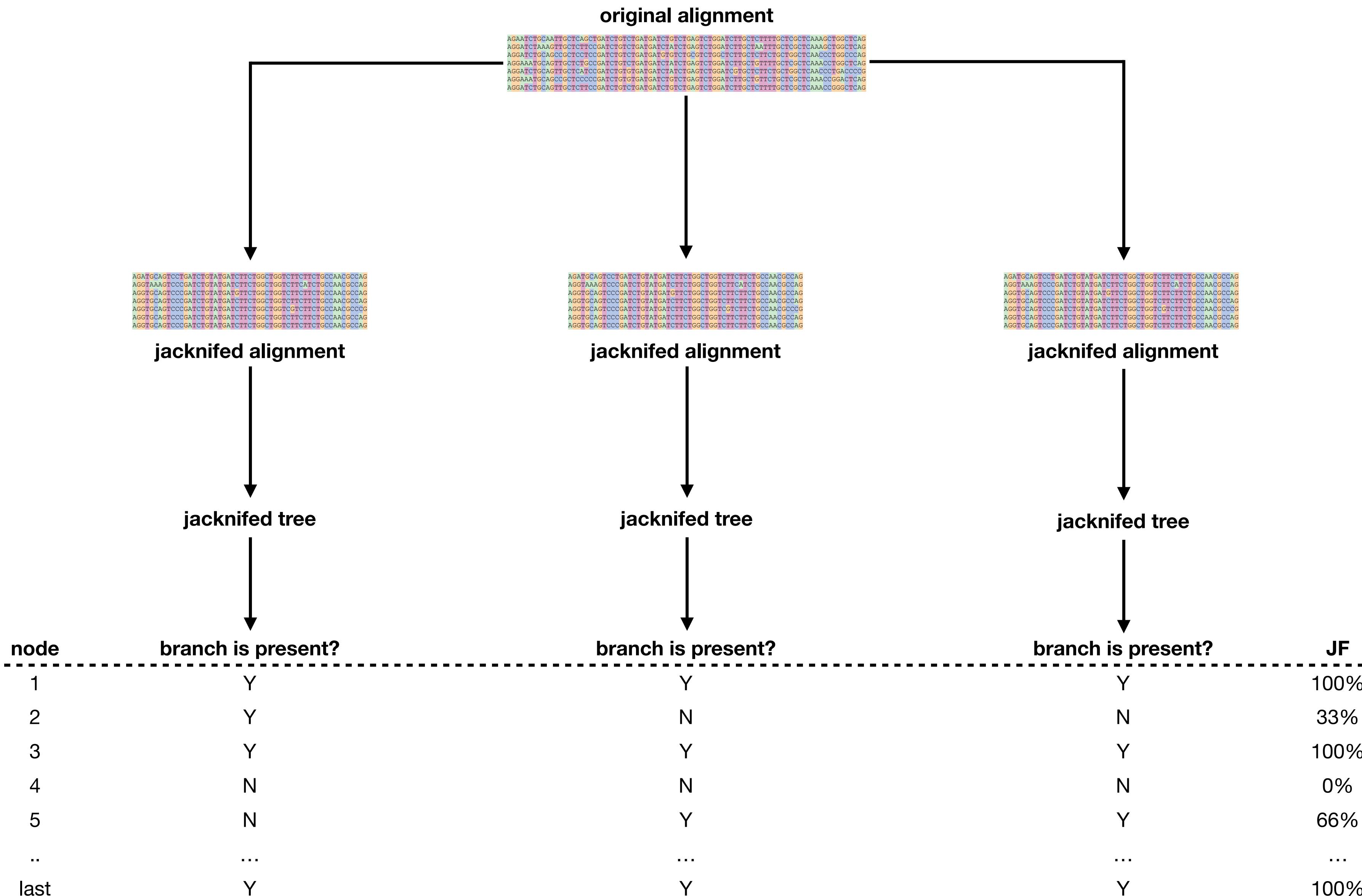
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Sampling without replacement!

Is the same information present in the jacknifed alignment?



approximate Likelihood Ratio Test (aLRT)

aLRT is a fast, branch-specific metric, related to the **conventional Likelihood Ratio Test (LRT)**.

The standard LRT uses the test statistics $2(L_1 - L_0)$:

L_1 - **alternative hypothesis**: is the log-likelihood of the current tree

L_0 - **null hypothesis**: is the log-likelihood of the same tree, but with the branch of interest collapsed

aLRT approximation: L_2 is the second best NNI configuration around the branch of interest

Why use L_2 in aLRT?

- **much faster** than evaluating a collapsed model or full likelihood surface
 L_2 is computed by optimising only over the branch of interest and the four adjacent branches
other parameters are fixed at their optimal values corresponding to the best ML tree
- allows efficient estimation of **branch-specific support**, especially in large trees
focuses on local rearrangements around a branch - just 4 adjacent branches!

⚠ Local rearrangements approach may miss topologies distant to current one but with higher lnL!

Posterior Probabilities (PPs)

Bayesian Inference is associated to **Posterior Probabilities** - also called clade credibility values.

- frequency that a bipartition appears in sampled trees ate the stationary phase of MCMC chain
- ranges from 0 to 1 - a PP of 0.95 means that the clade appeared in 95% of sampled trees

⚠ important:

- PPs tend to be higher than non-parametric BPs
- sensitive to model choice and priors

Concordance Factors (CFs)

Quantify how many genes or sites support each branch in a reference tree.

Two types of CFs:

- gene Concordance Factor (**gCF**):
proportion of **gene trees** that contain a specific branch (or split).
- site Concordance Factor (**sCF**):
proportion of **informative sites** in the alignment that support a branch

Interpreting CFs values:

- High (e.g., >70%) - strong signal and high agreement across loci/sites
- Moderate (40–70%) - moderate support; possible discordance
- Low (<40%) - weak support or substantial gene tree conflict

⚠ Different support **metrics** have different **pitfalls**:

- parametric supports assume the evolutionary model is the correct one.
- standard metrics - PPs or BPs - can support conflicting topologies.
- ...

😊 Good practices:

- different support metrics must be compared
- observe consistent outcomes from different approaches

FINISH