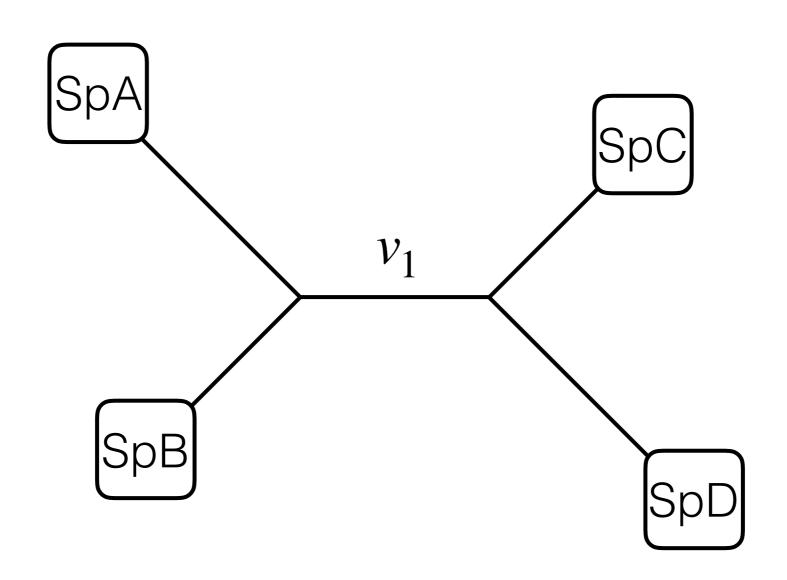
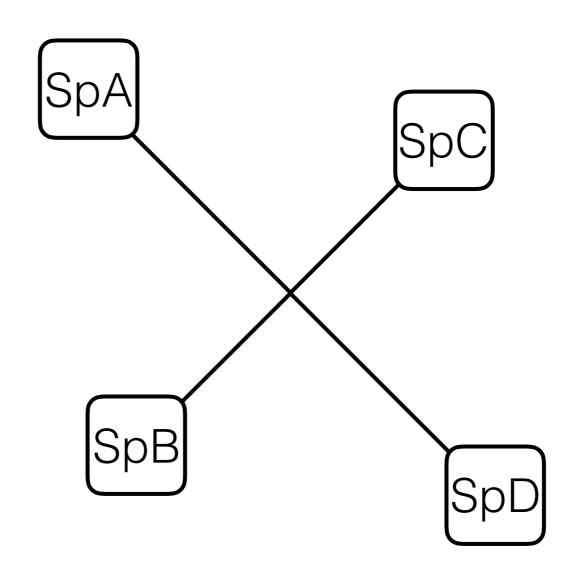
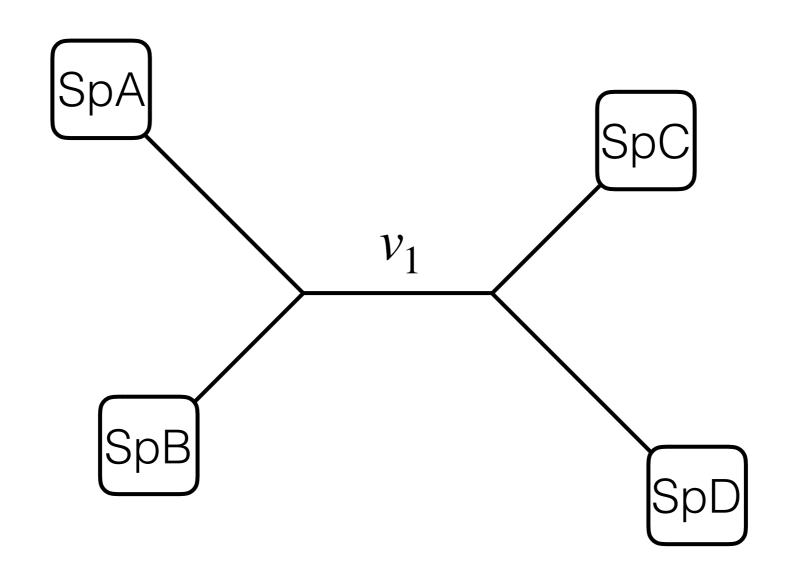
Testing Topological Hypotheses



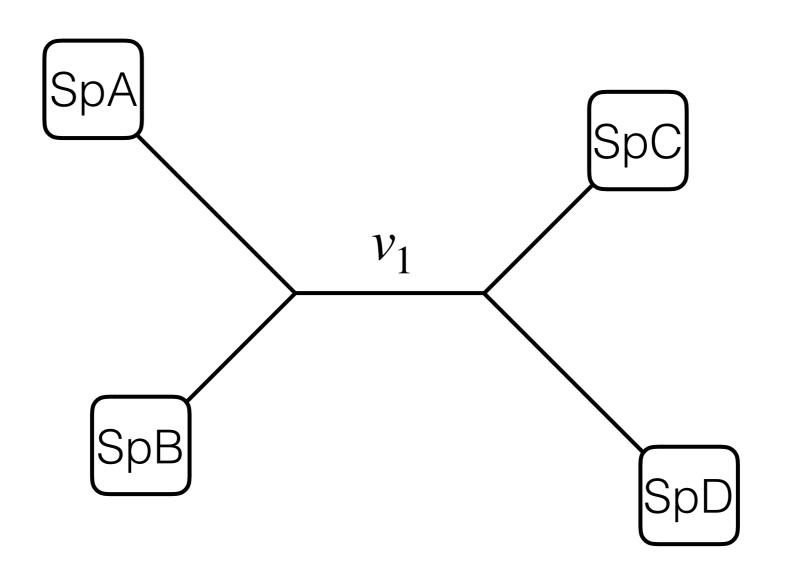
H₀: The length of this branch is 0 (effectively, it does not exist).



 H_1 : The length of this branch is > 0.



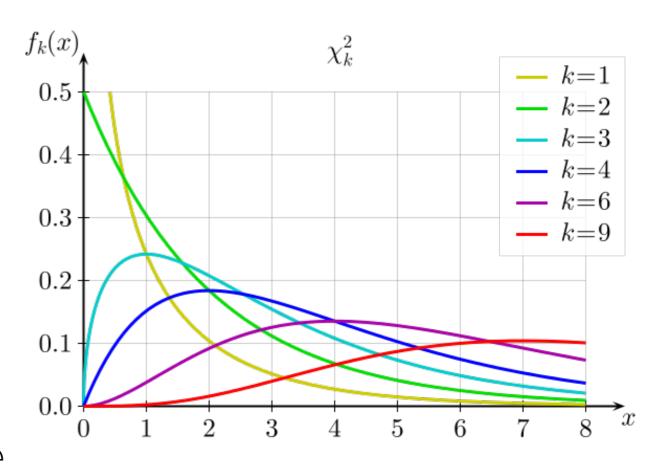
Ho and Ho are nested, so we can use an LRT.



Ho and Ho are nested, so we can use an LRT.

$$LR = \frac{\mathcal{L}(v_1 = 0)}{\mathcal{L}(v_1 > 0)}$$

Because the value of v_1 is at a boundary of parameter space, we should use a 50:50 mixture of χ_0^2 and χ_1^2 .

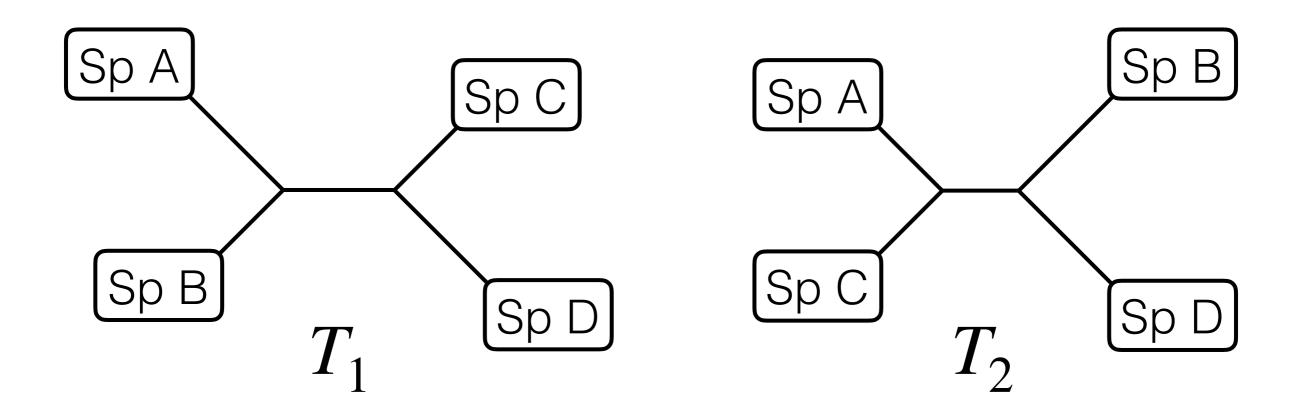


Challenges and Drawbacks

- Hypothesis not really specified a priori (only after inferring ML tree)
- Multiple tests if applied to all branches
- Not clear that H0 is actually correct/useful.
 Branch lengths may have expectations > 0 even for incorrect trees.

Challenges and Drawbacks





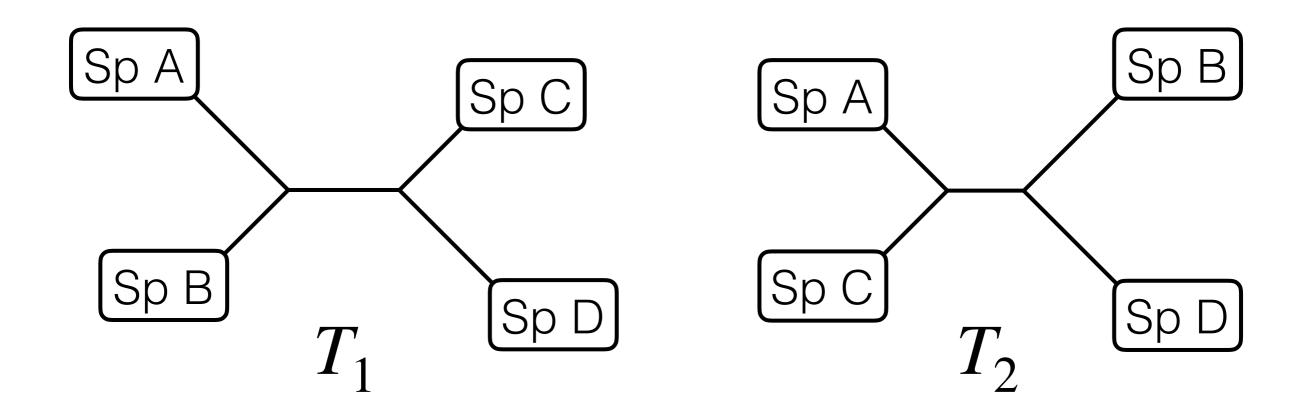
Test Statistic

$$\Delta = ln(\mathcal{L}_1) - ln(\mathcal{L}_2)$$

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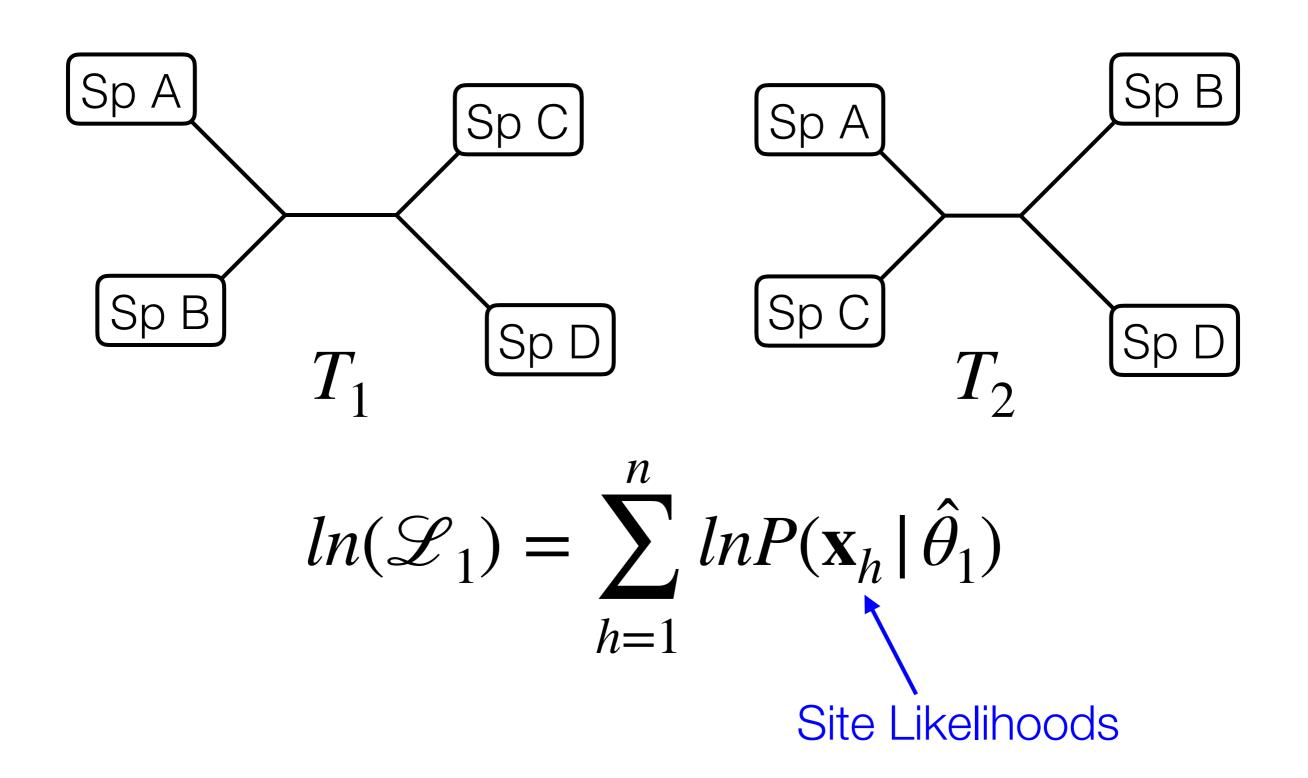
The Intuitive Approach (priNPfcd)

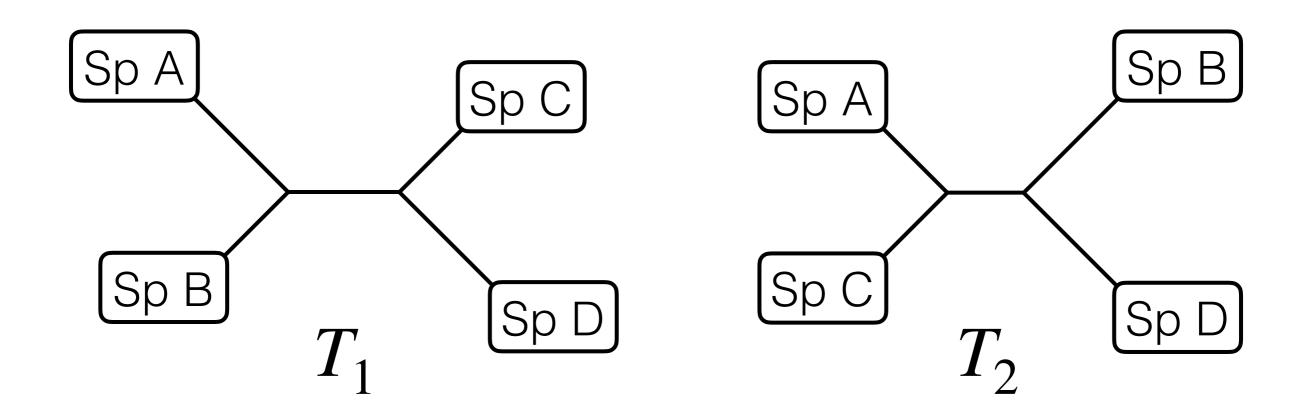
- 1. Bootstrap data
- 2. Reoptimize and recalculate likelihood differences
- After all bootstraps, take mean of differences and center distribution, so avg. difference is 0 (H₀).
- 4. Compare observed difference to centered, bootstrap distribution.



A Faster Approach (priNPnca)

This is the one described in Yang's book.

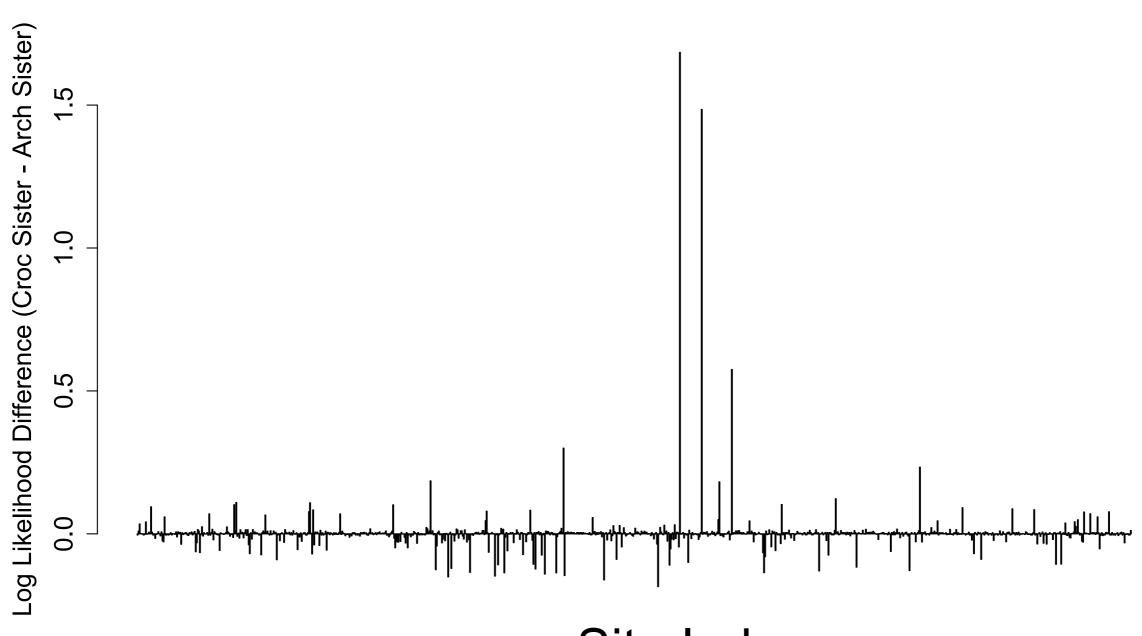




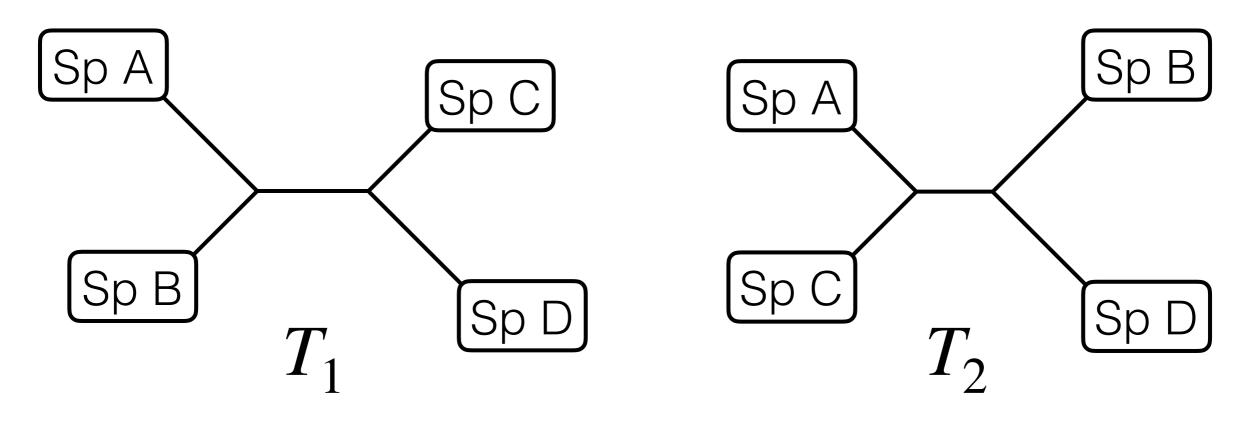
$$d_h = lnP(\mathbf{x}_h | \hat{\theta}_1) - lnP(\mathbf{x}_h | \hat{\theta}_2)$$

These can be used to estimate expected variance of Δ $\overline{d} = \frac{\Delta}{n}$ (with some assumptions)

Site Likelihood Example

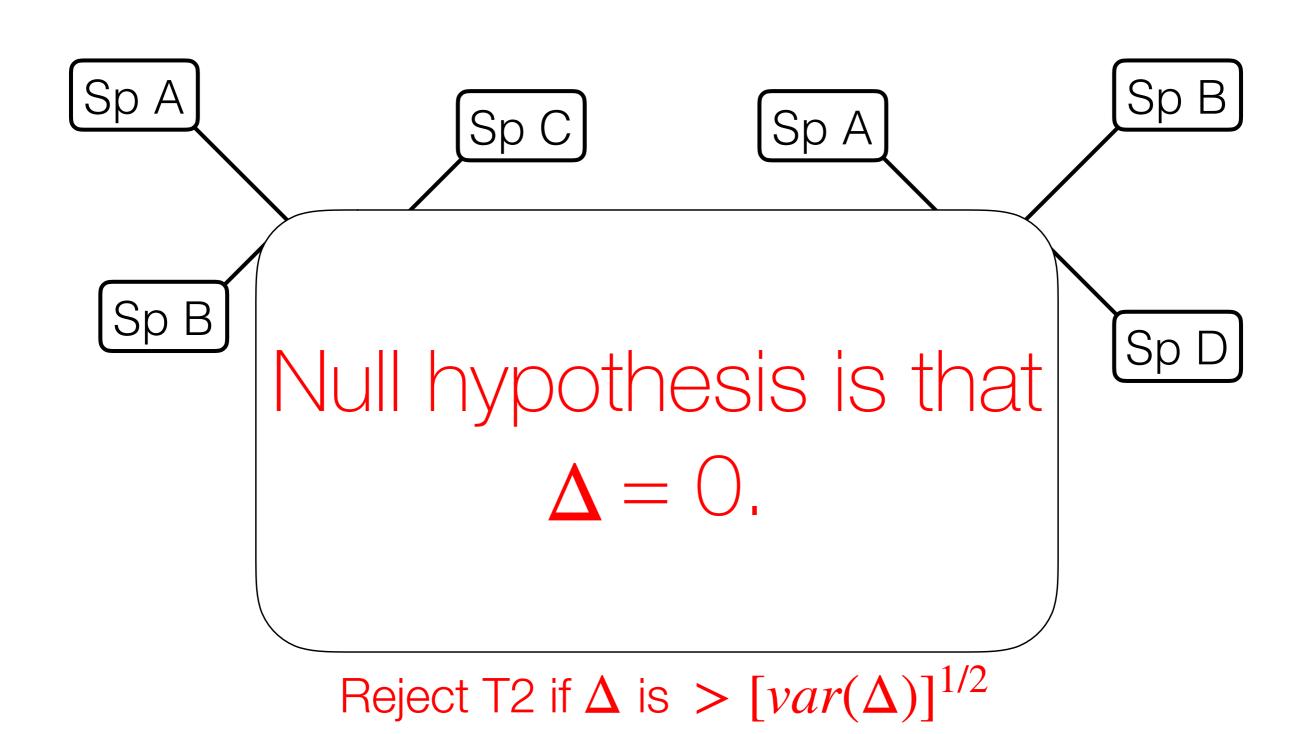


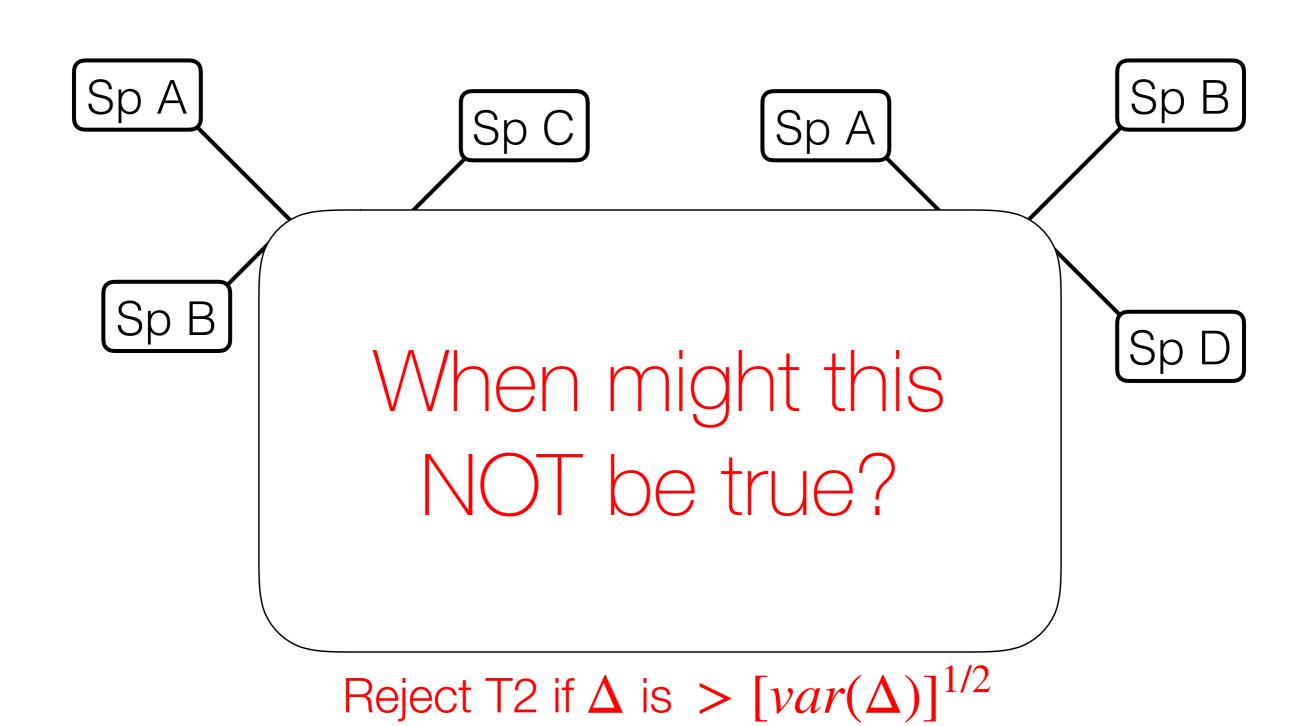
Site Index

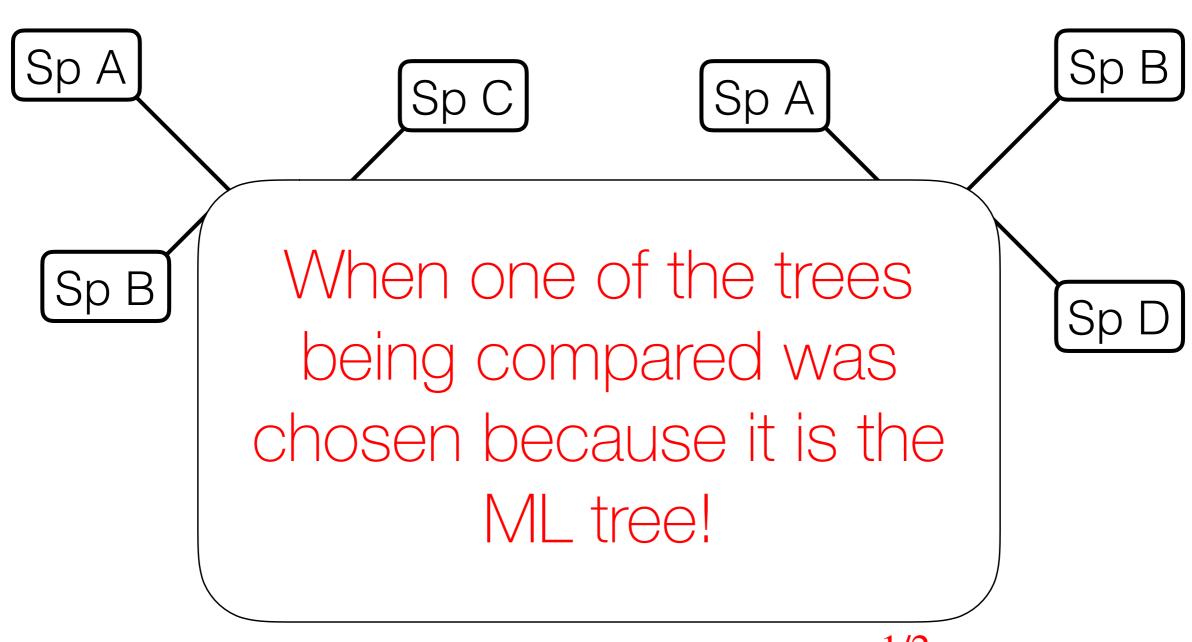


$$var(\Delta) = \frac{n}{n-1} \sum_{h=1}^{n} (d_h - \bar{d})^2$$

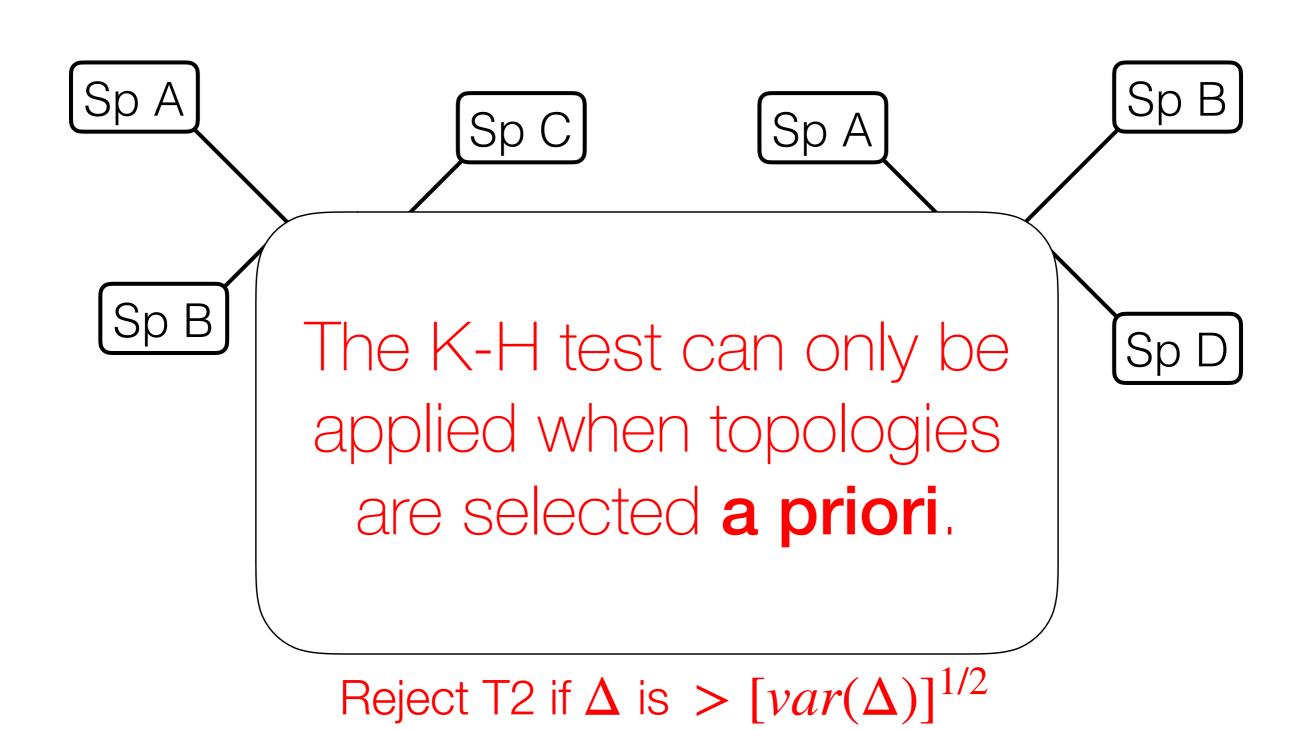
Reject T2 if Δ is $> [var(\Delta)]^{1/2}$



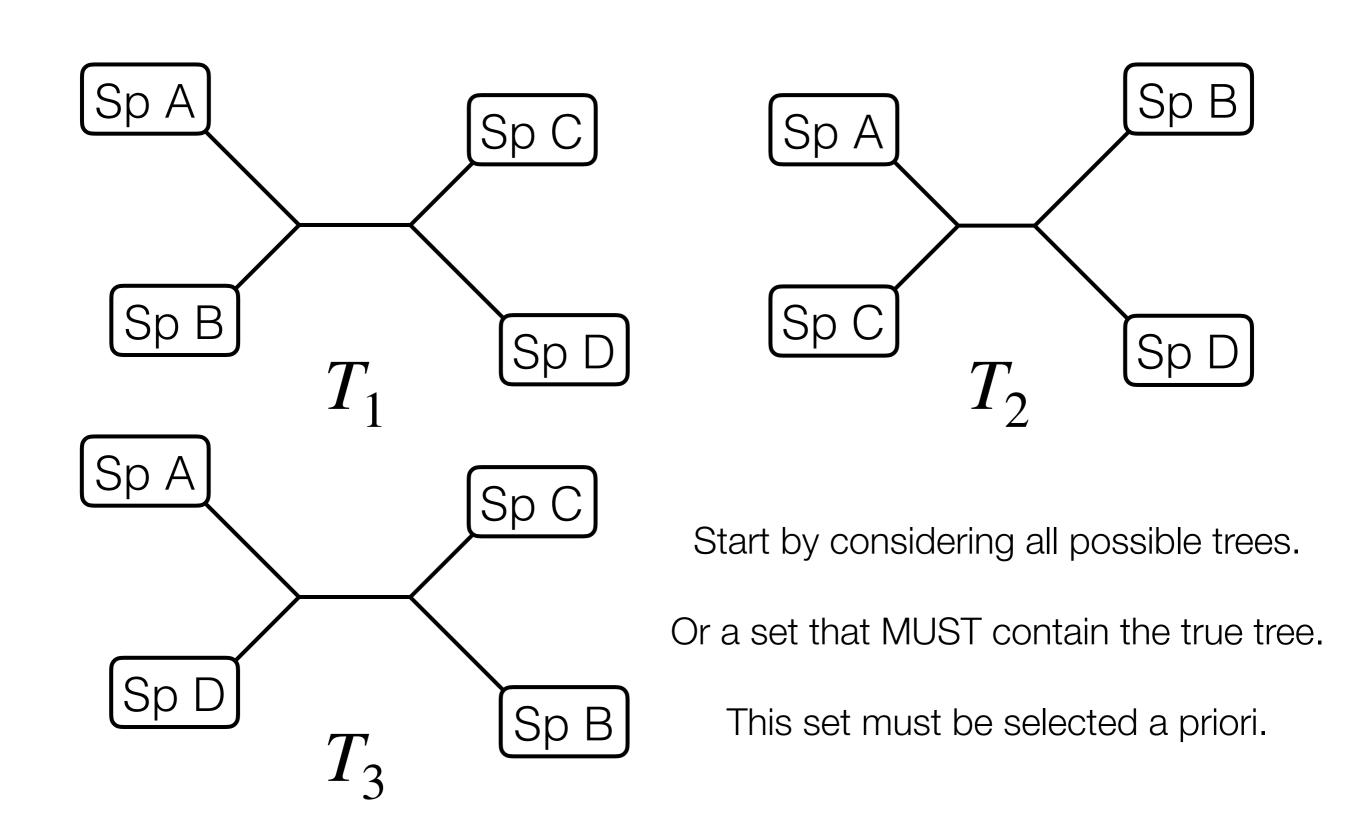




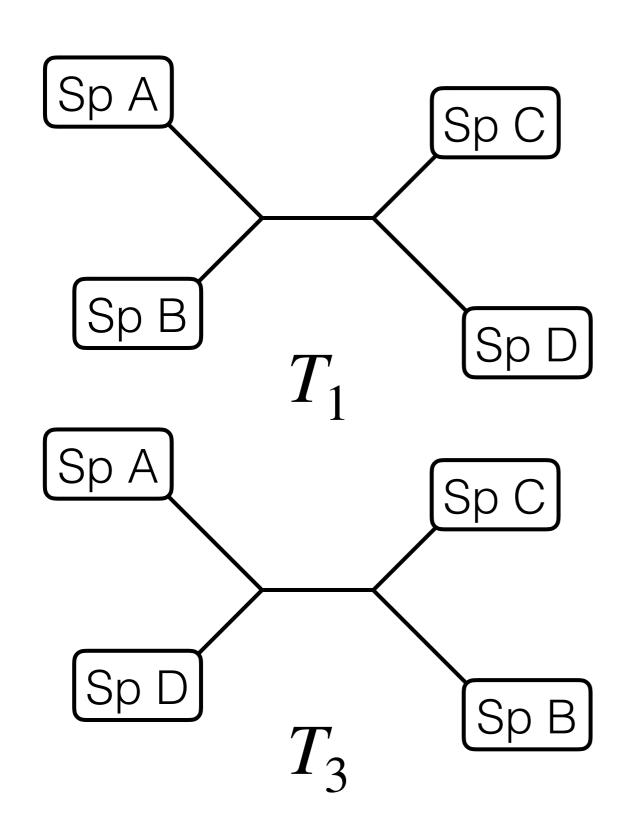
Reject T2 if Δ is $> [var(\Delta)]^{1/2}$

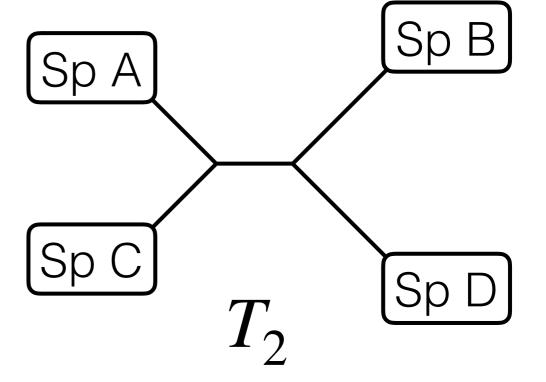


S-H Test



S-H Test





H₀: All *T* are equally good explanations of the data.

H_A: Some *T* are not equally good explanations.

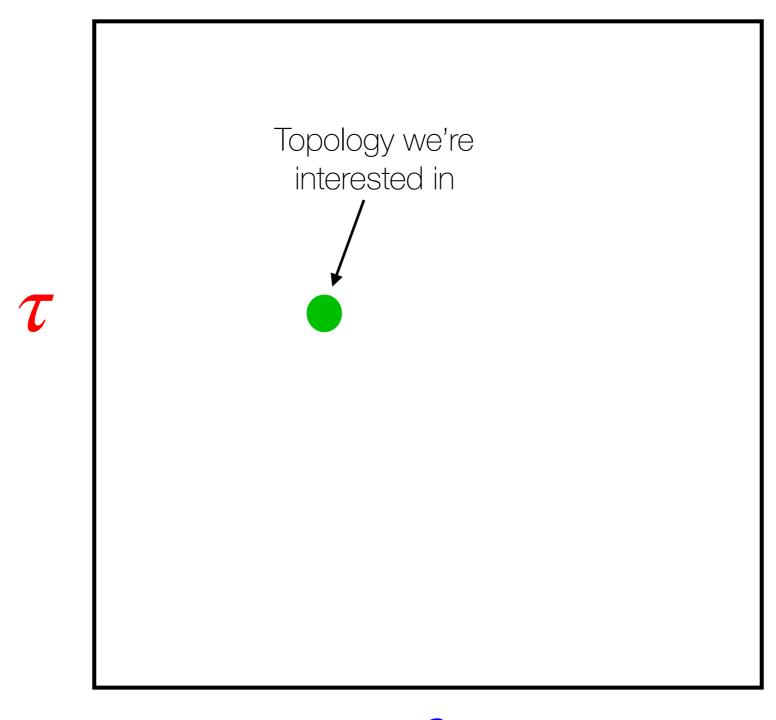
S-H Test

The Intuitive Explanation (posNPfcd)

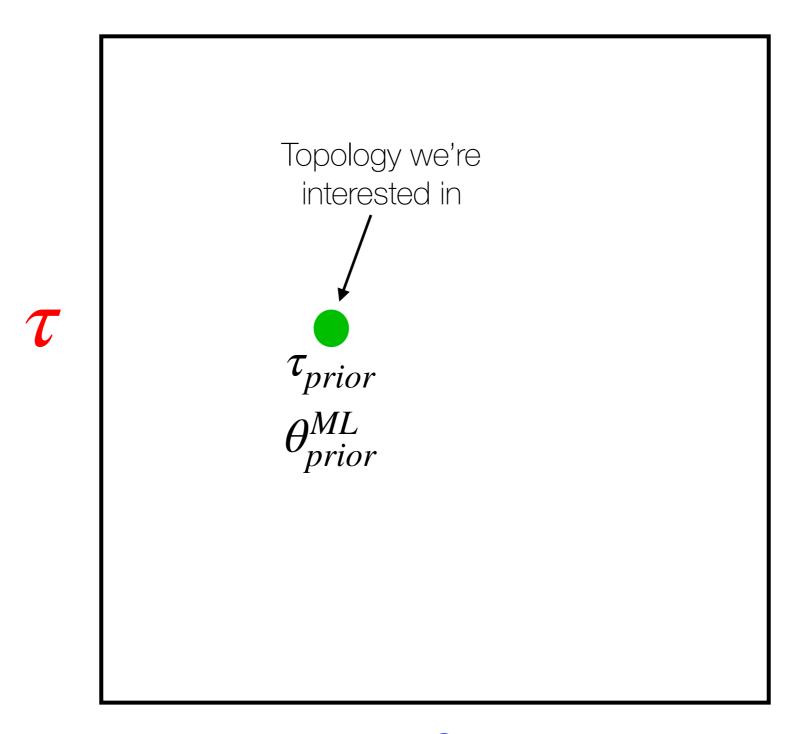
- 1. Calculate L_{ML} L_x .
- 2. Bootstrap
- 3. Reoptimize for each bootstrap
- 4. Center the bootstrapped likelihoods for each topology across replicates.
- 5. For each replicate, recalculate L_{ML} L_x from the recentered values.
- 6. For each topology, compare observed difference to the reentered, bootstrap distribution. This test is one-sided and gives a P-value for each topology.

T

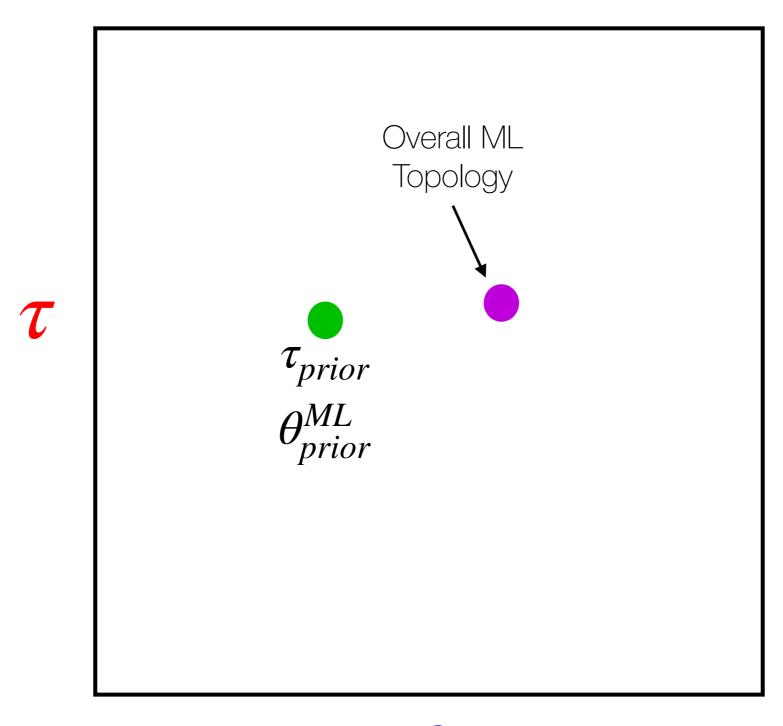
The space of all possible trees and model parameter values



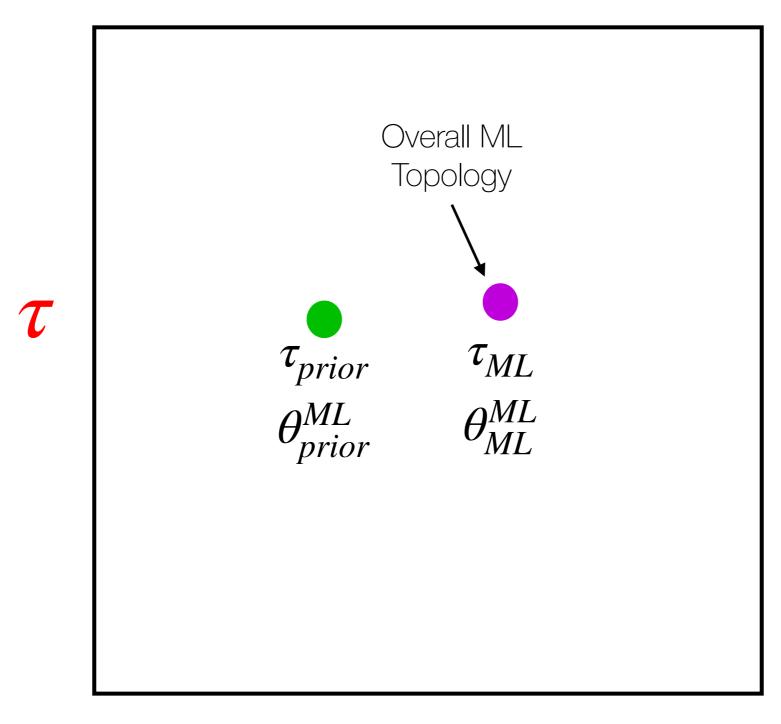








 θ





Is the likelihood of the overall ML tree sufficiently higher than the likelihood of our tree to reject it?

 \mathcal{T}

