Roch@SC: Probabilistic Techniques in Mathematical Phylogenetics:
Relating Combinatorial and Variational Distances Between Trees

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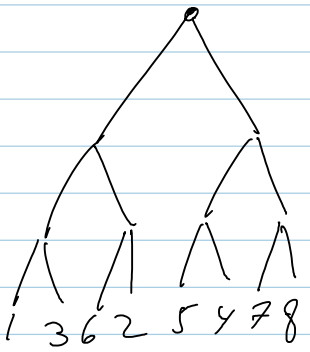
$[n]$-Tree: complete binary tree w/ $n=2^h$ leafs, with labeled leafs. Two are equivalent if the distance between labels is preserved.

Ising model: Every edge is "open" w/ probability θ; use to make connected components, then choose ± 1 per component uniformly & independently



$\underset{\sim}{Z}$ is the process

$\underset{\sim}{Z}_{[n]}$ the marginal on the leafs.

Z_v the value at the node.

The "swap distance" between T & T' is the minimal number of depth-preserving swaps to get from T to T'.

Goal: recover T from observations of $\underset{\sim}{Z}_{[n]}$