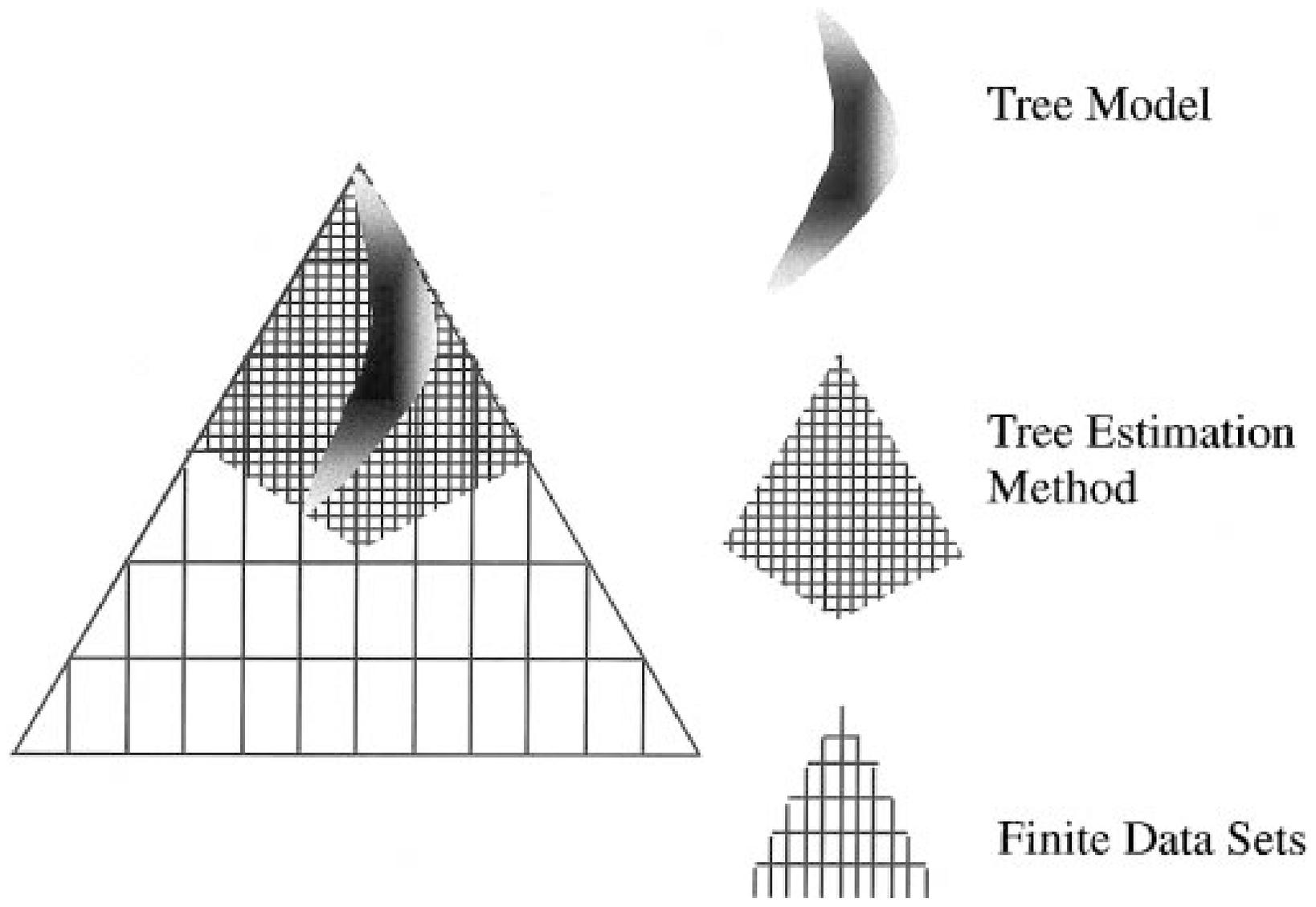
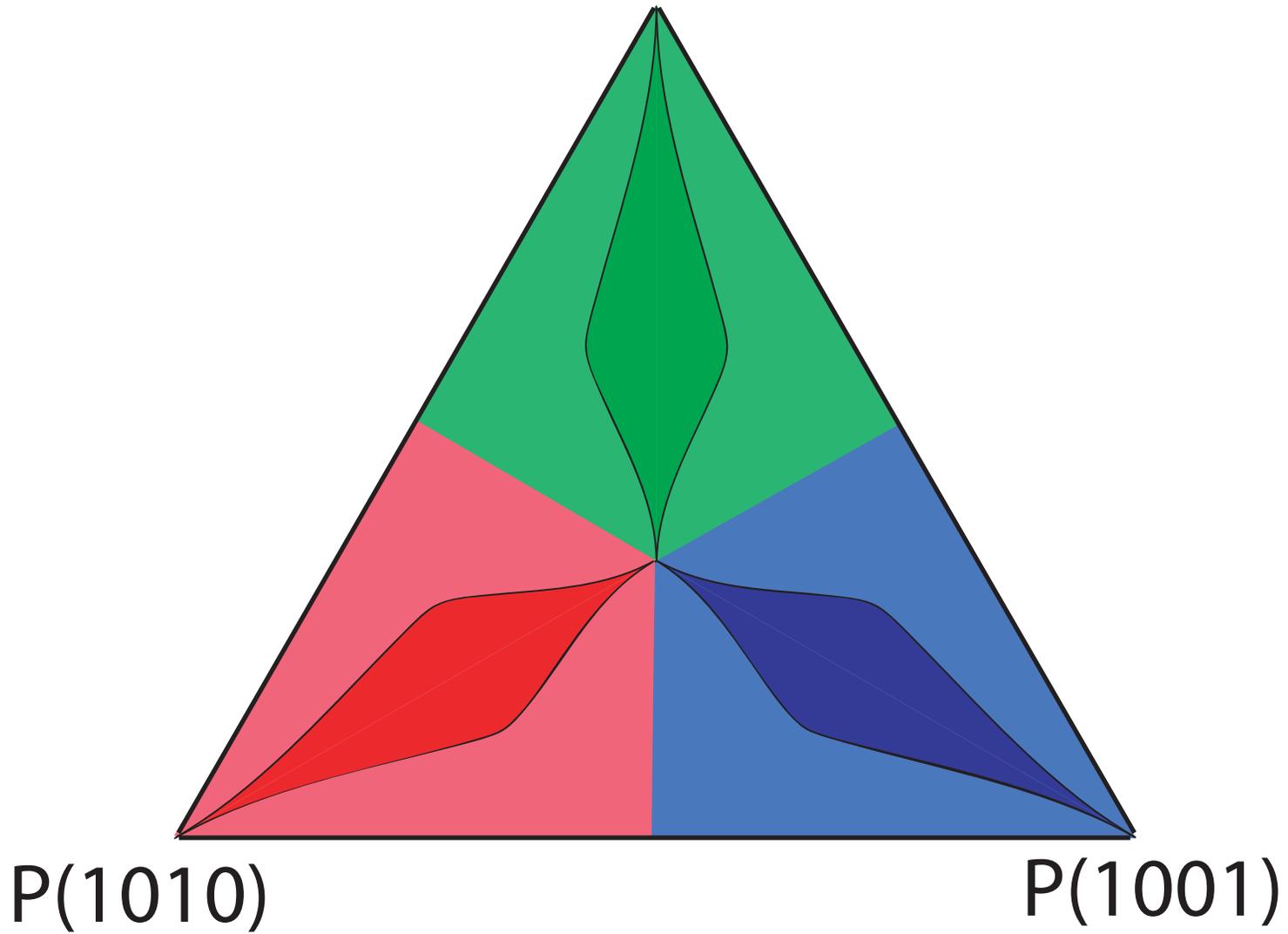


Cartoon time courtesy of the ? view of tree space



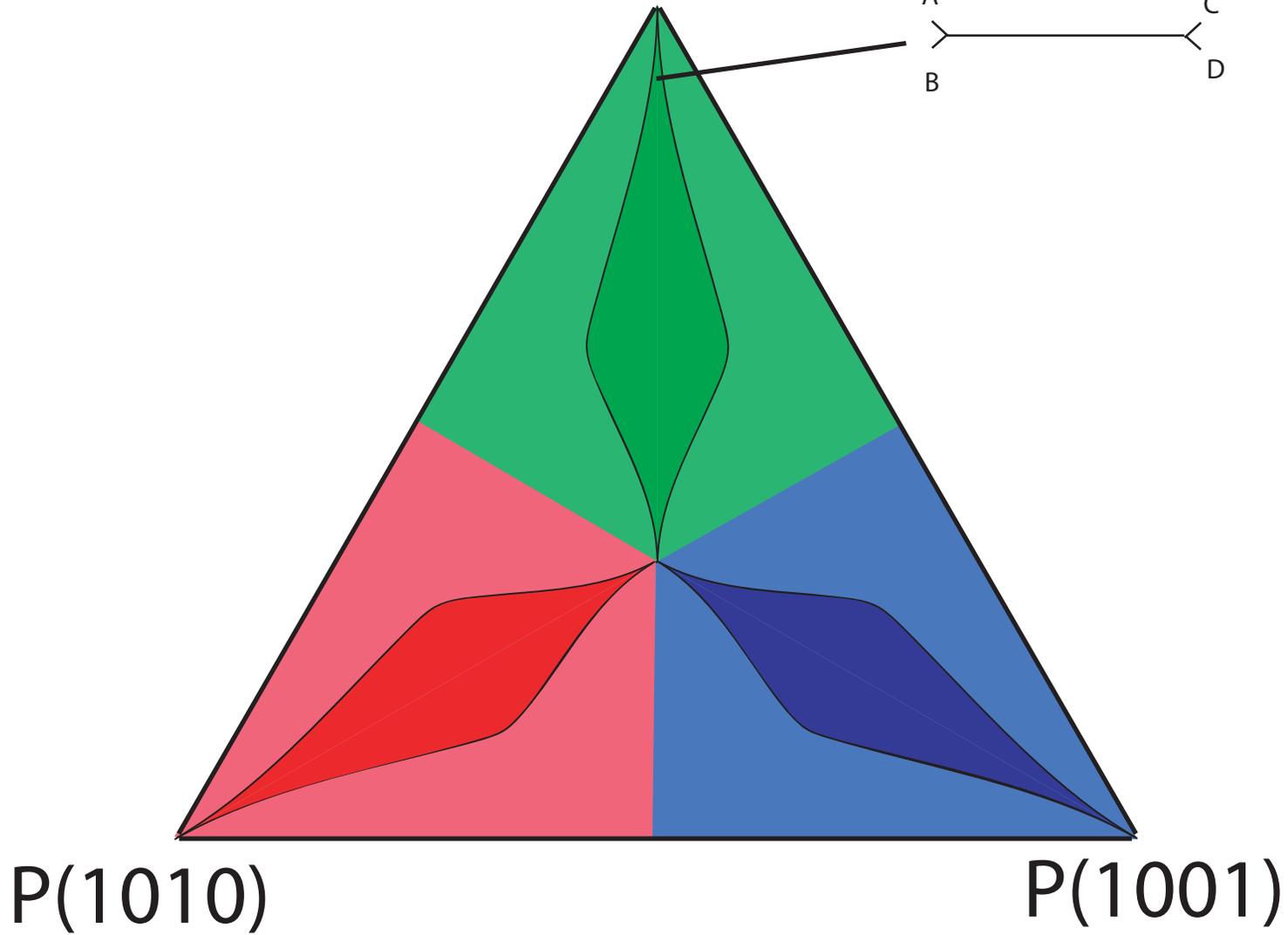
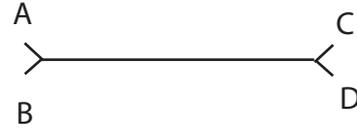
Parsimony-informative Pattern Frequency Space

P(1100)

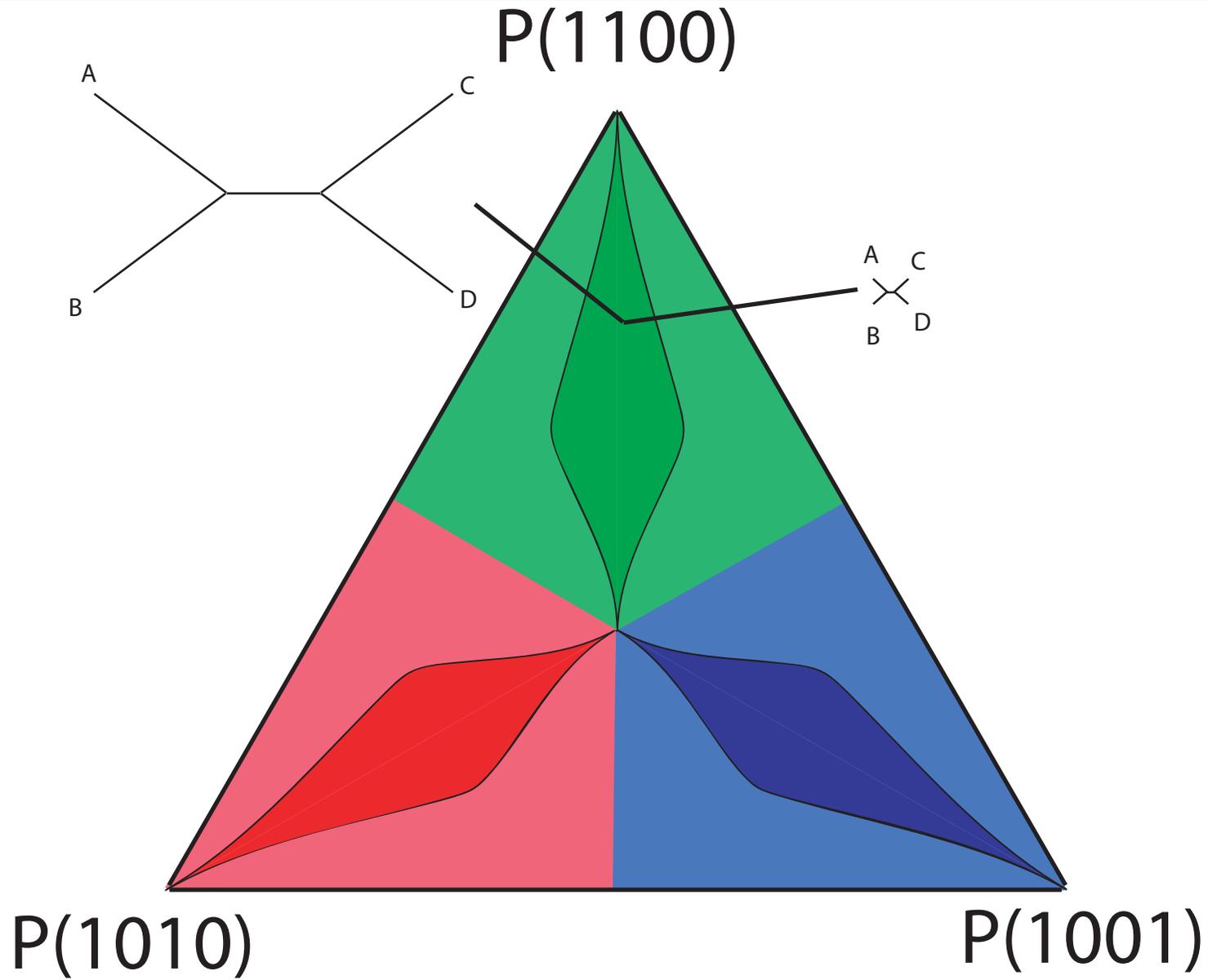


Parsimony-informative Pattern Frequency Space

P(1100)

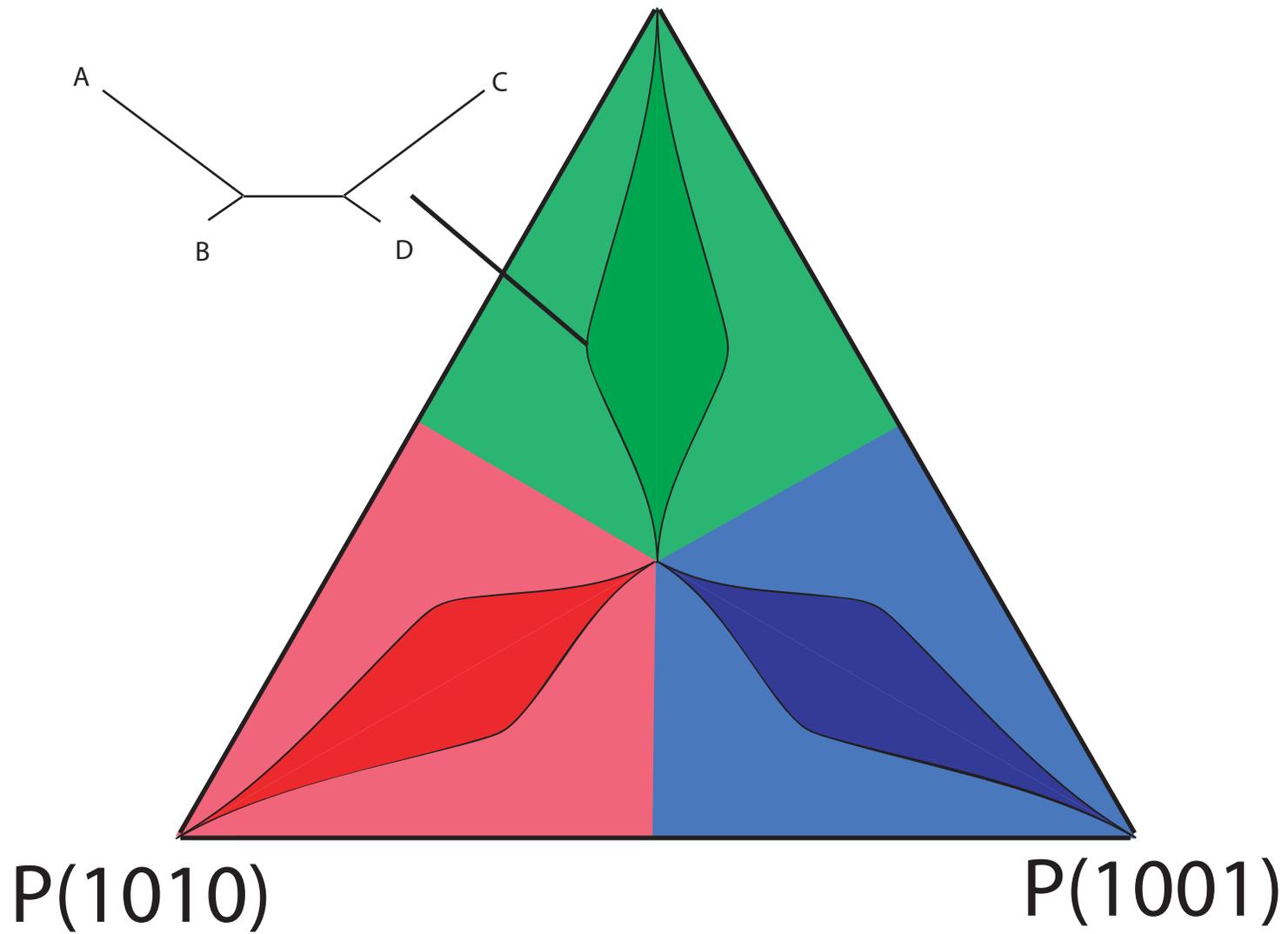


Parsimony-informative Pattern Frequency Space

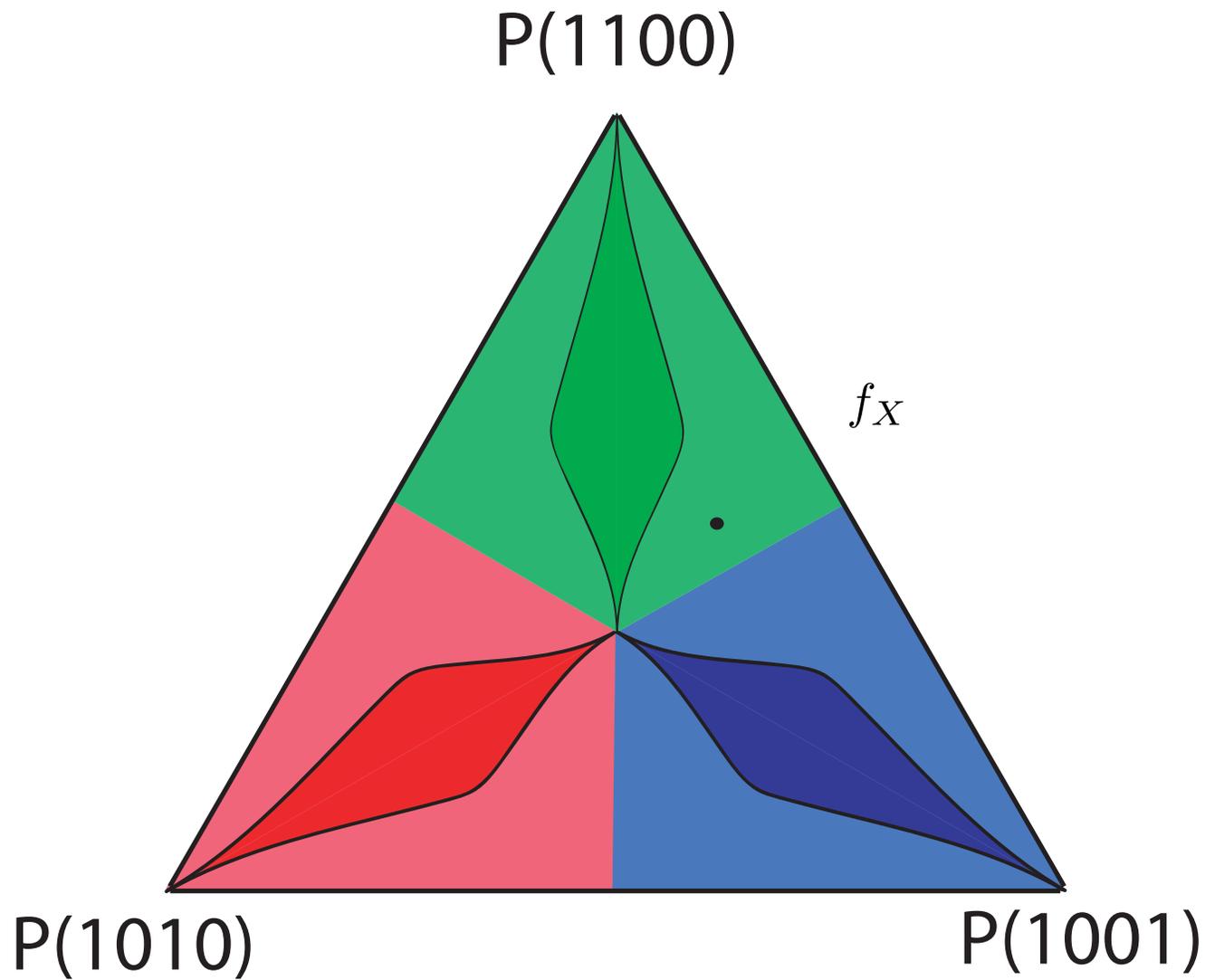


Parsimony-informative Pattern Frequency Space

P(1100)



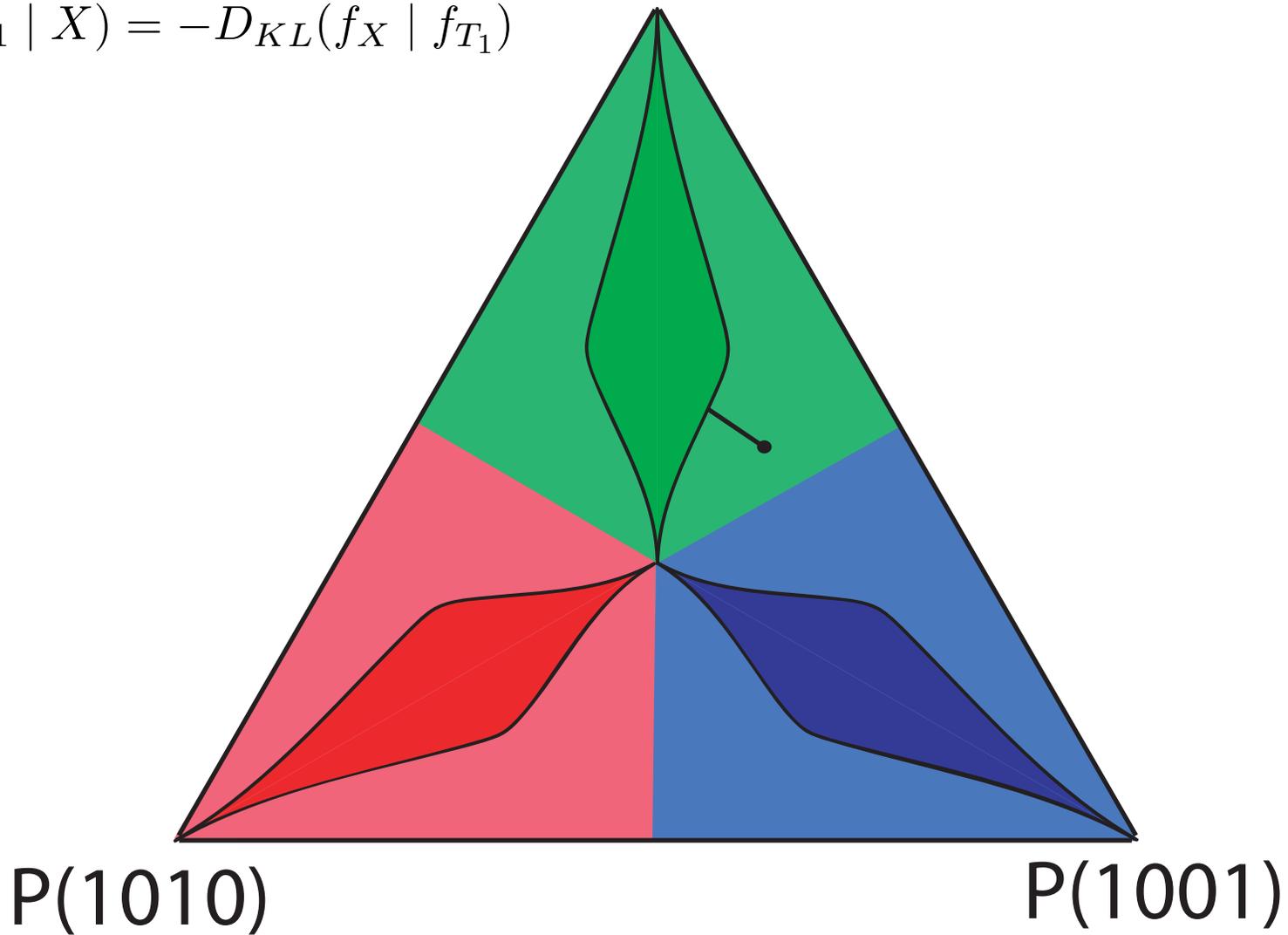
Pattern Frequency Space With Observed Data



ML scores in Pattern Frequency Space

P(1100)

$$\ln L(T_1 | X) = -D_{KL}(f_X | f_{T_1})$$

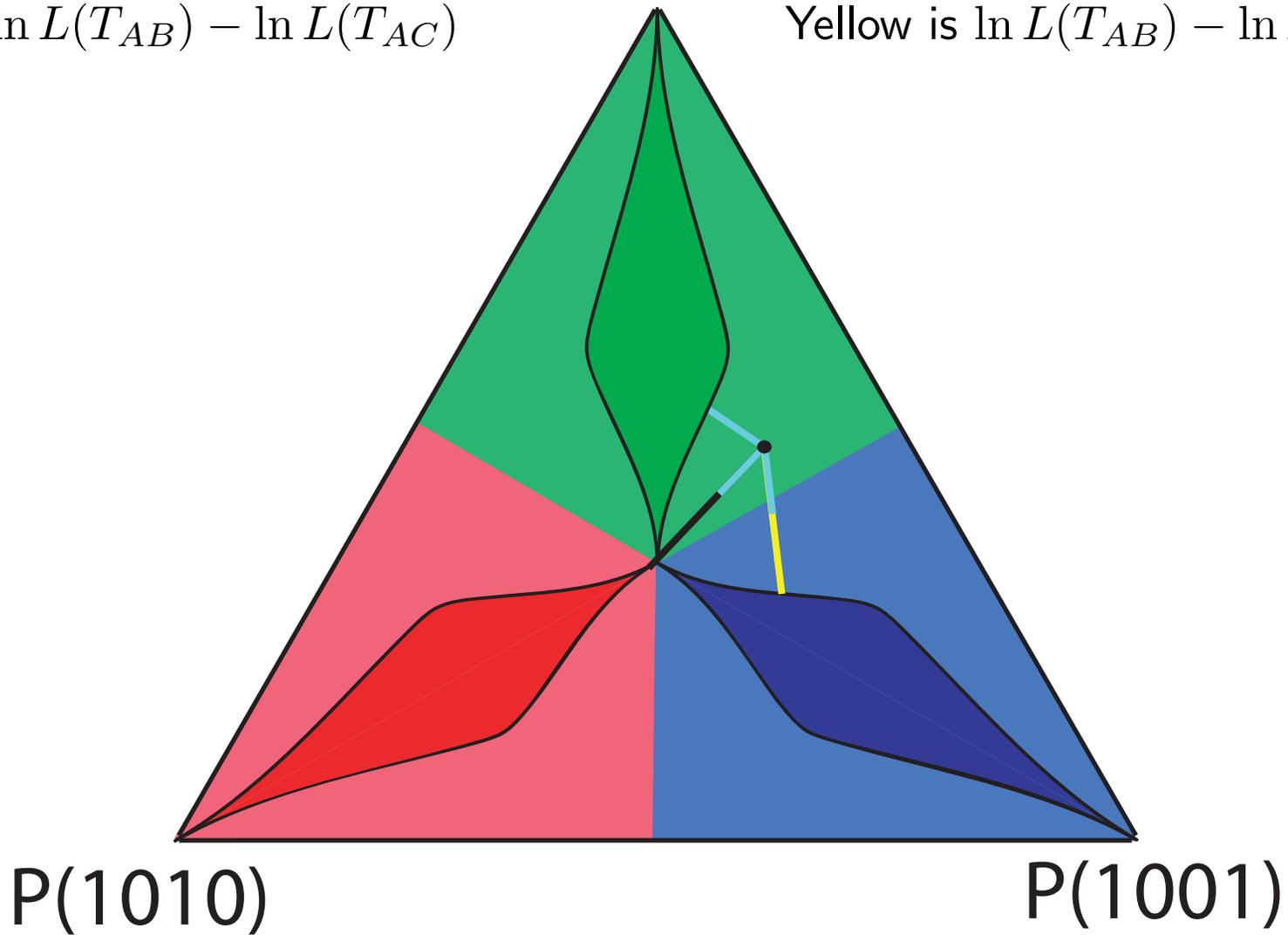


LR statistics in Pattern Frequency Space

P(1100)

Black is $\ln L(T_{AB}) - \ln L(T_{AC})$

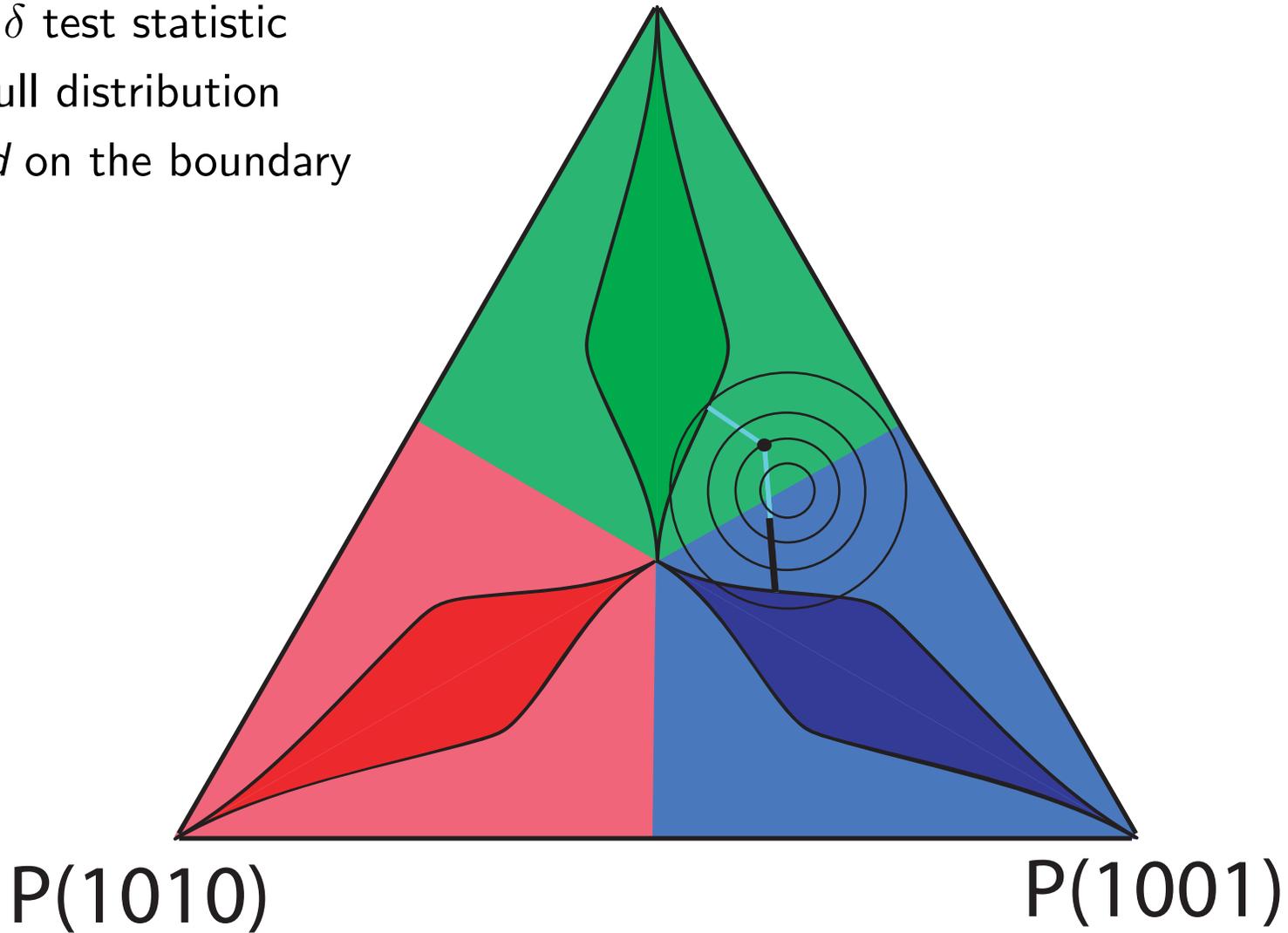
Yellow is $\ln L(T_{AB}) - \ln L(T_{AD})$



KH Test in Pattern Frequency Space

P(1100)

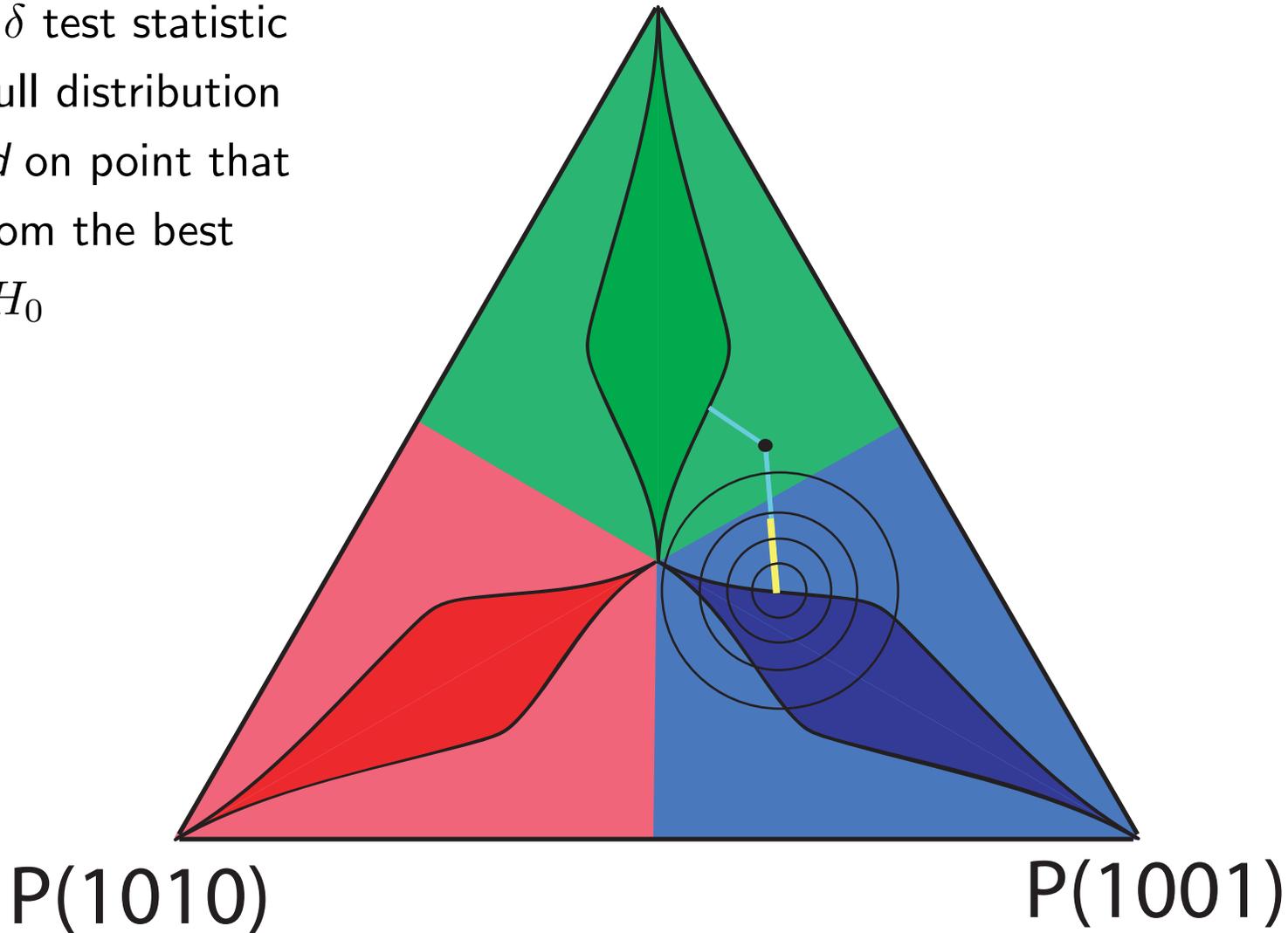
Uses the δ test statistic
and a null distribution
centered on the boundary



Parametric bootstrapping in Pattern Frequency Space

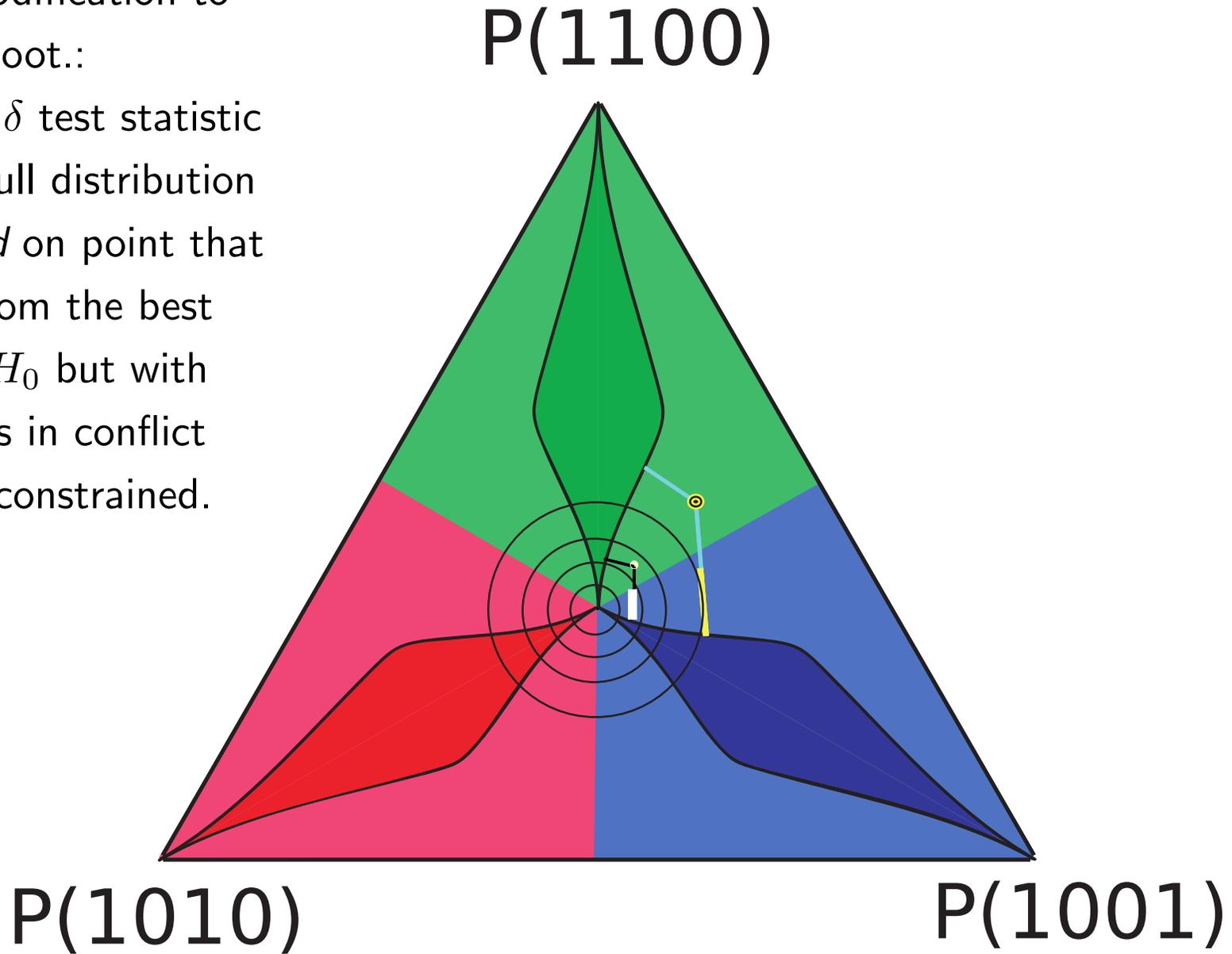
P(1100)

Uses the δ test statistic and a null distribution centered on point that arises from the best tree in H_0

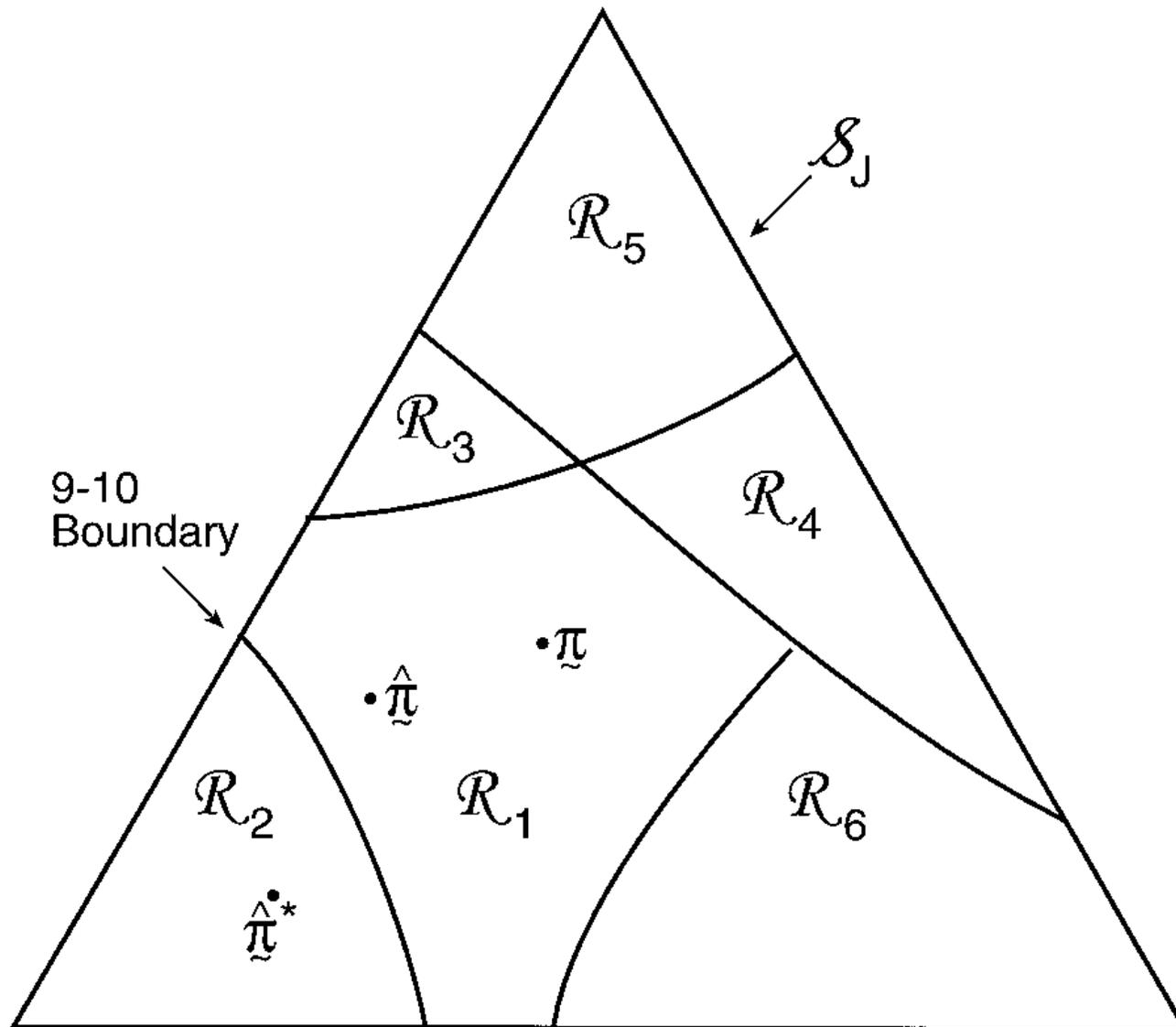


Susko modification to
param. boot.:

Uses the δ test statistic
and a null distribution
centered on point that
arises from the best
tree in H_0 but with
branches in conflict
with \hat{T} constrained
to be 0.

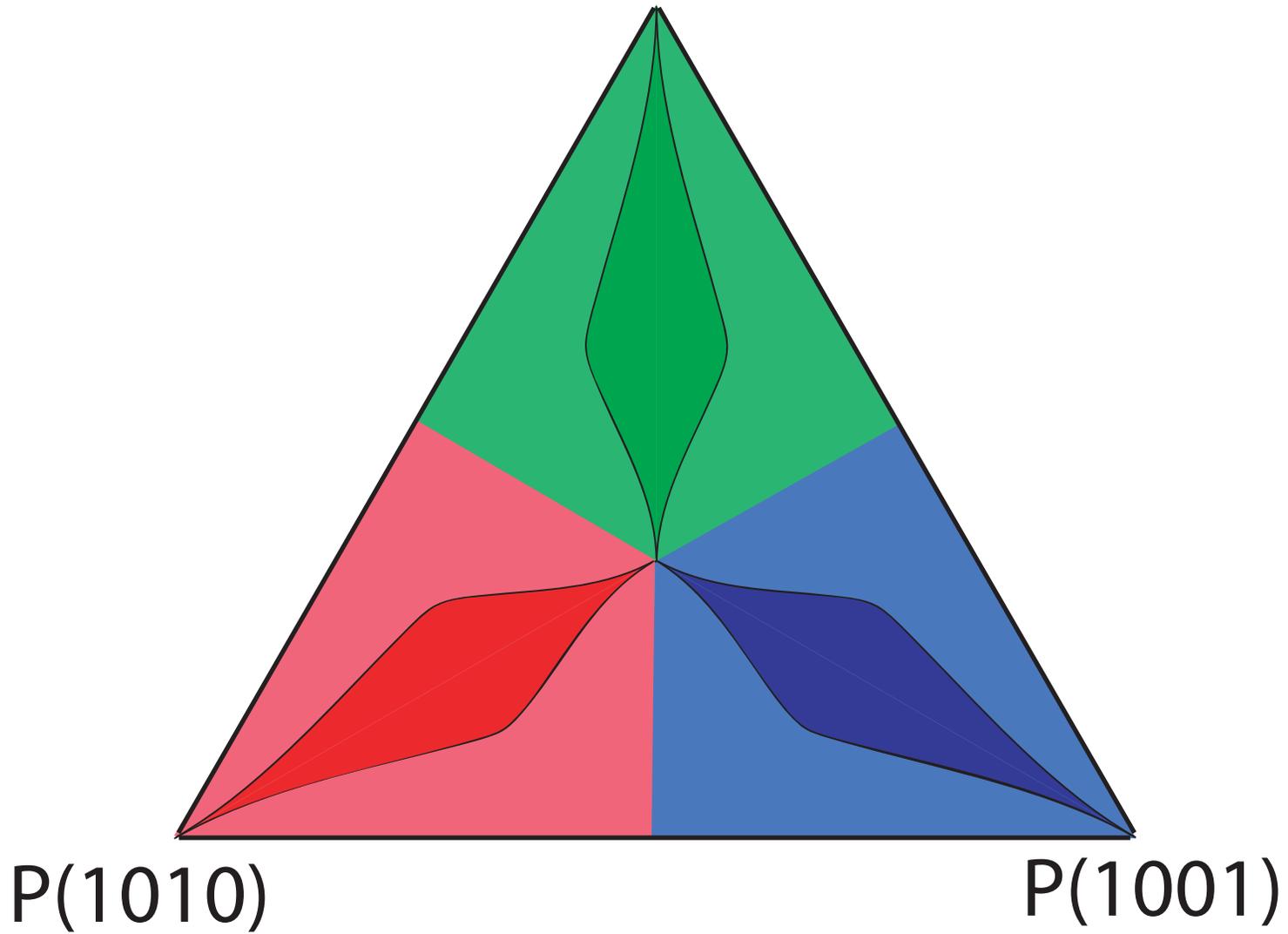


Efron et al. (1996) view of tree space

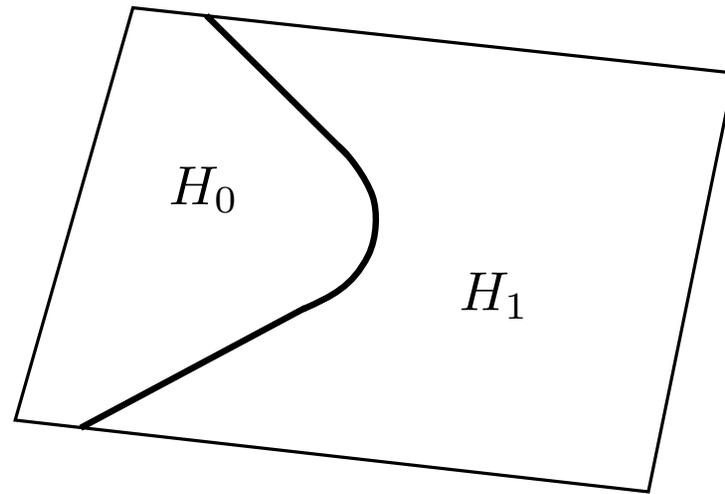
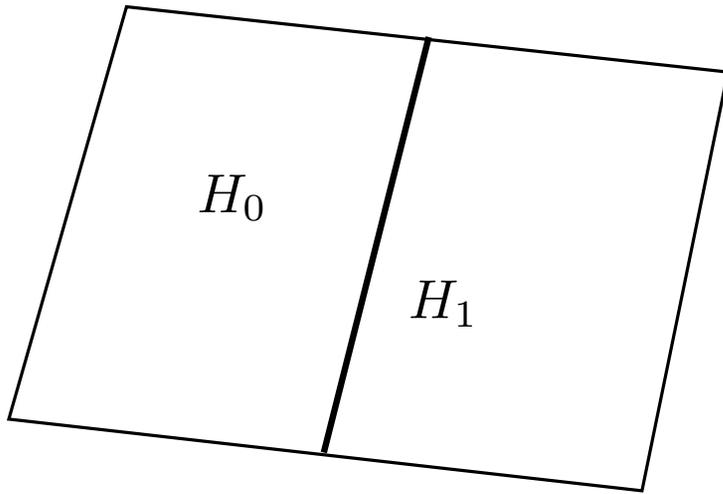


Parsimony-informative Pattern Frequency Space

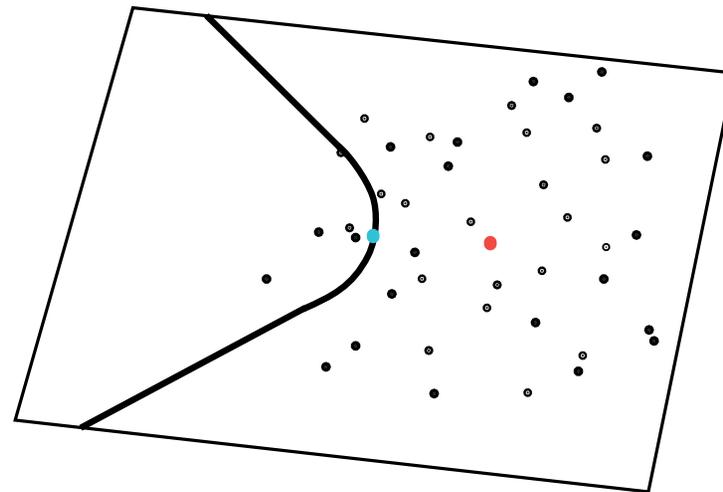
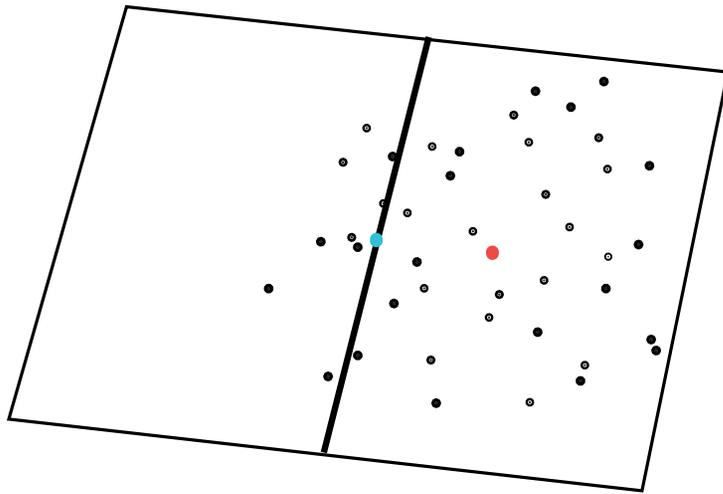
P(1100)



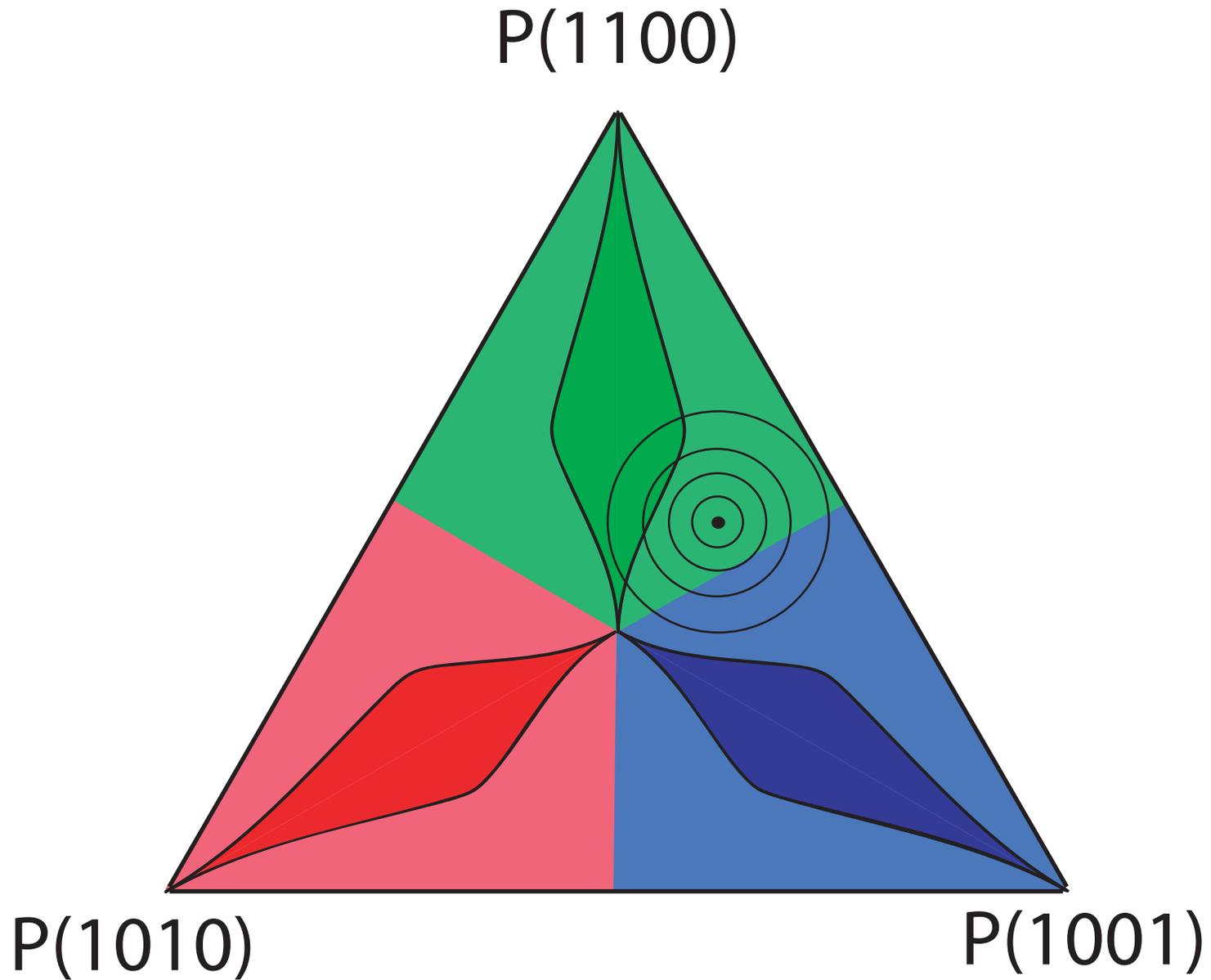
Imagine hypothesis tests of locations with different border shapes:



Similar dataset with point estimates (red dot) in H_1
Green dot is the hardest set of locations in H_0 to reject.

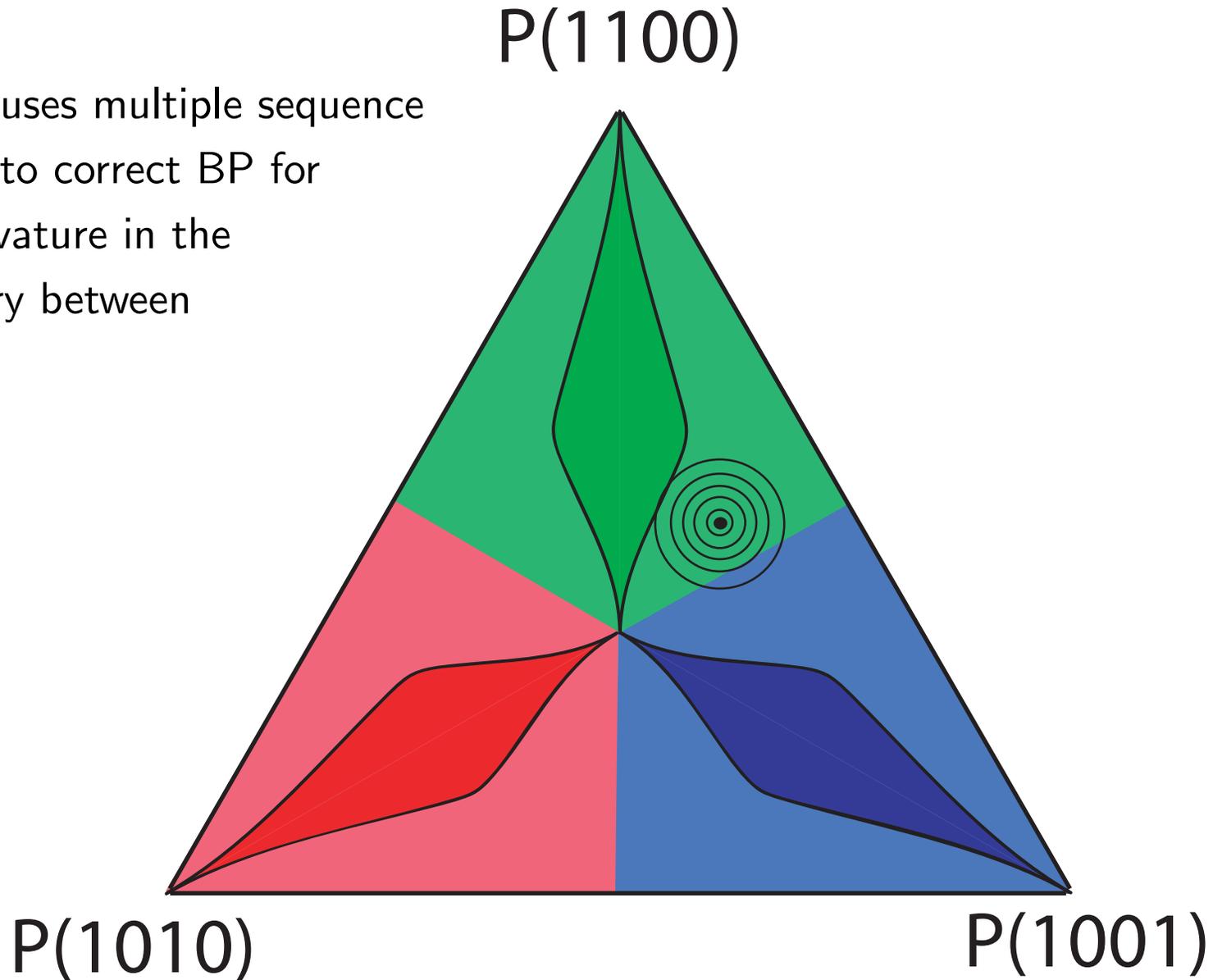


Non-parametric Bootstrapping in Pattern Frequency Space



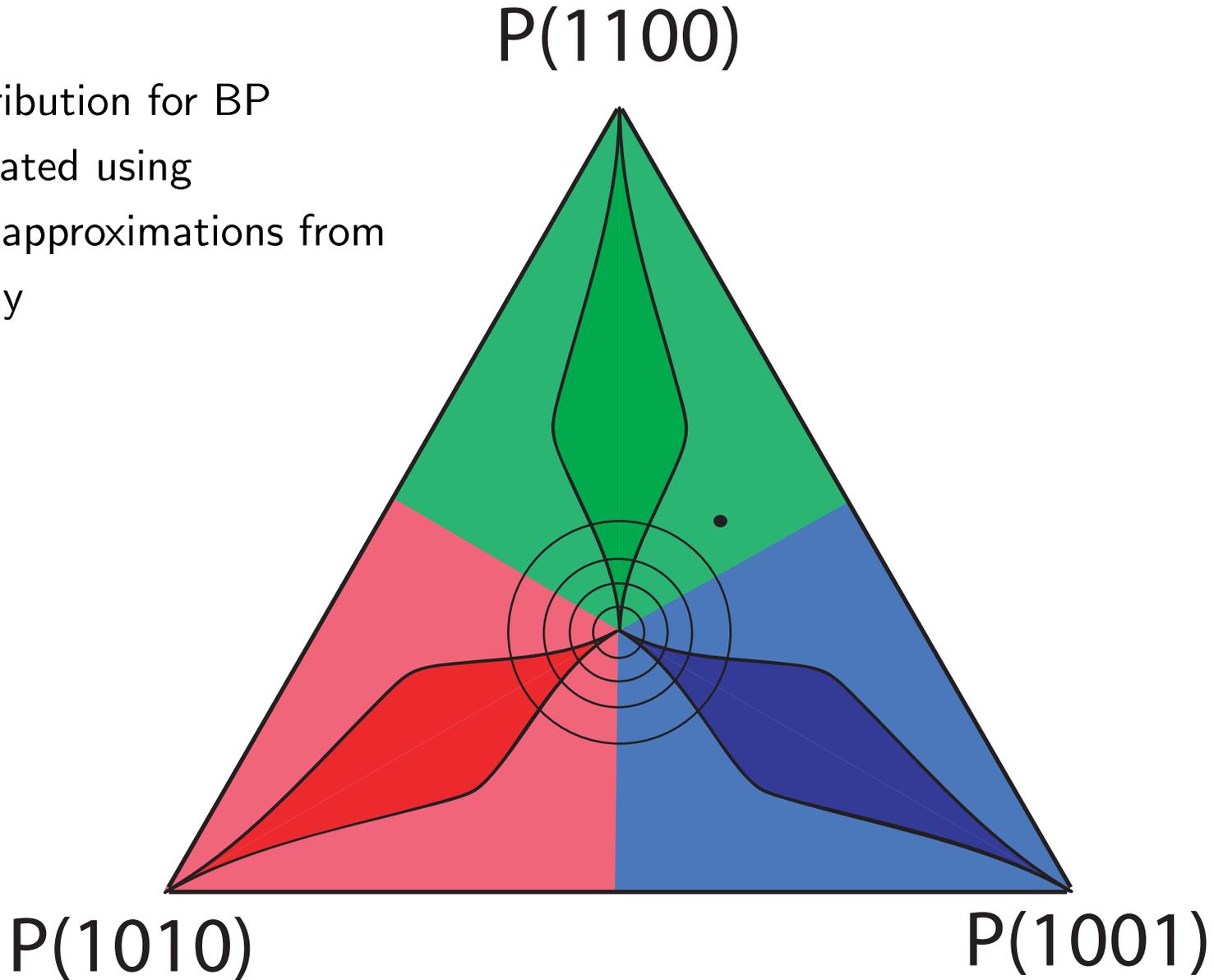
Bootstrapping in Pattern Frequency Space (if you had more data)

AU Test uses multiple sequence lengths to correct BP for any curvature in the boundary between trees



aBP in Pattern Frequency Space

Null distribution for BP
is calculated using
Normal approximations from
polytomy

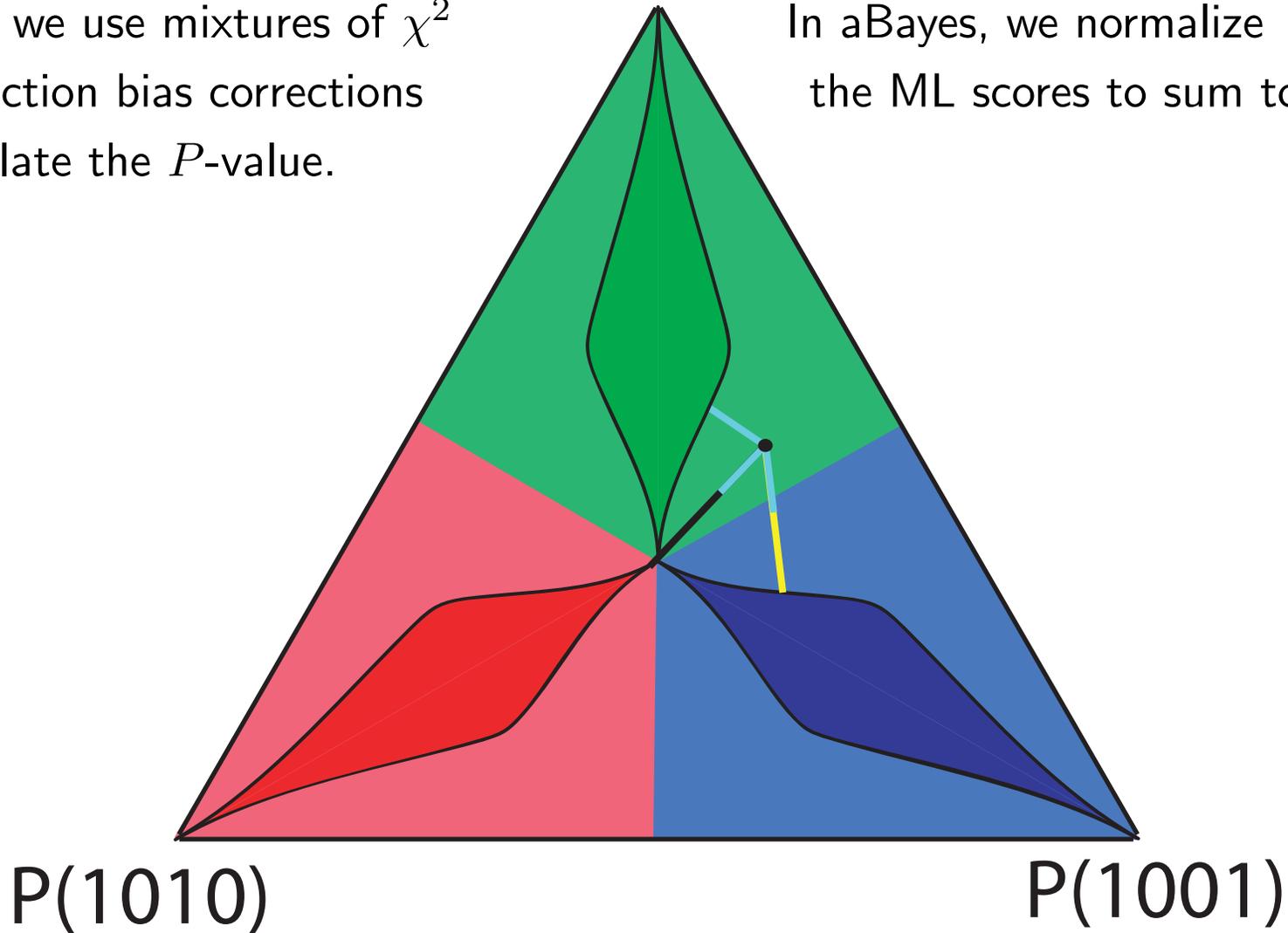


aLRT and aBayes in Pattern Frequency Space

P(1100)

In aLRT, we use mixtures of χ^2 and selection bias corrections to calculate the P -value.

In aBayes, we normalize the ML scores to sum to 1



References

Efron, B., Halloran, E., and Holmes, S. (1996). Bootstrap confidence levels for phylogenetic trees. *Proceedings of the National Academy of Science, U. S. A.*, 93:13429–13434.