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The correlation space of Gaussian latent tree models and model selection without fitting

In phylogenetics and lynguistics latent tree models are used to model evolutionary processes. Model selection procedures are employed to choose the best tree fitting the data. However, deciding if the tree hypothesis is consistent with the data is typically hard. We provide the full semialgebraic description of Gaussian latent tree models and link them to phylogenetic oranges. We then use this geometric description to propose a quick and robust way of choosing the best tree, or, of testing the tree hypothesis.

This is joint work with John Aston, Nat Shiers, and Jim Smith.