

A Flexible Bayesian Framework to Study Viral Trait Evolution

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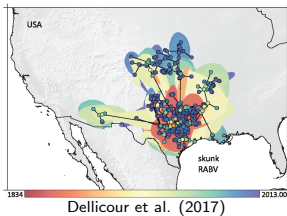
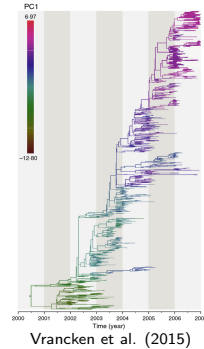
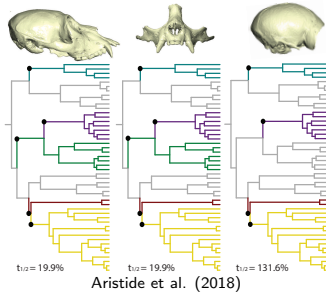
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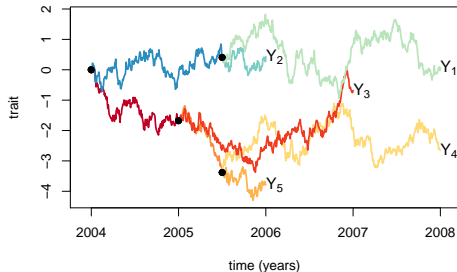
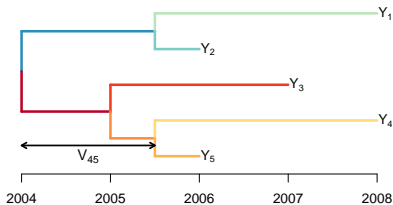
Phylogenetic Comparative Methods



- Various time scales: Myr – decade.
- Various traits: morpho, geo, viral.

Question: Trait dynamics for an evolving organism ?

BM on a Tree

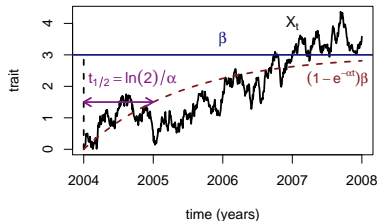


Variance: $\text{Cov}[Y_4; Y_5] = \sigma^2 \times V_{45}$ shared evolution time

Multivariate: $\text{Cov}[Y_{4k}; Y_{5l}] = R_{kl} \times V_{45}$

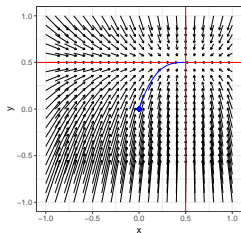
Distribution: $\mathbf{Y} \sim \mathcal{MN}(\mathbf{1}_n \boldsymbol{\mu}^T, \mathbf{V}, \mathbf{R})$ matrix normal

Multivariate OU Modeling

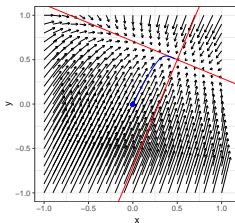


$$d\mathbf{X}_t = \mathbf{A}[\boldsymbol{\beta} - \mathbf{X}_t] dt + \boldsymbol{\Sigma} d\mathbf{B}_t$$

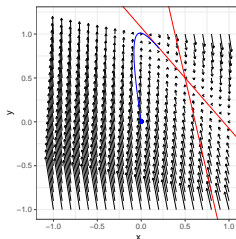
A Diagonal



Symmetric



Diagonalizable in \mathbb{R}



Distribution on a Tree: Still Gaussian. No nice Kronecker product.

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Sampling in constrained space

- Variance \mathbf{R} , selection strength \mathbf{A} .

Likelihood Computation

- One post-order traversal of the tree.

Gradient Computation: HMC

- One pre-order traversal of the tree.