Phylogenetic Gaussian processes for the Ancestral Reconstruction of Bat Echolocation Calls

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Acknowledgements





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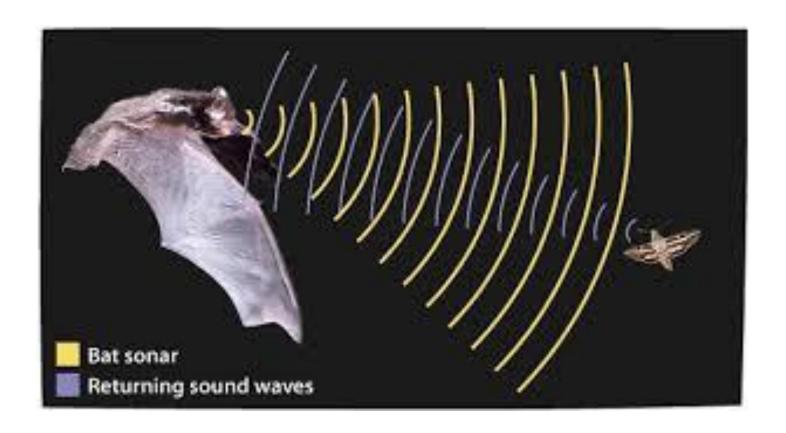


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Bats: Some Background



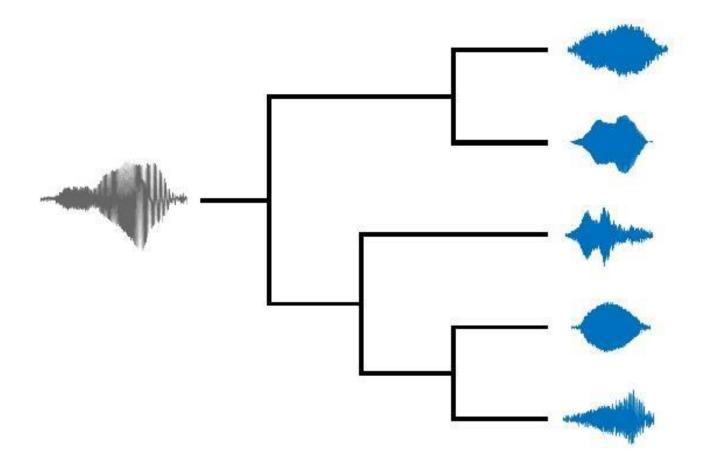
Bats: Engaging the Public



Bats: Non-invasive Monitoring



Research Project Summary

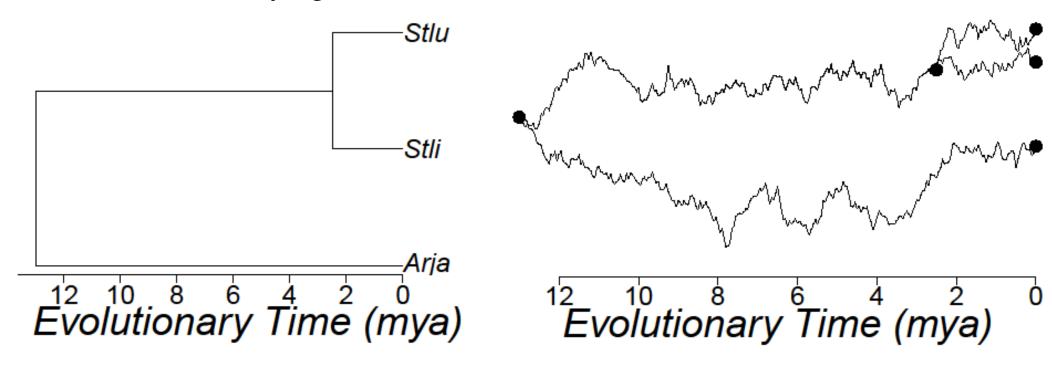


Ancestral Reconstruction: A Definition

The extrapolation back in time from measured characteristics of individuals (or populations) to their common ancestors.

Continuous Character Trait Evolution

Phylogenetic Ornstein-Uhlenbeck Process



Function-Valued Traits: A Definition

A trait that is repeatedly measured, along some continuous scale, where measurements can represent points on a curve, and both means and covariances along the trajectory can change, gradually and continually.

Gaussian Processes

A collection of random variables, any finite number of which have a joint Gaussian distribution.

$$f(\mathbf{x}) \sim \mathcal{GP}(m(\mathbf{x}), k(\mathbf{x}, \mathbf{x}'))$$

$$m(\mathbf{x}) = \mathbf{E}(f(\mathbf{x}))$$

$$k(\mathbf{x}, \mathbf{x}') = \text{cov}(\mathbf{x}, \mathbf{x}')$$

$$\mathbf{x} \in \mathbf{R}^p$$

Phylogenetic Gaussian Processes: Assumptions

- 1. Conditional on their common ancestors in the phylogenetic tree T any two traits are statistically independent.
- 2. The statistical relationship between a trait and any of its descendants in T is independent of the topology of T
- 3. The marginal GP along each branch of the phylogeny is space-time separable.

$$\Sigma((f,t),(f',t')) = K(f,f')k(t,t')$$

Phylogenetic Gaussian Processes: Theoretical Result

For a phylogenetic Gaussian Process Y with time-space separable covariance function, when K is a degenerate Mercer kernel, there exists a set of n deterministic basis functions $\phi_i: F \to \mathbf{R}$ and univariate GPs X_i for $i=1,\ldots,n$ such that

$$g(f, \mathbf{t}) = \sum_{i=1}^{n} \phi_i(f) X_i(\mathbf{t})$$

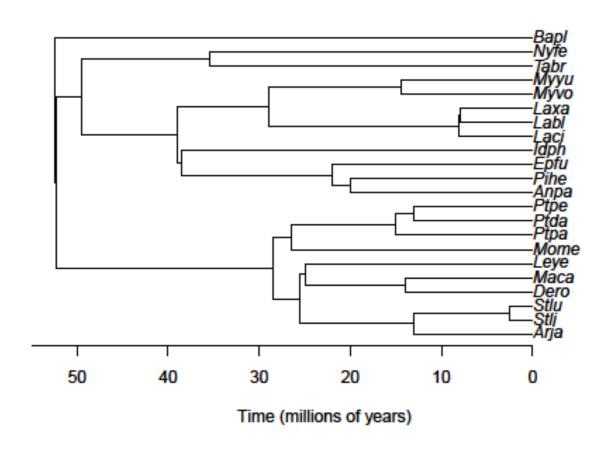
has the same distribution as Y. The full phylogenetic covariance function of this phylogenetic GP is

$$\Sigma_{\mathbf{T}}((f, \mathbf{t}), (f', \mathbf{t}')) = \sum_{i=1}^{n} k_{\mathbf{T}}^{i}(\mathbf{t}, \mathbf{t}') \phi_{i}(f) \phi_{i}(f'),$$

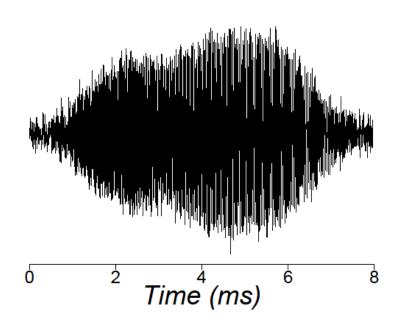
where $\int \phi_i(f)\phi_j(f)df = \delta_{ij}$, δ being the Kronecker delta, and so the phylogenetic covariance function depends only on $\mathbf{t}, \mathbf{t}' \in \mathbf{T}$.

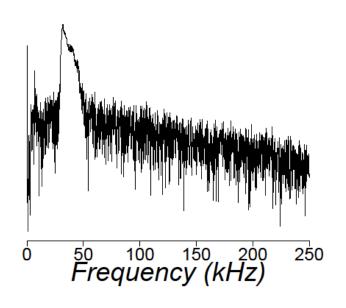
Bat Echolocation Calls: The Phylogenetic Tree

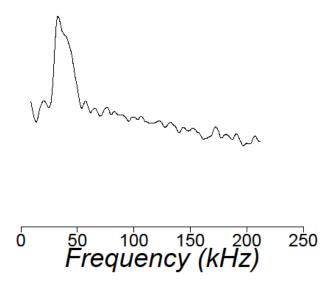
Mexican Bat Phylogeny



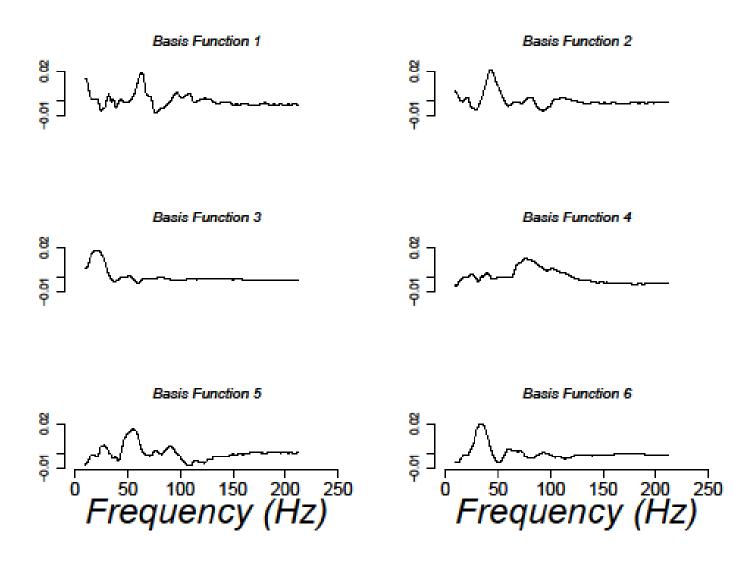
Bat Echolocation Calls: A Function-Valued Trait







Bat Echolocation Calls: Independent Basis



Results: Phylogenetic Ornstein-Uhlenbeck Process

$$k_{\mathbf{T}}^{i}(\mathbf{t}, \mathbf{t}') = (\sigma_{p}^{i})^{2} \exp\left(\frac{-d_{\mathbf{T}}(\mathbf{t}, \mathbf{t}')}{\ell^{i}}\right) + (\sigma_{n}^{i})^{2} \delta_{\mathbf{t}, \mathbf{t}'}$$

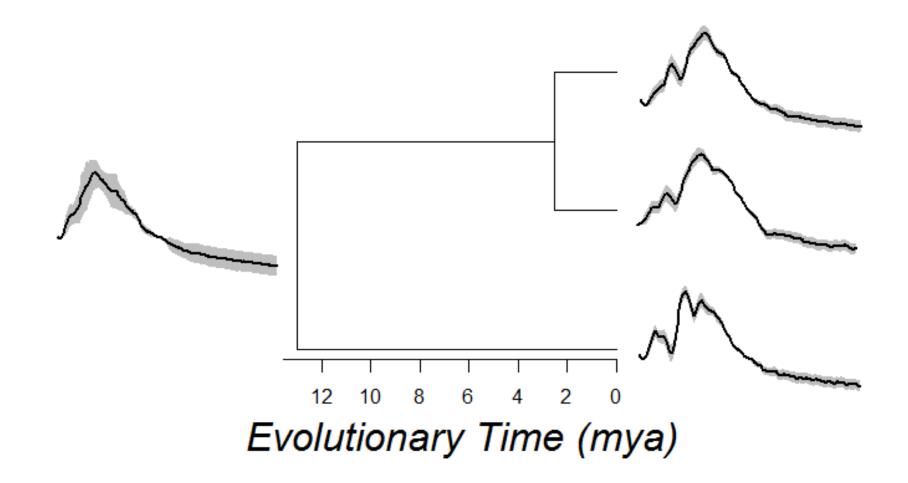
Results: Hyperparameter Estimates

Basis	$\hat{\sigma}_p$	$\widehat{\ell}$	$\hat{\sigma}_n$
1	2.30 (0.11)	12.27 (4.18)	1.18 (0.11)
2	3.17(0.11)	27.63 (3.70)	1.26 (0.13)
3	4.05 (0.32)	70.50 (20.31)	1.19(0.12)
4	3.32(0.17)	22.86 (8.95)	1.96 (0.19)
5	3.00 (0.13)	26.93 (2.85)	1.21 (0.11)
6	3.70 (0.14)	12.82 (4.52)	1.28 (0.15)

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Results: Posterior Predictive Distributions



Conclusions

- Phylogenetic Signal Identified
- Strong Phylogenetic signal at low frequencies.

Future Work

- Implement the Phylogenetic Gaussian Process Regression Model for Echolocation Call Spectrograms.
- Consider Alternative Echolocation Call Representations.
- Consider Alternative models for the evolutionary dynamics.

