Tests of Phylogenetic Signal on Networks

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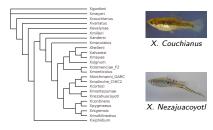








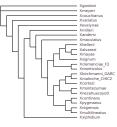
Introduction: Phylogenetic "Networks"



Phylogenetic Tree

Network: Solís-Lemus and Ané (2016)

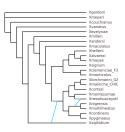
Introduction: Phylogenetic "Networks"



Phylogenetic Tree

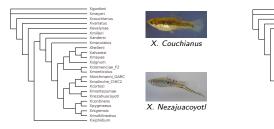


X. Nezajuacoyotl



Phylogenetic "Network"

Introduction: Phylogenetic "Networks"



Phylogenetic "Network"

Question: Can we see the effects of ancestral hybridization on the trait measured for present-day species ?

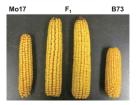
Network: Solís-Lemus and Ané (2016)

Phylogenetic Tree

Images: Xiphophorus Genetic Stock Center, Texas State University

Xclemenciae F2

Introduction: Heterosis



Heterosis: hybrid vigor

Image: Springer and Stupar (2007)

Introduction: Heterosis



Heterosis: hybrid vigor

Question: Can we see the effects of ancestral heterosis on the trait measured for present-day species ?

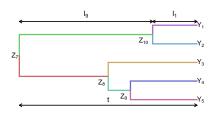
Image: Springer and Stupar (2007)

Outline

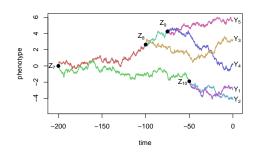
- 1 Trait Evolution on Networks
- 2 Tests of Phylogenetic Signal
- 3 Implementation and Example

Stochastic Process on a Tree

(Felsenstein, 1985)



The tree is known.
Only *tip* values are observed

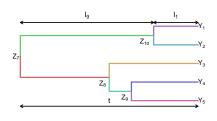


Brownian Motion:

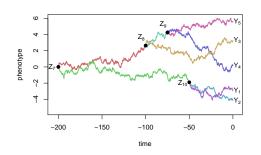
$$\mathbb{V}$$
ar $[Y_1] = \sigma^2 t = \sigma^2 (\ell_9 + \ell_1)$ \mathbb{C} ov $[Y_1; Y_2] = \sigma^2 \ell_9$

Stochastic Process on a Tree

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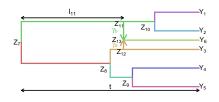


Brownian Motion:

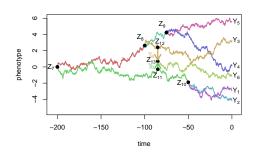
$$V_{ij}^{ ext{tree}} = \sum_{e \in p_i \cap p_i} \ell_e$$

Sum over shared edges. p_i : path from root to tip i

Stochastic Process on a Network



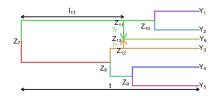
The *network* is known.
Only *tip* values are observed



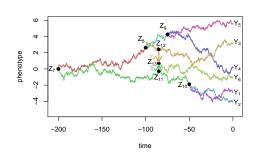
 $Z_{13} = \gamma_a Z_{12} + \gamma_b Z_{11}$ $\gamma_a + \gamma_b = 1$

Hybrid:

Stochastic Process on a Network



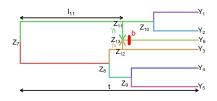
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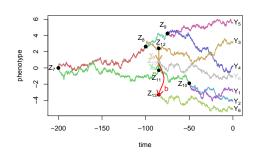
Hybrid:

$$V^{\mathsf{net}}_{ij} = \sum_{\substack{p_i \in \mathcal{P}_i \\ p_j \in \mathcal{P}_j}} \Big(\prod_{e \in p_i} \gamma_e \Big) \Big(\prod_{e \in p_j} \gamma_e \Big) \sum_{e \in p_i \cap p_j} \ell$$

Heterosis



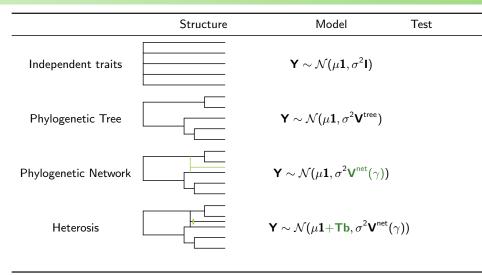
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Only *tip* values are observed

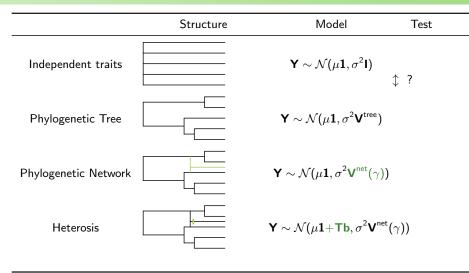


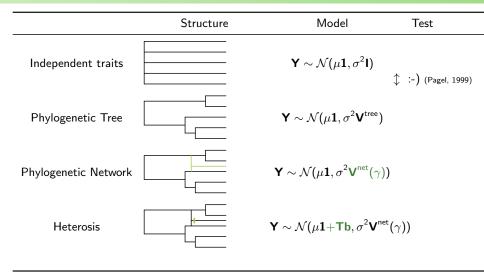
Hybrid:

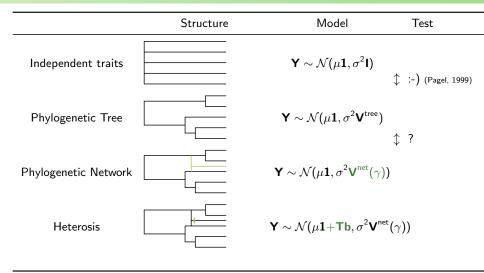
$$Z_{13} = \gamma_a Z_{12} + \gamma_b Z_{11} + b$$

b: Heterosis.

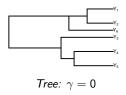


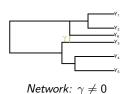






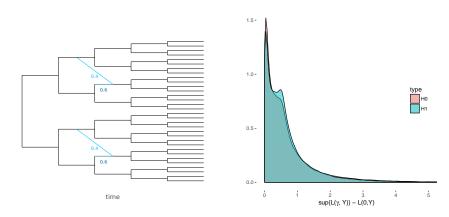
Tree vs Network



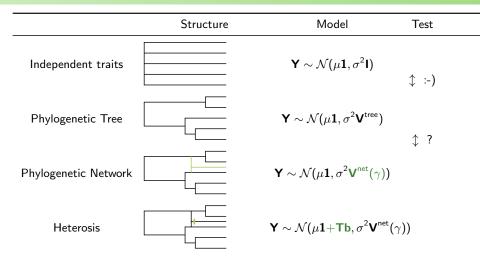


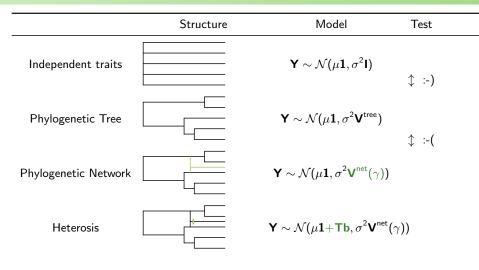
LRT:
$$T = 2 \left(\sup_{\gamma \neq 0} \{ L(\gamma, Y) \} - L(0, Y) \right)$$

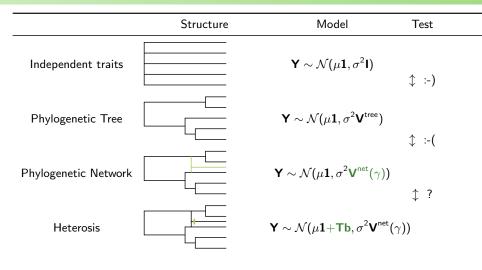
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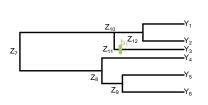
Empirical Distribution, 100000 simulations.







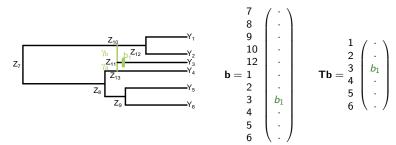
Linear Regression Model



$$\mathbf{Tb} = \frac{1}{2} \begin{pmatrix} \cdot \\ \cdot \\ \cdot \\ b_1 \\ \cdot \\ \cdot \\ \cdot \\ \cdot \end{pmatrix}$$

Model:
$$Y = \mu \mathbf{1} + \mathsf{Tb} + E^{\mathsf{tree}}$$

Linear Regression Model



Model: $Y = \mu \mathbf{1} + \mathbf{Tb} + E^{\text{net}}$

Heterosis: Testing Effect

Model:

$$\mathbf{Y} = \mu \mathbf{1} + \mathbf{T} \mathbf{b} + \sigma^2 \mathbf{E}$$
 , $\mathbf{E} \sim \mathcal{N}(\mathbf{0}, \mathbf{V})$

Tests: \mathcal{H}_0 : No heterosis

 \mathcal{H}_1 : Heterosis with one single effect

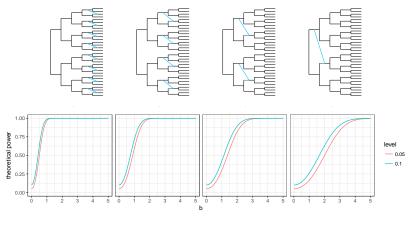
 \mathcal{H}_2 : Heterosis with heterogeneous effects

Stats.:

$$F_{10} \sim \mathcal{F}\left(1, n-2, \Delta_{10}(b, \sigma^2)\right)$$

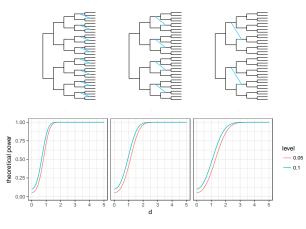
 $F_{21} \sim \mathcal{F}\left(h-1, n-h-1, \Delta_{21}(\mathbf{b}, \sigma^2)\right)$

Heterosis: Single Effect

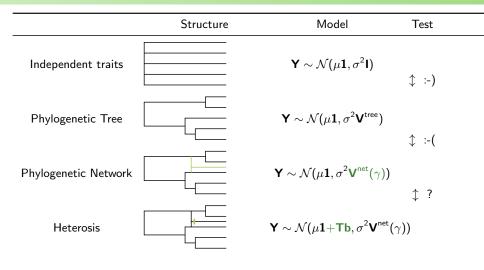


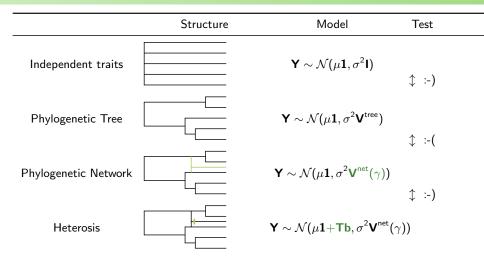
Detection Power ($\sigma^2 = 1$)

Heterosis: Several Effects



Detection Power ($\sigma^2 = 1$)



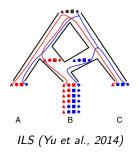


Phylogenetic Networks

- Inference is hard Kubatko (2009); Yu et al. (2012, 2014);
 Solís-Lemus and Ané (2016).
- Main issue: deal with Incomplete Lineage Sorting (ILS).
- ullet State of the art methods: up to \sim 15 taxa, with \sim 3 hybrids.
- → Need fast algorithms, and fast implementation

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julia package PhyloNetworks

julia

- "Julia is a high-level, high-performance dynamic programming language for numerical computing."
- "Julia use expanded dramatically in 2016, and 2017 is shaping up to be the year that Julia expands from early adopters into the mainstream."
- (source: julia website...)

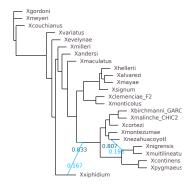
PhyloNetworks

- Inference of phylogenetic networks
- Interactive study of networks

Xiphophorus Fish Dataset

```
using PhyloNetworks

net = readTopology(fish)
plot(net, useEdgeLength=true, showGamma=true)
```



No branch length

Conclusion and Perspectives

A general inference framework for trait evolution on networks.

Conclusions

- BM model of evolution on networks
- Tests of hybridization / heterosis
- Phylogenetic regression

julia package

- Available on GitHub
- From network inference to trait evolution

Perspectives

- Getting a network
- Ornstein-Uhlenbeck
- Shifts detection

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Photo Credits:

- Xiphophorus Genetic Stock Center, Texas State University,

http://www.xiphophorus.txstate.edu/resources/galleries/comprehensive.html

Thank you for listening



Image: Hergé (1958)



Appendices