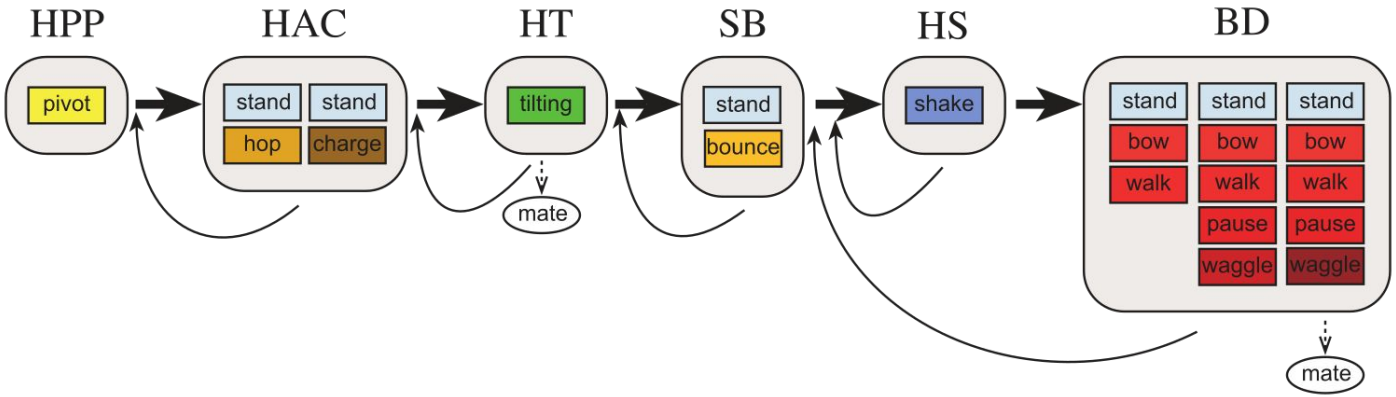
Comparative analyses of phenotypic sequences: a case study using cricket songs

Daniel Caetano and Jeremy Beaulieu
2019

UNIVERSITY OF ARKANSAS

What is a phenotypic sequence?



Biological Journal of the Linnean Society, 2008, **94**, 491–504. With 3 figures

Evolution of the courtship phenotype in the bird of paradise genus *Parotia* (Aves: Paradisaeidae): homology, phylogeny, and modularity

EDWIN SCHOLES III*
Cornell Laboratory of Ornithology, Cornell University, Ithaca, NY 14850, USA

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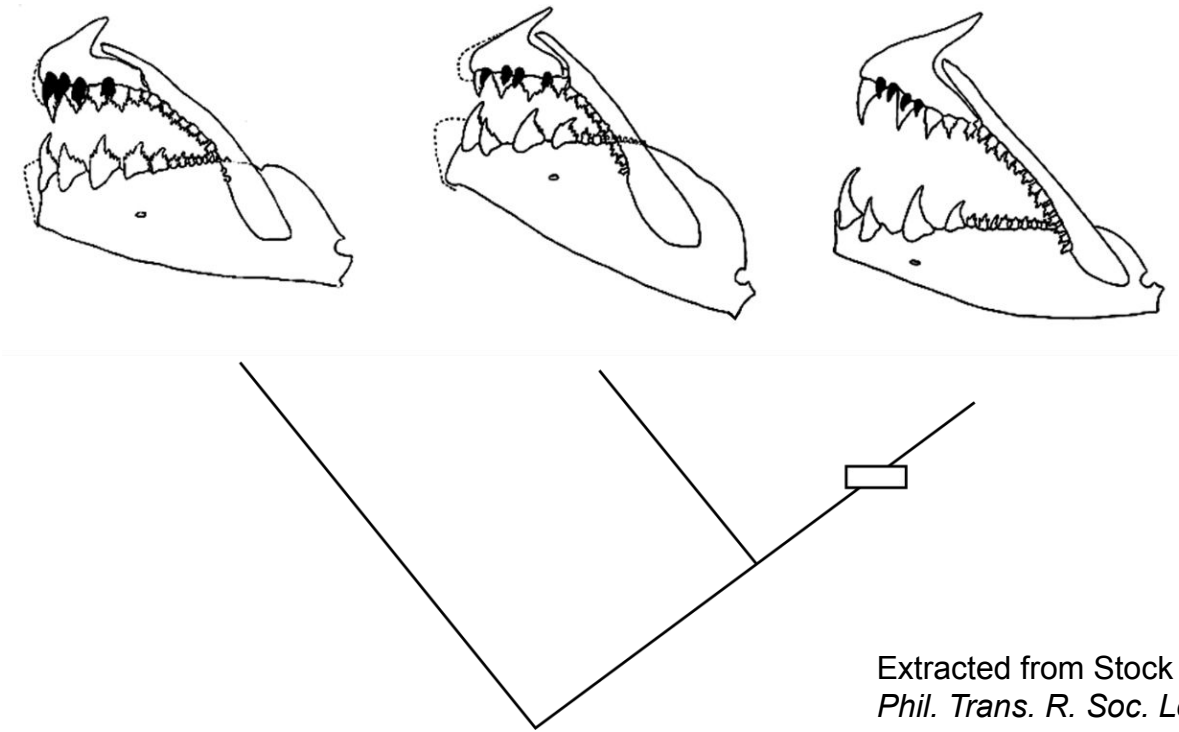
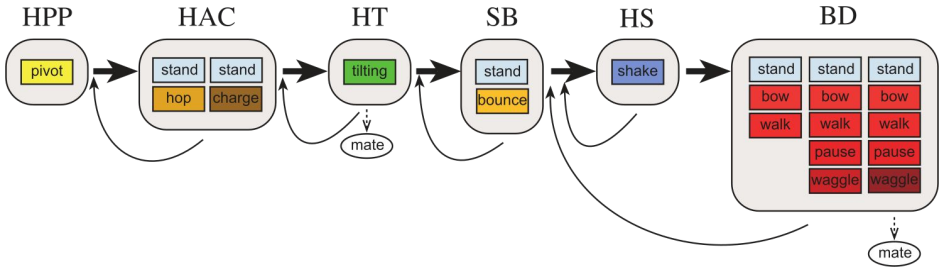
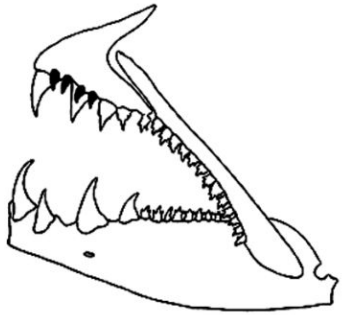


Extracted from Stock D. W. (2001)
Phil. Trans. R. Soc. Lond. B

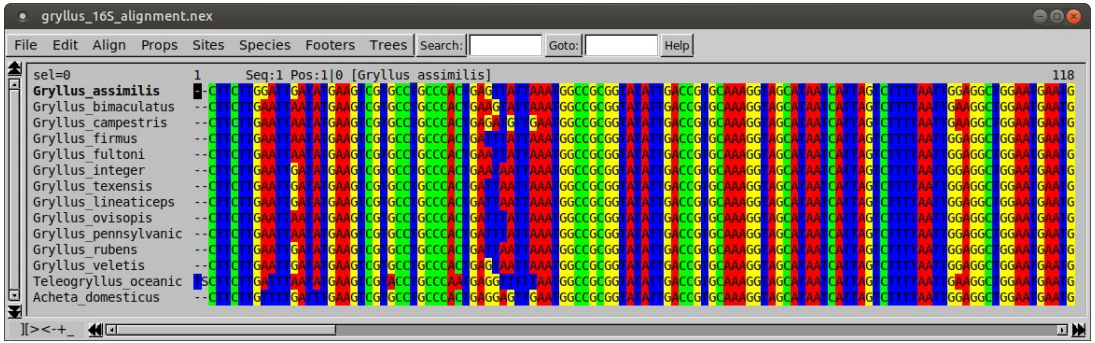
Caetano and Beaulieu caetanods1@gmail.com @ds_caetano



time sequence

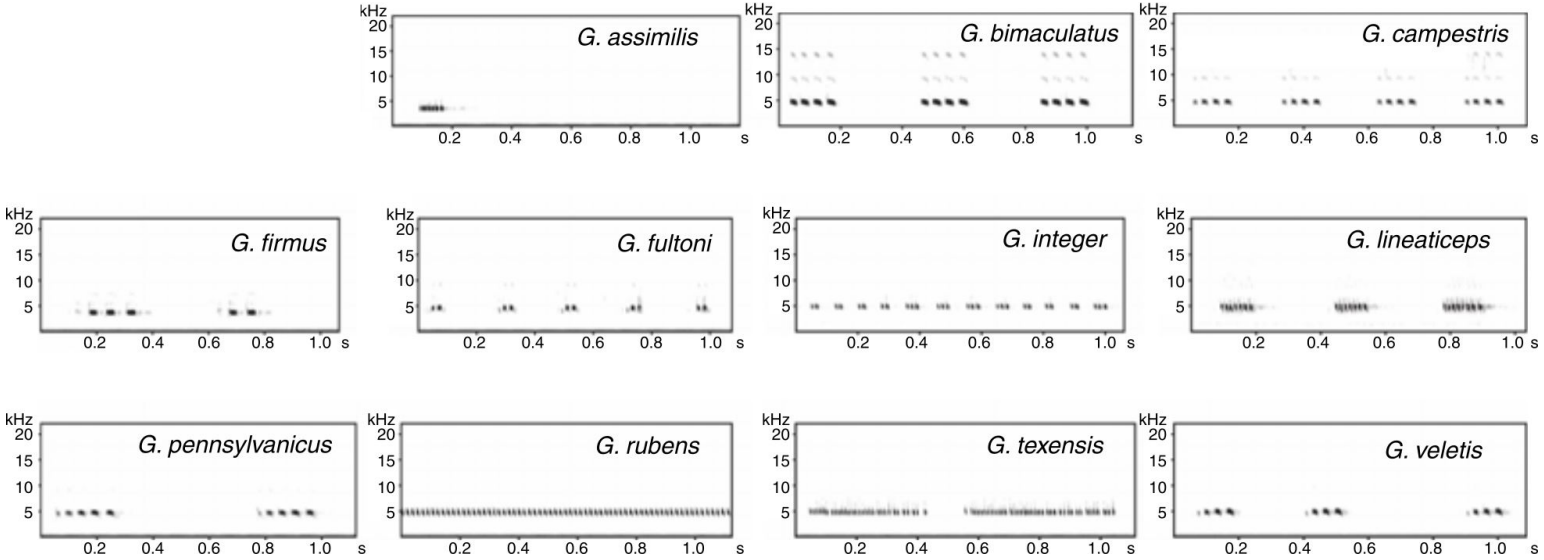


morphological position sequence



molecular sequence

Calling songs of *Gryllus* crickets (data from Robillard et al. 2006 *Cladistics*)



Questions

How rates of evolution vary along the sequence trait?

Are rates autocorrelated?

Do silent and chirp regions show similar rates of evolution?

Methods

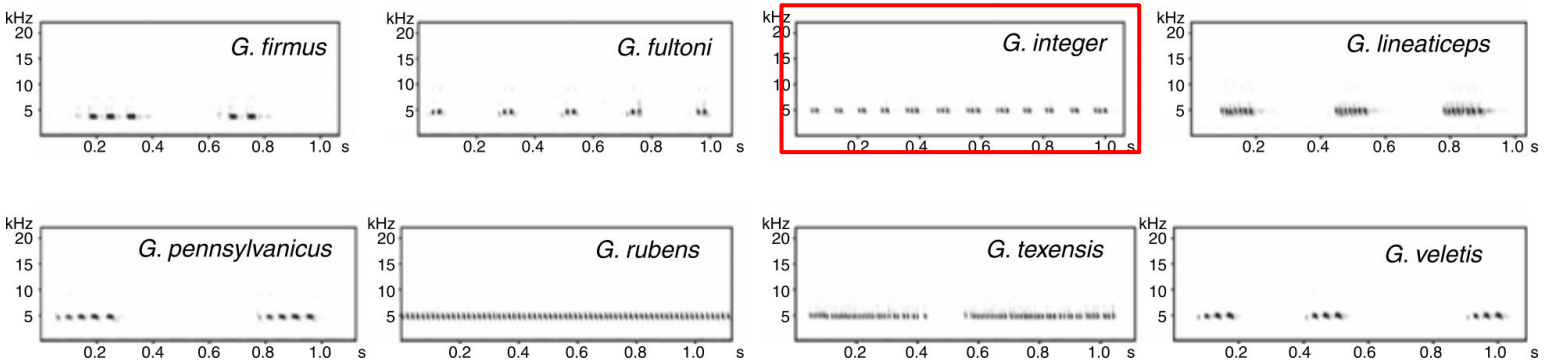
Estimate phylogeny **using molecular data**.

Estimate sequence alignment **conditioned on the phylogeny**.

Estimate rates of evolution along the sequence positions.

Contrast independent rates with autocorrelated rates.

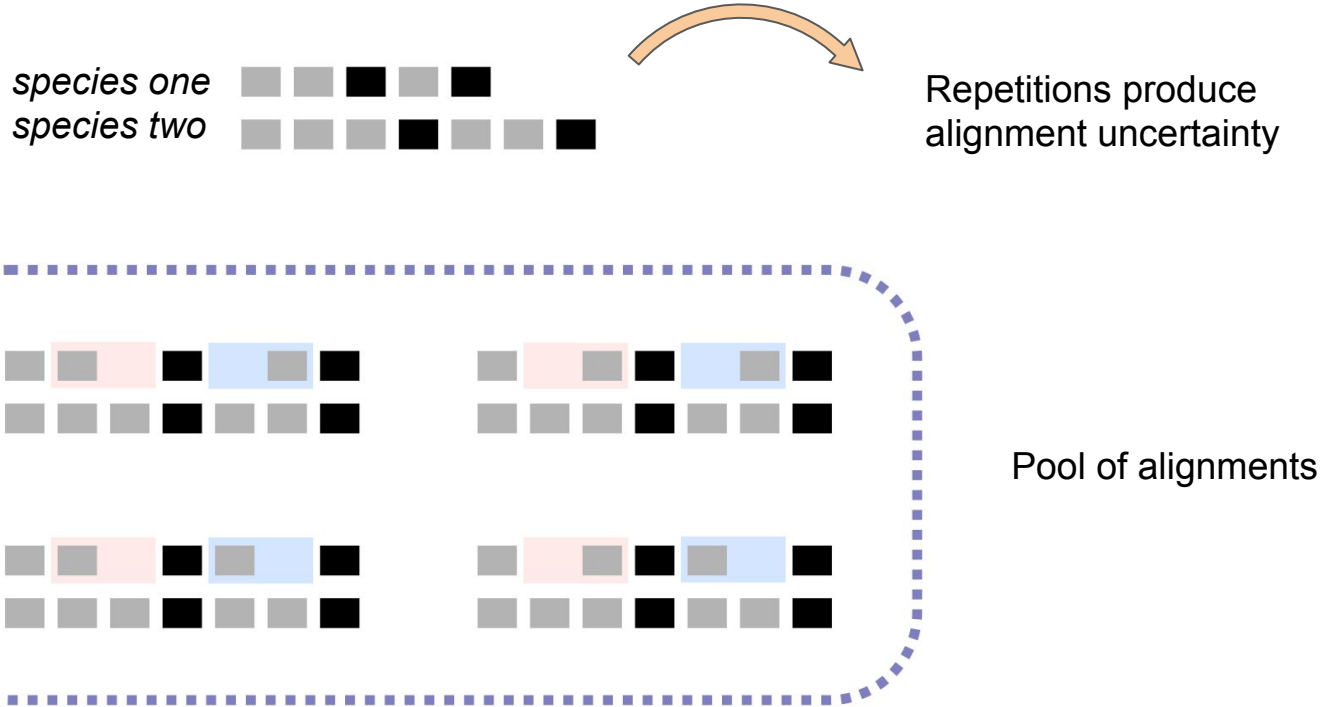
Calling songs of *Gryllus* crickets (data from Robillard et al. 2006 *Cladistics*)

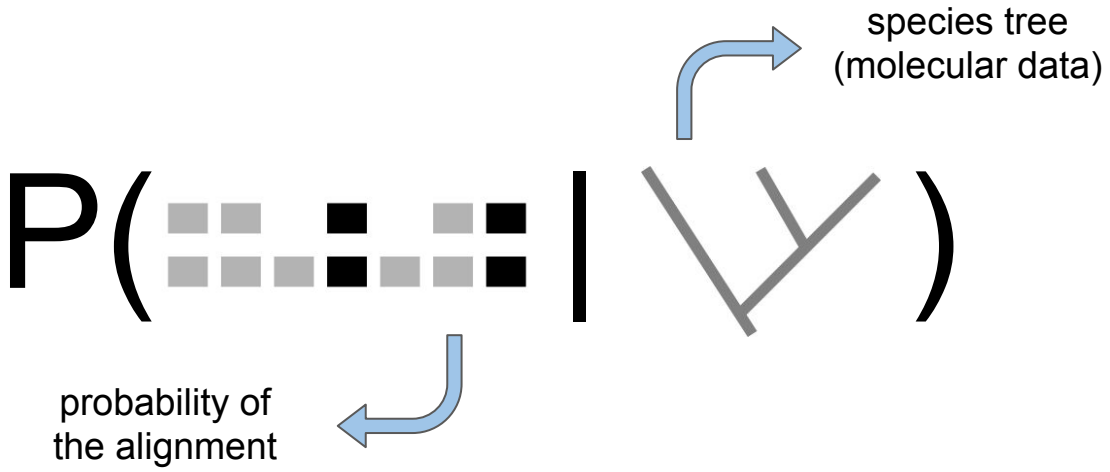


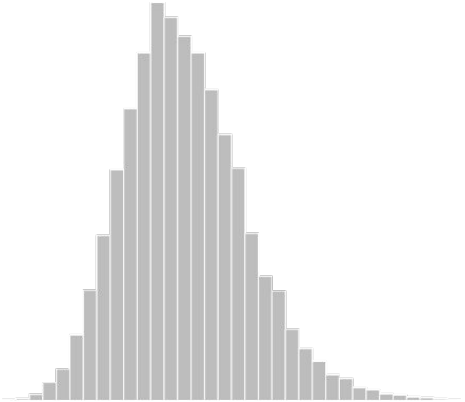
interchirp silence chirp (sound) unknown state

G. integer

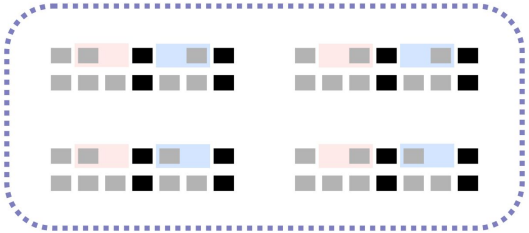
Alignment of non-molecular sequences







posterior distribution
of alignments



BAli---Phy

Suchard and Redelings (2006)

Distance-based alignment with custom distance matrices

MAFFT

Katoh and Standley (2013)

MAFFT version 7

Multiple alignment program for amino acid or nucleotide sequences

This feature is supported in versions ≥7.120.

Non-biological sequences

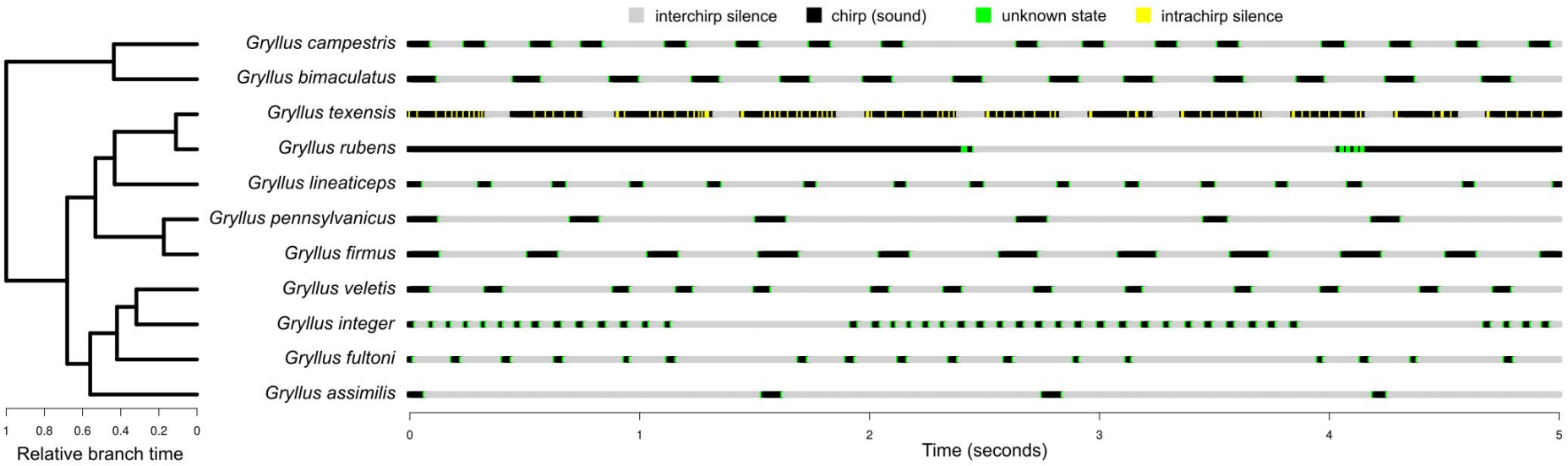
Non-biological sequences, or texts consisting of printable characters, can be aligned in the **--text** mode.

Input:

```
> text 1
2008~KATO~Toh
> text 2
2005~Katoh~Kuma~MIYATA~Toh
```

- Most printable characters, except for =<>, are accepted in the input sequences.
- Minus (-) is used to represent a gap in the output. If the input data has -s, they are removed.
- Spaces in the input data are also removed. They have to be converted to another symbol (~ in the

Calling songs of *Gryllus* crickets (data from Robillard et al. 2006 *Cladistics*)



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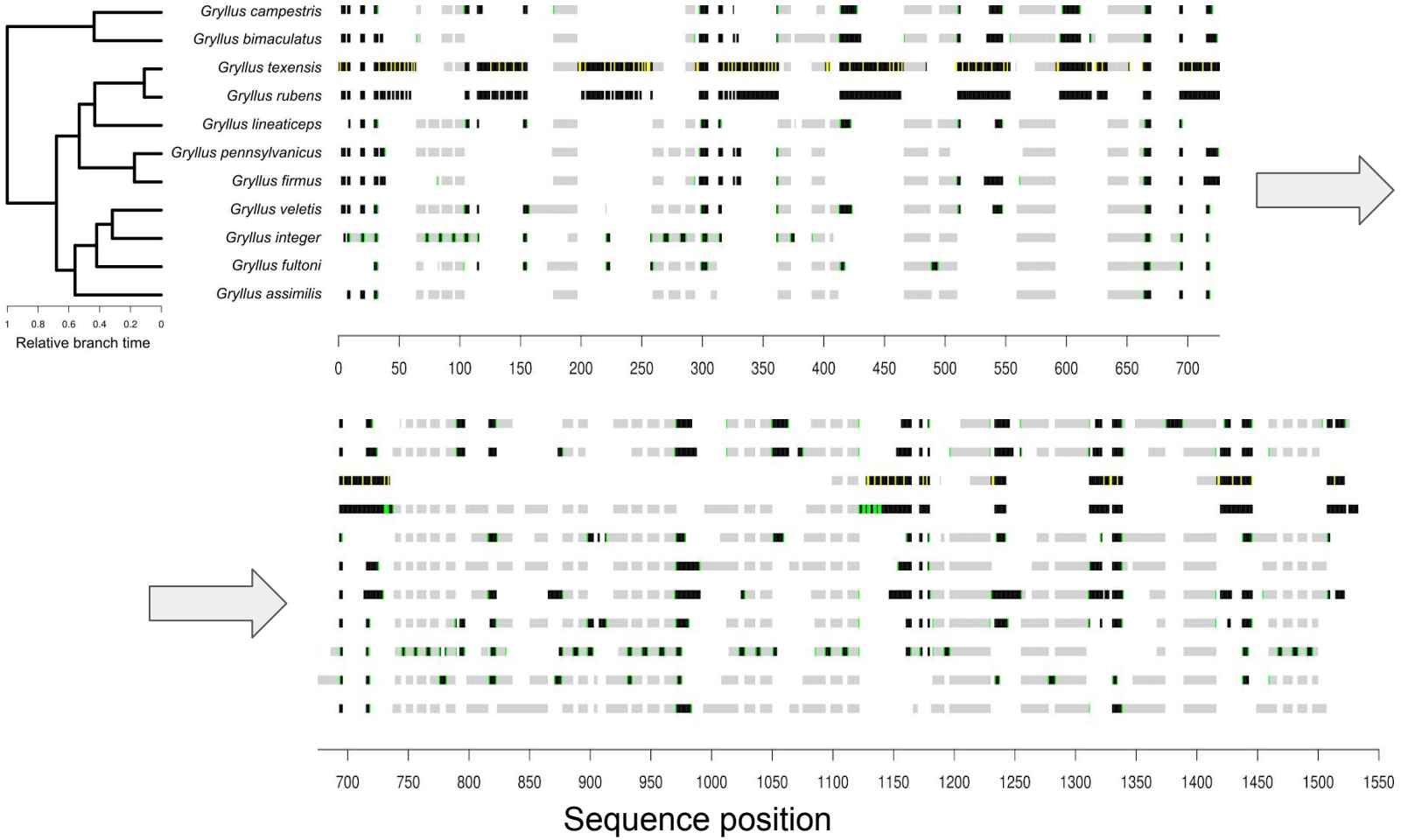

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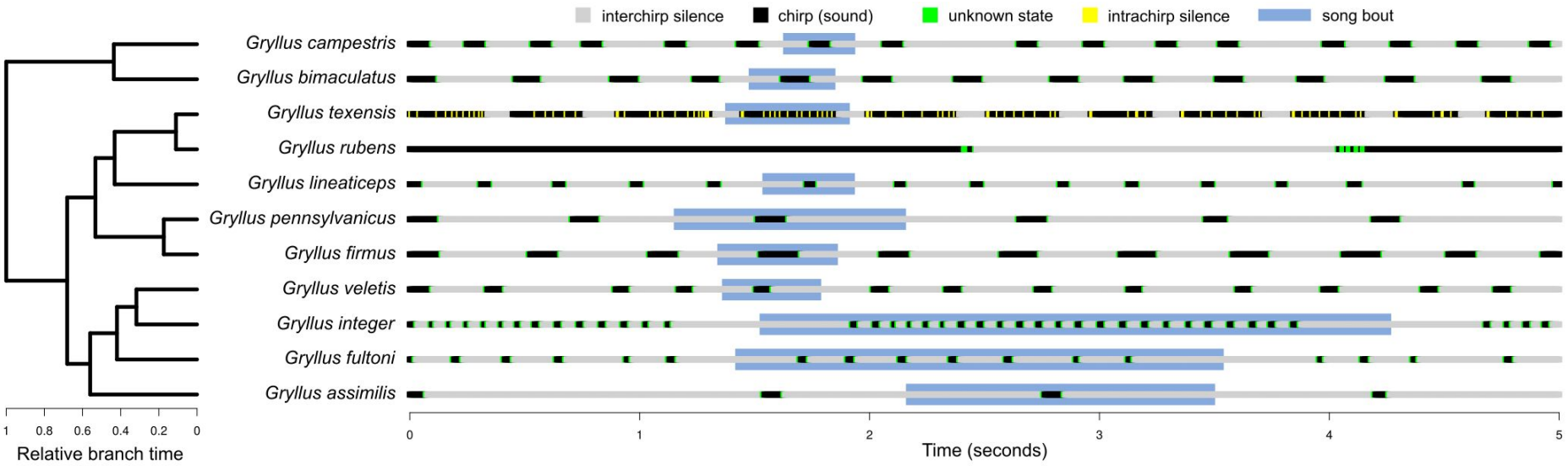
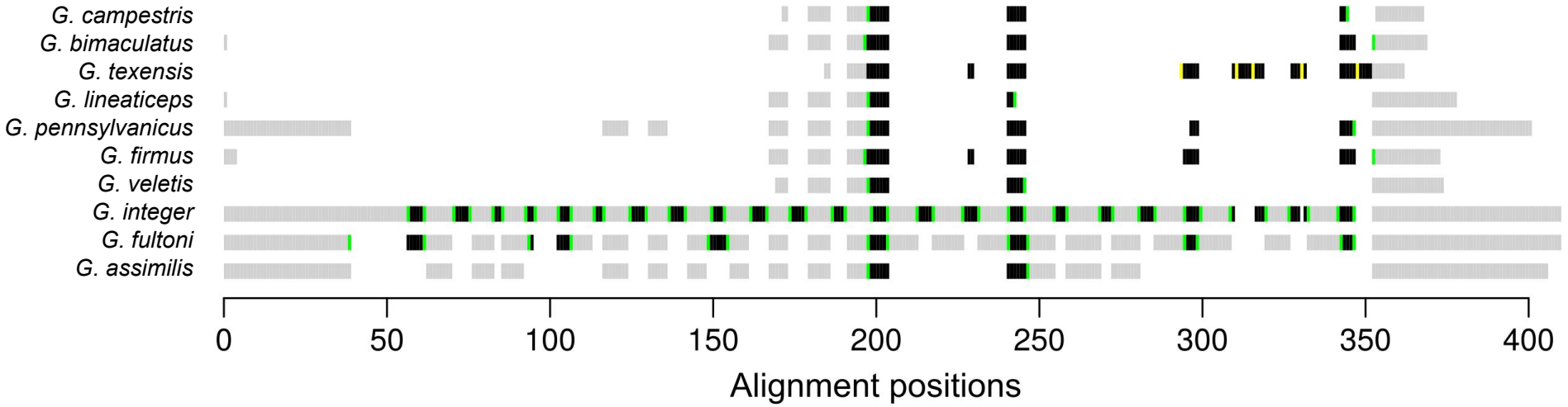


Alignment of song bout sequences



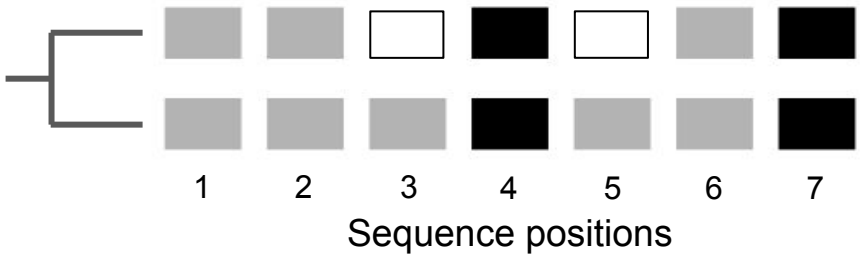
The model

The model

gap state (loss of trait)

sound (chirp)

silence



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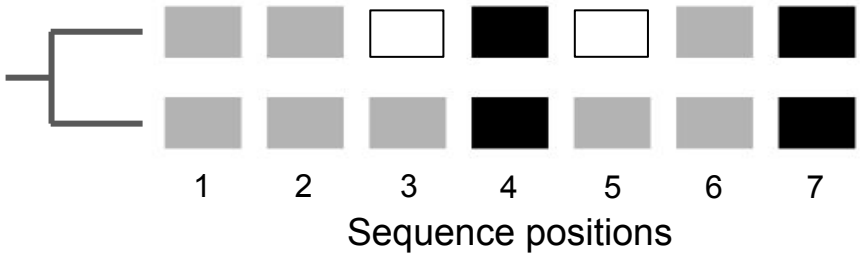
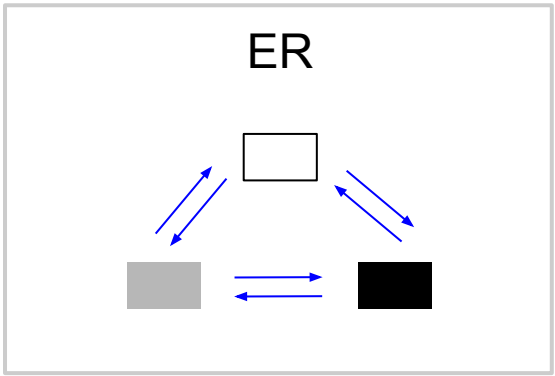
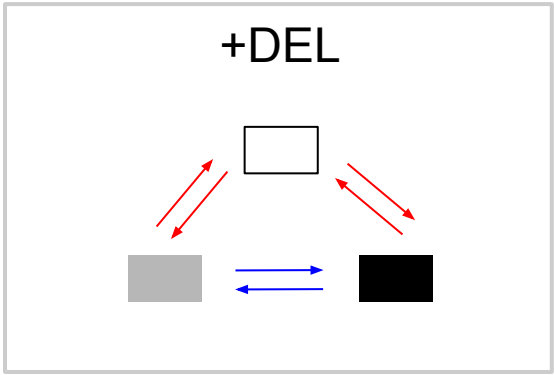
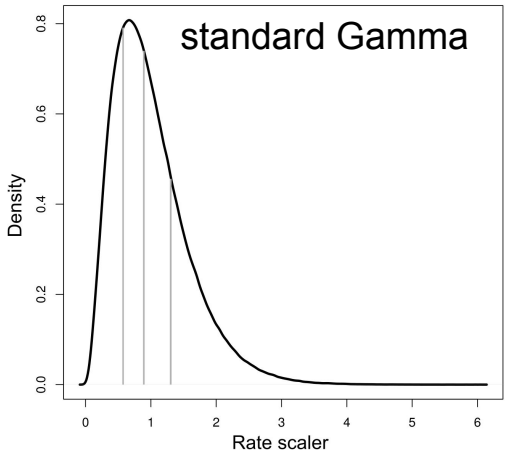
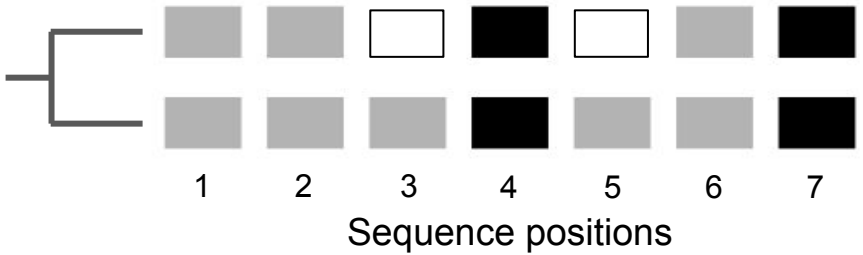


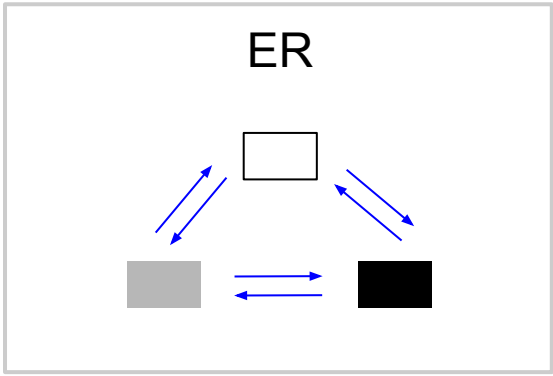


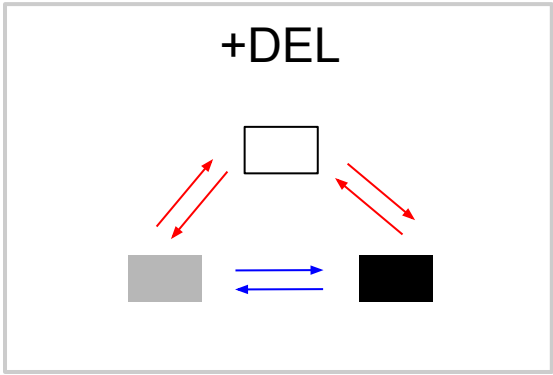


The model

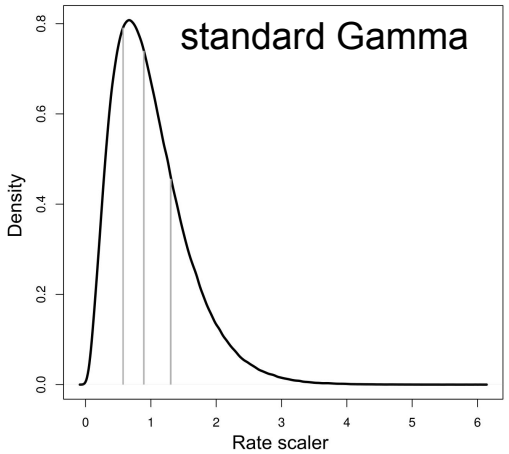

standard Gamma
Density
0.0
0.2
0.4
0.6
0.8
0
1
2
3
4
5
6
Rate scaler


1
2
3
4
5
6
7
Sequence positions


ER

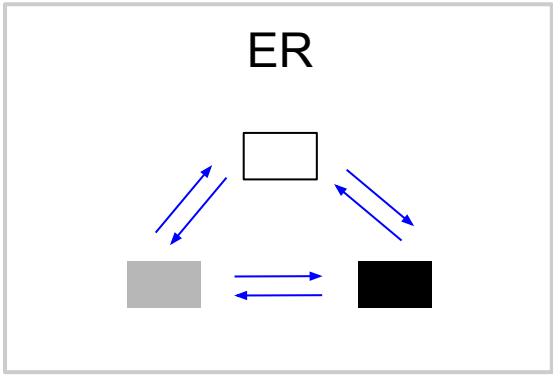

+DEL

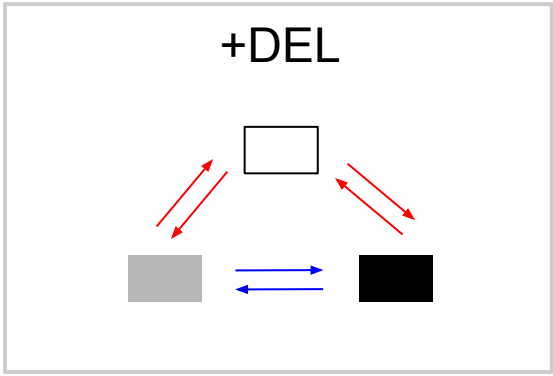
The model

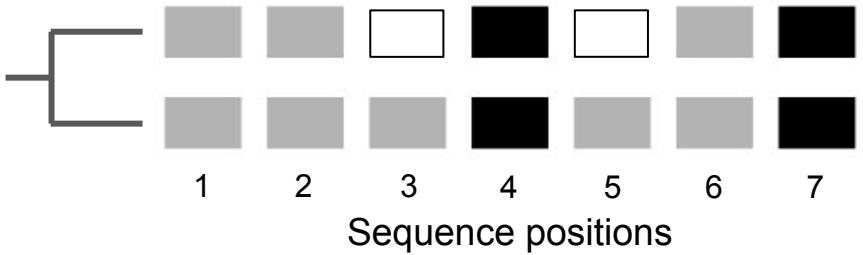


$r \cdot Q$

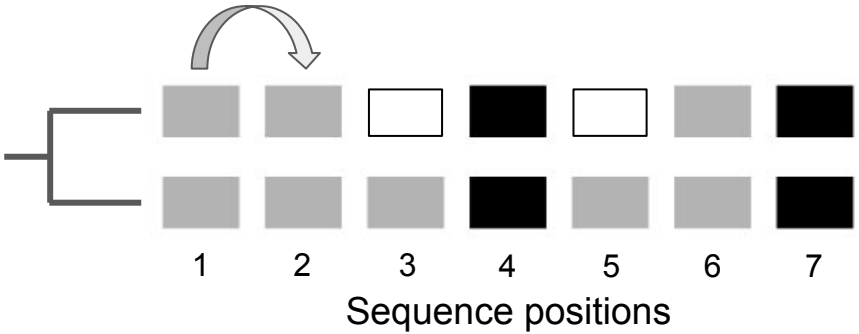
Yang (1994)







Including autocorrelation of rates



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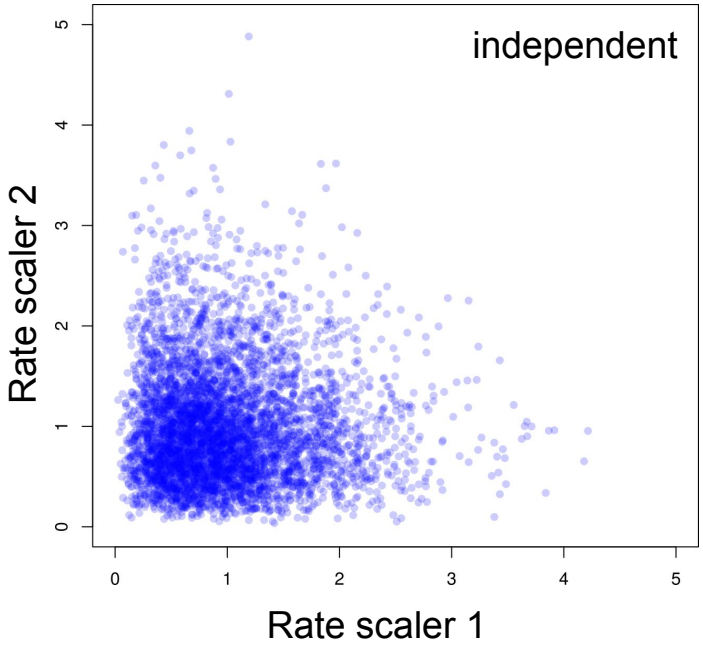
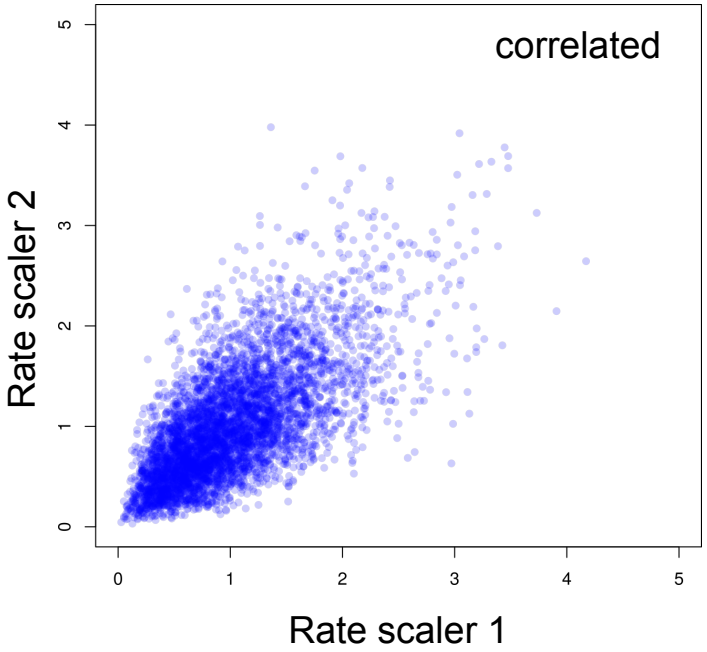
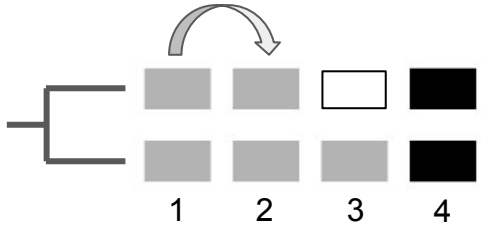
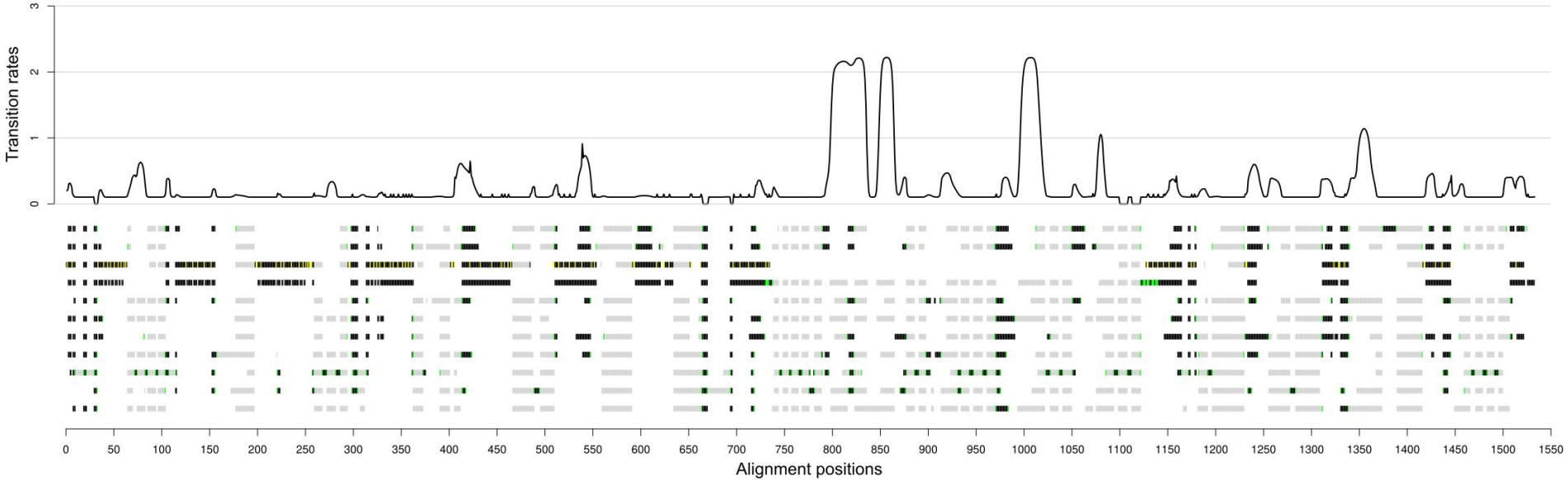






Yang 1995 - *Genetics*

Evolution of temporal pattern is autocorrelated



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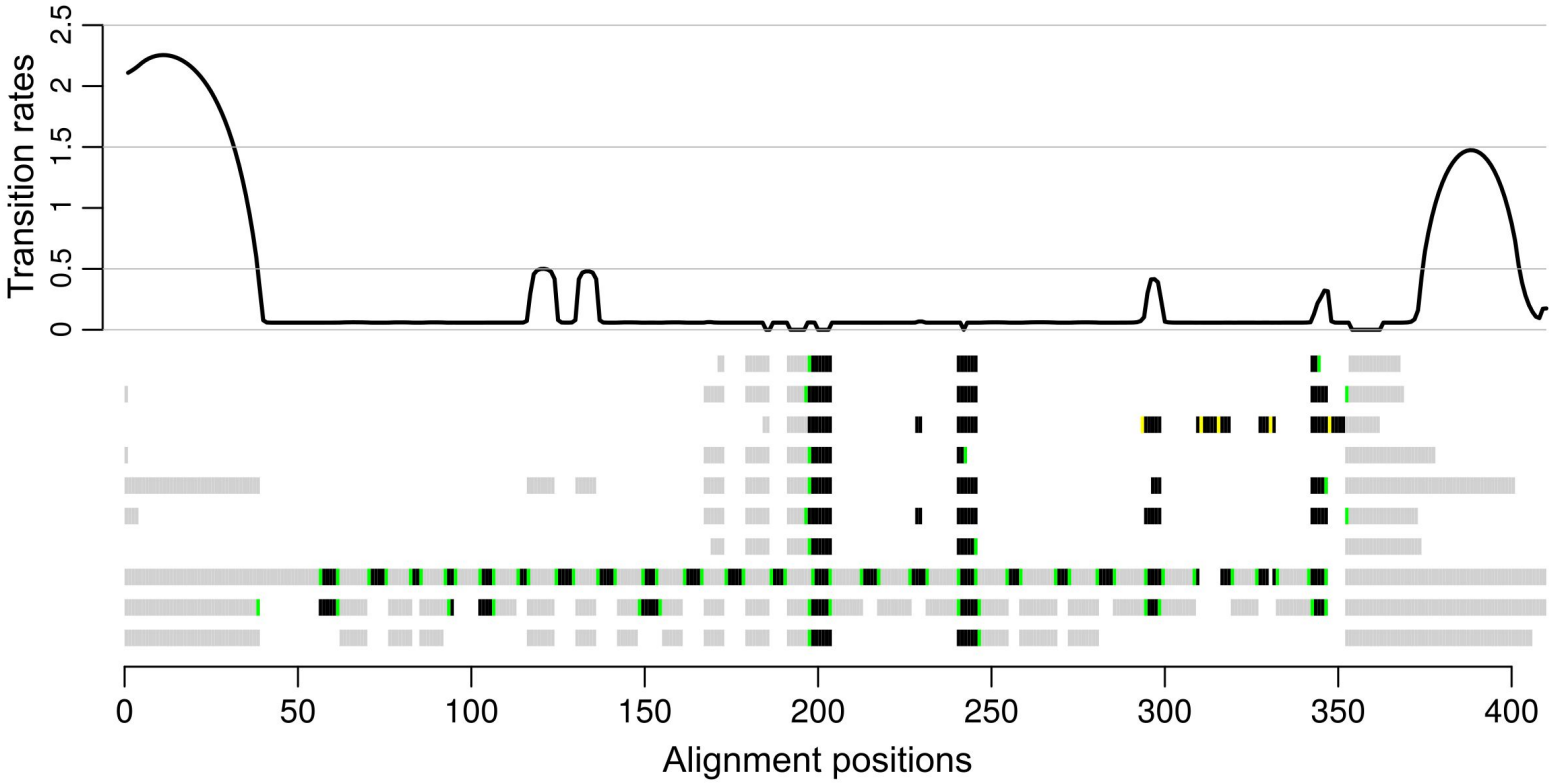

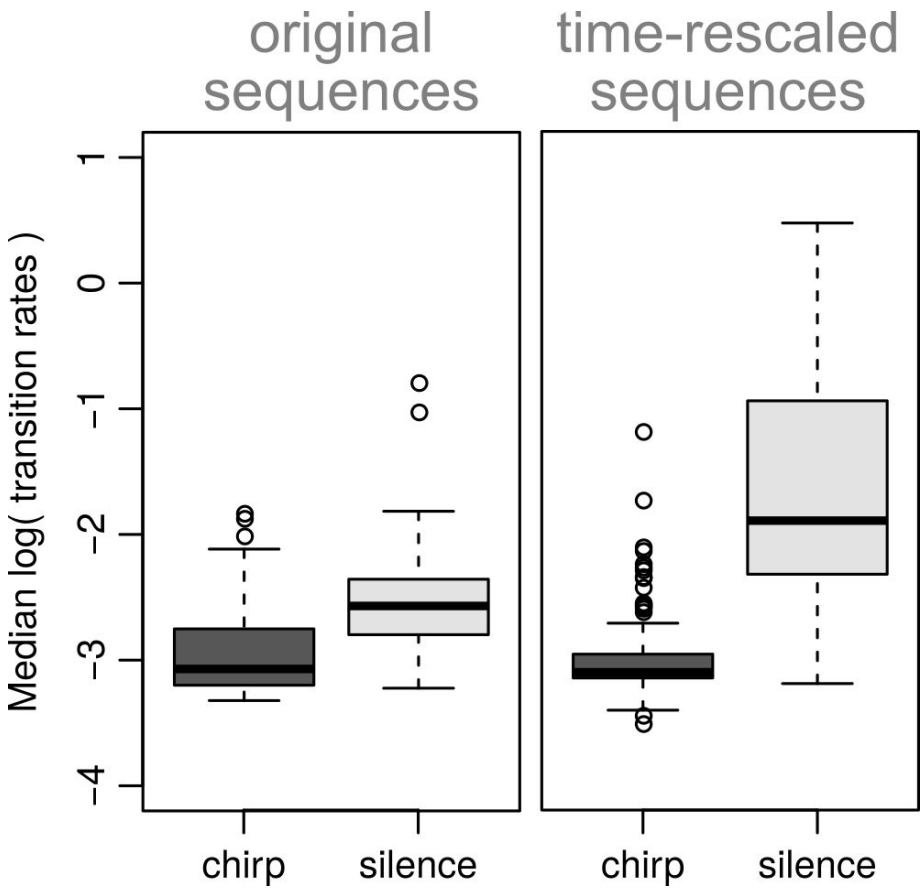

Wilcoxon signed-rank test ($p < 0.001$)

Conclusion

Sequence organization allows for context-dependent evolution

An underexplored axis of variation of multivariate traits

Faster rates of evolution for silent region suggests less constraints associated with predation and parasitism

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