Detecting heterogeneity in phylogenetic inference

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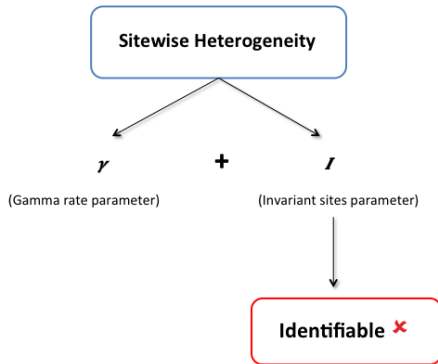
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- Heterogeneity - major challenge to the modelling process.

The Proposed Solution

Current Gamma Model

Weights: (0.25, 0.25, 0.25, 0.25)

Proposed Gamma Model

Weights: (0.10, 0.225, 0.225, 0.225, 0.225)
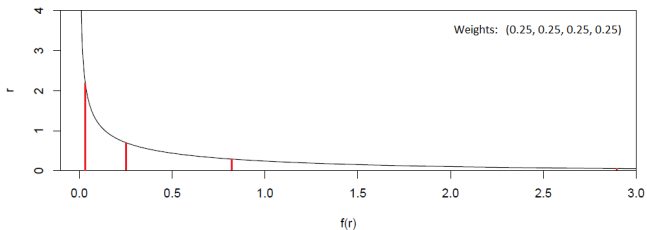
- Alignments simulated from Seqgen
- Model: JC69 $+ \gamma + I$
- 8 taxa
- Used three different topologies:
  a) Balanced, b) Caterpillar, and c) Intermediate
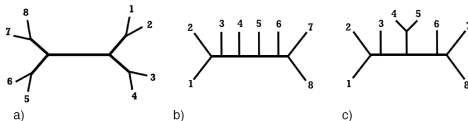
- Analysis in PhyML

Results
Difference in log-likelihoods

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Introduction
& Motivation

Methods &
Data

Results & Key
Findings

Current work
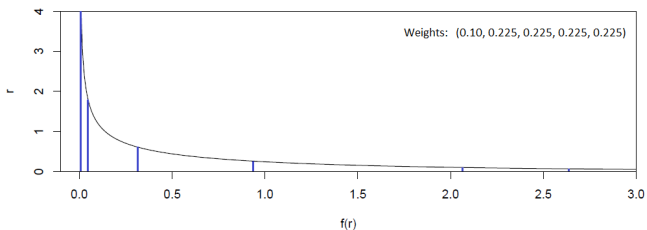
Results
Site likelihoods for individual trees
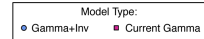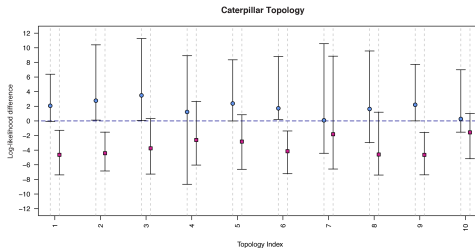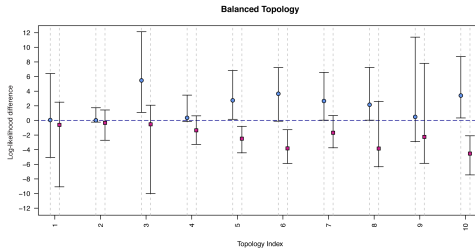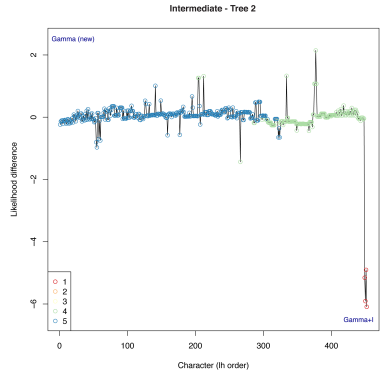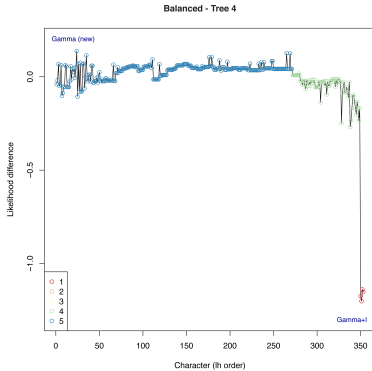
Key Findings

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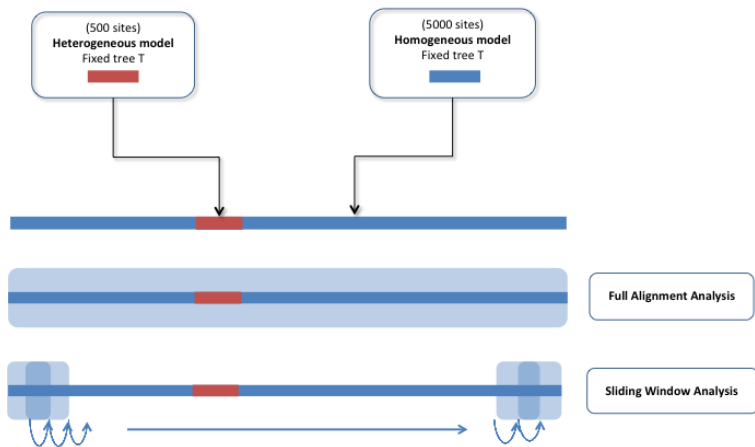Methods &
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Current work

- AIC, BIC suggested neither model consistently preferred.
- AIC favoured the simplicity of the proposed model.
- Wide CIs - Large variation.

But... Is it really necessary to implement the more complex model for little improvement?

Current Work
Main Ideas

- Ability to detect heterogeneity on a genomic scale
- Case Study: Sliding Window Approach

Preliminary findings & Future work

Full Alignment Analysis:
Heterogeneous model over Homogenous model 75% of time

Sliding Window Analysis:
Accurate in detection & parameter estimation

So where to next?

Acknowledgements

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