


GARD

Genetic Algorithm for Recombination Detection

 Export ▾

51

sequences in the alignment



2088

sites in the alignment



2087

potential breakpoints



5

inferred breakpoints



15725

models considered



2513.51

Δ c-AIC vs the null model



2136.11

Δ c-AIC vs the single tree multiple partition



GARD **found evidence** of recombination breakpoints. GARD examined **15725** models at a rate of **1.13** models per second. The alignment contained **2087** potential breakpoints, translating into a search space of **114269623460169630** models with up to **6** breakpoints, of which **0.00%** was explored by the genetic algorithm.

See [here](#) for more information about this method.

Please cite [PMID 16818476](#) if you use this result in a publication, presentation, or other scientific work.

Figures

Figure 1. Left: the best placement of breakpoints inferred by the algorithm for each number of breakpoints considered. Right: the improvement in the c-AIC score between successive breakpoint numbers (log scale).

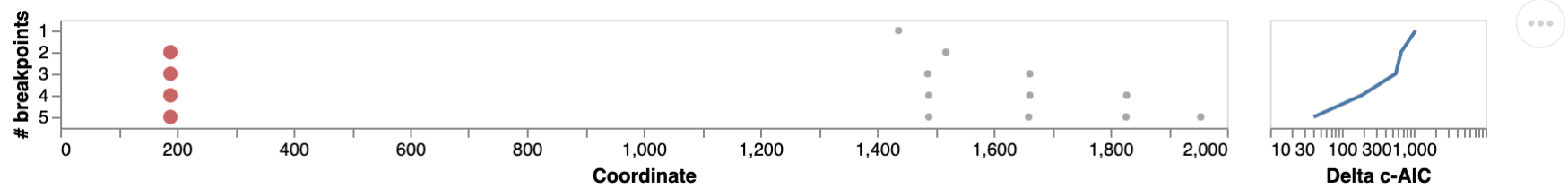


Figure 2. Model-averaged support for breakpoint placement

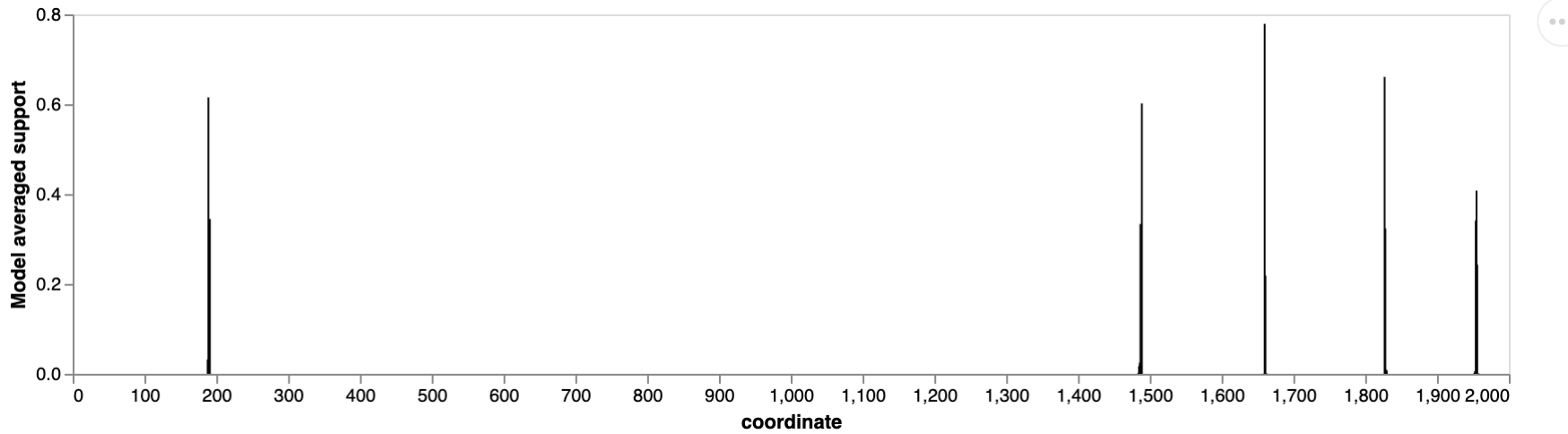


Figure 3. Total tree length by partition

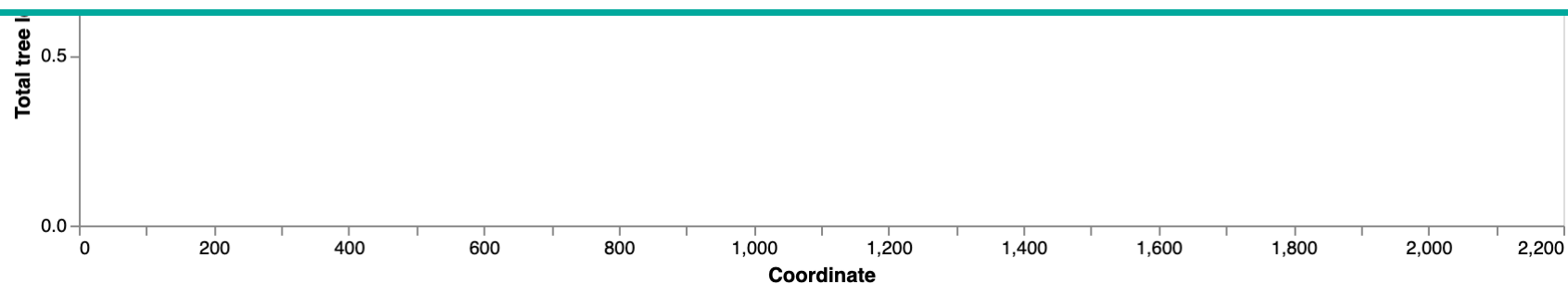
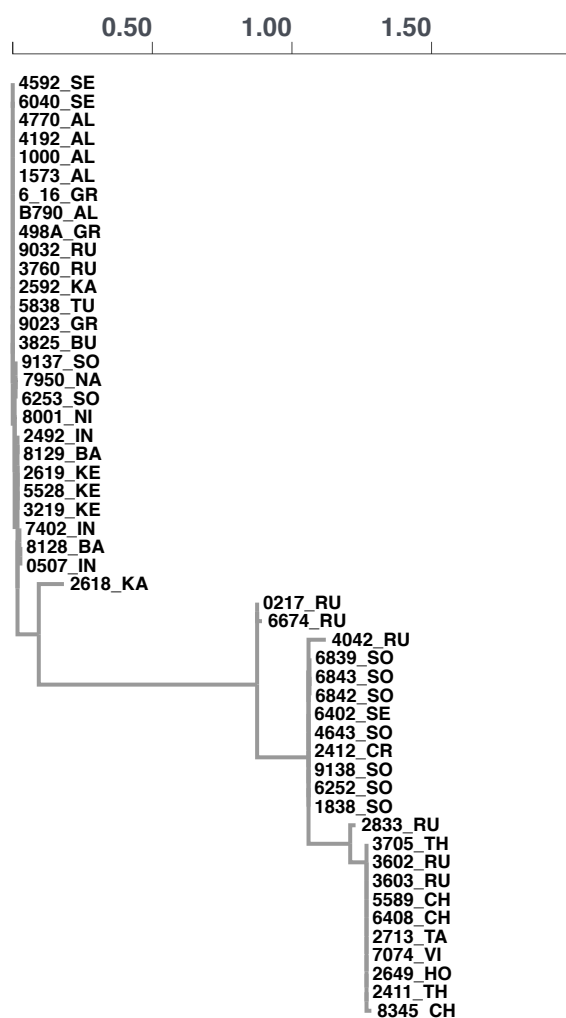


Figure 4. Trees for individual fragments

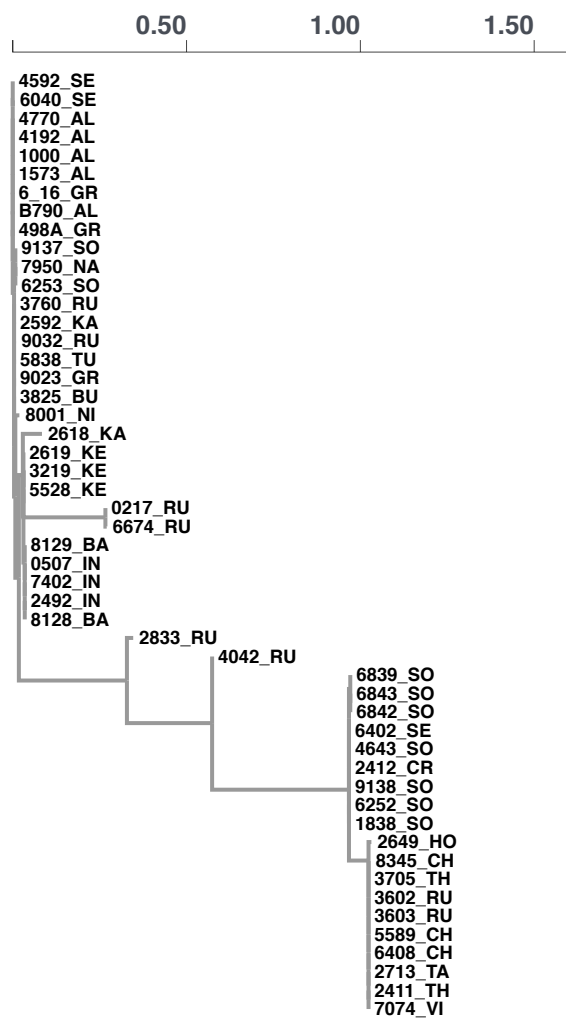
Select some sequences

```
variants = ▶Array(0) []
```

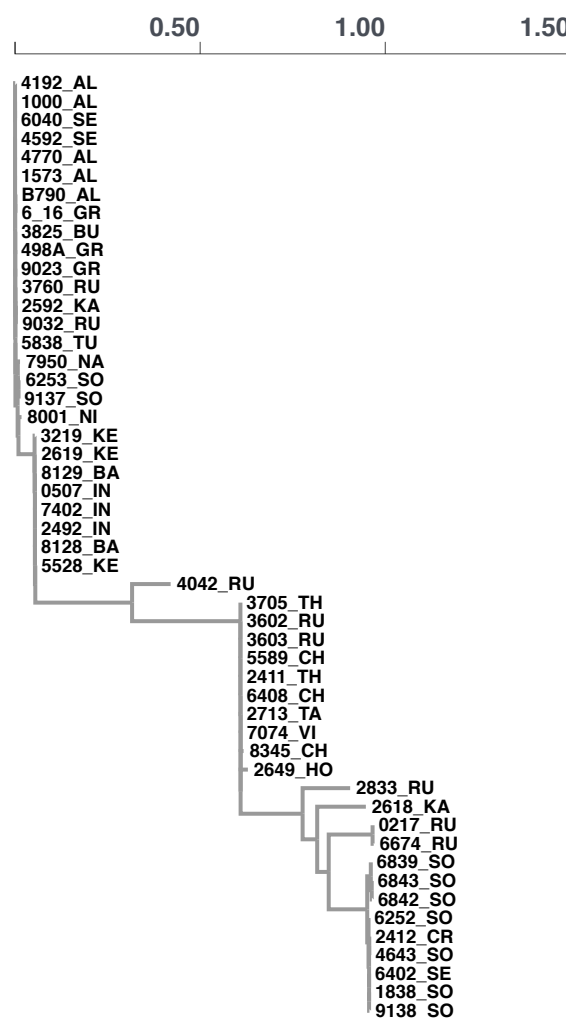
Tree 1, coordinate range 1-189

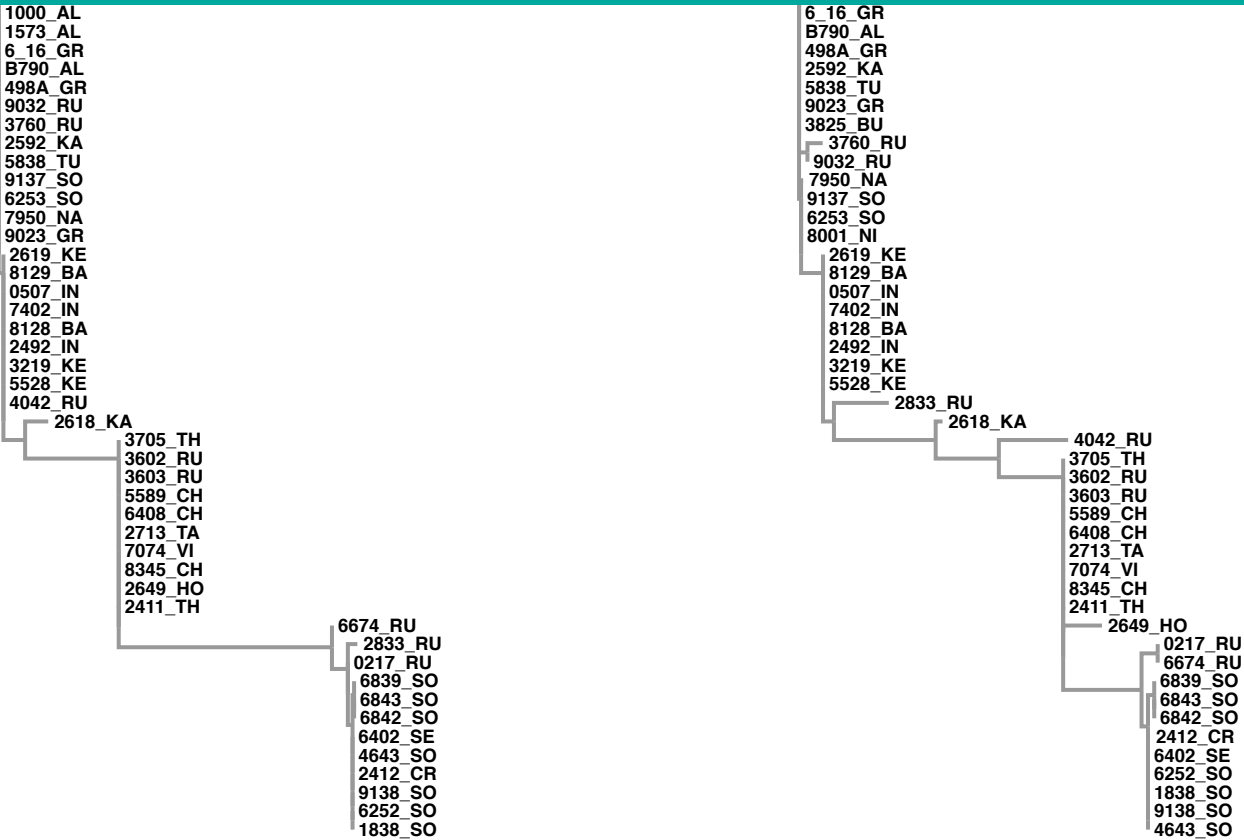


Tree 3, coordinate range 1490-1660



Tree 5, coordinate range 1828-1955






displayed_trees = ►Array(6) [Q, Q, Q, Q, Q, Q]


Topological incongruence report

Comparing the AIC_c score of the best fitting GARD model, that allows for different topologies between segments (30303.7), and that of the model that assumes the same tree for all the partitions inferred by GARD, but allows different branch lengths between partitions (32439.8) suggests that because the multiple tree model can be preferred over the single tree model by an evidence ratio of 100 or greater, *at least of one of the breakpoints reflects a true topological incongruence.*


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Tweets from
@hyphy_software

 HyPhy Retweeted

Brian Wasik
@BrianRWasik · Mar 24



Replying to @BrianRWasik

Our Bayesian and selection (Datamonkey, @hyphy_software) analysis of the genome segment ORFs show surprisingly little significant evolutionary divergence: the virus is not doing much special in one host vs another.
8/x