GARD

Genetic Algorithm for Recombination Detection

Export

11
sequences in the alignment

1277
sites in the alignment

43
potential breakpoints

1
inferred breakpoints

838
models considered

0.846631
Δ c-AIC vs the null model

7.91266
Δ c-AIC vs the single tree multiple partition

GARD **found evidence** of recombination breakpoints. GARD examined **838** models at a rate of **26.19** models per second. The alignment contained **43** potential breakpoints, translating into a search space of **946** models with up to **2** breakpoints, of which **88.58%** 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).

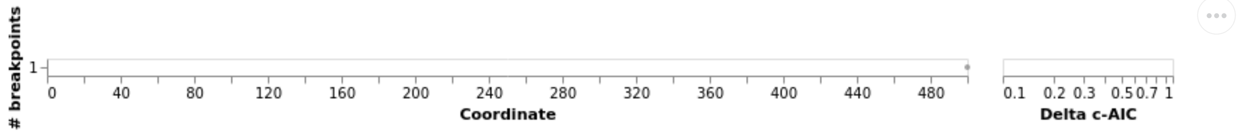


Figure 2. Model-averaged support for breakpoint placement

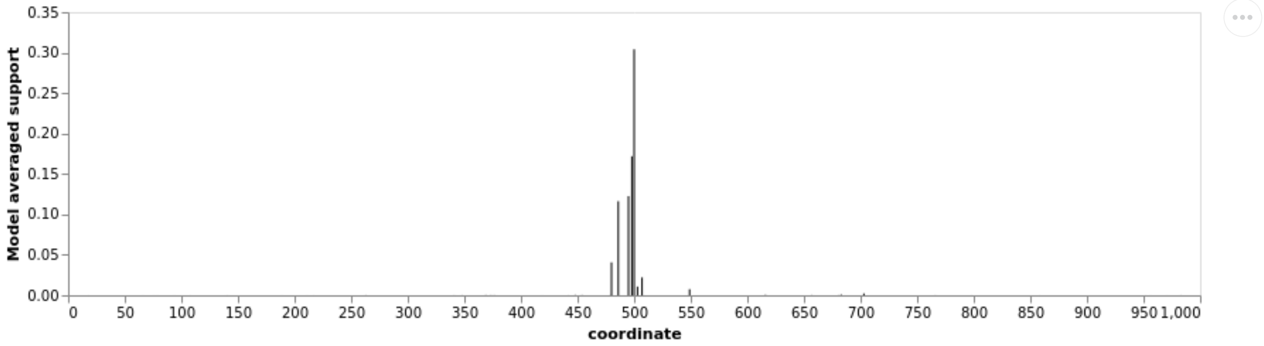


Figure 3. Total tree length by partition

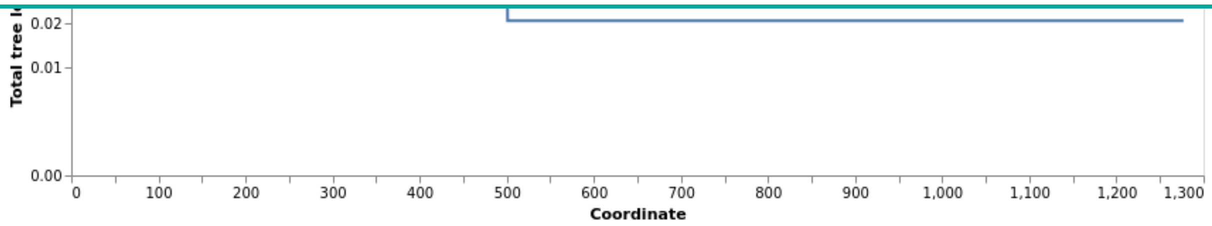


Figure 4. Trees for individual fragments

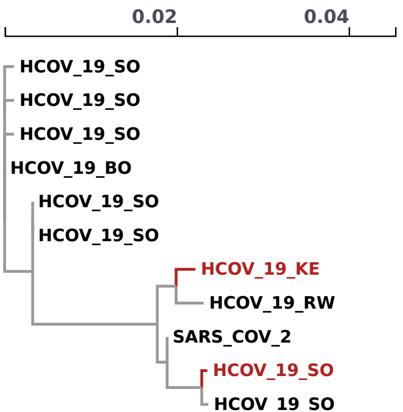
Select some sequences to highlight

Select some sequences

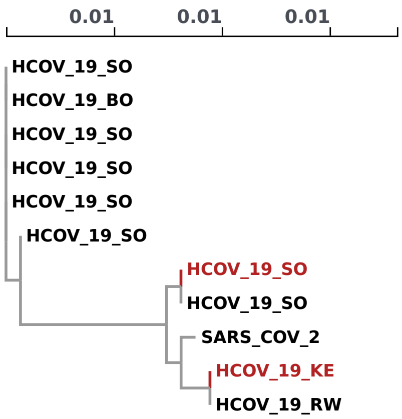
HCOV_19_KENYA_DELTA_EPI_ISL_3031406 ☒ HCOV_19_SOUTH_AFRICA_BETA_EPI_ISL_660629 ☒

variants = ▸**Array(2)** ["HCOV_19_KENYA_DELTA_EPI_ISL_3031406", "HCOV_19_SOUTH_AFRICA_BETA_EPI_ISL_660629"]

Tree 1, coordinate range 1-500



Tree 2, coordinate range 501-1277



displayed_trees = ▸**Array(2)** [Q, Q]

Topological incongruence report

Comparing the AIC$_c$ score of the best fitting GARD model, that allows for different topologies between segments (8275.3), and that of the model that assumes the same tree for all the partitions inferred by GARD, but allows different branch lengths between partitions (8283.3) suggests that because the multiple tree model cannot be preferred over the single tree model by an evidence ratio of 100 or greater, *some or all of the breakpoints may reflect rate variation instead of topological incongruence*.

Datamonkey is funded jointly by MIDAS and NIH award R01 GM093939

Tweets by @hyphy_software

HyPhy
@hyphy_software

Have a small dataset but still want to test for selection per-site? 🥵FEL with parametric bootstrap is now available in HyPhy 2.5.33 and Datamonkey. ♻️ Full description can be found here ➡️ hyphy.org/news/

Oct 15, 2021

HyPhy Retweeted

Spyros Lytras
@SpyrosLytras

Replying to @SpyrosLytras

We used an array of methods implemented in @hyphy_software to search for site-, branch- and ORF-specific selection in the phylogenetic clade SARS-CoV-2 emerged from (we refer to as the 'nCoV' clade) 9/18

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