

The Novel Coronavirus Is Evolving Gradually

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Here, we describe and compare the mode of SARS-CoV-2 genomic evolution to its tempo, which so far has been much slower than that of SARS-CoV [1] and the seasonal flu [2]. Once SARS-CoV-2 jumped and spread among humans, has it been evolving in a punctuated manner, so that a large proportion of their genomic divergences occurred during transmission events? Or has SARS-CoV-2 evolution been gradual?

To test for punctuated evolution [3,4], we regressed total phylogenetic path lengths of SARS-CoV-2 genomes (root-to-tip distances) on the net number of transmission events (nodes). We acquired a molecular tree of 3,958 genomes from [Nextstrain](#) [5,6]. And we used the maximum likelihood algorithm in BAYESTRAITS 3.0.1 [7], under a phylogenetic generalized least squares (PGLS), to estimate the parameters of the regression above. Punctuation would be consistent with a strong positive correlation.

We, however, find little evidence for a punctuated genome evolution (slope = $-0.0063 \pm .0038$; $R^2 = .064$; Figure 1). Diagnostics indicate no severe violations of linear regression assumptions (Figure A2). Additionally, the node-density artifact [3,8], an underestimation of branch lengths in tree regions with fewer taxa, does not seem to be present ($\delta = -.062$; Figure A3). Altogether, the evidence suggests that SARS-CoV-2 genomes are evolving gradually, with much of the mutations occurring in between net transmission events. The tempo and mode of SARS-CoV-2 evolution are likely linked. We expect the mutation rate of the novel coronavirus to be steady, and that drugs and vaccines (e.g. [9,10]) under development will still be effective in the future.

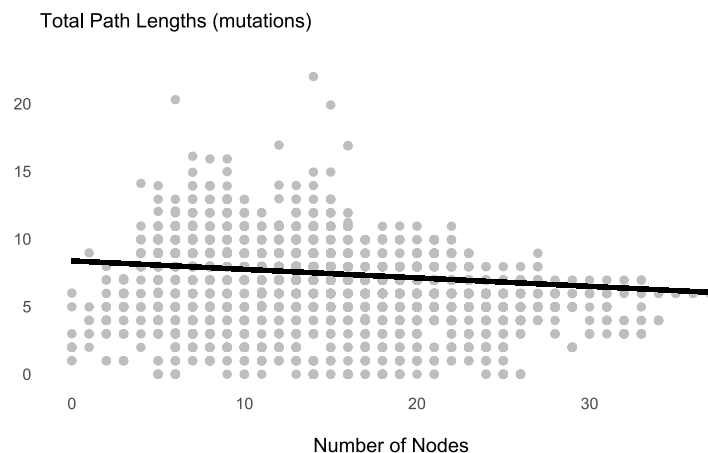


Figure 1. The number of nodes along the SARS-CoV-2 lineages (net transmission events) does not correlate with, nor does it explain the variation ($R^2 = .064$) in total path lengths (accumulated mutations in the genome). Equation: $y = 8.38 - .063x$.

References

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Appendix

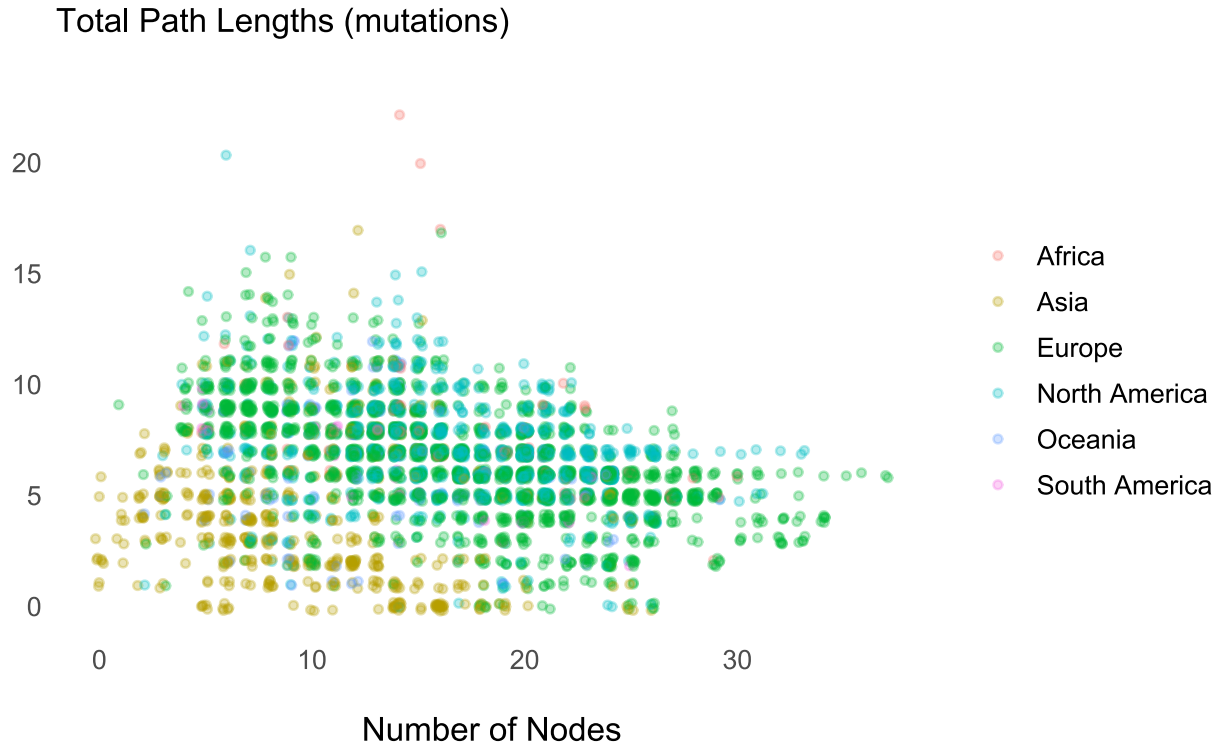


Figure A1. There may also not be punctuations of the SARS-CoV-2 genomic evolution at the continental level. See the interactive plot in the supplementary file folder to explore this data further. But, note that every continent has multiple introductions (see [Nextstrain](#)).

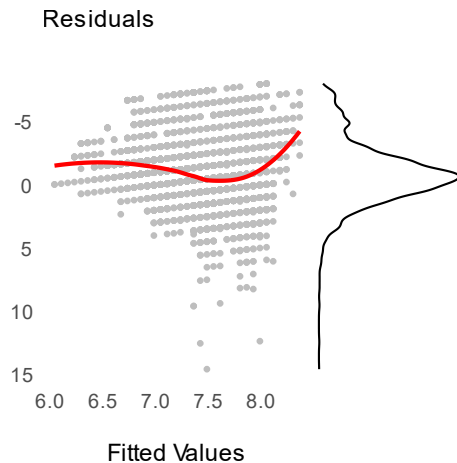


Figure A2. Regression diagnostics. The residuals vs. fitted values plot does not indicate a severe violation of residual homogeneity. The histogram shows that the residuals are normally distributed with a slight right skew.

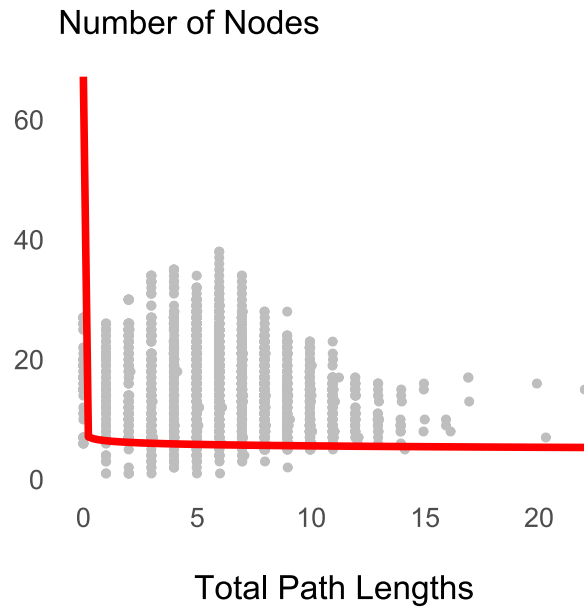


Figure A3. The node-density effect, which can bias our punctuation test, does not seem to be present ($\delta = -.062$). (A symptom of the artifact is a curvilinear relationship with $\delta > 1$.) Equation: $y = 6.46x^{-.062}$.