CoVtRec

TDALife

Topological Surveillance of Recurrent Mutations in SARS-CoV-2

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Abstract

The appearance of new variants in the evolution of the coronavirus SARS-CoV-2 underlines the importance of being able to quickly identify mutations that could confer some adaptive advantage to the virus, such as immune evasion or higher infectivity. Here we apply CoVtRec, a fast and scalable surveillance system based on Topological Data Analysis, for the identification of emerging potentially adaptive mutations in the ongoing evolution of SARS-CoV-2. CoVtRec is based on a new topological approach to the study of recurrent mutations in large genomic datasets developed in [1].

Results

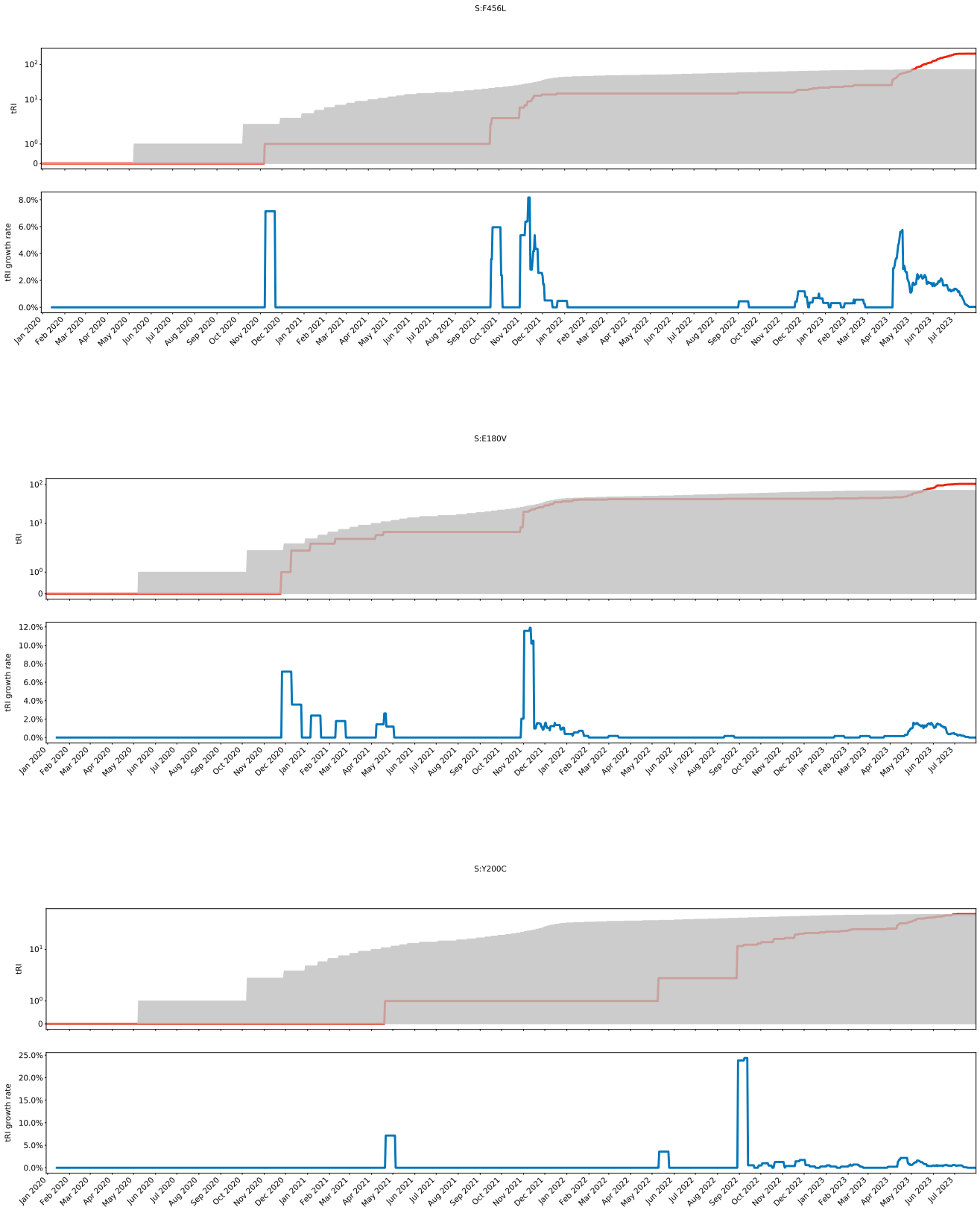
We analyzed topological signals for the ongoing convergent evolution of the coronavirus SARS-CoV-2 on the Spike gene from 15 January 2019 until 31 July 2023. To that end, we performed a topological recurrence analysis for a curated alignment of 14,286,081 high-quality SARS-CoV-2 Spike gene sequences shared via GISAID, the global data science initiative [2, 3]. For each Spike mutation we computed its topological recurrence index (tRI) and the corresponding time series analysis chart. The topological recurrence index is a topological measure for the potential adaptiveness of a given mutation (see [1, 4] for details).

We present a list featuring the top ten amino acid changes on the Spike gene with currently highest tRI growth rate in July 2023 (see Table 1). Here signals with tRI ≥ 71 are statistically significant ($p < 0.05$). It was demonstrated in [1] that these mutations are potentially adaptive and might therefore appear in future variants. We also present time series analysis charts (see Figure 1) showing (i) the development of the topological signal as well as its significance over time, (ii) major lineages containing the mutation, and (iii) the date from which on the topological signal became significant.

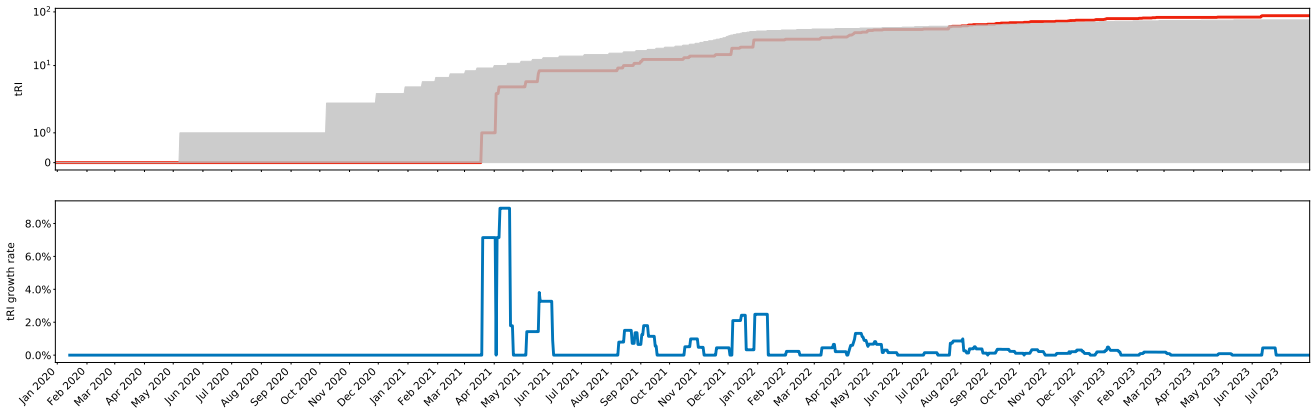
SAAV	tRI	notable variants
F456L	202	
E180V	104	
Y200C	72	
R214H	85	
N556K	72	
P521S	78	
T547I	504	
N148T	140	
G184V	90	
T51I	150	

Table 1. The top ten amino acid changes on the Spike gene with currently highest tRI growth rate in July 2023. For a given mutation, the table displays its topological recurrence index (tRI) and notable variants containing the mutation.

Figure 1. Time series analysis charts for the mutations listed in Table 1. Each chart shows the topological recurrence index (tRI, in red) and the tRI growth rate (in blue) from 15 January 2019 until 31 July 2023. In the upper diagram the shaded region marks the level of significance.



S:R214H



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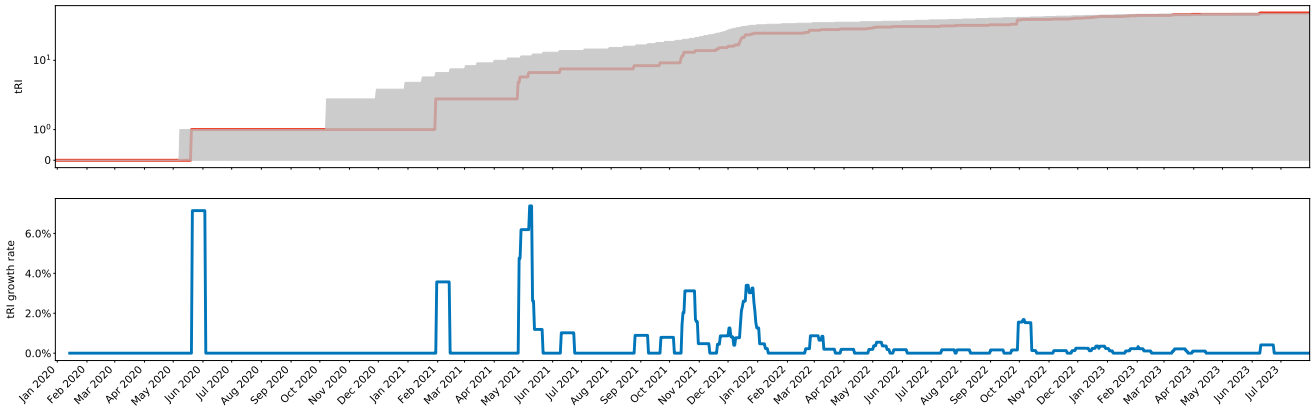
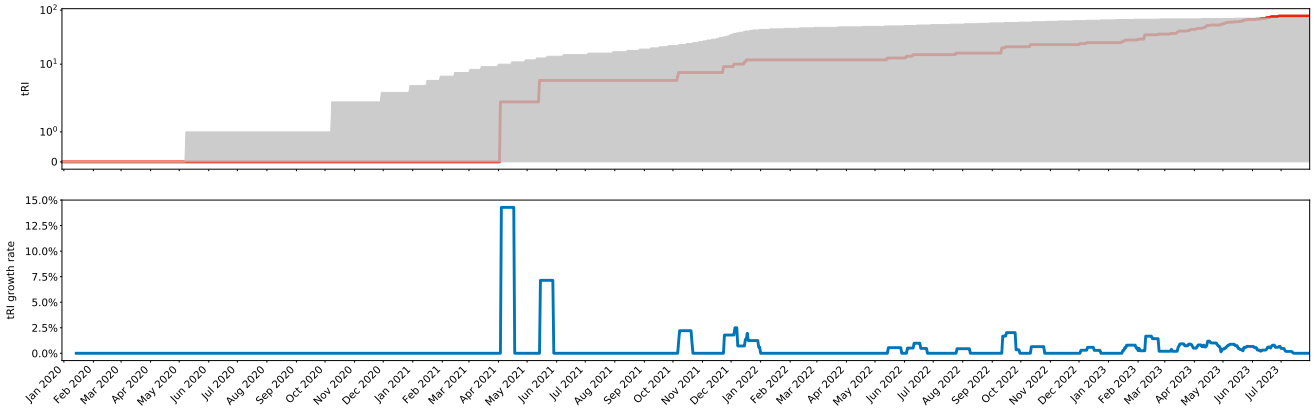
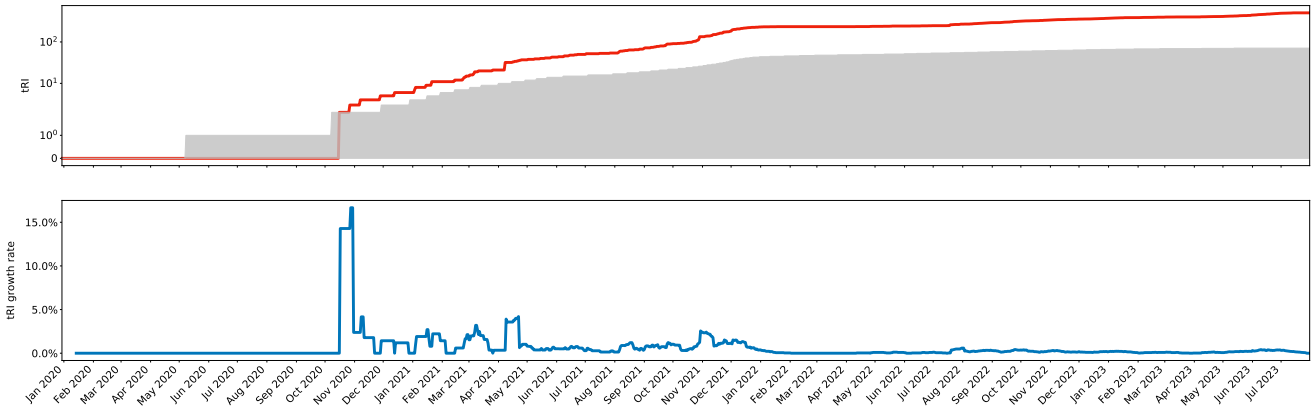


S:P521S



S:T547I



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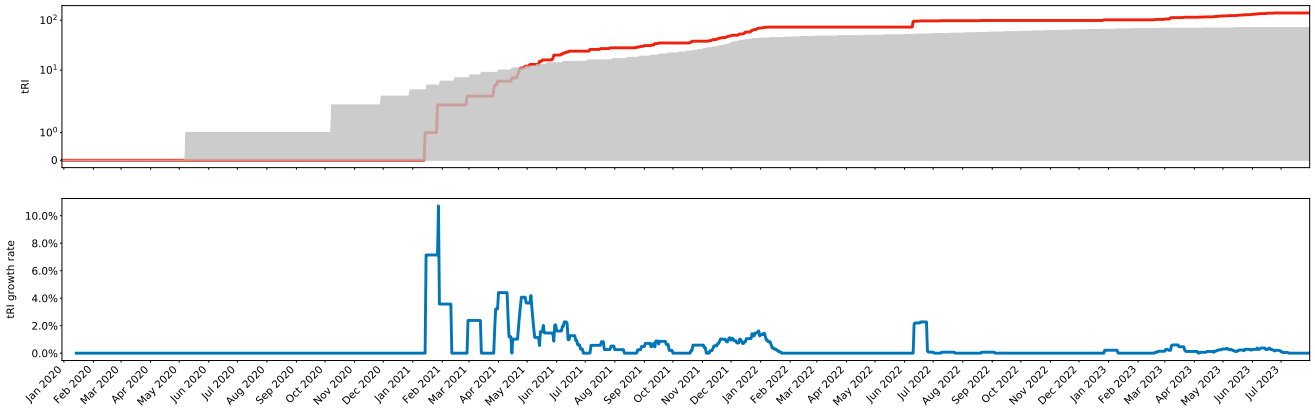

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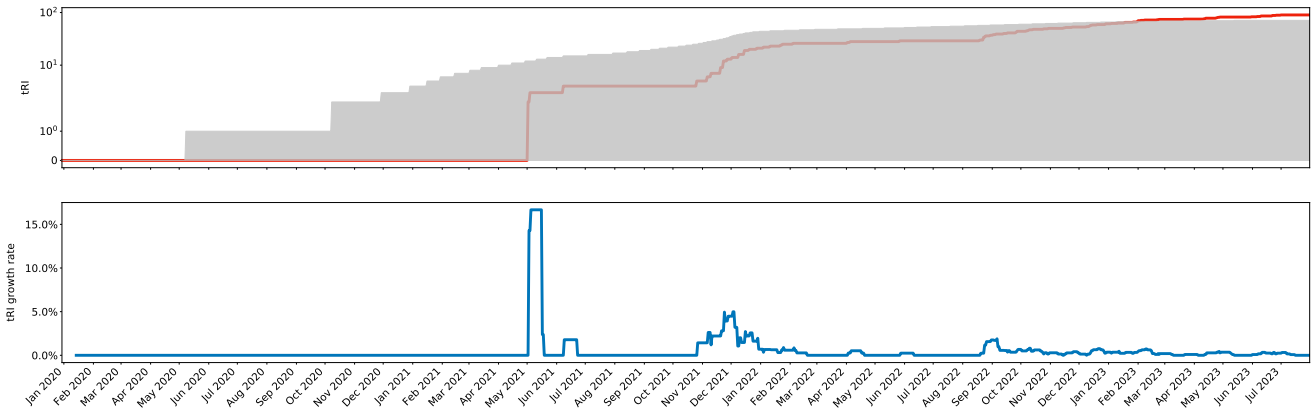

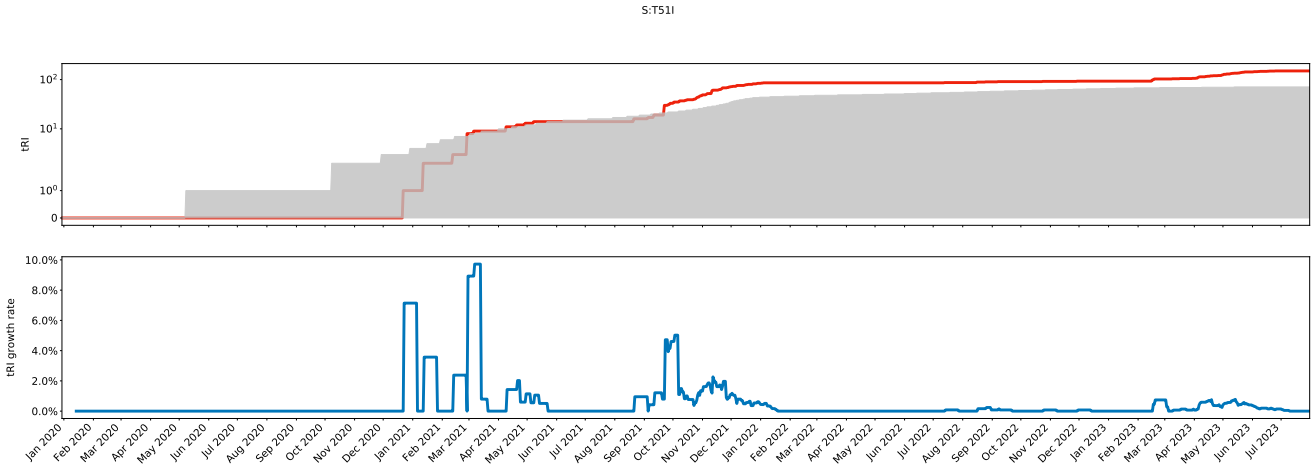

Methods

Data acquisition and data preparation

Our analysis is based on the alignment `msa_0731.fasta` downloaded from the GISAID EpiCoV Database [2, 3] on 5 August 2023. This alignment comprises 14,286,081 SARS-CoV-2 whole genome sequences that have been aligned to the reference sequence Wuhan/WIV04 with GISAID accession number `EPI_ISL_402124` using `MAFFT` [5]. Sequences in this alignment were truncated to the Spike gene (reference site positions 21,563 to 25,384). Subsequently the following sequences were removed: (i) sequences containing any characters other than A, C, T, G or -, and (ii) sequences that occur only once in the alignment. This resulted in an alignment comprising 9,250,719 complete SARS-CoV-2 Spike genes of length 8,054nt.

Topological recurrence analysis

The Spike gene alignment contains a subalignment comprising 231,541 genetically distinct sequences. A list of accession numbers of all sequences in this subalignment, along with an acknowledgement of the contributions of both the submitting and the originating laboratories, is accessible at https://doi.org/10.55876/gis8.230809tu. We used `Hammingdist (Version 0.19.0)` [6] to compute the genetic distance matrix of this subalignment. Subsequently we used `Ripser` [7] to compute the representative cycles for the persistent homology of the Vietoris–Rips filtration associated to the genetic distance matrix. The computation of persistence barcodes was restricted to small genetic distance scales (`Ripser` scale parameter threshold set to 2). Next a complete list of SNV cycles (topological cycles all of whose edges correspond to single nucleotide variations) in the given alignment was generated from the corresponding `Ripser` output. Then we used custom code implemented in Python to compute the *topological recurrence index (tRI)* for each such SNV. Summing over all SNVs determining an SAAV (single amino acid variation), we computed the tRI for each SAAV. Lastly, from the distribution of the tRI measurements over the whole Spike gene we inferred the level of significance for the tRI per SAAV. Using Vietoris-Rips transformations in multipersistent homology, we computed tRI time series analysis charts at daily resolution from the natural stratification by time of genomic data. We also computed the tRI growth rate (14 days moving average). For a more detailed description of the topological recurrence analysis see [1, 4].

Data availability

All SARS-CoV-2 genome data used in this work are available from the GISAID EpiCov Database [2, 3] at https://www.gisaid.org and are accessible at https://doi.org/10.55876/gis8.230809tu.

Code availability

Code used for the analyses is available at https://github.com/ssciwr/hammingdist and https://github.com/Ripser/ripser/tree/tight-representative-cycles. All other code is available from the corresponding authors upon request.

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Author contributions

M.B., L.H., M.N., A.O. designed the study; A.O. curated data; A.O. performed computational analyses; M.B., L.H., M.N., A.O., S.B., H.O., M.S., R.C. developed and implemented software; M.B., L.H., A.O. acquired computing resources; M.B., L.H., A.O., M.N. drafted the manuscript; all authors contributed to the final version of the report.

Competing interests

The authors declare no competing interests.

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