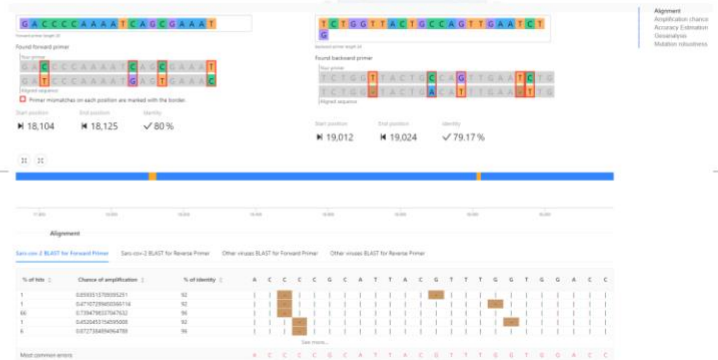


COVID GENOMICS

We are developing tools for large-scale in silico validation and the design of robust RT-PCR SARS-CoV-2 tests.

Our tool uses machine learning to predict the amplification of the PCR primer. It is run on a huge database of SARS-CoV-2 and other viruses collected around the world to estimate the sensitivity and specificity of the test.

We also provide spatial analysis about test accuracy in different countries, and predictions about test accuracy stability in the future, basing on virus mutations simulations.



PCR tests validation issues

- Experimental validation of PCR does not provide big picture about tests accuracy in the real world
- Due to the limitations in traveling, genomes of SARS-CoV-2 vary around the world, which can lead to lower tests accuracy in some countries
- Virus mutations can affect the sensitivity of the test over time

Our approach

- Testing PCR primes on over 600 thousand genomes of SARS-CoV-2 to measure how well the test is performing
- Evaluating test efficiency on different genomic samples to make tests customized for each country
- Stochastic simulation of virus mutations to predict future mutations - to determine the importance of each mutation, predicting if primer will amplify to the mutated sequence

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