

# VOE

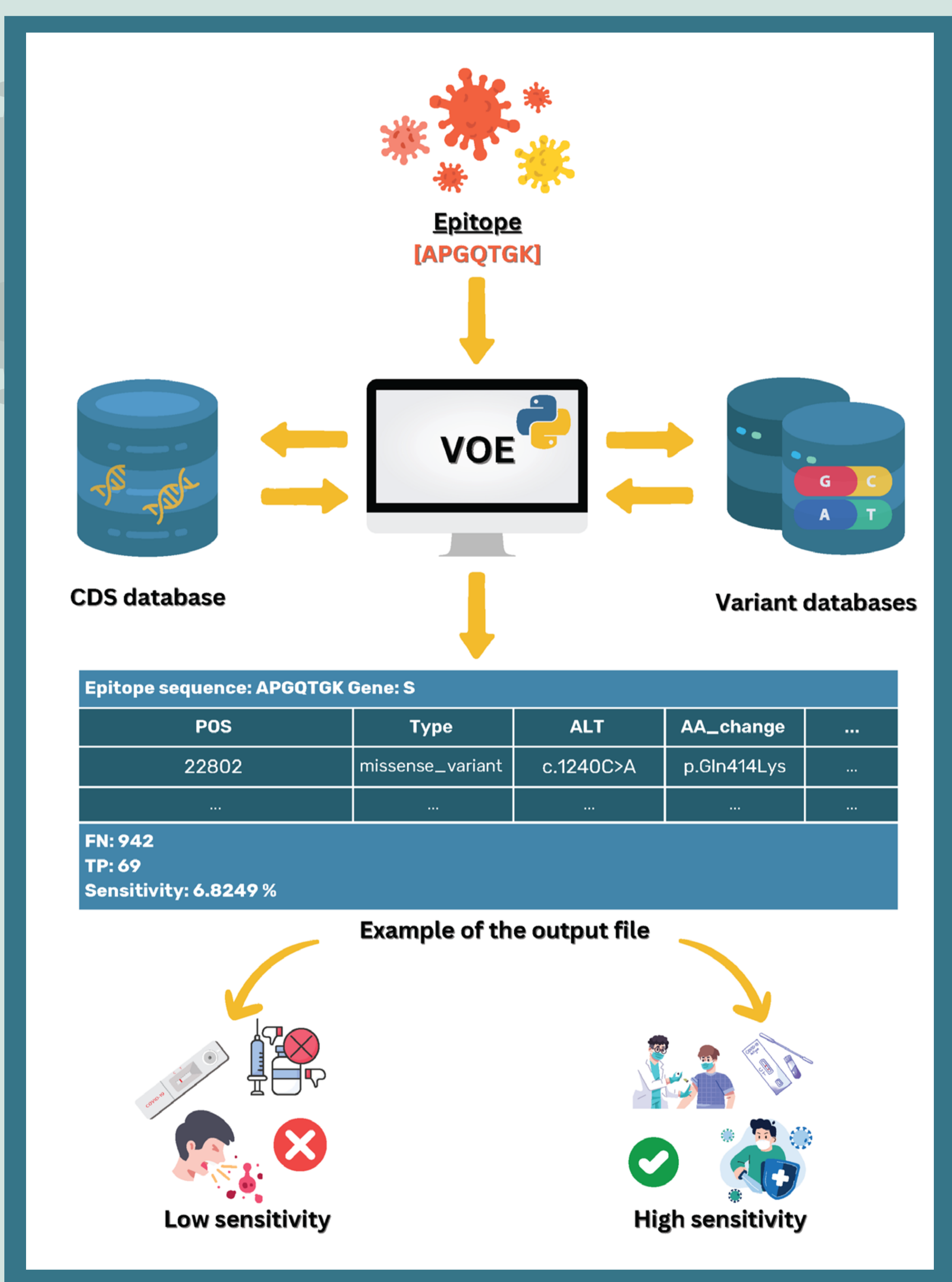
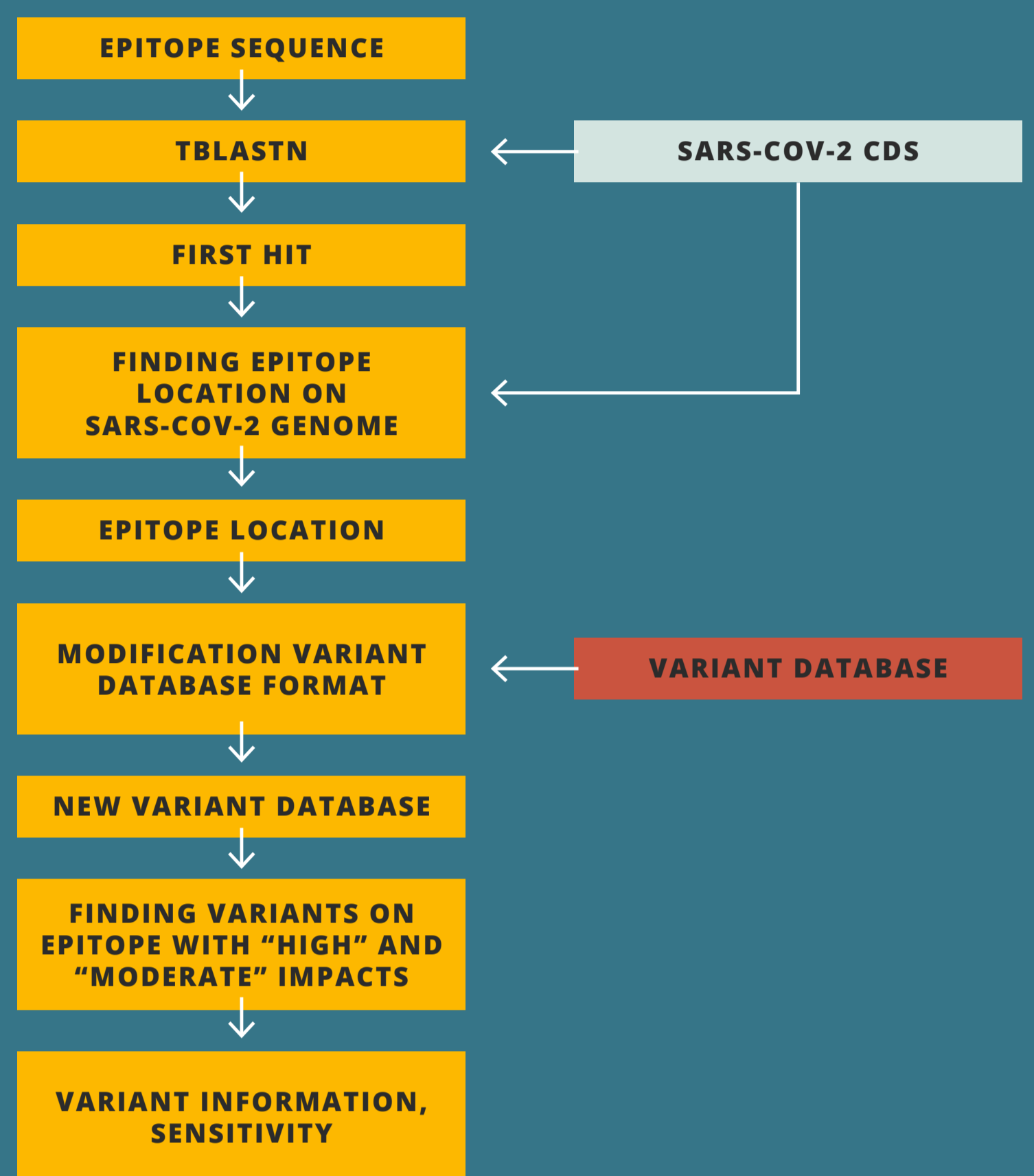
## Automated analysis of variant epitopes of SARS-CoV-2 for the development of diagnostic tests or vaccines for COVID-19

### BACKGROUND

The development of serodiagnostic tests and vaccines for COVID-19 depends on the identification of epitopes from the SARS-CoV-2 genome. An epitope is the specific part of an antigen that is recognized by the immune system and can elicit an immune response. However, when the genetic variants contained in epitopes are used to develop rapid antigen tests (Ag-RDTs) and DNA or RNA vaccines, test sensitivity and vaccine efficacy can be low.

### METHODS

Here, we developed a "variant on epitope (VOE)" software, a new Python script for identifying variants located on an epitope. Variant analysis and sensitivity calculation for seven recommended epitopes were processed by VOE. Variants in 1,011 Omicron SRA reads from two variant databases (BCFtools and SARS-CoV-2-Freebayes) were processed by VOE.



### RESULTS

A variant with HIGH or MODERATE impact was found on all epitopes from both variant databases except the epitopes KLNDLCFTNV, RVQPTES, LKPFERD, and ITLCFTLKRK on the S gene and ORF7a gene. All epitope variants from the BCFtools and SARS-CoV-2 Freebayes variant databases showed about 100% sensitivity except epitopes APGQTGK and DSKVGGNYN on the S gene, which showed respective sensitivities of 28.4866% and 6.8249%, and 87.7349% and 71.1177%.

Therefore, the epitopes KLNDLCFTNV, RVQPTES, LKPFERD, and ITLCFTLKRK may be useful for the development of an epitope-based peptide vaccine and GGDGKMKD on the N gene may be useful for the development of serodiagnostic tests. Moreover, VOE can also be used to analyze other epitopes, and a new variant database for VOE may be further established when a new variant of SARS-CoV-2 emerges.