Review of: "ASPICov: An automated pipeline for identification of SARS-Cov2 nucleotidic variants"

Sergey Senkin[1]

1 International Agency for Research on Cancer, World Health Organization

Potential competing interests: The author(s) declared that no potential competing interests exist.

The ‘ASPICov: An automated pipeline for identification of SARS-Cov2 nucleotidic variants’ paper represents a pipeline to detect and identify SARS-Cov2 mutations by analyzing raw reads data.

The pipeline is written in Nextflow DSL, making it reproducible in different computing environments, which is an undeniable asset. Starting with raw data, the pipeline outputs results in a user-friendly HTML report, combining the figures and quality reports of various tools incorporated within the pipeline. ASPICov comes across as a handy and helpful tool to aid researchers in identifying and analyzing whole genome variations of SARS-Cov2.

The tool appears to be under active development, hence a few hiccups may appear during running and testing, such as errors due to script permissions or problems with the download of the test dataset. However, the authors appear to be very responsive in addressing these issues on Gitlab, which is extremely important and adds value to the tool.

Overall, I would recommend this tool to researches working with SARS-Cov2 genomes, and wish the authors continue developing it, perhaps making it of broader use, e.g. scaling it to support other genomes.