Enhancing pathogen surveillance of *Candida auris* using MycoSNP and Nextflow: an update

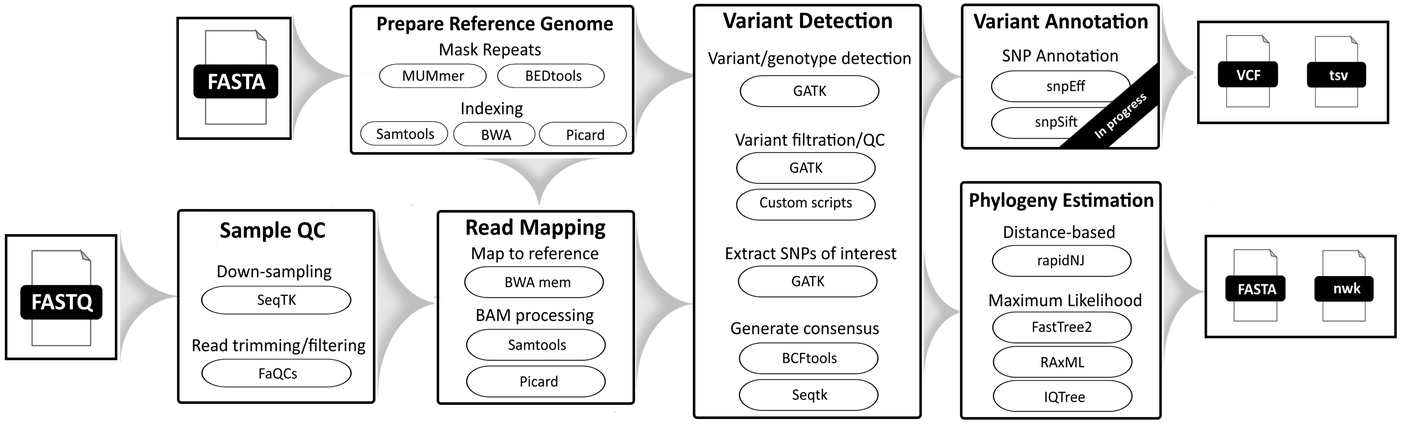
nf-core/mycosnp

MycoSNP is a bioinformatics best-practice pipeline for analyzing fungal genomes, including *Candida auris*.

Connect with the MycoSNP development team on Github!

https://github.com/CDCgov/mycosnp-nf

Problem: The fungal pathogen *Candida auris* is an emerging global health concern that can cause invasive infections, can spread rapidly in healthcare settings, and is characterized by high rates of antifungal drug resistance.



In response, CDC developed MycoSNP to support national-scale *C. auris* surveillance. MycoSNP has now been converted to Nextflow DSL2 using nf-core principles to maximize portability and reproducibility for public health partners

More reliable information can be provided to public health officials using DSL2 updates to MycoSNP, leading to faster outbreak detection and action.

Check out the MycoSNP paper for more details

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