
Swab-Seq: Detecting Pathogens using Sequencing

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Abstract:

At UCLA we developed one of the only novel technologies for COVID-19 diagnostic testing that was deployed on a large scale. The assay, which we named SwabSeq, performs genomic sequencing of pooled samples tagged with sample-specific molecular barcodes and then uses computational approaches to deconvolve the pooled samples into individual diagnoses, enabling the testing of thousands of nasal or saliva samples for SARS-CoV-2 RNA in a single run without the need for RNA extraction. The efficiency of SwabSeq has enabled a small facility with a handful of staff to perform close to 2,000,000 tests, with an analytical sensitivity and specificity comparable to or better than traditional qPCR test with turnaround times of less than 24 h. SwabSeq has been recently adapted for the detection of other pathogens.

Bio:

Dr. Eleazar Eskin is the founding Chair of the Department of Computational Medicine at UCLA. He is also a Professor in the Computational Medicine, Computer Science and Human Genetics departments. His research focuses on developing computational methods for the analysis of genetic variation and discovering the genetic basis of human disease. He was a founding faculty of multiple academic programs at UCLA including the Bioinformatics Ph.D. Program, the Undergraduate Minor in Bioinformatics, the Bruins in Genomics Summer Research Program and the Computational Genomics Summer Institute. He is a Fellow of the International Society of Computational Biology and a Alfred P Sloan Foundation Research Fellow.

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