



New website supports genetic understanding of COVID-19

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A new website to facilitate analysis and interpretation of SARS-CoV-2 genomic data is aimed at improving the global response to the COVID-19 pandemic by helping researchers to detect and identify the virus and to analyze its evolution and how mutations impact diagnostic assays.

The [COVID-19 Genome Analytics](#) site launched by the Los Alamos National Laboratory Bioscience Division comprises several tools, including a tailored bioinformatics workflow based on the fully open-source [EDGE Bioinformatics](#) platform developed at Los Alamos. This mini-version of EDGE consists of a user-friendly interface that accommodates multiple different types of raw genomic sequencing data from COVID-19 patient samples as input, such as data being generated by the CDC and public health labs around the world. If the virus is present within the sample, EDGE COVID-19 can generate a complete SARS-CoV-2 genome that is ready to be shared with public data repositories such as GenBank, the nation's primary repository for genomic data.

Currently, over 13,000 SARS-COV-2 genomes have been sequenced, and with every new sequence comes a more comprehensive understanding of the virus and its evolution. The COVID-19 Genome Analytics site not only facilitates the assembly and addition of more high-quality genomes, but it also helps scientists analyze how the virus is evolving and how these changes impact our ability to detect and identify the virus.

For instance, Los Alamos scientists are also computationally screening published diagnostic assays against the increasing number of SARS-CoV-2 sequences to determine the most reliable assays for diagnosis. This computational assay validation is also available on the COVID-19 Genome Analytics site, as well as information tracking both the growth in genomic data and in confirmed COVID-19 cases in the USA and around the globe.

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Keep up to date on the latest information and media coverage of the Lab's scientific response to the emergency [with this news page on the Laboratory site.](#)