BIOMÉRIEUX

BIOMÉRIEUX **EPISEQ®**

NGS data analysis platform providing easy-to-use applications for clinical microbiologists.

NOT FOR DIAGNOSTIC USE

PIONEERING DIAGNOSTICS

ACTIONABLE ANSWERS, FAST.

THE BIOMÉRIEUX EPISEQ® PLATFORM WORKS IN 3 EASY STEPS:

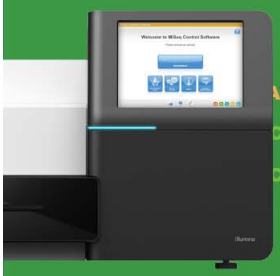
Import **raw data** directly from Next Generation Sequencing instruments.

Fast and intuitive workflow, **in a few clicks**, from data to actionable results.

BIOMÉRIEUX EPISEQ® combines state-of-the-art bioinformatics pipeline and meaningful microbiological data to **answer meaningful microbiological questions**.

EPISEQ® SARS-COV-2

for SARS-CoV-2 variant identification



BIOMÉRIEUX

EPISEQ® SARS-COV-2

www.biomerieux-episeq.com

- ✓ QUALITY CONTROL INFORMATION
- ✓ VARIANT IDENTIFICATION (BASED ON NEXTSTRAIN & PANGO)
- ✓ GENOME ASSEMBLY
- ✓ SAMPLE REPORT
- ✓ MUTATION LIST
- ✓ MAPPED ALIGNMENT BAM

With a **WEEKLY UPDATE** of the variant of concern (VOC) list from the WHO* and CDC**

The microbiology expertise of bioMérieux allows this solution, which identifies SARS-CoV-2 genomic variants from FASTQ files, to report the list of mutations detected in the spike gene and other genes of the variant sequenced.

A consensus sequence is created from the reads after alignment against the reference genome and solid results can be downloaded as BAM files.

BATCH
download of results

For easy submission to public health

COMPATIBLE
with three platforms

Illumina®, Thermo Fisher, Ion Torrent® or Oxford Nanopore Technologies®

*World Health Organization **US Center for Disease Control and Prevention

www.biomerieux-episeq.com/sars-cov-2

SARS-COV-2

EPISEQ® CS

for clinical pathogens outbreak monitoring

Contains **14 BACTERIAL SPECIES** covering the majority of all HAI-related organisms.

EPISEQ® CS performs Whole Genome Sequencing bacterial typing and Multi Resistant Bacteria characterization. It helps to detect HAI outbreaks early & accurately.

It reports decisive data to further investigate a potential outbreak or cluster, thus triggering infection prevention and controlling protocols at an early stage.

wgMLST
at the core of the analysis

A **phylogenetic analysis** based on the wgMLST schemes. It provides a very discriminant relatedness between strains.

>4000
resistance genes

Microbiological expertise extracted from public databases and bioMérieux proprietary knowledge.

598
point mutations

Display all **resistance** and **virulence genes** and their presence on an identified **plasmid**.

www.biomerieux-episeq.com/cs

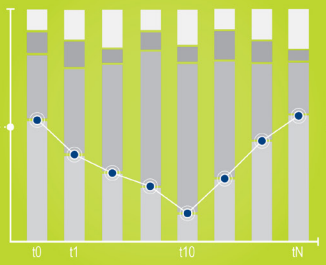
EPISEQ® 16S

for microbiome profiling studies

BIOMÉRIEUX

EPISEQ® 16S

www.biomerieux-episeq.com



- ✓ OTU ASSIGNMENT
- ✓ OTU ABUNDANCE
- ✓ ALPHA & BETA DIVERSITY
- ✓ CLUSTERING
- ✓ STATISTICAL ANALYSES
- ✓ TIME-SERIES ANALYSIS

Helps to investigate the role of **MICROBIOME** on patients' health.

The microbiology expertise of bioMérieux allows this solution to cover full diversity of bacteria and archaea with alpha and beta diversity parameters. This solution supports users to investigate the use of microbiome to define predictive biomarkers.

TRENDS SERIES
your sample compared with others through time

QIIME
state of the art pipeline

SILVA
state of the art database

TRUST
your results with the embedded statistical analysis

www.biomerieux-episeq.com/16s

ALSO DISCOVER
BIOMÉRIEUX VISION SUITE
DATA-DRIVEN DECISION MAKING

BIOMÉRIEUX VISION SUITE turns laboratory and hospital data into insightful, actionable information to support diagnostic and clinical decisions at all stages to **better support antimicrobial stewardship**.

By providing a **comprehensive suite of software solutions** that collect, analyze, and merge various sources of data, BIOMÉRIEUX VISION SUITE empowers you to make the right decisions at the right time.

BIOMÉRIEUX
EPISEQ®

MORE RESOURCES AT
www.biomerieux-episeq.com

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