Oxford NANOPORE Technologies™

GENEYX'S SCALABLE SOFTWARE SOLUTION TO ADVANCE THE FUTURE USE OF NANOPORE SEQUENCING

The new platform is designed to enable the end-to-end analysis and variant interpretation for nanopore sequencing data, empowering researchers, and other users with an advanced, "one-click" solution.

Oxford Nanopore and Geneyx teamed up to create a comprehensive analysis tool for interpretation of nanopore sequencing data. The research use-only solution offers valuable insights to aid in critical workflows such as newborn screening and rare disease research.

Geneyx offers an ideal solution for swiftly identifying candidates and complex variants with a focus on high-throughput and user-friendly operation. The future of Long-Read data analysis with Geneyx is here.

EFFICIENT VARIANT INTERPRETATION AND REPORTING FOR LONG-READ SEQUENCING:

» Comprehensive tertiary analysis platform
» Processing of Long-Read sequencing data
» Streamlined interpretation

ENHANCING RESEARCH:

» Complete transparency and customization
» Seamlessly automated working environment
» Powerful analytics tools for research purposes

GENEYX
Better Data for Better Health™

The European Human Genetics Conference
JUNE 1- 4, 2024 Berlin, Germany
We Are Exhibiting at Booth Number 400
email: sales@Geneyx.com

ESHG

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KEY FEATURES:

- Repeat Expansion
- Connecting Geneyx to EPI2ME
- Phasing Analysis
- Visualization of methylation data
- Support multi-sample VCF (joint calling)
- Streamlines workflow through seamless integration SMART filtering for genomes including CNVs, SVs, repeats, fusions, and enhancer analysis

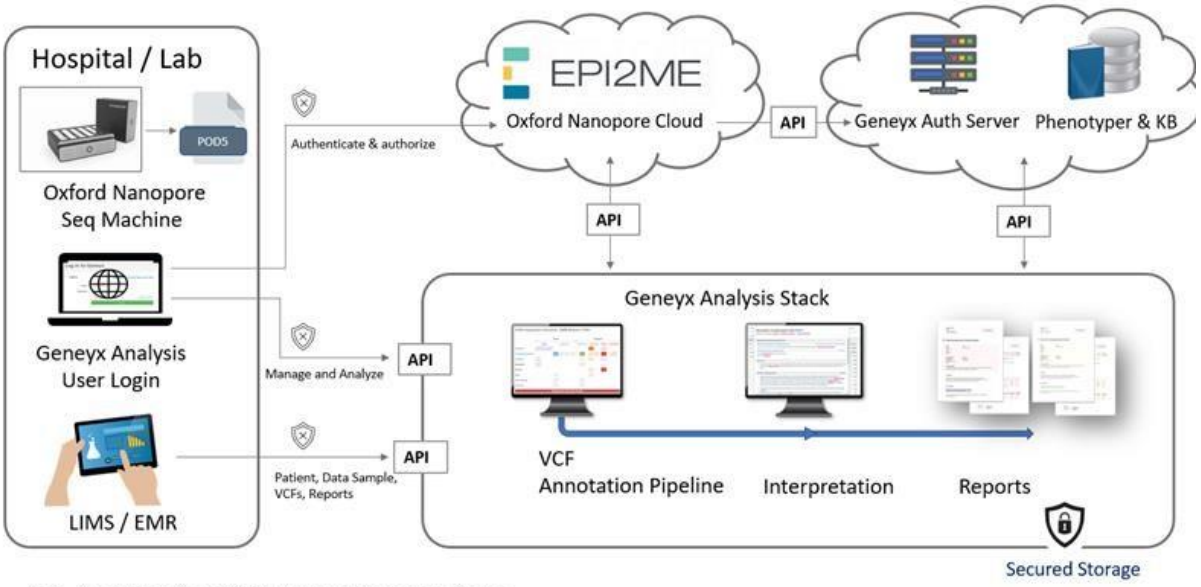

Fig 1. Geneyx Analysis and Oxford Nanopore Component Diagram

Don't miss out on the transformative potential of Long-Read sequencing. Upgrade your capabilities with Geneyx Analysis and unlock a wealth of information hidden in your genetic data. Contact us today to learn more.

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