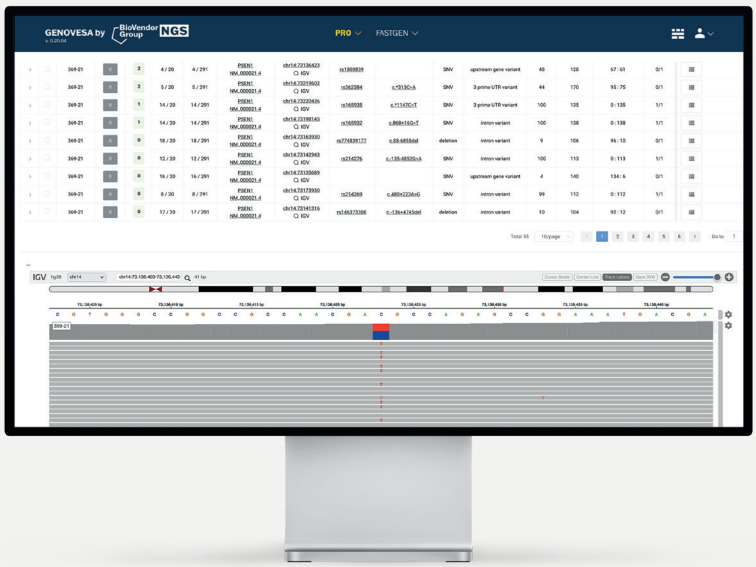
BioVendor Group NGS



GENOVESA – cloud-based database bioinformatics and interpretation system

Analysis of NGS genetic data can be a challenging task that often requires specialized user skills. We developed a cloud-based bioinformatics software – GENOVESA as an easy solution for everyone and for all NGS data regardless of the sample preparation kit used.

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Key features

- **User friendly**
- **Automatized bioinformatics analysis of NGS data**
- **Advanced quality control of sequencing data**
- **Easy variants filtration**
- **Local Clinical Variants Database**
- **Visualization of NGS data**
- **Internal interpretation of variants and sharing between clinics**
- **Clinical report generation**

From FASTQ to clinical report

GENOVESA enables evaluation of data from small panels, through clinical exome (CES) whole exome data (WES) to whole genome sequencing (WGS) data. It includes a wide range of annotation databases and the possibility of individual customization. FASTQ, BAM and VCF data quality control. Possibility of own interpretation of variants and comments. Complete clinical management with integration of International Classification of Diseases (ICD) and HPO terminology.

Sequencing technology

GENOVESA enables analysis of conventional sequencing data (FASTQ, BAM, VCF) regardless of what sequencing technology was used – Illumina, MGI, PacBio, Oxford Nanopore Technologies, Genapsys and many others.

Databases and data sharing

GENOVESA also serves as a database for storing variants, with the possibility of sharing data between individual clinics.

Security

GENOVESA prioritizes data security through HTTPS encryption. We do not rely on third-party providers like Google or Amazon; instead, we host your data in our secure data center located in Prague. We do not collect any sensitive patient data, GENOVESA is fully GDPR compliant.

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Genovesa is a joint project of the companies:

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