Convince yourself of the benefit of the SEQUENCE PILOT modules by analysing your own data or demo data provided on our homepage. Free trial licenses + software introduction (WebEx session) are available upon simple request.

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General product features

- Collection of patient data independent of input format and SEQUENCE PILOT module in one order
- Technical and medical validation, secured by the user rights management
- Detailed and customisable analysis reports
- Available as single and multiple user application
- Runs on Unix and Windows server systems (32 and 64 bit)
- Efficient use of all available computing resources by parallel data analysis on multiple cores and computers
- Automated data import (ListenMaster) and export (TalkMaster) to LIMS systems

A customer-oriented company with customised solutions developed individually for your needs

JSI medical systems GmbH, the market leader in the field of DNA sequence analysis is a software company with decades of experience in developing software in the field of clinical diagnostics. The company philosophy is to place customer satisfaction at the core of each of its business decisions. Thus competent support, availability, short response times, intensive on-site or online trainings and the implementation of customer demands are only some of JSI’s key strengths.

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MLPA®

The MLPA® module is a convenient and powerful tool for detecting copy number changes.
- Pre-configured SALSA MLPA® kit descriptions for download and import
- Different analysis modes for each MLPA® kit
- Configurable control settings and RPA limits
- Data correction for probes with "tailing-off-effect"

SEQPATIENT

The SEQPATIENT module facilitates the convenient and powerful analysis of Sanger sequencing data.
- Peak area statistic based on previously analysed data (internal data base) for a sensitive detection of heterozygous positions (mosaics, somatic mutations etc.)
- Configurable base caller with sequence dependent thresholds; self-adaptive algorithm based on peak area statistic
- Definition of reference electropherograms from previously analysed orders
- Sophisticated tools for frame shift and indel detection

SEQUENCE PILOT

The utilisation of the SEQUENCE PILOT software as stand-alone tool or as a seamlessly integrated part of existing analysis pipelines, allows you to address current and future challenges related to the understanding, integration and use of biomedical and clinical diagnostic data. These challenges include the need to streamline the clinical testing process, manage the vast amounts of data generated in genetic testing, generate clinically useful interpretations from these data and channel this information efficiently and effectively to clinicians to impact patient care.

SEQNEXT

The SEQNEXT module facilitates the convenient and powerful analysis of next-generation sequencing data.
- Fast and easy definition of regions of interest (ROIs) via bed, manifest or CSV files
- Manual generation / import of specific gene lists addressing your interests
- Customizable filters for variants in pseudogenes and homologous regions
- Efficient standards for mapping, alignment and quality control
- Variant calling against specific reference sequences (e.g. somatic, UMA etc.)
- Patient identification via SNP IDs
- For small panel to Whole Exome Sequencing analysis
- High speed analysis: Complete WES in 2.5 hours* (dependent on your server hardware requirements, 28 Cores à 3.1 GHz, 64GB RAM)

SEQHLA & SEQNEXT-HLA

The SEQHLA and SEQNEXT-HLA module are convenient and powerful tools for the interpretation of your HLA typing data.
- Availability of all IMGT HLA database versions and updates for download and import
- Constant positions can be ignored
- Display of results in different resolutions (2-digits, 4-digits and max. resolution)
- Intron sequences can be displayed (not used for result calculation)
- Extended UMI check against pseudogenes
- Splice site mutation warning
- High sensitivity and specificity for detection of SNPs, deletions and insertions as well as detection of CNV and fusion genes
- Analysis of FFPE samples and processing of Tags (e.g. smMIPs, UMIs etc.)

28 Cores à 3.1 GHz, 64GB RAM