Sequence Navigator™ for Automated DNA and Protein Sequence Comparisons

Automated sequence comparison for mutation detection.
As comparative sequencing becomes more and more popular as a research technique, automated analysis tools are essential. Sequence Navigator™ software is the ideal tool specifically designed to address the unique needs of researchers performing comparative sequencing, as it accurately aligns sequences to a standard or a population and identifies sequence variants. Whether you’re studying HIV epidemiology, mutagenesis, cancer-related mutations, or mitochondrial DNA variants, Sequence Navigator quickly and effortlessly guides you from raw sequences to research results.

Optimal system integration.
Sequence Navigator integrates seamlessly with data collected on the Applied Biosystems automated DNA Sequencer, as well as text files from other sources. Sequence Navigator identifies vectors, regions of ambiguities, and even heterozygotes. With Sequence Navigator’s ability to perform fast, efficient feature identification and multiple sequence alignment, mutation analysis has never been easier.

Factura’s automated batch processing for feature identification saves you valuable time as it easily recognizes features such as the vector, primer, and heterozygote/IUB base positions.

Once you have processed your sequence files in Factura, you can import Factura’s batch worksheet into the second software module, Sequence Navigator. Here you have all the tools needed to analyze sequences for mutations. You can perform basic sequence editing, use pair-wise alignments to assemble contigs, select multiple alignment to identify sequence variants, and even display the electropherograms collected by the automated sequencer.

Simplicity and flexibility on your desktop. Sequence Navigator was designed around the familiar, user-friendly Macintosh® platform to provide intuitive ease of use.
Heterozygote detection is easily controlled by selecting a peak-height to peak-height ratio of the heterozygote composition.

**Set-up.** Factura provides databases of more than 140 vectors and over 300 enzymes. These libraries can be customized by creating smaller subsets or by adding your own sequences.

**Features Table.** Heterozygotes in sequences can be identified and labeled as features. These labeled mutations can be marked and graphically displayed allowing you to easily see relationships.

**Electropherogram.** Your data is displayed in full-color enabling quick and accurate verification of mutations.

**Automation**

**Factura’s automated batch worksheet offers flexibility and power.** Allow Factura to do the hard work for you. Once you have imported your sequence data into Factura’s batch worksheet, you can effortlessly edit your data, verify base calls, and mark features. Automatic feature identification in batch mode saves time and ensures accuracy.

**The power of automation at your fingertips.** Engineered to achieve seamless integration with the Model 373 DNA Sequencer, Sequence Navigator reliably handles vast amounts of sequence data in batch mode. At the touch of a button, all the files from a 373 results folder can be automatically added to a Factura worksheet. Powerful algorithms detect and mark vector ambiguity and heterozygotes for all of the sequences. Reports are electronically generated. All the prepared sample files can then be effortlessly imported into Sequence Navigator where you can learn more about the sequences you’re investigating.

**Rely on Factura for superior data integration.** Factura software performs labor-intensive tasks in batch mode, saving time and ensuring accuracy. Then, after Factura sorts and marks your 373 files, your edited data effortlessly integrates with Sequence Navigator software which fosters profound sequence analysis.

**Sequence Navigator—your key to comparative sequencing.** To characterize sequence mutations, you need to compare and analyze sequences, create small contigs, and edit data. Sequence Navigator is the tool for you as it provides unprecedented versatility enabling you to manage a number of different types of projects. When you need to find, analyze and discover, turn to Sequence Navigator.
Integration

When you're ready to move forward with your research, you can save your edited data from Factura and import it into Sequence Navigator for more in-depth analysis.

Sequence. Graphically display the base calls made by the automated sequencer. Vector and 3' ambiguities are grayed-out for quick identification. Heterozygotes are marked in color.

Compute a consensus sequence with a click of the mouse.
Whether you are comparing your sequence to a reference sequence or a new set of data, Sequence Navigator has the tools you need. Align multiple sequences with the powerful multiple alignment algorithm and display the associated electropherograms. A quick click of the mouse produces a consensus sequence which can be used as a reference sequence for future analysis. Sequence Navigator guides you from raw sequences to a consensus sequence in a matter of minutes.

Ensured accuracy with automation. With Sequence Navigator, you can use your computer to create dynamic sequences which allow you to visually combine, translate, or compare data sequences without compromising the integrity of your original data. The benefits of automation here are twofold—not only is the pace of your research accelerated, but our proven algorithms ensure you of accurate results, time after time.

Interpret your research results with ease. Sequence Navigator automatically assigns differentiating symbols to your sequence so insertions and deletions are easily identifiable. You can detect ambiguities and similarities between sequences as the powerful software computes ambiguities or consensus sequences for you. Colored highlighting, combined with readily displayed electropherograms, allow you to interpret your data with ease and confidence. Comparative sequencing projects have never been easier.

Comparative Sequencing. If you're looking for areas of mutation or conserved regions, Sequence Navigator will quickly find them for you. Features, such as heterozygotes found by Factura, will be displayed in color and underscored. Verifying mutations is critical: Sequence Navigator ensures your accuracy by displaying the electropherograms.

• p53 data provided courtesy of Stephen Friend and Peggy Romero, Massachusetts General Hospital, Boston.
Sequence Navigator™ Specifications

Macintosh Requirements

• Macintosh II-class computer or higher (≥ 16 MHz 68030)
• 8 Megabytes RAM (20 MB recommended)
• 40 Megabyte hard drive (≥ 80 MB recommended)
• 13" RGB color monitor (≥ 16" recommended)
• Macintosh System 7.0 or later

Input

• 373 sample files
• INHERIT AutoAssembler files
• INHERIT Analysis sequence files
• Macintosh text files
• SeqEd layouts

Output

• Heterozygote quantitative ratio information
• Vector/feature identification report
• Edited sequences
• Project layout
• Printed electropherograms with graphically marked features
• Sample files with vector, ambiguities, and heterozygotes marked

*Alignment Algorithms

• Comparative—Myers & Miller implementation of Gotoh’s Alignment
• Overlap—Myers’ Dovetail Alignment
• Needleman-Wunsch Pairwise Alignment
• Multiple—Kececioglu MultiWeight Trace Multiple Alignment
• ClustalV—Higgins Multiple Alignment

Compatibility with Other Programs

Data can be exported to standard Macintosh desktop publishing software and can be exported as text data to database and sequence analysis software packages.

Performance

• Alignment of more than 100 sequences of typical 400–500 base length each
• Alignment of more than 25 sequences of typical 3 kb base length each
• Automatic heterozygote screening and IUB assignment

Included in Purchase


References