You’re in control with Sequencer’s powerful, user-friendly tools and features

Sequencer is intuitive, so each step from importing your reads to assembly to searching for SNPs and heterozygotes is straightforward. Sequencer is flexible. You can adjust parameters and preferences and save them to easily standardize your workflow.

Sequence editing and trimming tools

» Sequencer makes it easy to clean up raw data by trimming vector, low quality base calls, and other artifacts. Rapid editing tools let you correct sequencing errors before or after they have been incorporated into alignments.

Assembly and alignment

» Perform de novo or reference-based assembly with flexible, understandable parameters. Take advantage of your laboratory’s naming conventions to assemble multiple samples from multiple sources using Assembly by Name. Use available Clustal or MUSCLE programs for multiple-sequence alignment.

Detect SNPs and produce reports

» Analyze traces locally or globally to find secondary, uncalled peaks. Use the Sequencer Variance Table to navigate your assemblies, discover SNPs, and more. Generate reports that quickly and clearly document your findings.
Sequencer Connections allows you to run multiple analyses in parallel

Sequencer Connections is your portal to local and remote analyses. Connections allows you to run multiple analyses on one or more sequences in parallel. The Connections control panel updates in real time to show you the progress of each analysis on each part of your data, so you can explore them as they complete. Simultaneously run multiple instances of the same application with different parameters and see how the results compare graphically.

Run multiple BLAST searches simultaneously

» Connections links to the NCBI BLAST server to search for sequence similarity against the broad availability in the GeneBank database. In addition, you can run the same query sequences using different parameters, and simultaneously use Local Blast to search databases stored on your machine. Run PrimerBlast to design primers and check their specificity and then save your predicted primers to your Sequencer Connections sessions to view your results later, even after they have expired on the NCBI website.

Perform multiple-sequence alignments with MUSCLE

» Another example of using Connections is trying different variable settings for multiple-sequence alignments and comparing the resulting phylogenetic trees. You can run the same sets of sequences at the same time with different parameter settings, or test the impact of adding or removing some samples from your alignment. As each alignment completes, the indicator in the Connections control panel turns green to let you know that the data is ready to review, even while other analyses are still running.
Use the top tools developed by bioinformatics researchers with an easy-to-use interface

Most NGS tools utilize the command line. Sequencher provides an interface that gives access to all of the power of those tools, without the command line. For each algorithm, Sequencher uses recommended settings or you can set up Advanced parameters. Each Advanced parameter is accompanied by a description and setting it is as easy as a single click and changing the values to suit your data.

Perform de novo assembly or reference-guided alignment without the command line

Sequencher has a plugin lineup featuring Velvet for de novo assembly and Maq, GSNAP, and BWA for reference-guided alignment. With GSNAP you can perform SNP-tolerant alignments and SNP analysis, generate methylation reports from bisulfite-treated DNA, and perform A-to-I RNA-editing tolerant alignments.

Multiplex ID for barcoded data

Use Multiplex ID barcodes with GSNAP, BWA-MEM, or Velvet to sequence a mixture of DNA samples in a single run.
Check the quality of your FastQ reads files

» A new plugin added for Sequencher 5.4.6 is FastQC which allows you to produce quality control reports of your data. Check up to 11 different metrics including per base and per sequence quality and GC content.

Variant calling

» With Sequencher 5.4.6 you can now utilize SAMtools to analyze the output from your GSNAP or BWA-MEM alignments for variants, saved in the standard VCF format. Then explore the alignments and the variants in the Tablet genome browser.

Viewing assemblies and alignments

» View your NGS results using Tablet in a number of different modes. Get information on individual reads and read pairs and arrange the stacking of the reads to reveal pairings. Customize the color of the individual bases, variants, read types, and read groups. Annotate alignments with GTF and VCF files. Tablet has controls to enable translations, zoom in and out, as well as highlight variant bases, making it a cinch to explore your reads.

genecodes.com
Easily perform powerful RNA-Seq analyses with Sequencer’s user-friendly interface

Extend Sequencer with more options for RNA-Seq analysis. Plug-in algorithms from the Cufflinks’ suite can be downloaded right from the Gene Codes website (www.genecodes.com), including tools for normalizing and quantifying NGS data. In addition, the graphical user interface lets you have complete and easy-to-understand control of Advanced options that would require you to set flags and in-line parameters if you were using the same tools from the command line. Add annotated replicates to your workflow with ease using Sequencer’s Conditions and Replicates editor.

Unique tools to help you organize and streamline your analyses

Sequencer’s External Data Browser makes it easy to track and organize your NGS runs. Add free-form text annotations to each run to remind you about data and parameters. View any alignment in Tablet without opening its project and delete old space-consuming runs without having to spend time searching for them.

Design publication-quality plots and charts with Sequencher’s customizable visualization tools

Sequencher has easy-to-use visualization tools that allow you to produce high-quality charts and plots without worrying about command-line statistical programming or forcing your data into a spreadsheet. Choose your data and view your results as a Scatter Plot, Volcano Plot, or Bar Chart.

Interactive charts and plots

» The charts and plots are linked to the underlying data. Search by gene name or geneID to locate your data of interest. Click on a bar or data point to view more information in the data table, or click on a line in the data table to locate that data point in the graph.

Customize and export charts and plots

» Sequencher allows you to select and plot on only the genes you want to focus on. Sort the data and then choose which rows you want to include or exclude from your plot. Once you have the graph you want, you can export it as a high-resolution png file.

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Make the move to Sequencher 5.4.6 for powerful, user-inspired and lab-tested functionality, facilitating accurate and rapid assembly and down-stream analysis

With applications inclusive of the following fields of study:

» Forensics
» Genetics
» Microbiology
» Pathology
» Systematics
» Virology

Choose your best-fit license option

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Extensive tutorials and videos show you how to get the most out of your data with Sequencher

» Sanger DNA sequencing tutorials
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» RNA-Seq tutorials
» Sequencher Connections tutorials for single and hybrid analyses

Visit www.genecodes.com to learn more and to download a free 15-Day trial of Sequencher 5.4.6.

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