SEQUENCHER® 5.3
with SEQUENCHER CONNECTIONS

Power with Simplicity

Gene Codes Corporation
TCA GENE
AGT CODES

The Premier DNA Sequence Analysis Software for Sanger and NGS Datasets

Try Sequencher 5.3 with Sequencher Connections™ if your research involves DNA sequencing. You will see increases in the speed, quality, and consistency of both Sanger and Next-Generation Sequencing (NGS) data analysis. Sequencher is known for its short learning curve and powerful editing tools. It is lightning fast and easy to use.

Sequencher is the standard around the world for Sanger sequencing. For Sanger analysis, Sequencher's cutting edge technology has brought the scientific community features such as an interactive variance table and assembly by sample name. Sequencher is the most widely used, commercially available DNA analysis program. Gene Codes has constantly met the needs of Sequencher users from the days of autoradiograms to capillary instruments to NGS technology.

NGS analysis tools are advancing at a rapid pace. Many of the cutting-edge algorithms are developed by and for bioinformaticists and computer scientists. Sequencher's latest NGS technology gives bench scientists as well as computer and bioinformatics scientists access to superior algorithms, offering an easy-to-use point and click interface as well as command line options. Easily load your NGS data and quickly organize, align, and analyze it with Sequencher. RNA-Seq analysis is the latest addition to Sequencher.

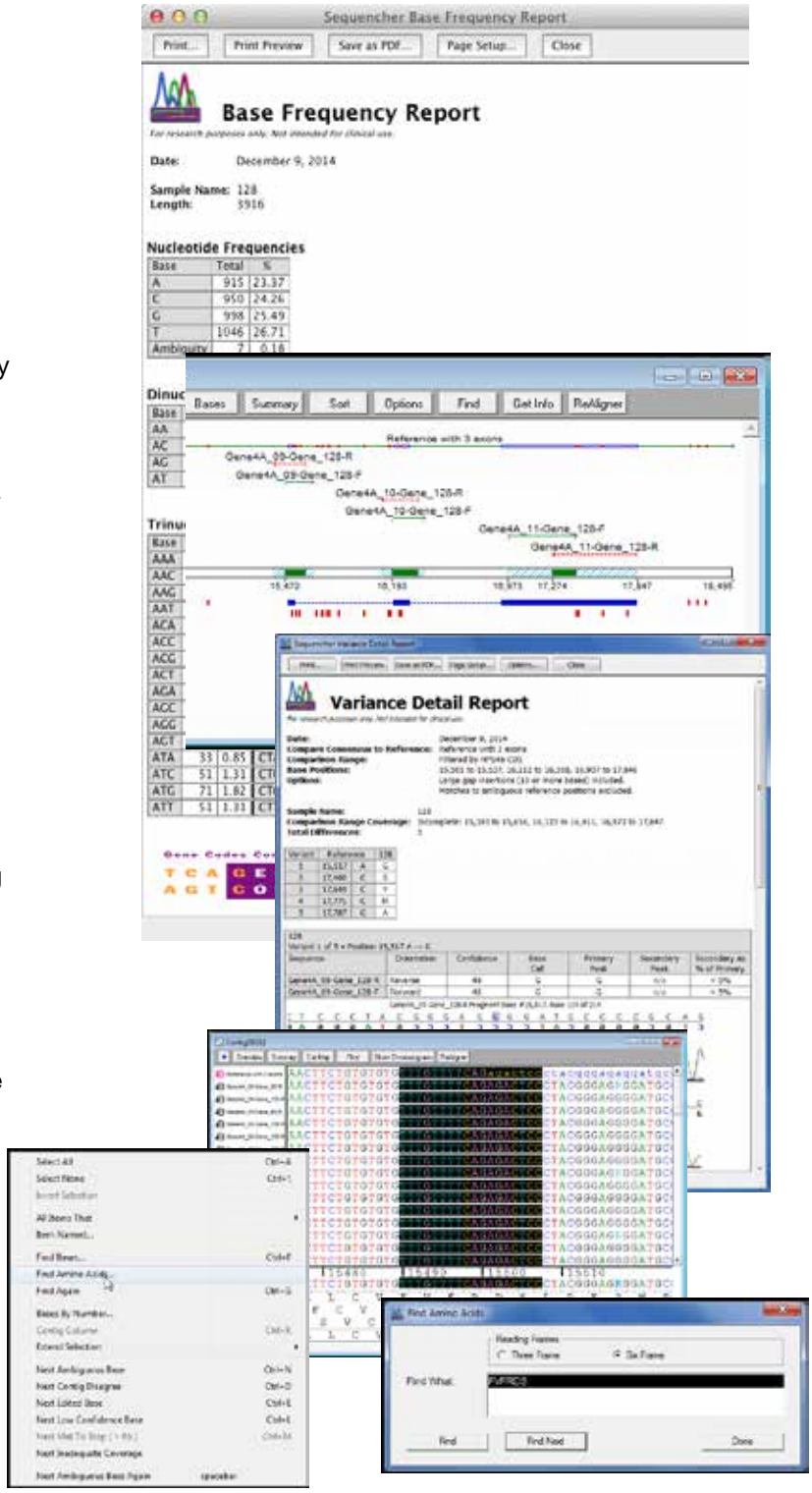
Sequencher is the best software for labs working with DNA data, whether Sanger or NGS. It is used across a wide range of disciplines including genetics for SNP discovery, systematics for evolutionary analysis, forensics for human identification, epidemiology for vaccine development and treatment selection, and mutation detection for clinical HIV analysis to name a few.

Quick to learn, easy to master with low IT overhead, Sequencher comes with industry leading technical support to help you make the most of the time and resources you've invested. Gene Codes provides flexible licensing, including unlimited support, and the option to receive all future upgrades on licenses that never expire. Connect with the new Sequencher.

Sequencher 5.3 for Sanger Sequencing Analysis

Sequencher gives you total control over the tools and features you need while being user friendly and powerful.

- Import data from any of the major CE instruments.
- Clean up raw data by trimming vector, low quality base calls and other artifacts.
- Perform alignment, de novo, or reference-based assembly with flexible, understandable parameters.
- Perform multiple-sequence alignment using Clustal or MUSCLE algorithms and several custom assembly modes.
- Move easily between aligned data and electropherograms. Analyze traces locally or globally to find secondary, uncalled peaks.
- Instantly and intuitively move between raw data to primary sequence to multiple-sequence alignments.
- Move smoothly between alignments and multi-frame translations at the base level to assembly overview and restriction analysis.
- Take advantage of your laboratory's naming conventions and organize all of your data processing using Assemble by Name.
- Save set up time by creating reusable templates for common projects.
- Use base numbering and features from the reference sequence to annotate new alignments.
- Generate reports that quickly and clearly document your findings.
- Refer back to raw data to eliminate sequencing artifacts.
- Use the Sequencher Variance Table to navigate your assemblies, discover SNPs, and more.



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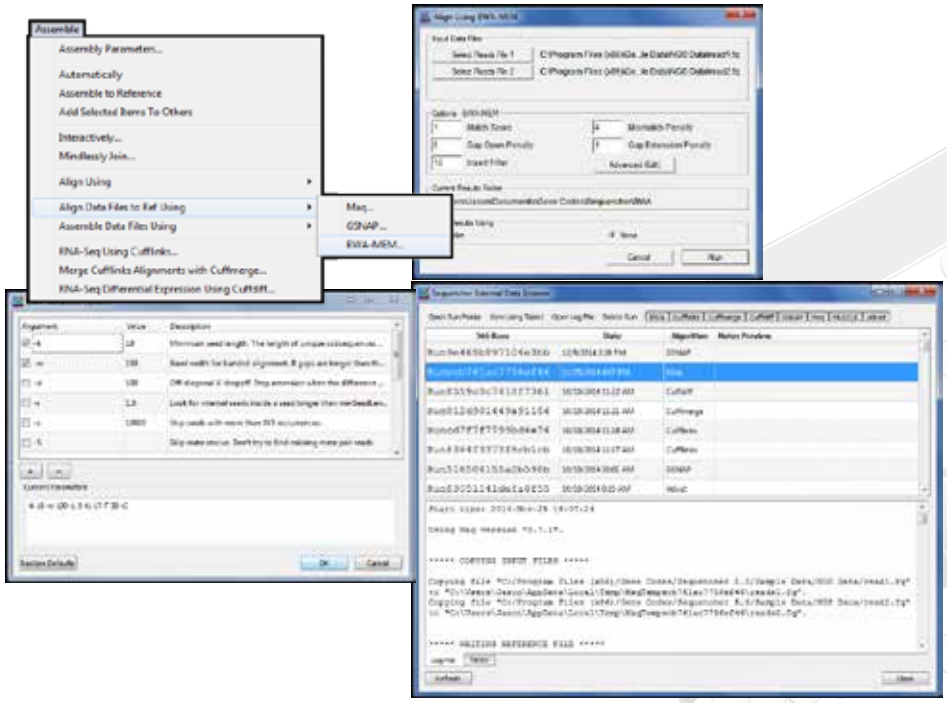
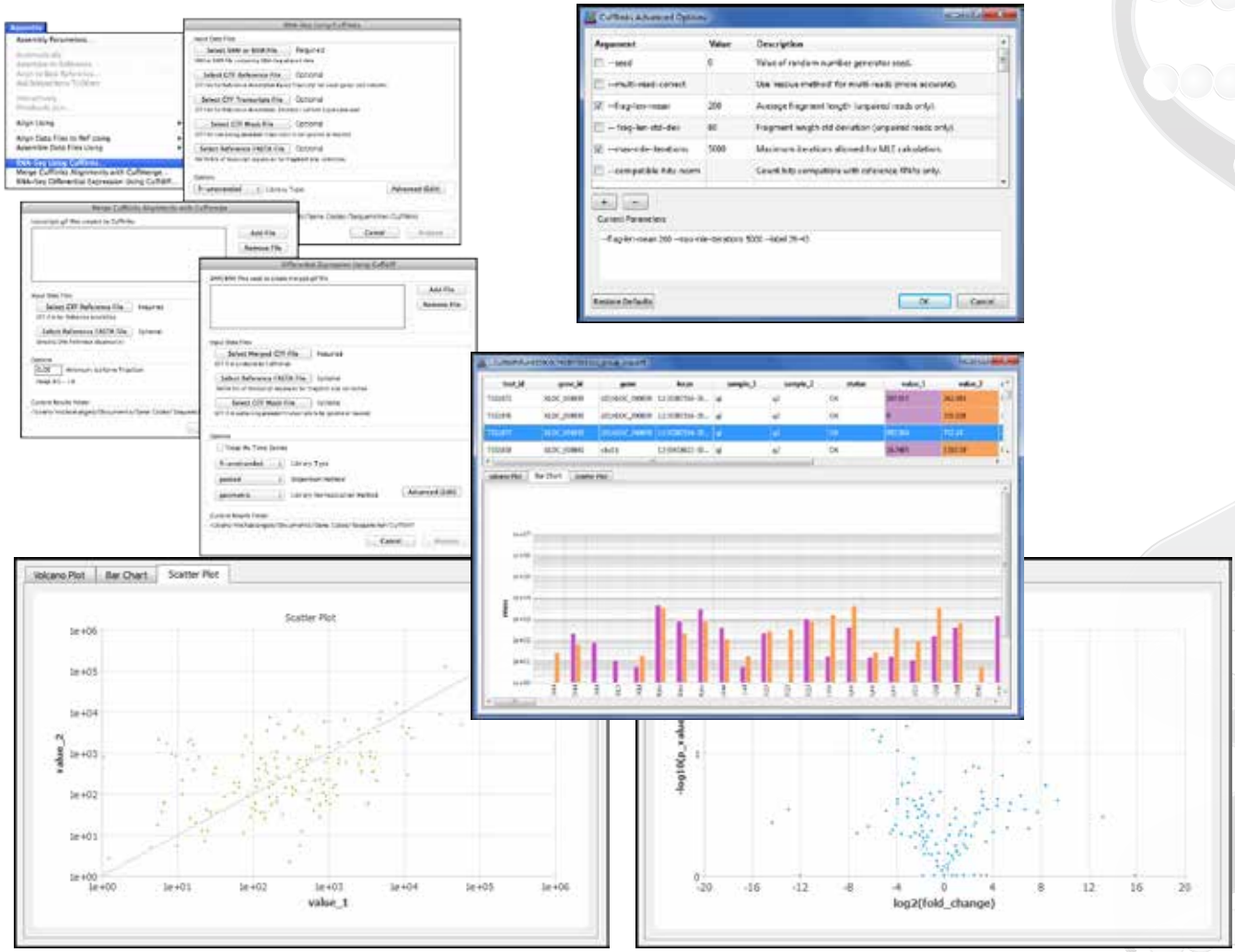
Alignment and assembly

- Easily import your NGS reads with Sequencher.
- Use Velvet for de novo assembly and Maq, GSNAP, and BWA for reference-guided alignment.
- With Sequencher's easy-to-use interface, you can use top tools developed by bioinformatics researchers without the command line.
- Use recommended settings or set up advanced parameter values for BWA, GSNAP, and Velvet to get the most out of your NGS datasets.
- Use Multiplex ID barcodes with BWA, GSNAP or Velvet to sequence a mixture of DNA samples in a single run.
- View your results using Tablet in a number of different modes, highlighting bases in different colors and read directions. Get information on individual reads and read pairs and arrange the stacking of the reads to reveal pairings. Tablet has controls to enable translations, zoom in and out, as well as highlight variant bases, making it a cinch to explore your reads.
- Perform SNP-tolerant alignments and SNP analysis with GSNAP and generate methylation reports from bisulfite-treated DNA.



RNA-Seq

- Sequencher now features the Cufflinks suite for the analysis of RNA-Seq data.
- Investigate differential expression using Cufflinks, Cuffmerge, and Cuffdiff, along with Sequencher's Display tools.
- Sequencher's graphic interface gives you access to the advanced command-line functions of the Cufflinks suite and lets you view the results as plots from within Sequencher without the need for the command-line.
- Choose from Volcano Plot, Scatter Plot and Bar Chart. Each spot or bar is linked to its underlying data to help you explore the results in detail.



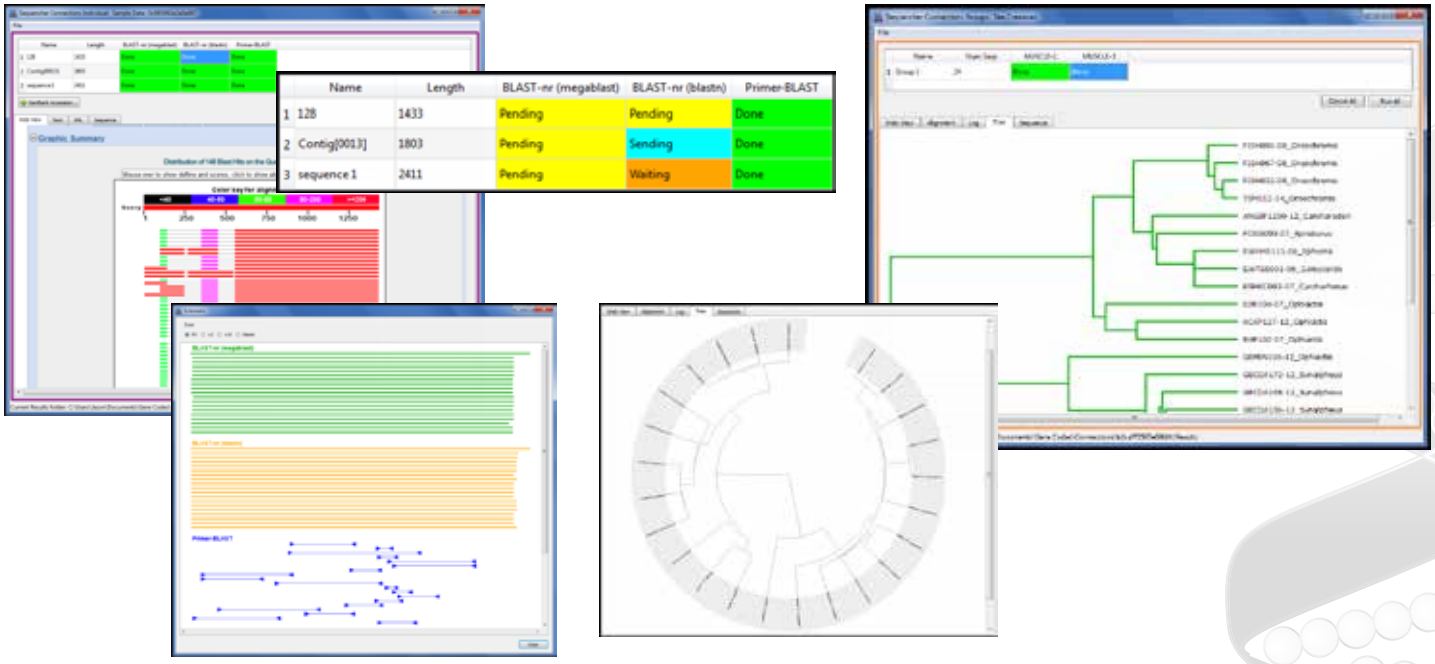
Sequencher 5.3 with Sequencher Connections

Sequencher 5.3 features enhancements to our latest innovation, Sequencher Connections.

The concept behind Sequencher Connections is straightforward but far reaching. It is a vision of taking a desktop application like Sequencher and integrating it with third-party plugin tools in your environment and remote tools over the internet. In short, connecting data, algorithms, and a scientist-centered user interface in a single platform that connects **you** to the rest of the world's resources.

Sequencher Connections gives you the power to:

- Run multiple analyses in parallel and monitor the progress of each in a control panel that updates in real time
- Simultaneously run multiple instances of the same application with different parameters and see the different results graphically
- Connect to NCBI over the internet and BLAST your DNA sequences against multiple GenBank databases
- Use Local-BLAST to search databases stored on your machine
- Use Primer-Blast to design primers
- Do multiple-sequence alignments with MUSCLE and create a phylogram to visualize the results



Sequencher is available for Windows, Macintosh or as a dual platform, dedicated or shared license and comes with:

- Unlimited Technical Support for one year
- Free upgrades for one year
- Optional network licensing capability
- Low-cost maintenance

Don't just take our word for it. See what your peers are saying about Sequencher.

"Sequencher is not just the best sequence analysis program I have used; it is one of the best pieces of software I have used. Period. It is intuitive: it does exactly what I want it to do in pretty much the way I would expect it to work. "

Wilson Clements, Ph.D.
St. Jude Children's Research Hospital, Memphis

"Whether it has been for building contigs in the search for novel causative mutations, verifying proper vector construction, or simply aligning large numbers of samples for typing of a single SNP, it has been an invaluable tool. With the advent of next-generation sequencing technologies, it becomes even more necessary to have trustworthy, user-friendly software."

Rob Loechel
Chief Scientific Officer, Vetgen, L.L.C.

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