Fast, complete automation for sequence assembly. The new, affordable, easy-to-use, AutoAssembler™ software for the Macintosh® performs labor-intensive tasks for you, saving valuable time while providing the most accurate results. AutoAssembler simplifies sequence assembly by automating each step of the process—from vector deactivation, sequence “cleanup”, and assembly, to easy resolution of sequence ambiguities. With full automation, any DNA sequencing project moves from primary sequences to a consensus sequence in record time.

Perkin-Elmer’s Applied Biosystems Division is dedicated to creating total sequencing solutions. AutoAssembler is the most recent addition to our suite of integrated bioinformatics products designed to manage complex sequencing projects. The flexible and powerful AutoAssembler software package is ideal for researchers performing small to medium size sequencing projects.

Accurate results and reliable data management. AutoAssembler’s powerful algorithms deliver the most accurate results, making it the most reliable approach to sequence assembly. AutoAssembler automatically examines all possible relationships between sequences, in both orientations. Dynamic programming is used to determine the optimum sequence order, resulting in a precise consensus sequence.

Multiple projects are efficiently managed and easily updated. Convenient sequence and project reports monitor sequence quality and project progress. In addition, data integrity is always maintained because AutoAssembler allows you to go back and review all stages of your project at any time. No data is ever lost and original sequence information is always preserved. Deactivated vector and ambiguity sequence regions, as well as edited base calls, can be easily viewed or reactivated as original primary base sequences. Moreover, unlike other software programs, this information is preserved within the original sequencer data files, making data management easier and more reliable.

Flexible, graphical access to data for viewing results and effortless editing. AutoAssembler works efficiently to deliver results, find ambiguities, and access primary data throughout your sequence assembly project. Results can be graphically viewed and quickly interchanged as project layouts, bar and sequence alignments, and aligned, multiple, four-color electropherograms, allowing you to analyze your data from several different perspectives. The unique statistics view helps you quickly identify ambiguous sequence regions. Electropherograms, features tables, sequence annotations, and edited and primary sequence data are accessible and easily edited directly from within any part of the program and for any sequence.
Simplicity and automation means results in three easy steps. With complete automation, your sequence assembly project is accurately and quickly completed in three simple steps. AutoAssembler integrates seamlessly with data collected on the ABI 373 DNA Sequencer, as well as text sequence files. You can simply process your data after every sequencer run, updating your projects on a day-by-day basis. What’s more, automated assembly is accomplished right from your desktop with the user-friendly Macintosh platform; and the AutoAssembler software comes standard with “Balloon Help” so you have quick access to valuable reference information.

Step 1

Automatic, batch-mode sequence cleanup and feature identification. AutoAssembler consists of two software applications that work in tandem. The first application, Factura, operates to identify features automatically in batch-mode. Up to 1,000 ABI 373 DNA Sequencer sample files or text files can be processed in batch-mode to de-activate vector/primer cloning sites and areas of ambiguity according to user-set criteria. Factura can also assign IUB characters to ambiguous bases, simplifying downstream sequence editing. Impressive feature identification design provides information pertaining to feature location and feature type, such as vector, ambiguous sequence regions, and IUB character positions, to be written to the original sequence file. No data is ever lost, so any deactivated data can be reactivated at any point along the process. The “cleaned up”, edited sequences are then submitted as a batch worksheet for assembly in the second software application, AutoAssembler.

Step 2

Just click on “assemble” to assemble your sequences. All of the batch sequences are assembled using either the convenient default parameters or according to user-defined criteria.

Step 3

Easily view and edit results. AutoAssembler’s versatile methods of viewing your data are linked and work effortlessly together so that you can be confident that, when you switch from the electropherogram view to the alignment view, for example, you are not compromising data integrity. No other program offers data viewing and editing capabilities that are this easy to use and highly integrated! Informatively, four-color electropherograms, graphical views of assembled results and primary sequence are shown. Flagged sequence ambiguities shown in the statistics, layout, and alignment views may be directly edited or quickly viewed as multiple, aligned electropherograms for on-screen correction of base calls. In addition, edited sequences, as well as new sequences, may be added to the project for automated incremental assembly.

Easily view and manage assembly results. Zoom features and view buttons (layout, alignment, statistics) allow you to effortlessly analyze your assembly project from a variety of perspectives. Start with the layout view of the entire project:

Then click on the statistics view, which shows level of ambiguity across the whole project and locate areas that need editing or more sequence coverage.
Factura: Automatic sequence cleanup and feature identification. Factura provides easy setup for user-defined screening criteria to automatically deactivate vector sequence, identify sequence ambiguities, and assign IUB characters for all sequences in batch-mode. Simply add all of your ABI 373 files into a batch worksheet for fast, reliable data processing. Electronically generated reports define sequence quality and feature locations. These processed files are then effortlessly imported into AutoAssembler for sequence assembly.

On-line tools make AutoAssembler quick and easy to learn. AutoAssembler was designed to be an easy-to-use tool, and comes standard with unique features to help you quickly learn how to take advantage of the powerful features built into the software. In addition to “Balloon Help,” an on-line tutorial teaches you program operation to get you up and running in no time.

Easily upgrade for large scale sequencing projects. AutoAssembler can be easily upgraded to address large scale sequencing projects. The Macintosh-based AutoAssembler is an affordable first step into the powerful client-server based INHERIT® AutoAssembler. With INHERIT, any number of Macintosh clients are networked with a SUN Microsystems® server and FDF® Data Search System® to provide shared-use efficiency and faster performance when addressing any size sequencing project. Upgrading is worry-free since the user-interface for the INHERIT AutoAssembler Macintosh client and Macintosh-based AutoAssembler are identical.

Commitment to cutting-edge software tools and total system solutions. Perkin-Elmer’s Applied Biosystems Division is committed to developing labor-saving tools to address the analysis and management of sequencing and genetic-based data. We now offer several easy-to-use, affordable Macintosh products that work together effortlessly to create reliable, integrated data analysis systems. Our suite of complementary data products include: AutoAssembler automated sequence assembly software; Sequence Navigator® DNA and protein comparison software; Genotyper™ automated genetic analysis software; and the powerful shared-use, client-server INHERIT Sequence Analysis System for high performance assembly, sequence analysis, and motif and DNA/protein homology database searching. These powerful software products offer compelling solutions to all aspects of your research.

Build Consensus

Highlight an ambiguous area and click on alignment. The alignment view shows base sequence alignment of all sequences, as well as the consensus sequence. Now, highlight an ambiguous region in the consensus sequence and show multiple aligned, four-color electropherograms. You can directly edit the base calls on the electropherograms or consensus sequence. Easy-to-use vertical and horizontal zooming cursors help expand the data for viewing.

Now, build a consensus sequence, reassemble with more sequences or export to other packages, such as INHERIT® Sequence Analysis System and Sequence Navigator® comparative sequencing software.
AutoAssembler Specifications

Macintosh® requirements/printer compatibility

Compatible with Apple® Macintosh® IIci, IIfx, Centris and Quadra line. For optimal performance, use Quadra (Centris) 650 or above. 13" RGB color monitor; 16" or larger color monitor facilitates easier editing. Minimum 80 Mbyte hard disk storage and 8 Mbyte RAM required. Recommend 16 Mbyte RAM for optimal operation. Print with Apple-compatible printers, including LaserWriter, ImageWriter, StyleWriter, and Tektronix ColorQuick or Phaser 200E. Compatible with Macintosh system 7.0 and 7.1.

Input/output

- ABI 373 sample files
- Macintosh ASCII text files
- INHERIT files
- Consensus sequence file
- Layout file (Sequence Navigator™, SeqEd™)

Reports/printouts

- Factura Batch Report with vector/feature identifications
- Project Report
- Assemble Report
- Printed 4-color electropherograms with graphically marked features
- Sample files with annotations, features table, and sequence

Assembly algorithms

Based on collaborative work with Applied Biosystems and the following:
- Contig Assembly Program (CAP) for local assembly on the Macintosh
- Meyers-Kececioglu algorithm for remote assembly on the SUN server product

Packages

AutoAssembler Software Package

Macintosh-based software as standalone or client to INHERIT AutoAssembler client-server system. Includes application software, on-line tutorial, user manual, tutorial data files, and reference mousepad. 90-day limited warranty on parts. Single-user license.

AutoAssembler Multipacks for the Macintosh

- AutoAssembler, 1-pack: 401725
- AutoAssembler, 2-pack: 401406
- AutoAssembler, 5-pack: 401407
- AutoAssembler, 10-pack: 401408

INHERIT AutoAssembler, Client-Server, Kit

Includes AutoAssembler Macintosh software for three users and SUN® Server Software, user manuals. 90-day limited warranty on parts.

Service Installation: 700025
User Installation: 401567

INHERIT AutoAssembler SUN Server Software

Includes user manual. One year limited warranty on parts and technical support.

Runs on SUN Microsystems® Workstation®: minimum 16 Mbyte RAM, 424 Mbyte hard disk. Ethernet network required.

670 Data Search System

- FDF® hardware for fast sequence comparisons. One year limited warranty on parts.
- Service installation.

References


Specifications are subject to change.

AutoAssembler™, PRISM™, Sequence Navigator™ and Genotyper™ are trademarks and INHERIT® is a registered trademark of the Perkin-Elmer Corporation.
All brand names and product names are trademarks of their respective holders.

© 1994 Applied Biosystems, Inc.
A Division of the Perkin-Elmer Corporation

For more information: