



BIOVIA PIPELINE PILOT SEQUENCE ANALYSIS COMPONENT COLLECTION

Datasheet

The BIOVIA Pipeline Pilot Sequence Analysis offers essential bioinformatics tools and algorithms for creating practical sequence analysis workflows that complement any laboratory research. With over 100 different component functions, you can analyze and annotate nucleotide and protein sequences using a variety of industry accepted methods.

BENEFITS OF BIOVIA PIPELINE PILOT FOR SEQUENCE ANALYSIS:

- Automate your routine analysis of new sequence data
- Compare genes and genomes across species
- Prototype new algorithmic processes
- Annotate nucleotide and protein sequences using several databases
- Integrate your own algorithms into any protocol

SEQUENCE SIMILARITY SEARCHING

For uncomplicated sequence similarity searching, use the Smith-Waterman component or any of our standard BLAST components, including BLASTn, BLASTp, BLASTx, tBLASTn, and tBLASTx. Display the results of these searches with our Similarity Search Viewer, and extract or fetch to further analyze the individual hits. BIOVIA Pipeline Pilot also makes it easy to build custom BLAST databases on-the-fly, providing more targeted and intelligent sequence similarity searches.

MANIPULATION AND ANNOTATION

An assortment of sequence manipulation and annotation components are available. For nucleotide sequences, these components include functions such as primer identification, GC content, six-frame translations, reverse complement, and siRNA target site prediction. For protein sequences, you can back translate, predict secondary structure, and calculate isoelectric point.

ALIGNMENT AND PROFILE SEARCHING

To identify potential homologs among a collection of different organisms and quickly select variants among nucleotide sequence regions, you can use our alignment and profiling

components. To allow for multiple sequence alignments of either nucleotide or protein sequences, MUSCLE, ClustalW, and Clustal Omega algorithms are provided. For profiling tasks, HMM Build, Align, Search, and Pfam are available.

PATTERN MATCHING

A variety of standard tools are implemented so you can search for interesting patterns or motifs within a biological sequence.

These algorithms enable the identification of potential PROSITE regions, GC rich regions, proteolytic cleavage sites, restriction enzyme sites, signal peptide cleavage sites, open reading frames, or regular expression patterns.

RESULT VIEWERS

You can also visualize sequence information and related features with our sequence viewers. These viewers include a custom report (PDF or HTML), plain text view, or Artemis viewer (for nucleotide sequences). Also, multiple sequence alignments can be displayed in a custom report (PDF or HTML), plain text, or JalView.

THIRD-PARTY TOOL INTEGRATION

The BIOVIA Pipeline Pilot Sequence Analysis includes examples of integration with BioPerl, NCBI BLAST, EMBOSS tools, and BioJava. You can use these examples as templates to extend the available functionality to include other programs of interest. Your BIOVIA Pipeline Pilot integration options include Python, Java, Perl, web services, C#, .NET, VB Script, or writing simple command-line wrappers.

LEARN MORE

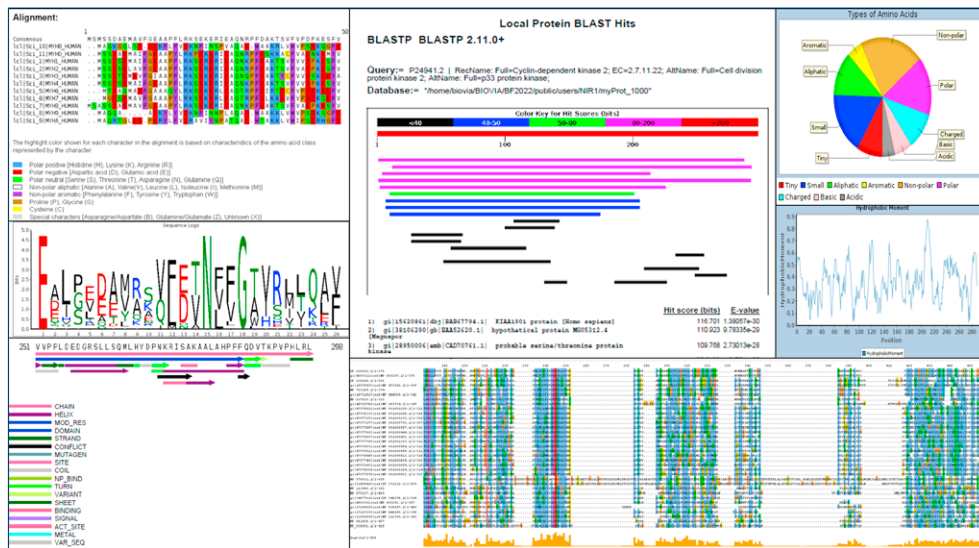
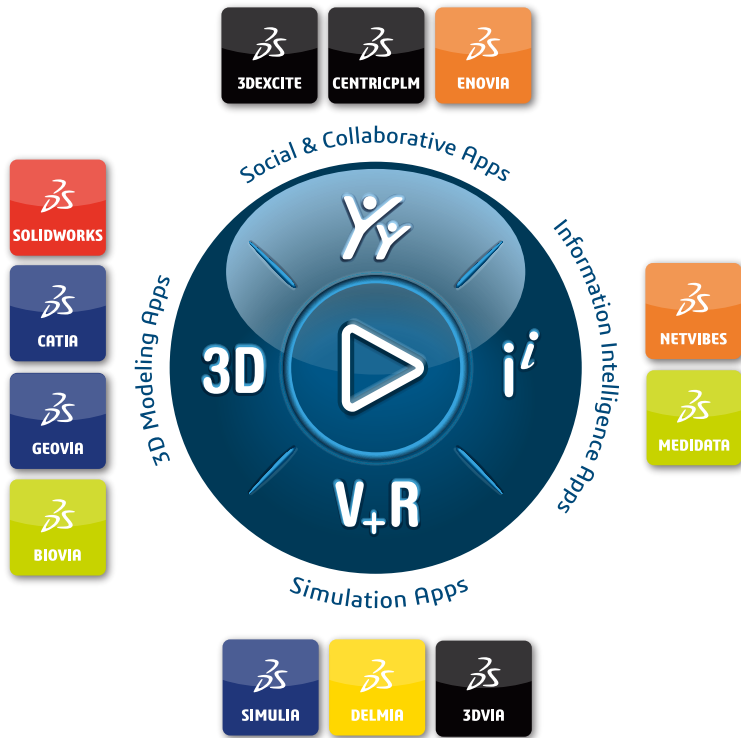


Figure 1. BIOVIA Pipeline Pilot Sequence analysis collection automates nucleotide and protein sequence similarity searches, annotation, manipulation, alignment, profile searching, pattern matching with multiple viewing and reporting options.



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Europe/Middle East/Africa
 Dassault Systèmes
 10, rue Marcel Dassault
 CS 40501
 78946 Vélizy-Villacoublay Cedex
 France

Asia-Pacific
 Dassault Systèmes K.K.
 ThinkPark Tower
 2-1-1 Osaki, Shinagawa-ku,
 Tokyo 141-6020
 Japan

Americas
 Dassault Systèmes
 175 Wyman Street
 Waltham, Massachusetts
 02451-1223
 USA



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