

# ANGIS and BioManager:

Tools for discovery and diagnostics

## What is ANGIS?

The Australian National Genomic Information Service (ANGIS) provides access for biologists to a comprehensive system of bioinformatics software, databases, documentation, training and support, on a subscription basis.

In excess of 5000 scientists from over 160 biological, medical and biotechnological organisations depend on ANGIS's flexible and dedicated facility. With **WebANGIS** and **BioManager**, researchers throughout Australia access ANGIS, through the internet, to analyse their data and search the many nucleotide, protein, structure, and reference databases available.

ANGIS supports and encourages the use of the Service in undergraduate and postgraduate university courses and regularly conducts introductory and advanced courses and workshops in applied bioinformatics and BioManager.

## BioManager: Your Bioinformatics Workspace

BioManager is an integrated bioinformatics workspace with a user-friendly and intuitive graphical interface. BioManager provides easy access to a complete suite of tools so that, regardless of your bioinformatics experience, all operations from uploading data from your desktop through to running programs and downloading results and figures for reports and publications, are easily accomplished.

- You can easily upload or paste your data into BioManager or use **Text Search** to extract data from one of the available databases including GenBank, SWISS-PROT, Blocks, Prosite, Enzyme, Pfam and StackDB.
- BioManager's **History View** records all your analyses to provide a "virtual lab book". Use the History View to create a **Macro** and automate and standardise your regular analyses.
- If you are new to bioinformatics, BioManager's **Protocols** will guide you through unfamiliar analyses.
- An extensive **on-line help** system is available by clicking the **HELP** button from any screen within BioManager or by clicking hyperlinked text within BioManager.



BioManager provides access to over **170 programs** which include functions for:

- Sequence database similarity search
- Pairwise sequence comparison
- Nucleic acid structure and analysis
- Sequence file management
- Gene detection and translation
- Multiple sequence analysis
- Statistical analysis
- Motif and pattern analysis
- Protein structure and function
- Molecular Modelling
- Molecular evolution
- PCR primer design
- Set Operations
- Mapping

## How do I get started with BioManager?

BioManager is available to all ANGIS users who have a current ANGIS subscription. Contact ANGIS at [help@angis.org.au](mailto:help@angis.org.au) for subscription information.

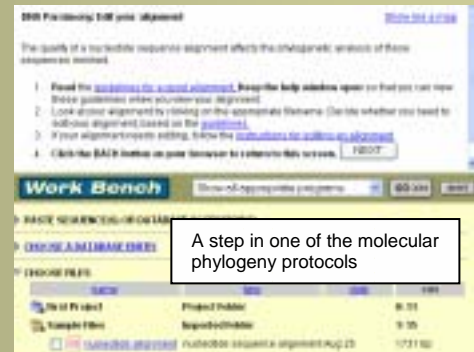
Use your ANGIS account name and password to log in from the ANGIS home page at <http://www.angis.org.au>.

- Try the "How to use BioManager" **Protocol** for an introduction to essential BioManager features.
- For more detailed exercises in BioManager, two BioManager tutorials, "Getting started with BioManager" and "Getting more out of BioManager" can be downloaded in PDF format.

# More BioManager Features

**Not sure how to do an analysis? Let BioManager's Protocols show you how.**

BioManager's **Protocols** make complex multi-step bioinformatics analyses, such as the **phylogenetic analysis of sequence data**, available to novice users. Protocols have an extra window containing step-by-step instructions (with links to appropriate help) to direct you which steps to perform in the BioManager window below. At any time you can click on a map to see how far you've progressed through the protocol.



A step in one of the molecular phylogeny protocols

**Do you have hundreds of sequences to analyse? Create sets to analyse them in one step.**

BioManager allows you to automate the analysis of large groups of data by creating sets of files. Sets allow you to run a program on every sequence (or file) in that set with the same simple process that you would run a program on a single sequence (or file). Sets of up to **10,000 sequences** can be reliably analysed. Sets can be uploaded from your desktop and/or created and edited within BioManager using the various set operation tools.

**Do you routinely perform the same analyses? You can automate them with Macros.**

Over 20 BioManager **Macros** have been included in the **Program Index** to automate common series of bioinformatics analyses. For example, the **Identify an unknown DNA sequence** macro will run the programs GenScan, blastn and blastx on a nucleotide sequence and generate a report summarising these results. You can create your own macros from a file's **History View** to automate your own analyses and program settings.



History View tracks all your analyses, including program options.

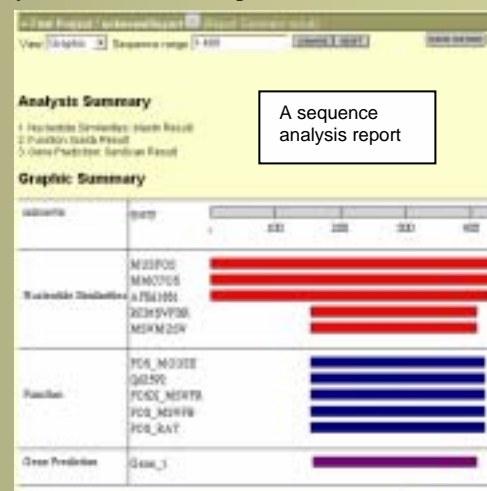
**Keep track of your work and automate repetitive analyses using History View and Macros.**

All inputs, outputs, programs run and parameters used are recorded in BioManager's on-line bioinformatics lab-notebook, the **History View**.

A file's **History View** can show all the analyses that led to the creation of that file as well as all those analyses that have since been performed on that file. You can save all or only some of these steps as a **Macro**, so that you can simply and **quickly reproduce an experiment on any input**. Macros can also be shared with any nominated collaborators or colleagues.

**Automatically generate sequence analysis reports with Report Generator.**

BioManager's program, **Report Generator**, allows you to quickly summarise in a report, the results of a range of bioinformatics analyses on an unknown sequence. This graphical summary report file can be easily exported ready for publication. Programs in BioManager supported by this feature include: BLAST, BlockSearcher, CoilScan, FASTA, FindPatterns, Flip ORFs, Garnier, GenScan, HMMpfam, HTHScan, Motifs, Secondary Structure Prediction, SPScan, and Ssearch.



A sequence analysis report

**Download publication quality diagrams for your reports.**

Use BioManager to generate publication quality diagrams and figures for your publications and presentations. These can then be downloaded in a format suitable for printing and editing using a range of desktop graphic editing packages, or simply imported directly into your documents.