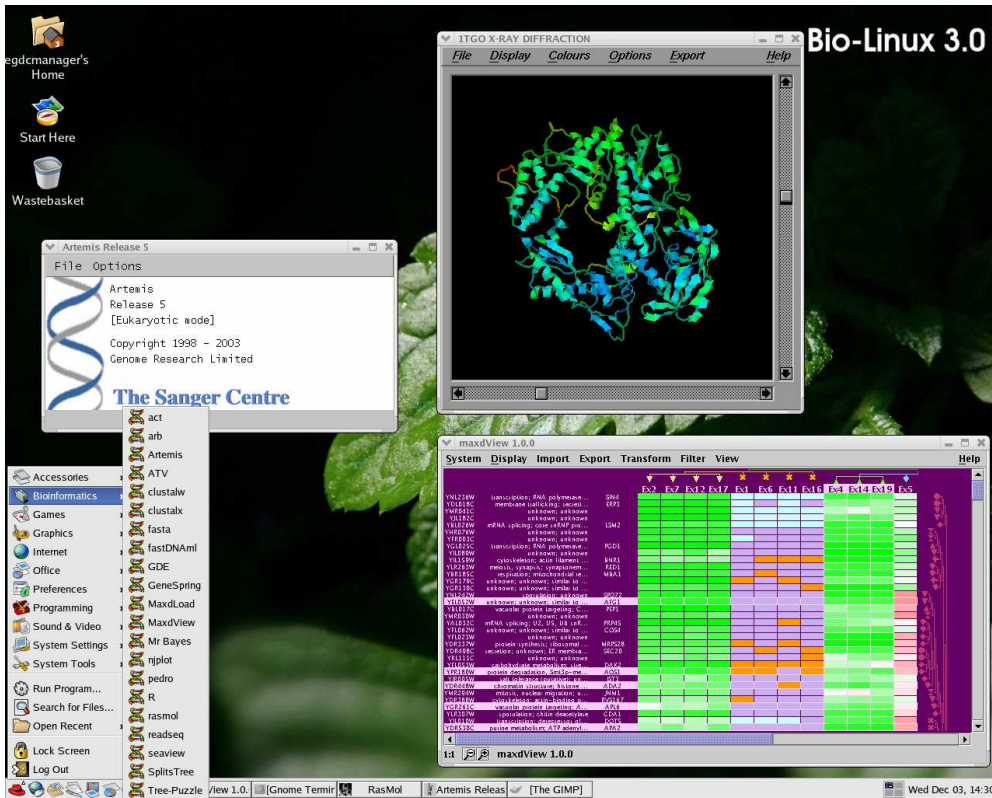# Bio-Linux 3.0

Bio-Linux - an integrated, bioinformatics-centric computer system

New Features

Bioinformatics

- QTL software
- integrated EST pipeline
- new versions of maxd and maxdLoad
- latest versions of bioinformatics software
- new software including Stars and Pedro

System

- based on RedHat 9.0
- improved automatic system update mechanism
- easier system administration
- ready for clusertering using Condor
- more development tools including BioJava and Eclipse IDE

By providing standard favourite and cutting edge bioinformatics tools on a Linux-based system, Bio-Linux combines the benefits of being powerful, configurable, and easily updatable, with the ease of use and potential for software integration required for the handling and analysis of biological data.

Version 3.0 includes many new features including new software for bioinformatics analysis, the improved system handling provided by RedHat 9.0, and being ready to cluster with other machines running the Condor package.

To get Bio-Linux, or to upgrade from an earlier version of Bio-Linux, please refer to the information at the key websites listed below, and book an install date by emailing the EGTDC helpdesk at
helpdesk@envgen.nox.ac.uk

Key web pages:

Bio-Linux main page	envgen.nox.ac.uk/biolinux.html
How to upgrade to Bio-Linux 3.0	envgen.nox.ac.uk/envgen/software/archives/000409.html
How to request Bio-Linux	envgen.nox.ac.uk/envgen/software/archives/000426.html
Major changes between Bio-Linux 2.x and 3.0	envgen.nox.ac.uk/envgen/software/archives/000425.html
Bioinformatics software versions on 3.0	envgen.nox.ac.uk/envgen/software/archives/000430.html

Bio-Linux Mailing List: www.bioinf.ceh.ac.uk/mailman/listinfo/bio-linux