



## Information Document for Undergraduate Teachers using BioManager

The following document is designed to assist teachers who wish to use BioManager as a tool in their undergraduate classes.

**Setting up an account:** Any university department that has an ANGIS subscription is able to ask for a temporary set of class accounts in order to run a practical class in bioinformatics. These accounts can be used ONLY for the undergraduate class and must be cleaned out at the completion of the class period. These accounts cannot be used as research accounts. Periodic checks on the accounts will be made to ensure compliance with this requirement.

To request a class account you need to contact [help@angis.org.au](mailto:help@angis.org.au) at least 5 working days before the class begins. You will then be provided with a list of logins and passwords in which to use. A class account request MUST be accompanied with the time table details of the class (day and time). We will then be able to keep an eye on the jobs during the class (provided the class is held during EST business hours). Only two (2) classes' national wide can be scheduled at any particular time. We cannot guarantee the jobs of any classes run without our knowledge or in addition to the two scheduled in a session. Passwords will be changed at the end of the semester.

From feedback on previous courses, we have identified the following ways in which to ensure your class runs smoothly.

- Each student must use a unique login as multiple accesses to a single account will cause problems in running programs and viewing the results.
- When using Blast and FastA database searching programs, please use where possible the Course DNA and Course protein databases. This will reduce search times significantly as these programs are the first to suffer (in speed) when the user load is high. If the sequences that you need are not in these databases, provide us with a list of accession numbers and we will enter them into the database (send list to [help@angis.org.au](mailto:help@angis.org.au)).
- Do not use any of the Maximum likelihood programs as these often take a day to run.
- If you require Bootstrapping, reduce the number of iterations/bootstraps to 10. (The time taken for this analysis is 10x the time it takes for a single analysis).
- If you are familiar to the QUERYDB system in the old WebANGIS, TextSearch Advanced gives you the same type of options.
- The heavy load from classes sometimes gives problems and the server needs to be restarted. When this happens you may find the screen goes white and a PROXY ERROR appears. Within 2 minutes of this happening the system would be fixed automatically. If this does not occur, please contact support (02 9351 8619).
- You can use the SHARE/IMPORT options to share folders between the teachers account and the students (if you wish everyone to have the same starter files). Select the relevant folder and SHARE with all the student logins. The students then IMPORT from your login. The IMPORTED folder needs to be COPIED into a new folder in order for any analysis to be done.

Please note:

- Inform your students not to be impatient as clicking on the Go button several time actually sends out additional jobs (see note below) and will slow the whole class significantly.
- A maximum of three (3) jobs per login will be run simultaneously. Any additional jobs will have to wait for these jobs to be completed before they will start. If the system is moderately busy, the maximum number of jobs run at a time will more likely be two (2).

If you run into any problems during the class, contact us on 02 9351 8619 or email us at the completion of the class on [help@angis.edu.au](mailto:help@angis.edu.au) with any comments/suggestions.