

The ever increasing amount of data flowing into biological databases shows no signs of leveling off. Sequencing technology is improving at an unprecedented rate, bringing down the time it takes to decipher entire genomes to a matter of days. Making sense of this data by predicting molecular function is a time-consuming and tedious manual task.

Our group which is part of the Biomolecular Function Discovery Division at the Bioinformatics Institute (BII) is developing an advanced tool for functional characterization of sequences and strives to establish the ANNOTATOR software environment as the de-facto standard in this field.

We are looking for a

## **Software Engineer - Infrastructure**

The successful candidate will be responsible for installing and maintaining the ANNOTATOR software as well as components it depends upon. This includes the following task:

- Setup and maintain ANNOTATOR instances:
  - Setup and upgrade of ANNOTATOR instances.
  - Periodical update of sequence and pattern databases of individual ANNOTATOR instances.
  - Implement build system to automate the above mentioned tasks.
  - Maintain ANNOTATOR import scripts for individual databases.
  - Setup and upgrade database software (Postgres).
- Actively participate in the development of import scripts for new databases.
- Maintain and enhance test suite.
- Maintain Batch Queuing System interface.
- Setup and maintain Version Control Software (subversion).
- Setup and maintain Bug-Tracking software.

Qualifications needed:

- A strong background in Unix(Linux) is essential.
- Java
- C/C++
- Shell-scripts
- Perl
- SQL
- Postgres maintenance

Please submit your detailed resume via email to [recruit@bii.a-star.edu.sg](mailto:recruit@bii.a-star.edu.sg) or send it to the HR Department, Bioinformatics Institute, 30 Biopolis Street, #07-01, Matrix S(138671).