In collaboration with the TAMU Supercomputing Facility, we have deployed a local instantiation of Galaxy.

Why Galaxy?
- Galaxy is Open Source Certified and is Free!
- Galaxy is a top representative of the Next Generation of Genome Analysis Tools
- Galaxy combines data analysis and data display
- Galaxy makes Bioinformatic pipelines reproducible
- Galaxy allows you to share pipelines of analysis
- Galaxy is modular and expandable
- Galaxy has LIMS modules available
- Galaxy has both public and private environments
- Galaxy makes Bioinformatics Social Networking a reality

Formed in the Spring of 2009 with support from the Office of the VPR, the COS, Chemistry and Biology.
The LGB is physically located in, and affiliated to, the Institute of Developmental and Molecular Biology (IDMB).
We have eight workstations that have been configured to run the most popular Bioinformatics tools. These workstations are used in the teaching of Genomics (BIOL/BICH450 and BIOL/BICH650) and have been informally open to selected members of the campus community for testing and will soon be open to the campus community at large.

Our workstations have:
- Tools for Alignment of DNA and Proteins
- Tools for Expressed Sequence Tags Analysis
- Tools for Finding Genes
- Tools for Designing Oligonucleotides
- Tools for Phylogenetic Analysis
- Tools for Sequence Format and Analysis
- Tools for the Identification of Repeat Families
- Tools for Comparative Genomics
- Tools for MS/MS Analysis
- Tools for the Manipulation of Small Reads
- The EMBOSS Package
- Tools for Genome Data Display (Genome Browsers)

We have also developed and tested configuration protocols for the installation and use of Open Source Bioinformatics software.