In September, 2011 GSAF staff presented a three-section training on using the GSAF at UT to get NGS projects done. The full presentation can be found here. In outline, we presented:

**What the GSAF does** - from helping with experimental design through QC and library prep and into data analysis, see what the GSAF does day-to-day.

**Application examples:**

1. Finding variants using "short-read" NGS platforms (Life Technologies SOLiD and Illumina HiSeq)
2. Analyzing transcriptomes for gene expression and gene variants using short-read NGS platforms and de novo sequencing using both 454 and Illumina data
   a. describe starting material requirements
   b. discuss a schematic of the prep method
   c. plot prep time, run time, and costs, and
   d. show a typical bioinformatic analysis pipeline (command names, what data looks like, etc.)

**Training and links for our new Galaxy Workflow & Sample Submission system: a "How to work with the GSAF"**

1. Discussing projects & experimental design
2. Getting a quote/checking the queue via Galaxy
3. Submitting your samples
4. Getting your results
5. Analyzing your data on the GSAF server and at TACC
6. Getting help