In this specific project using the software mentioned on a remote HPC has greatly helped by using parallelization strategies to achieve faster runtimes of the analysis and providing more storage and computing power than available on other platforms. Transcriptional profiling of the tests after changes in the JAK/STAT pathway has made this experiment the first in its kind of RNAseq transcriptional profiling experiments in flies.

### Future Directions
- Comparison of transcriptional profiling of this study with transcriptional profiles done with other fertility mutants.
- Confirm transcript expression using qPCR.
- Analyzing expression of specific transcripts that are known to be binding sites for STAT.
- Functionally analyze candidates that are target for individualization during spermiogenesis.

### Use of HPC
Because of the high data volume of Next-generation sequencing experiments, analyses are time-consuming and high-performance computing clusters like the DLX provide great advantages for such research.

In this specific project using the software mentioned on a remote HPC has greatly helped by using parallelization strategies to achieve faster runtimes of the analysis and providing more storage and computing power than available on other platforms. Transcriptional profiling of the tests after changes in the JAK/STAT pathway has made this experiment the first in its kind of RNAseq transcriptional profiling experiments in flies.

### Experimental pipeline
- Dissecting tests and RNA extraction
- Sequencing
- Performing differential expression

### Bioinformatic pipeline
- RSEM
- EbSeq
- JMP

### Differential expression analysis
- Hierarchical clustering Heatmap showing different expression levels in transcripts of control vs experiment

### Expression profile
- 35044 transcripts showed expression
- 1508 transcripts were up-regulated in A90:UAS-lat relative to A90 control more than two-fold
- 0.5% of all transcripts were down-regulated in A90:UAS-lat relative to A90 control more than two-fold

### Transcriptional profiling
- Comparison of transcriptional profiling of this study with transcriptional profiles done with other fertility mutants.
- Confirm transcript expression using qPCR.
- Analyzing expression of specific transcripts that are known to be binding sites for STAT.
- Functionally analyze candidates that are target for individualization during spermiogenesis.
Use of HPC to analyze changes in gene expression during fruit fly spermiogenesis
Sepideh Dadkhah, Douglas Harrison, Jeremiah J Smith
Department of Biology, University of Kentucky

• **Research Category:** Bio-informatics, NGS, Development, Spermiogenesis, JAK/STAT Pathway

• **Description of research:** This study has compared transcriptional profiles of testes in which JAK/STAT signaling has been genetically arrested prior to individualization during spermiogenesis to testes from wild type flies using RNA-seq methods.

• The main goal of this project is to characterize the events downstream of JAK/STAT signaling in spermiogenesis and more specifically to determine the mechanism by which JAK/STAT activation regulates individualization, a later stage in spermiogenesis where 64 individual spermatids are formed from a 64-interconnected spermatid bundle.