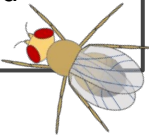
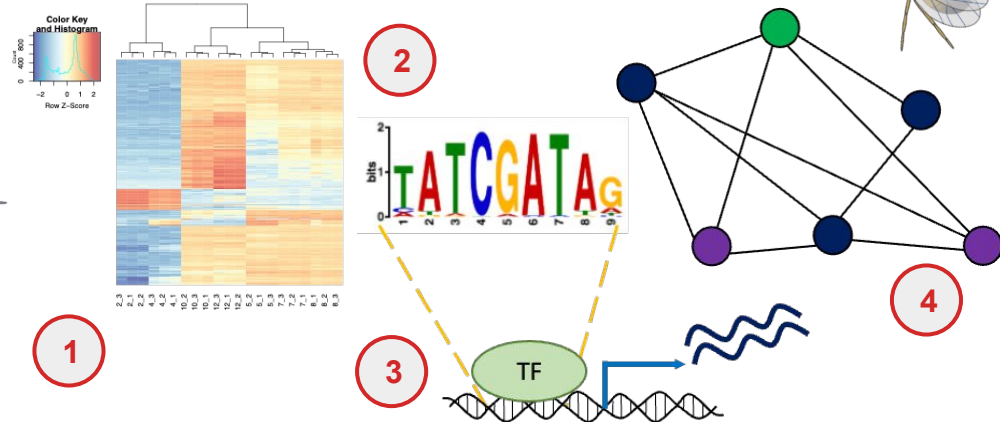
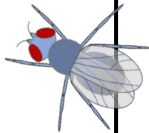


## Overview:

- Students will use publicly available *Drosophila* transcriptome data to identify patterns of gene expression across conditions
- Using identified groups of genes, students will complete motif enrichment analysis to examine regulatory sequences in upstream regions of the genes
- Students will synthesize findings to construct a model of gene regulation and outline future experimental testing and hypotheses

## Topics:

1. Introduction to differential gene expression and RNA-sequencing
2. Bioinformatics tools for identifying enriched sequences in gene regulatory regions
3. Transcription factors and transcription factor binding sites
4. Gene regulatory network analysis: GO analysis and KEGG pathways



The course will be designed to allow students to explore RNA-sequencing data, build confidence using computational tools for analysis, and connect findings from sequencing data to regulatory networks!

