

Comparative Plant Transcriptomics: Designing course-based research experiences for RNA sequencing analysis.

Clear advancements in undergraduate research training have been shown by designing course-based undergraduate research courses (CUREs). I have designed and implemented NCSU BIT 495/595 Comparative Plant Transcriptomics, a CURE that trains student researchers to analyze RNA-seq data sets comparing plant tissues of various crop species. This course is structured with Open Pedagogy by designing course assignments that are collaborative, generate research deliverable to disseminate to the scientific community and public, and promote student's metacognition and emotional intelligence. Upon completion of this course, student researchers are expected to meet the course objectives (COs). Through a biology education research study I am assessing whether instructional materials support student achievement of the COs:

CO1. Justify the use of variables, sequencing approach, and reference genome selection when designing RNA-seq experiments for comparing transcriptomes.

CO2. Describe the different data outputs from various NGS technologies and their utility in research discovery.

CO 3. Interpret Linux-based bioinformatic code to align plant RNA sequencing reads to a reference.

CO 4. Quantify plant RNA sequencing reads and **determine** differentially expressed genes.

CO 5. Compare the expression patterns of orthologous gene families across model and crop species.

CO 6. Evaluate the use and limitations of a model species as a genetic resource.

CO 7. Navigate course materials, **recognize** how course assignments measure attainment of course objectives, and **assign** affective domains of learning (feelings, values, motivations, and attitudes) associated with each objective.

CO 8. Develop a research proposal using an innovative NGS approach.