

Selecting Data for GEMmaker

Construct a Query for the NCBI Short Read Archive

1. Navigate to [SRA advanced search](#).
2. Construct a query that has the following:
 - a. oryza sativa
 - b. Illumina transcriptome data
 - c. SRA project data
3. From those query results, find a project and its **accession number**.
 - a. A project accession number should begin with PRJN...
4. Navigate to the [run selector](#).
 - a. Enter the project accession number you selected previously.
 - b. Select all associated runs, and download the associated metadata and accession list.
5. Move both of these files into your home directory on Kamiak.
6. Consult the [GEmmaker documentation](#), and read about creating:
 - a. a nextflow.config file.
 - b. An SBATCH submission script.