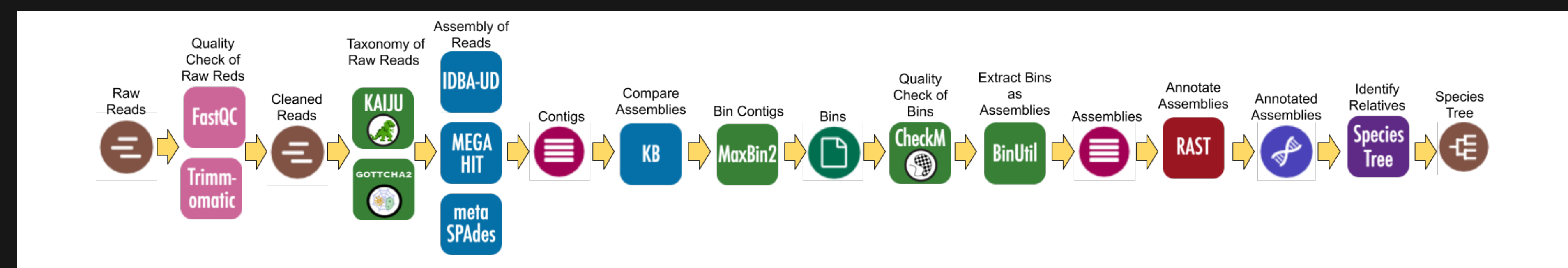
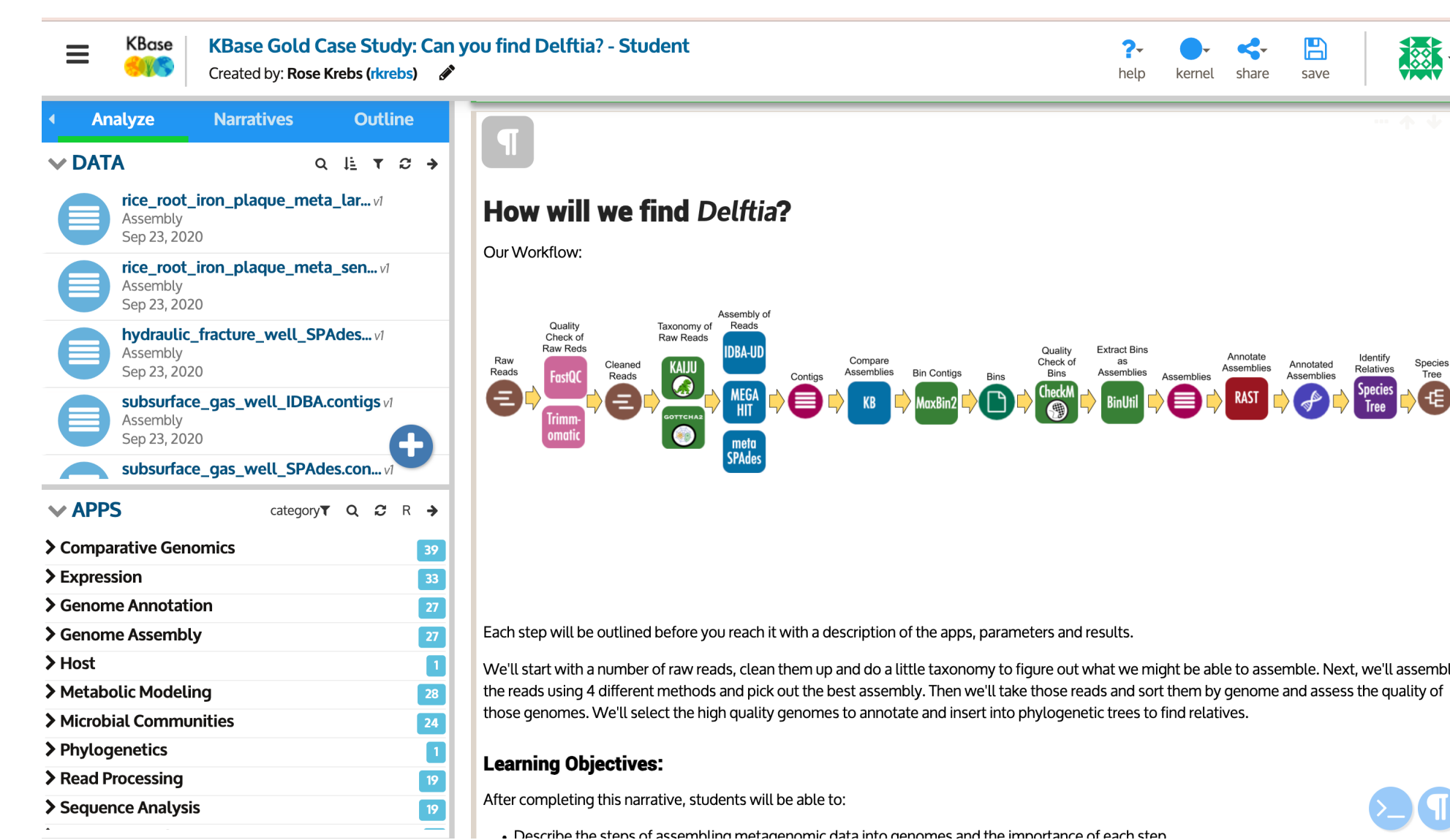


Assembling Knowledge of Metagenome Assembled Genomes (MAGs) through Annotation and KBase



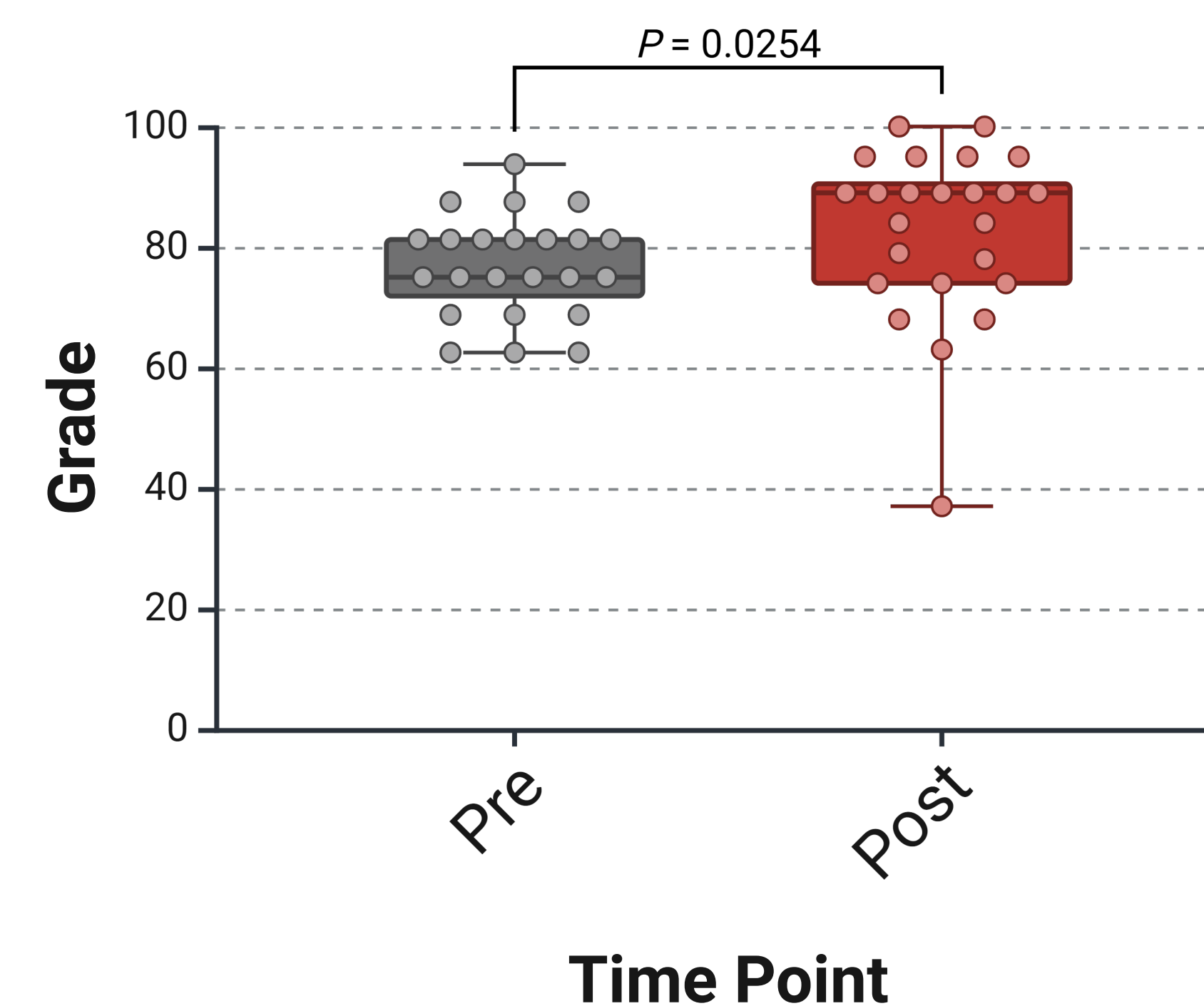
We used a combination of **primary literature**, **pre/post quizzes**, **bioinformatics attitude surveys**, and **KBase narratives** to learn how students perform and analyze fundamental metagenome assembled genomes (MAGs).

FIGURE 1: KBase Narrative case studies engage students in assembly and binning of sequences for taxonomic analyses.



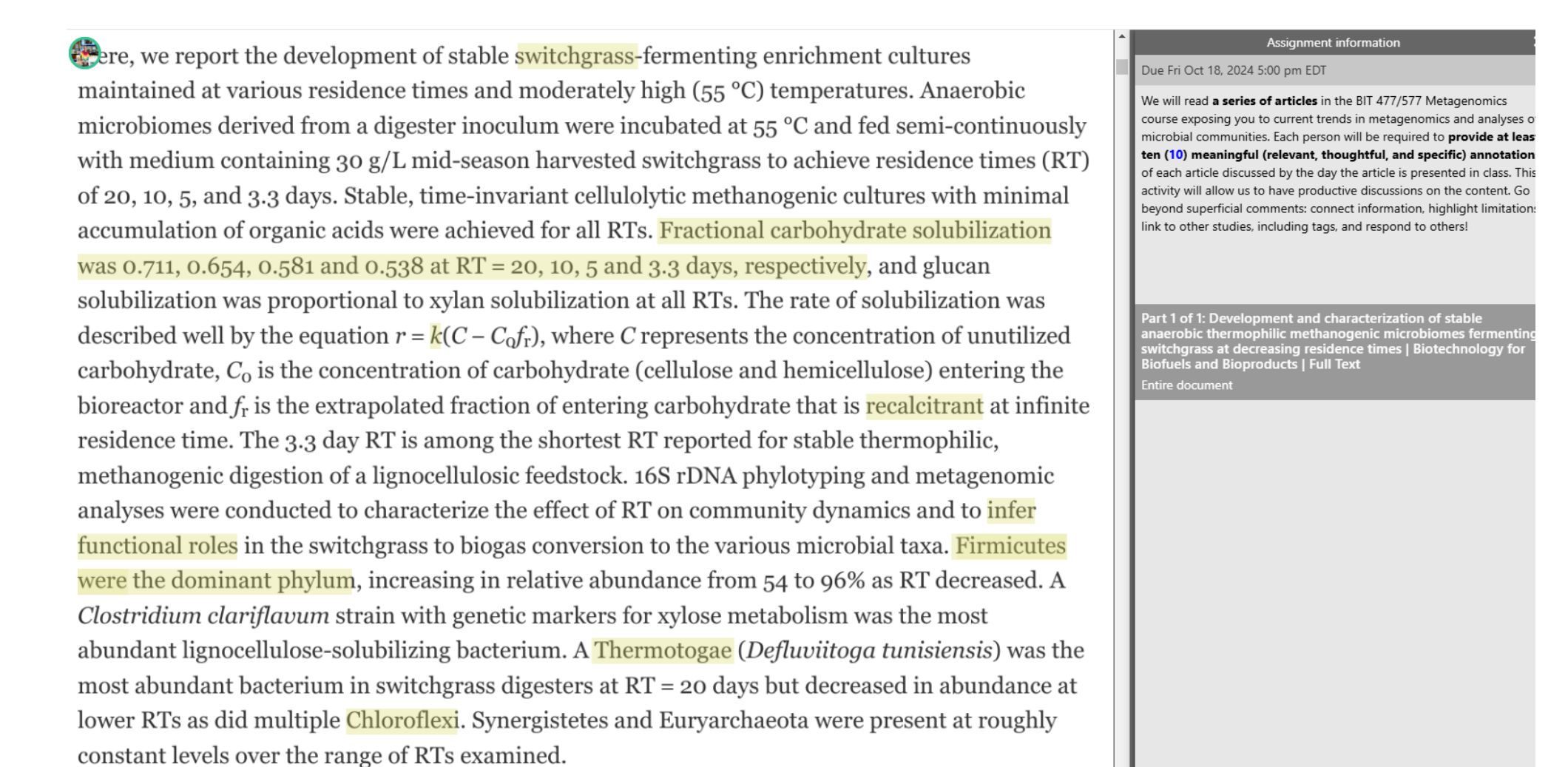
Participants learn about metagenome assembled genomes (MAGs) through a step-by-step KBase Narrative that introduces trimming, assembly, binning, annotation, and phylogenetic trees. Next, participants are challenged to find *Delftia acidovorans* MAGs (above).

FIGURE 3: Students complete pre and post quizzes about MAGs and metagenomics.



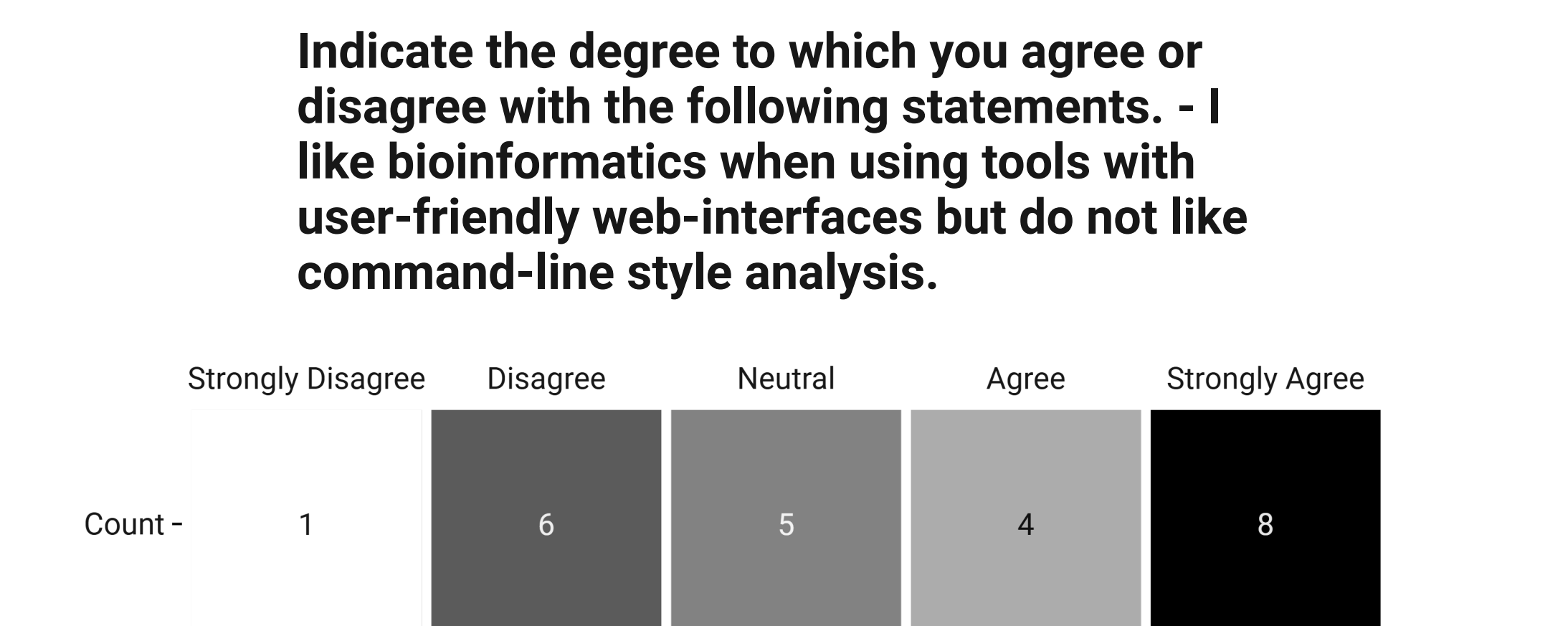
Students complete **multiple-choice pre** (n=24) and **post** (n=23, fall 2021, fall 2022, and fall 2023) **quizzes** aligned with the learning objectives and addressing concepts from the articles and KBase narratives. Questions include analyses, definitions, and the purpose of tools (e.g., MetaBat2 and CheckM). Pre/post differences are ns at this time.

FIGURE 2: Students annotate three articles related to the bioinformatics tools and applications of MAGs.



Scholars annotate texts collaboratively to learn about MetaBAT2 (Kang *et al.* 2019 above) and tools for metagenomic assembly. Two articles discuss the application of metagenomic assembly and binning (Ling *et al.* 2018 and Mason *et al.* 2014).

FIGURE 4: Students share their thoughts on how they approach computational challenges.



Participants complete **post surveys** with questions about their confidence with **bioinformatics tools** and how they approached annotation and web-based computational assignments.



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