



Enhancing Student Engagement with Online Annotation of Bacteriophage Genomes

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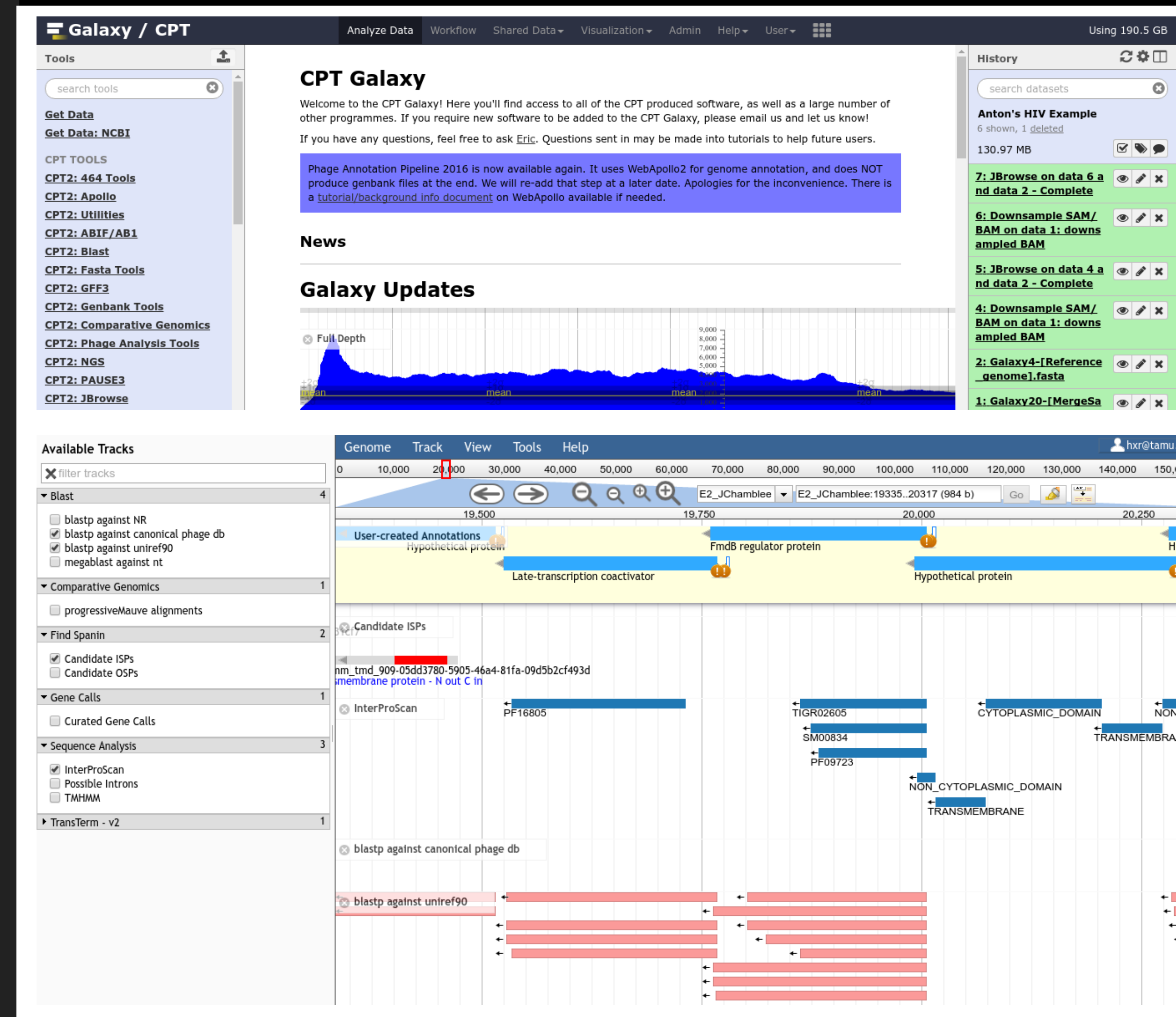
Why Phage Genomics?

- ▶ Whole genome sequencing is more accessible than ever before
- ▶ We can sequence and assemble as many phages as are needed for students
- ▶ Phages are ideal; small size, high coding density
- ▶ Able to be annotated in the span of a single semester

Previous Course Iterations

- ▶ Previously, much time was spent manually moving data around
- ▶ **Students hated the command line!**
- ▶ Students struggled to correctly copy command line statements, and struggled to understand the relationship between the instructions and their (possibly differently named) files.
- ▶ Staff struggled to keep up with changing interfaces and progress of bioinformatics tools
- ▶ *Completely Unreproducible Annotations*

Galaxy & Apollo



The future

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