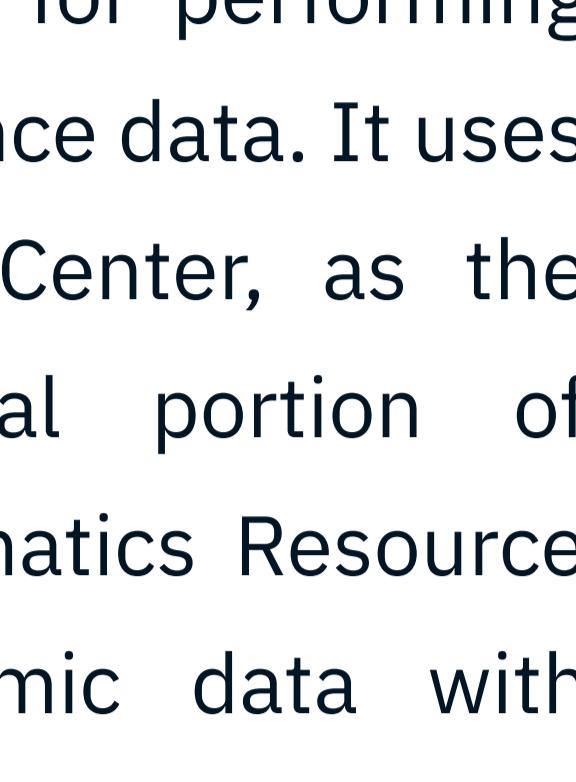


Bacterial Bioinformatics using PATRIC

Taught by:

Rebecca Wattam
Biocomplexity Institute
University of Virginia

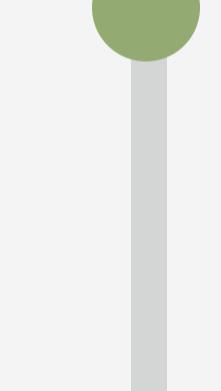


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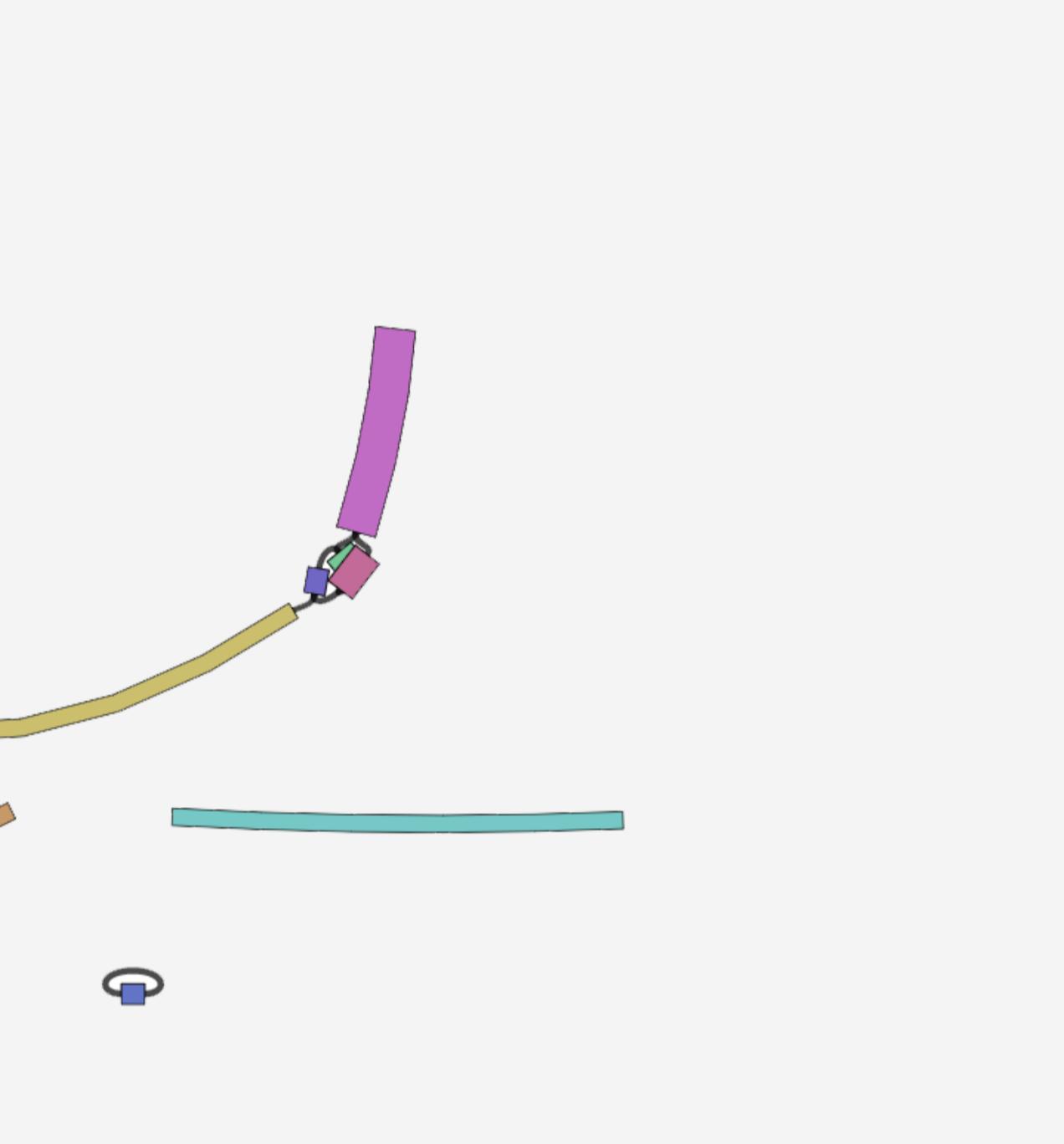
WHAT IS GENOMICS-BASED ANALYSIS?

This course provides demonstrations and exercises for performing common genomics-based analysis of bacterial sequence data. It uses PATRIC, the PathoSystems Resource Integration Center, as the platform for analysis. PATRIC is the bacterial portion of the NIH/NIAID-funded Bacterial and Viral Bioinformatics Resource Center (BV-BRC), providing comprehensive genomic data with integrated analysis tools and visualizations along with a private workspace where users can upload and analyze their own data.



ONLINE LEARNING

Course participants will gain skills needed to do comparative analysis of bacterial genomes, starting with raw sequence data. The lessons in the first module cover genome assembly, annotation, phylogenetic tree construction, and protein family/proteome comparisons. Each lesson builds on the previous, creating a complete baseline analysis workflow.



WEEK ONE

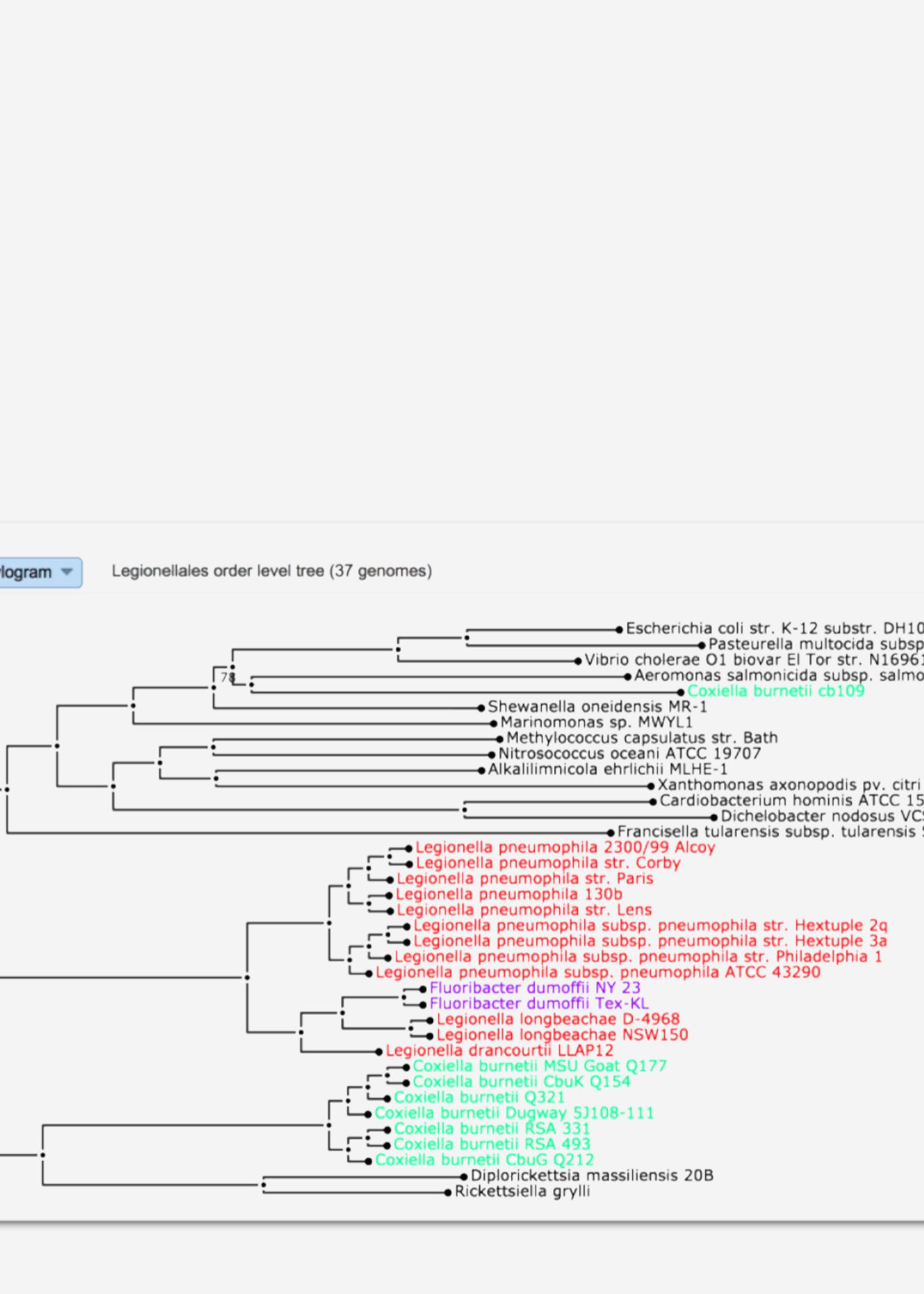
INTRODUCTION

This lesson provides an introduction to PATRIC, including an overview of the resource. It also explains how to register to get access to a private workspace and all analysis tools and how create a shared workspace so that you can share data with other users/collaborators.

WEEK TWO

ASSEMBLY

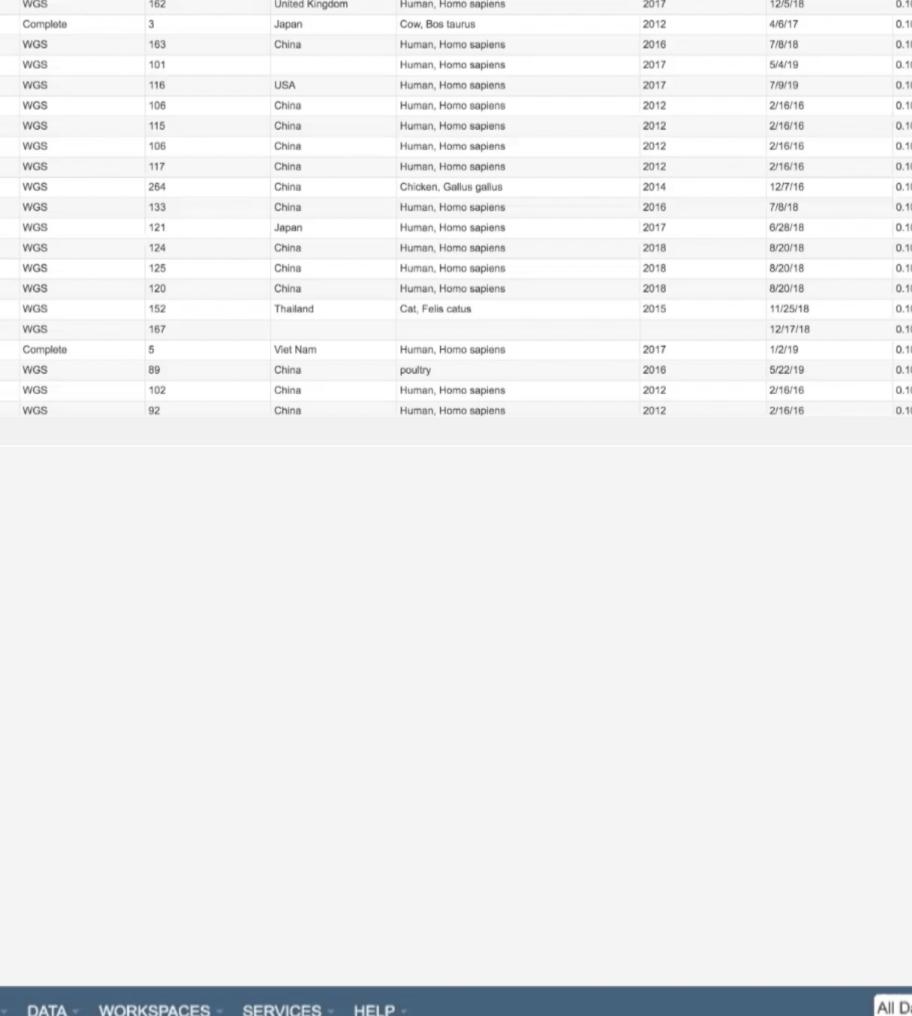
This lesson provides step-by-step instructions for assembling a genome from a set of bacterial sequence reads using the Genome Assembly Service. Exercises are included to enhance comprehension and build proficiency in using the assembly process.



WEEK THREE

ANNOTATION

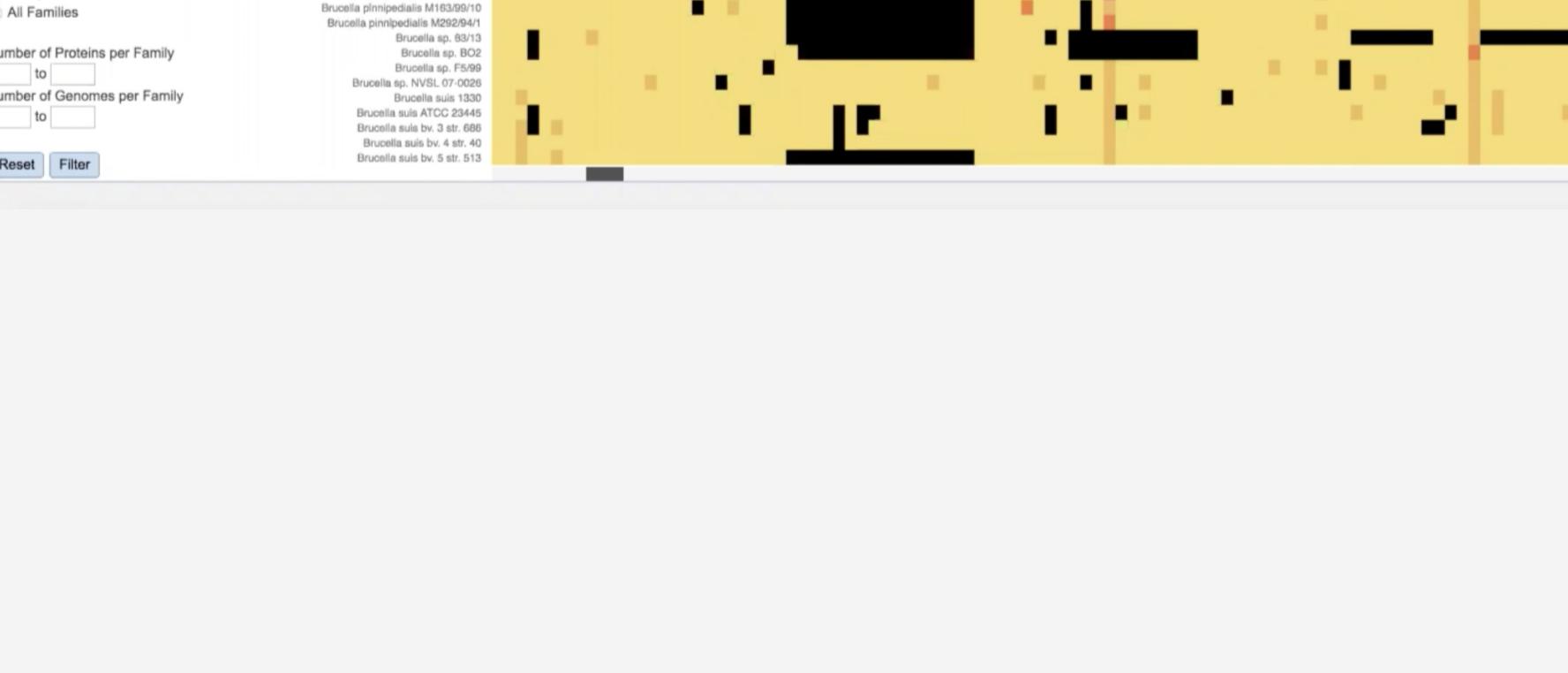
This lesson provides step-by-step instructions for annotating a genome from contigs using the Genome Annotation Service. Exercises are included to enhance comprehension and build proficiency in using the annotation process.



WEEK FOUR

COMPREHENSIVE GENOME ANALYSIS

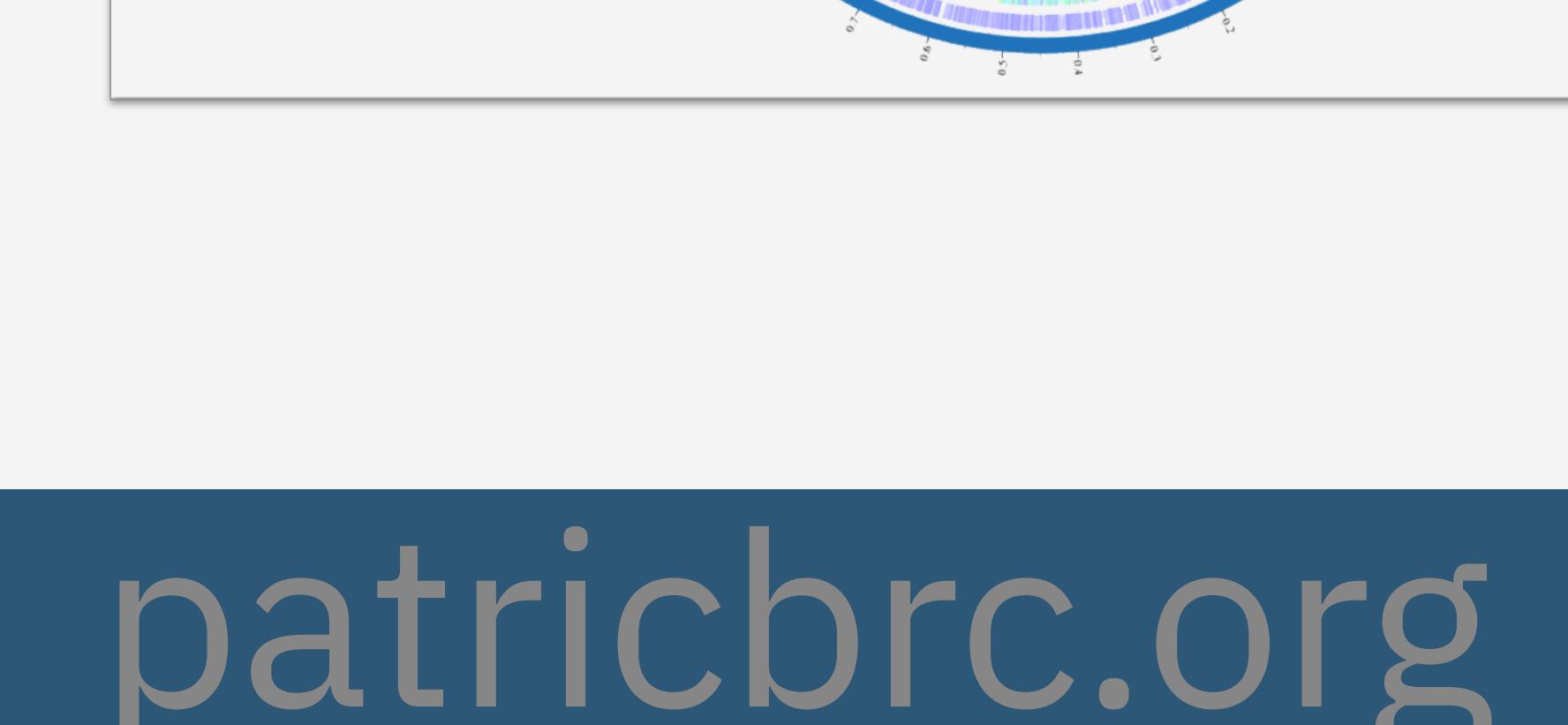
This lesson provides step-by-step instructions for assembling, annotating, and performing an automated analysis of a genome from a set of bacterial sequence reads using the Comprehensive Genome Analysis Service. Exercises are included to enhance comprehension and build proficiency in using the service.



WEEK FIVE

CODON-BASED PHYLOGENETIC TREES

This lesson provides step-by-step instructions for generating a codon-based phylogenetic tree from a set of genomes using the Codon Tree Service. Exercises are included to enhance comprehension and build proficiency in using the service.



SIMILAR GENOME FINDER

This lesson provides step-by-step instructions for finding genomes (and associated taxonomy) in similar to your genome or sequences using the Similar Genome Finder Service. Exercises are included to enhance comprehension and build proficiency in using the service.

WEEK SIX

PROTEIN FAMILY SORTER

This lesson provides step-by-step instructions for using the Protein Family Sorter to compare presence, absence, and counts of proteins in protein families across a set of genomes. Exercises are included to enhance comprehension and build proficiency in using the tool.

WEEK SEVEN

PROTEOME COMPARISON

This lesson provides step-by-step instructions for using the Proteome Comparison Service to compare a set of genomes against a reference genome, feature group, or FASTA file. Exercises are included to enhance comprehension and build proficiency in using the tool.

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patricbrc.org

