

Auburn University Bioinformatics Bootcamp 2014

May 19-23, 2014

Science Learning Center Building 231

Course run by:

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Course assistance by:

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This syllabus is a starting point for the course, but it may be adjusted as needed.

Sunday PM

Arrive in Auburn.

Monday May 19

8:45 – 12:15

*Introduction, review of sequence technologies,
crash course in the commandline of Linux OS
Seq Data formats, Sequence QC*

12:15-1:30 Lunch

1:30-5:00

*Assembling genomes & transcriptomes
Ray and Trinity*

Tuesday May 20

8:45 – 12:15

*Assessment of Assemblies
BLAST at the command line*

12:15-1:30 Lunch

1:30-5:00

*Annotation via Trinotate
Parsing data with awk, grep and sed*

Wednesday May 21

8:45 – 12:15

*More on orthology determination
HaMStr, OrthoMCL
EMBOSS, sequence alignments & trimming*

12:15-1:30 Lunch

1:30-5:00

*Mapping reads to references and visualization
Bowtie2, Tablet, Artemis*

Thursday May 22

8:45 – 12:15

*SNP and INDEL calling from mapping
Analyses of Expression Data*

12:15-1:30 Lunch

1:30-5:00

*Inferring phylogenetic trees
FastTree, RAxML, PhyloBayes*

Friday May 23

8:45 – 12:15

Phylogenetic/Phylogenomics Pipeline

12:15-1:30 Lunch

1:30-5:00

Questions and Review

7:00

End of Course Social