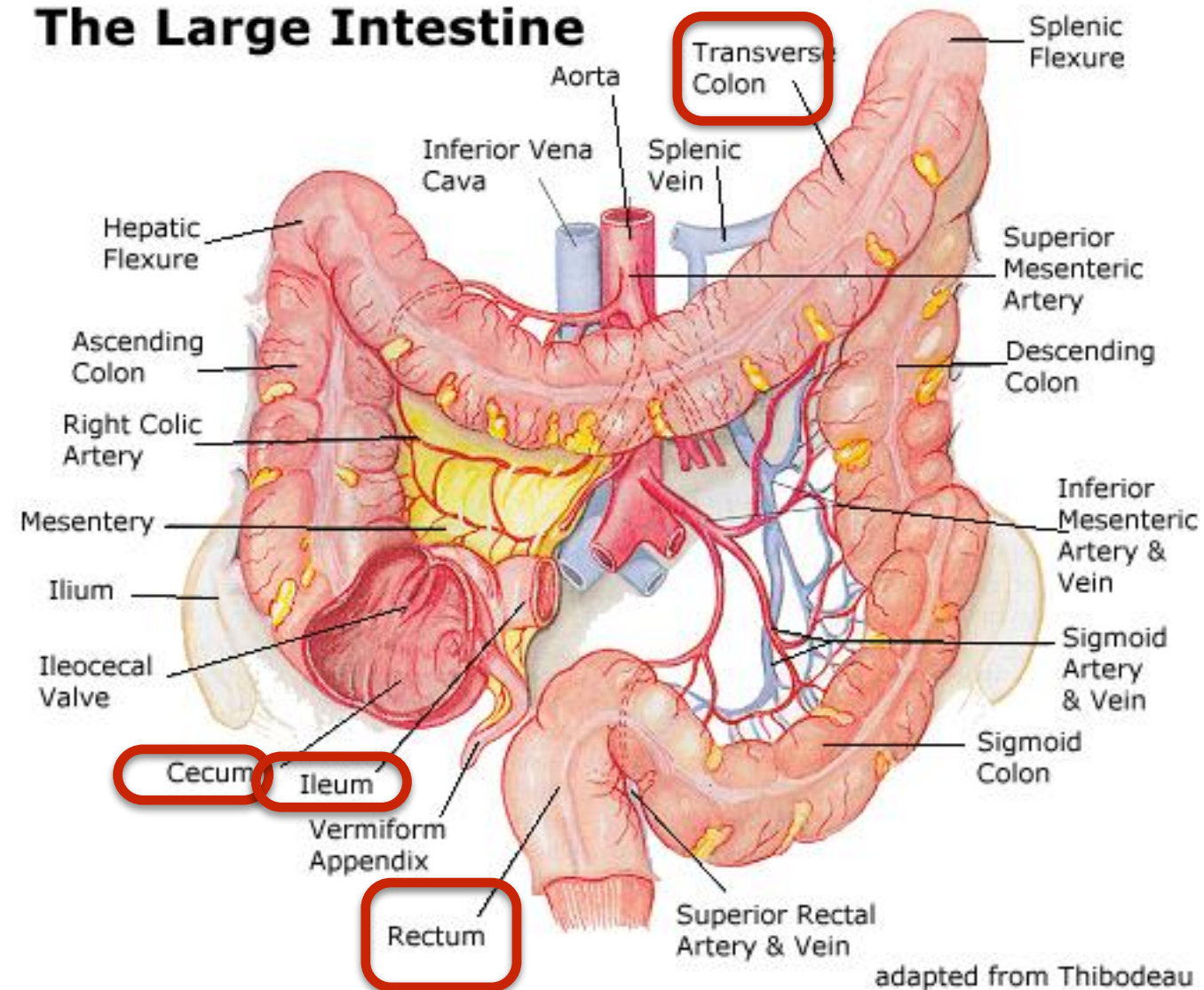


Metagenomic Visualization

Using MEGAN

<http://ab.inf.uni-tuebingen.de/data/software/megan6/download/manual.pdf>

The Large Intestine

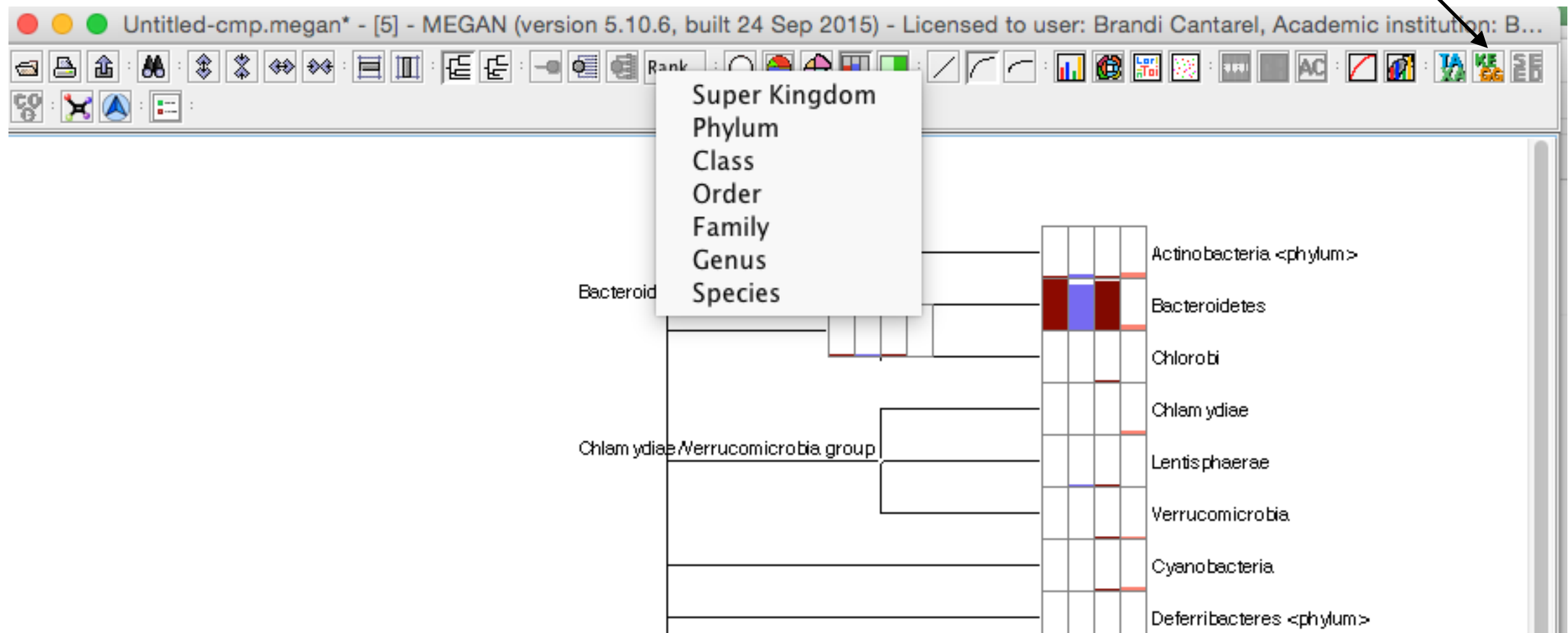


16S Taxonomic Comparison

- What are the dominate phyla, family and genera for each sample?
- Are sites that are closer (spatially) also closer taxonomically (use cluster analysis)?
- What fraction of each samples is “unclassified” taxonomically?

Some Tool Options

Gene Annotation

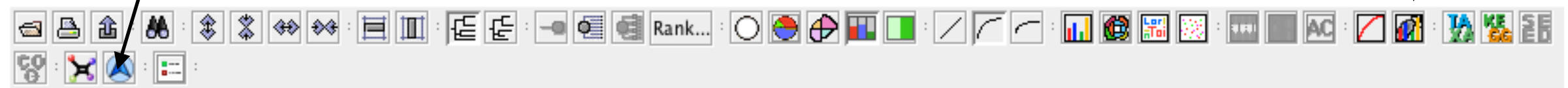


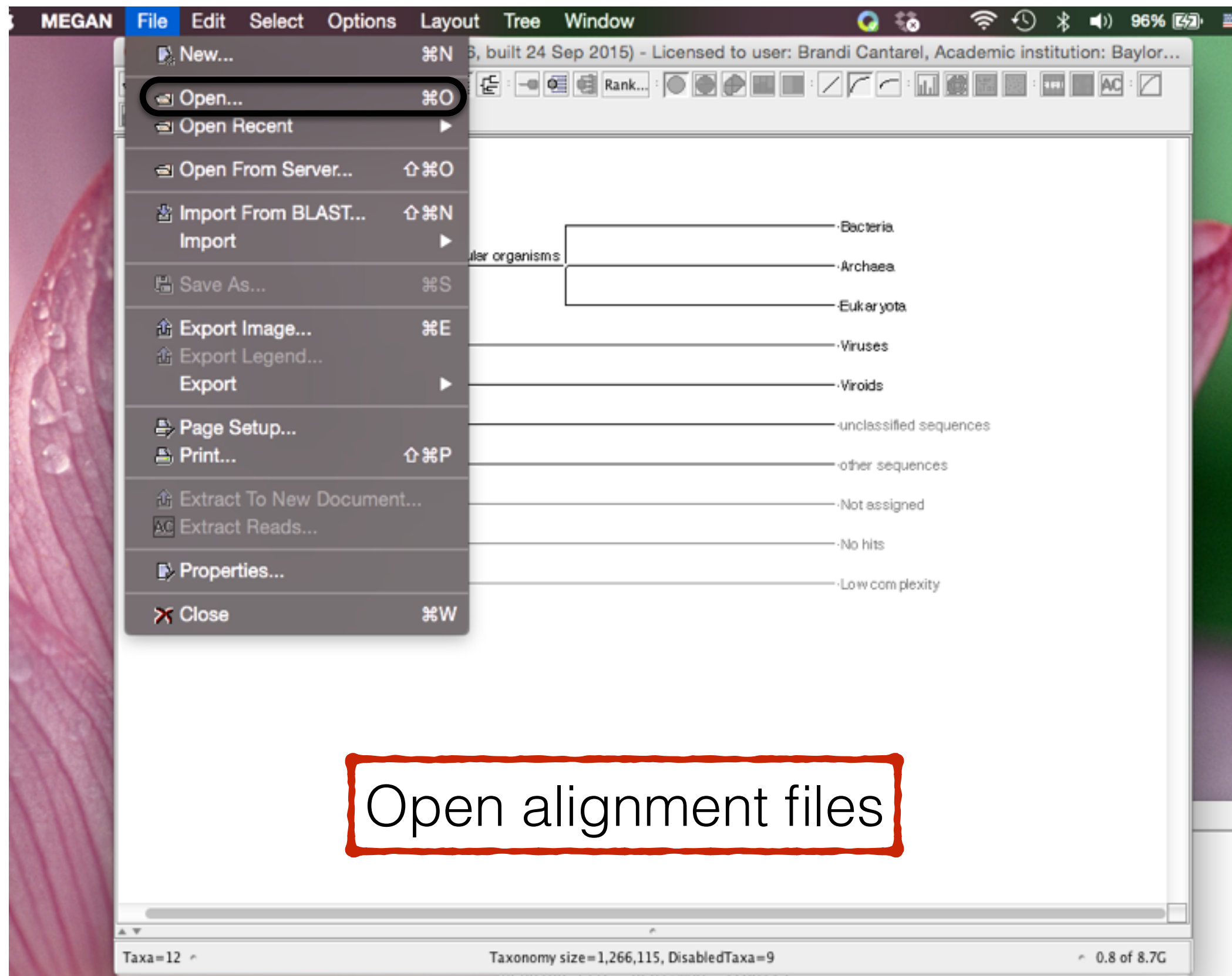
Organism Annotation

Rarefaction

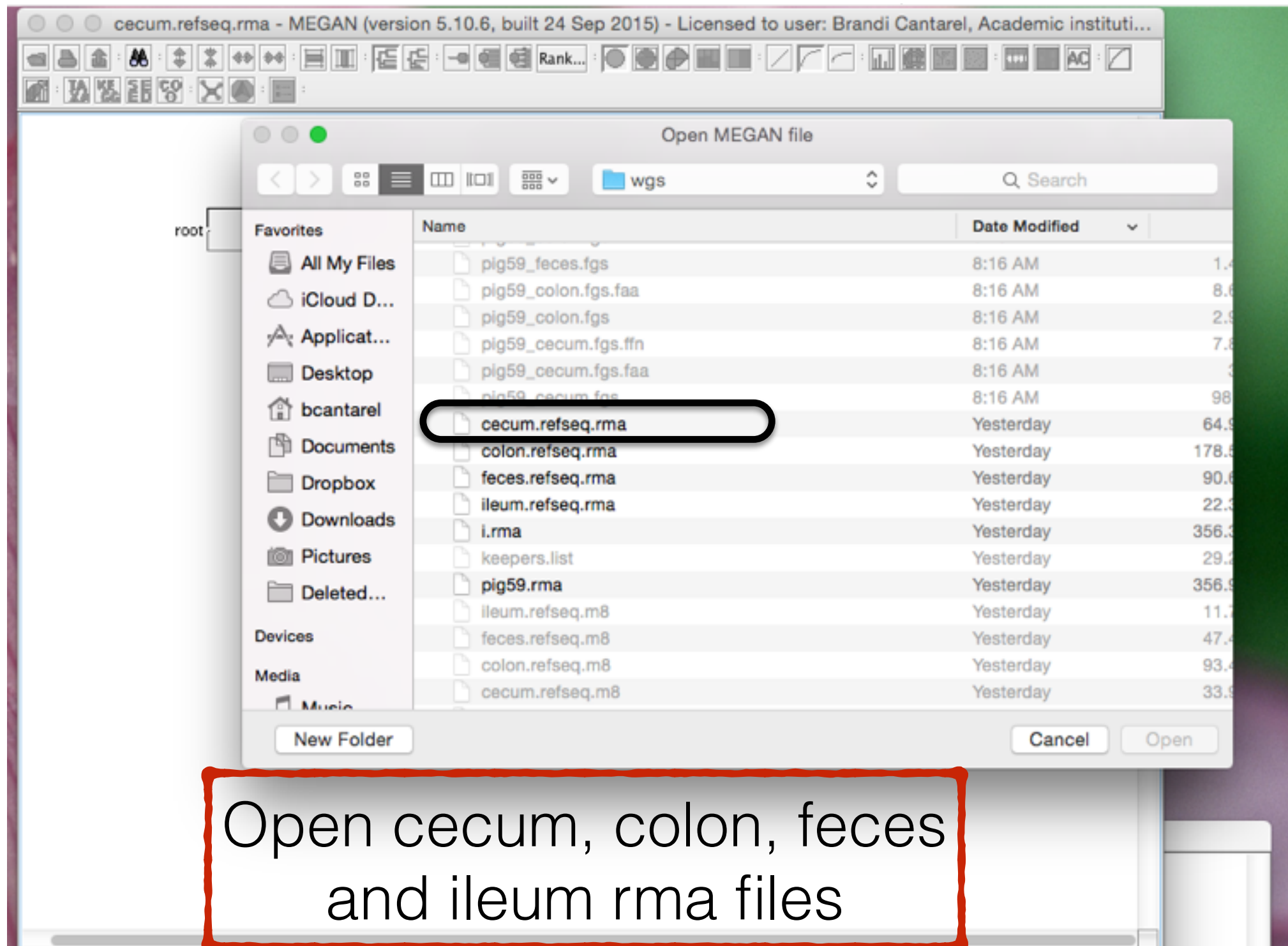
Visualization Options

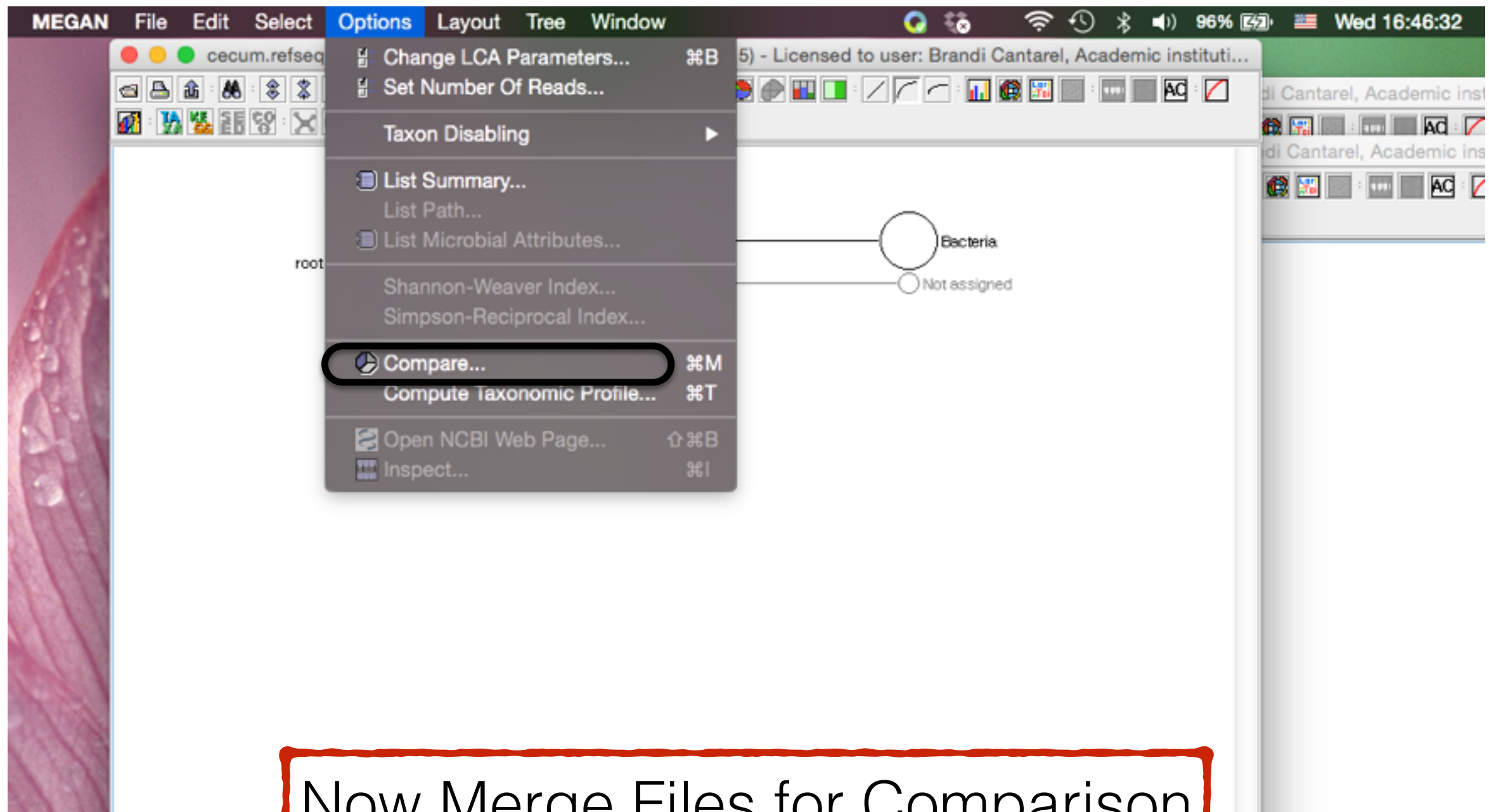
Cluster Analysis



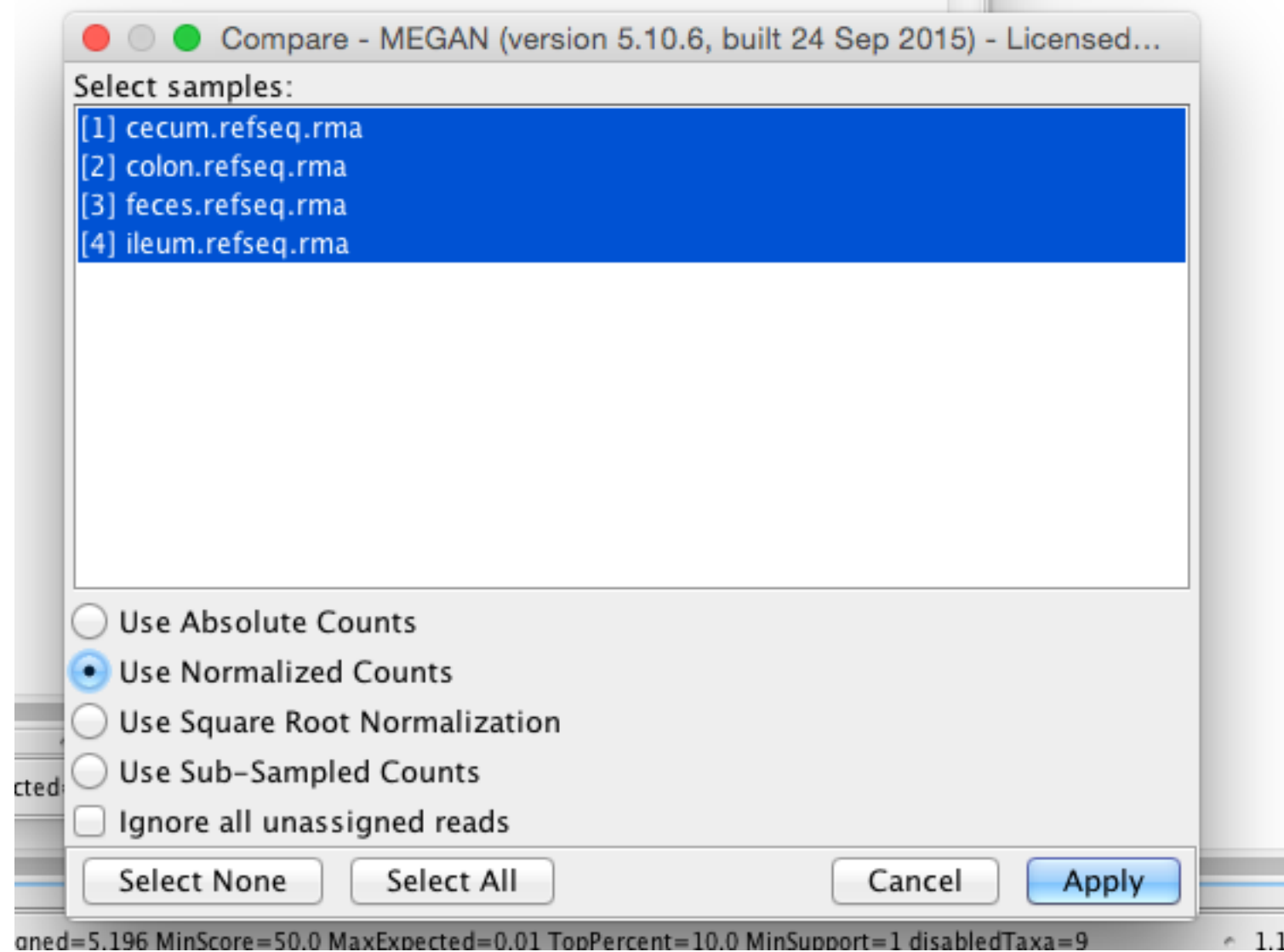


Open alignment files





Now Merge Files for Comparison

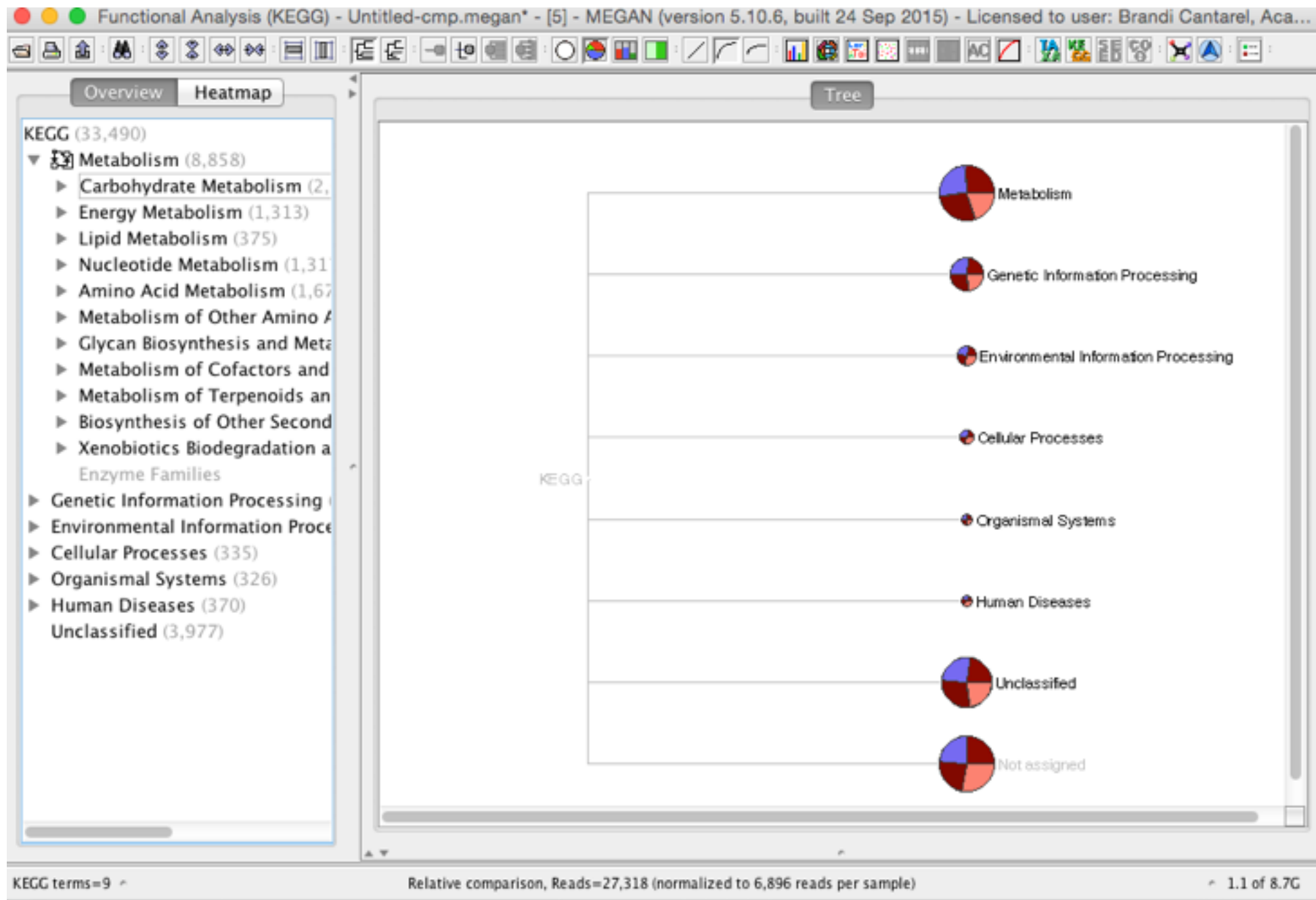


Select all files and select normalized counts

WGS Taxonomic Comparison

- What are the dominate phyla, family and genera for each sample?
- Are these dominate taxa consistent with 16S results?
- Are sites that are closer (spatially) also closer taxonomically (use cluster analysis)?
- What fraction of each samples is “unclassified” taxonomically?

Functional Exploration



Functional Exploration

- Pick a pathway from Carbohydrate Metabolism or Glycan Biosynthesis and Metabolism.
- How does the abundances of the genes in your pathway compare between the 4 body sites?
- Now pick a pathway from Genetic Information Processing
- Are the abundances more or less similar between body sites in your chosen sugar metabolism pathway compared to Genetic Information Processing?
- Run KEGG Cluster analysis, how does functional clustering compare to clustering by Taxa?
- What fraction of each samples is “unclassified” functionally?