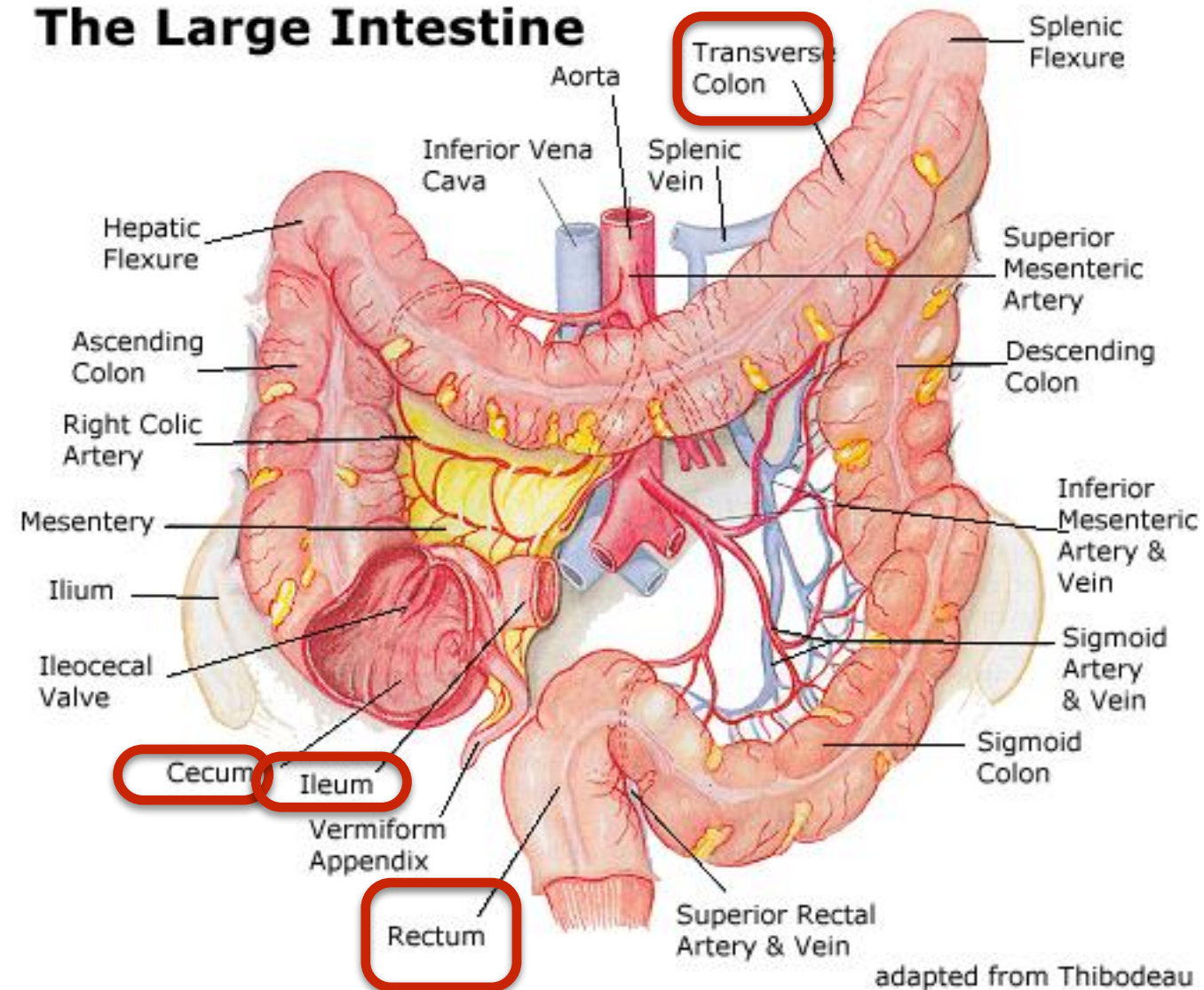


# Metagenomic Visualization

Using MEGAN

<http://ab.inf.uni-tuebingen.de/data/software/megan5/download/manual.pdf>

## The Large Intestine



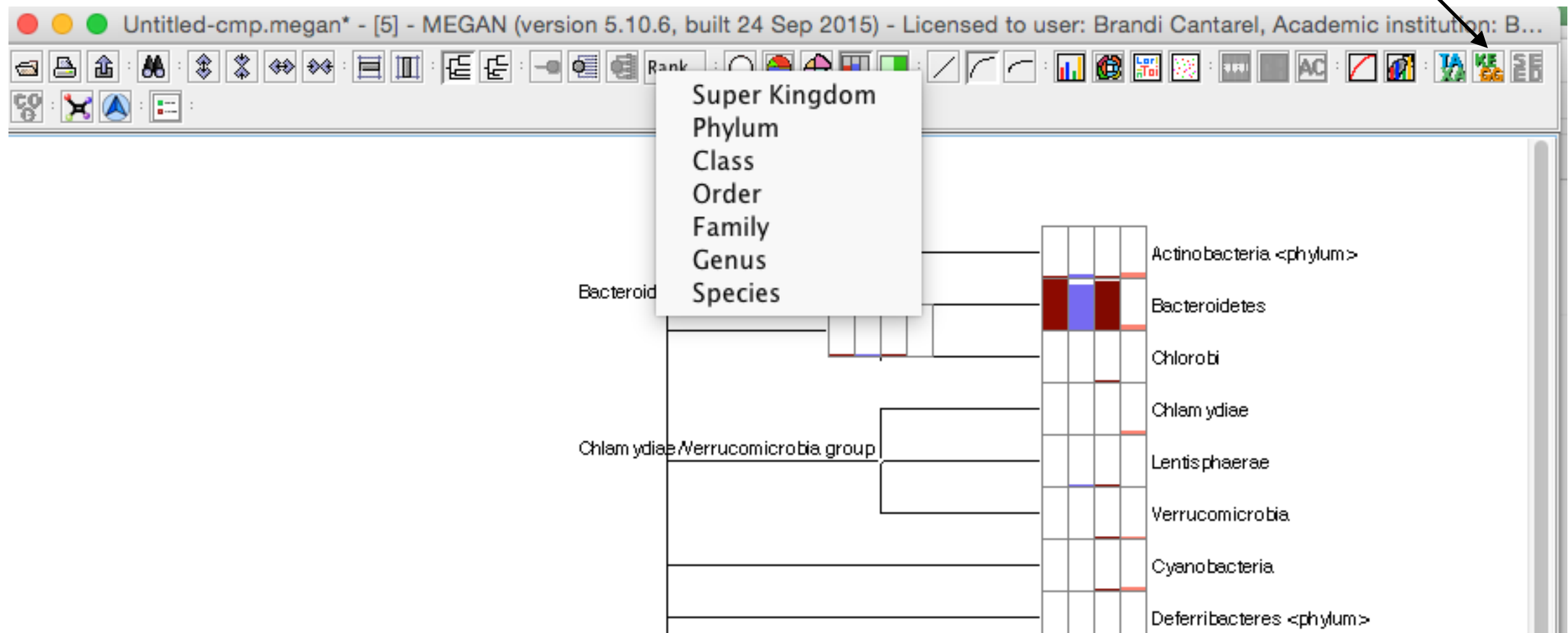


# 16S Taxonomic Comparison

- 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



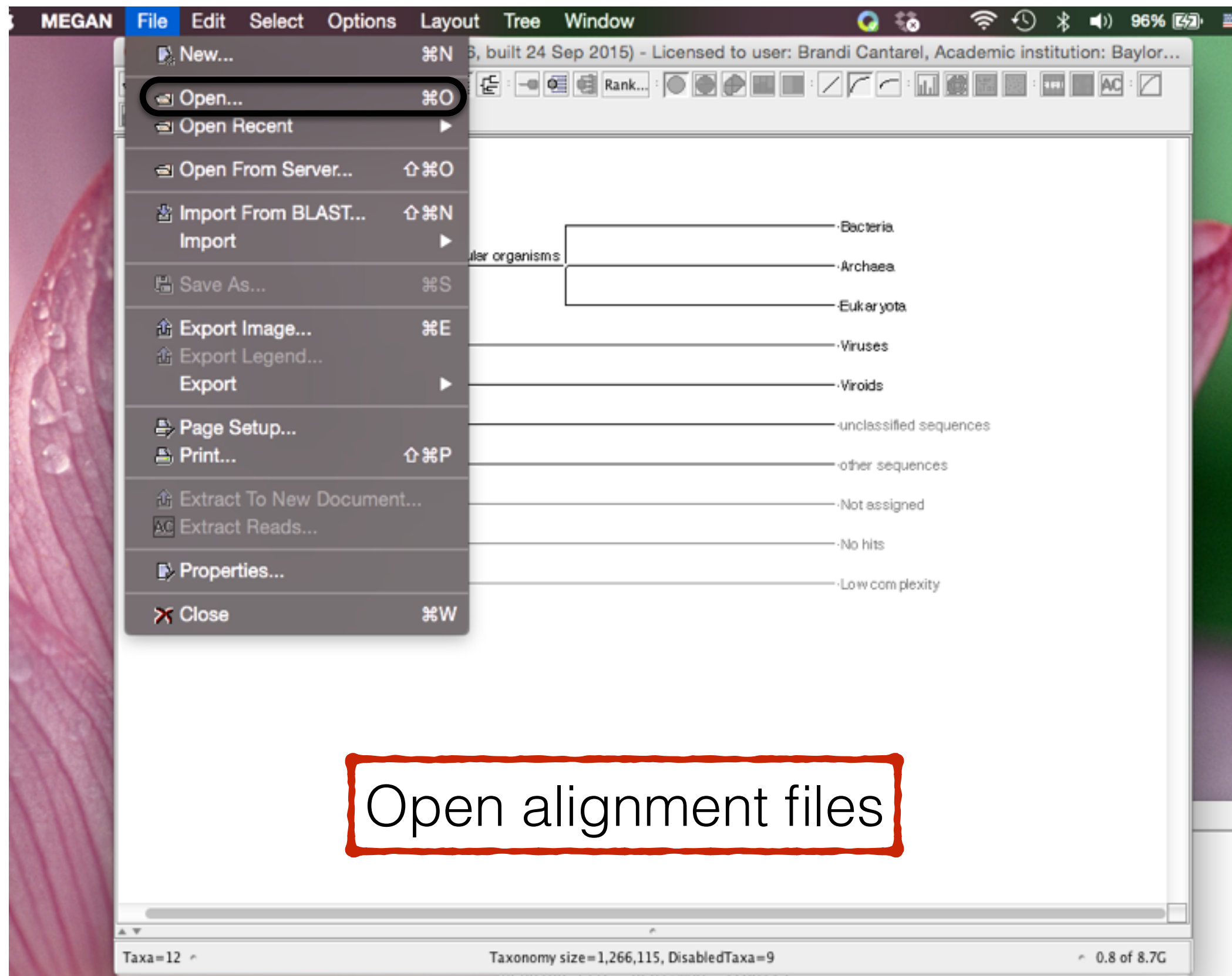
## Organism Annotation

## Rarefaction

## Visualization Options

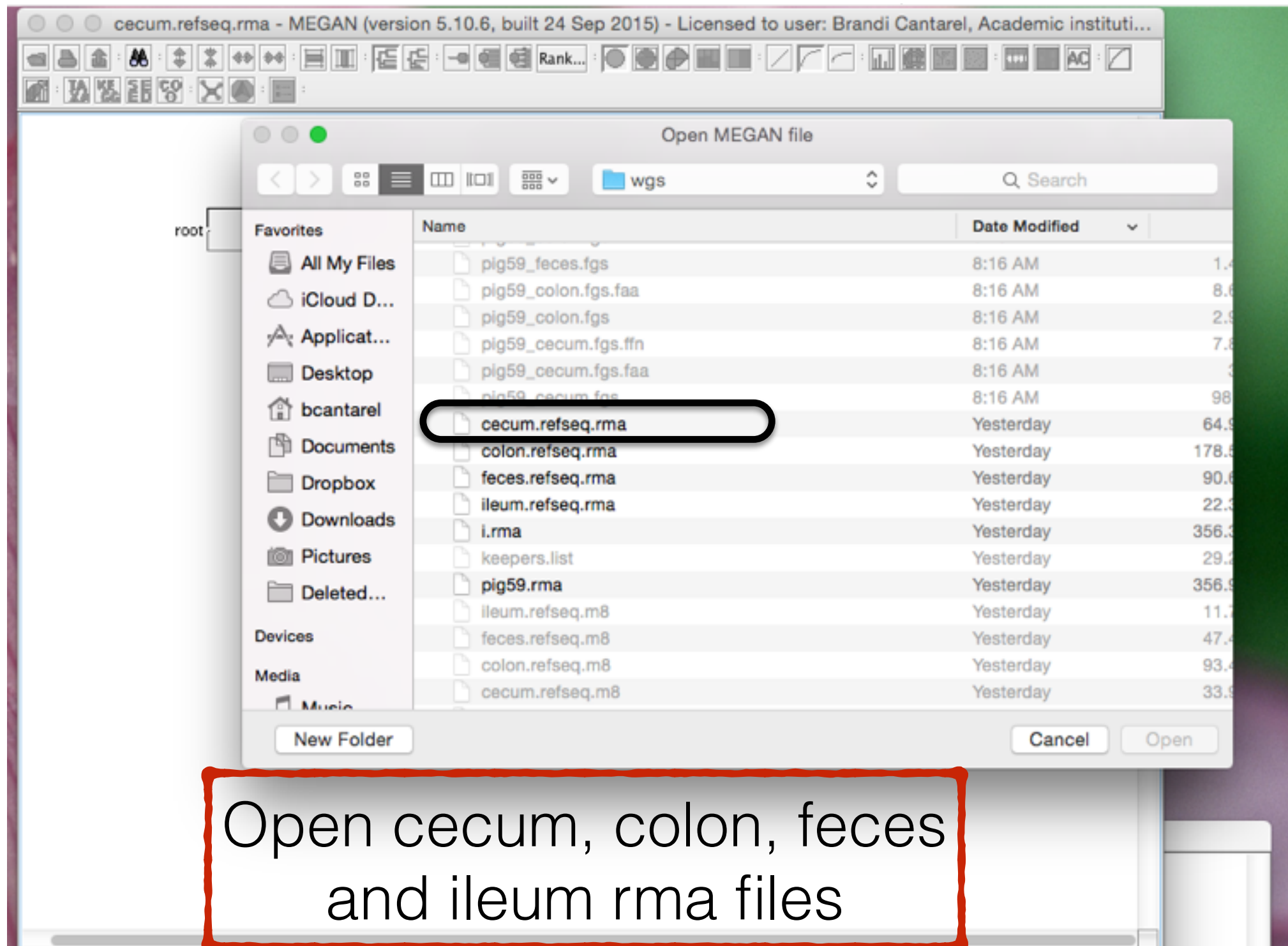
# Cluster Analysis

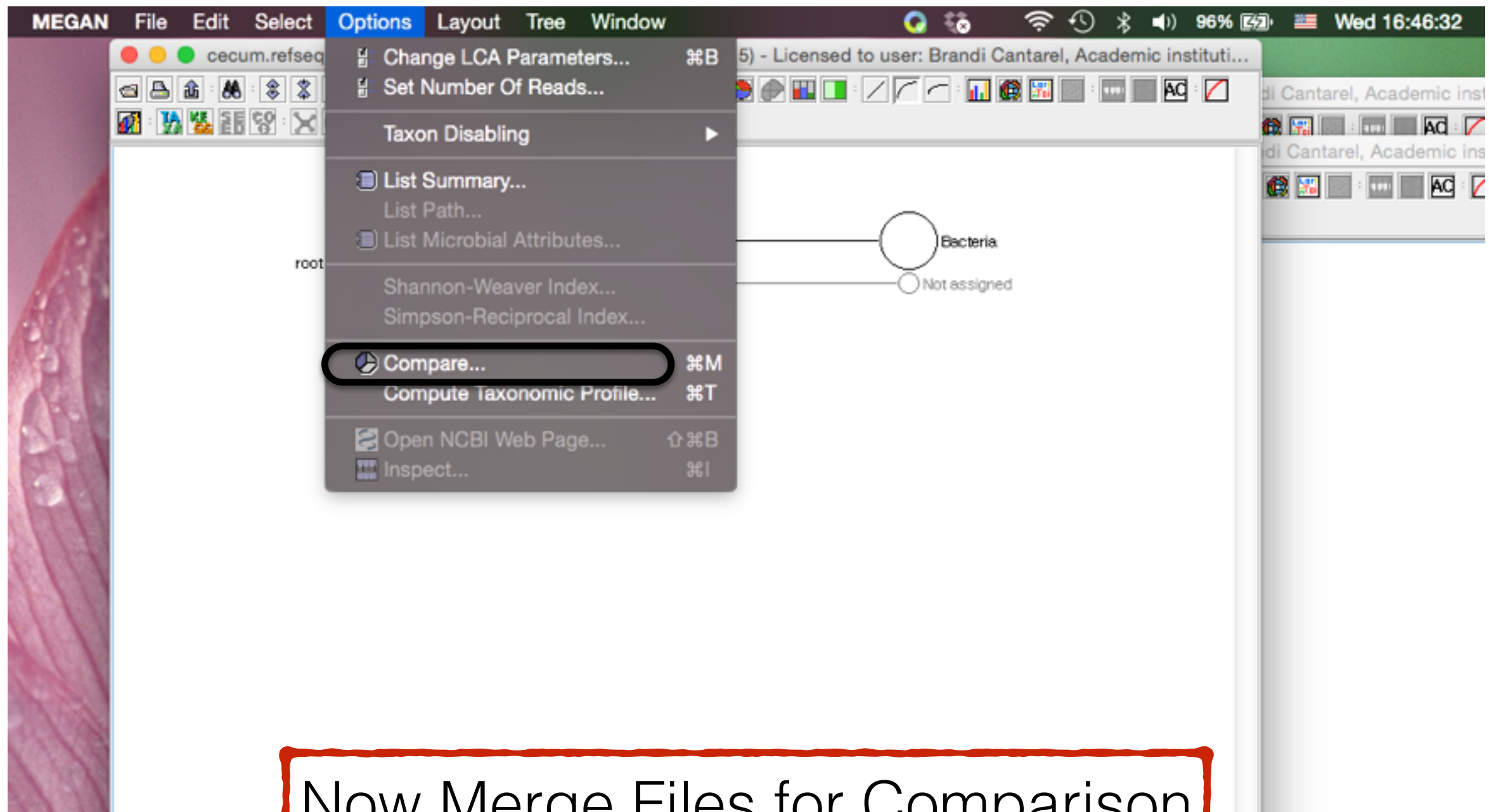




Open alignment files

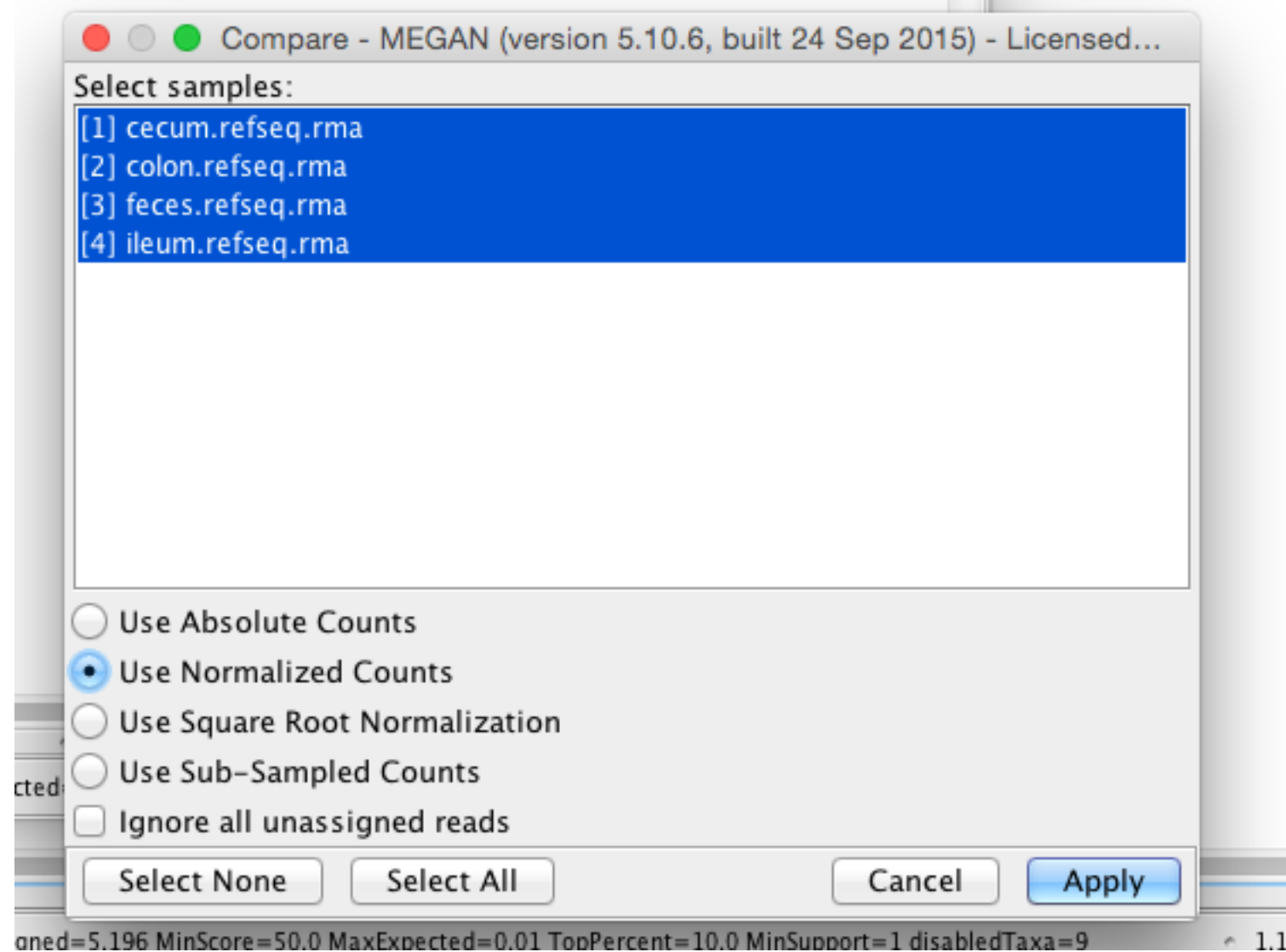






Now Merge Files for Comparison



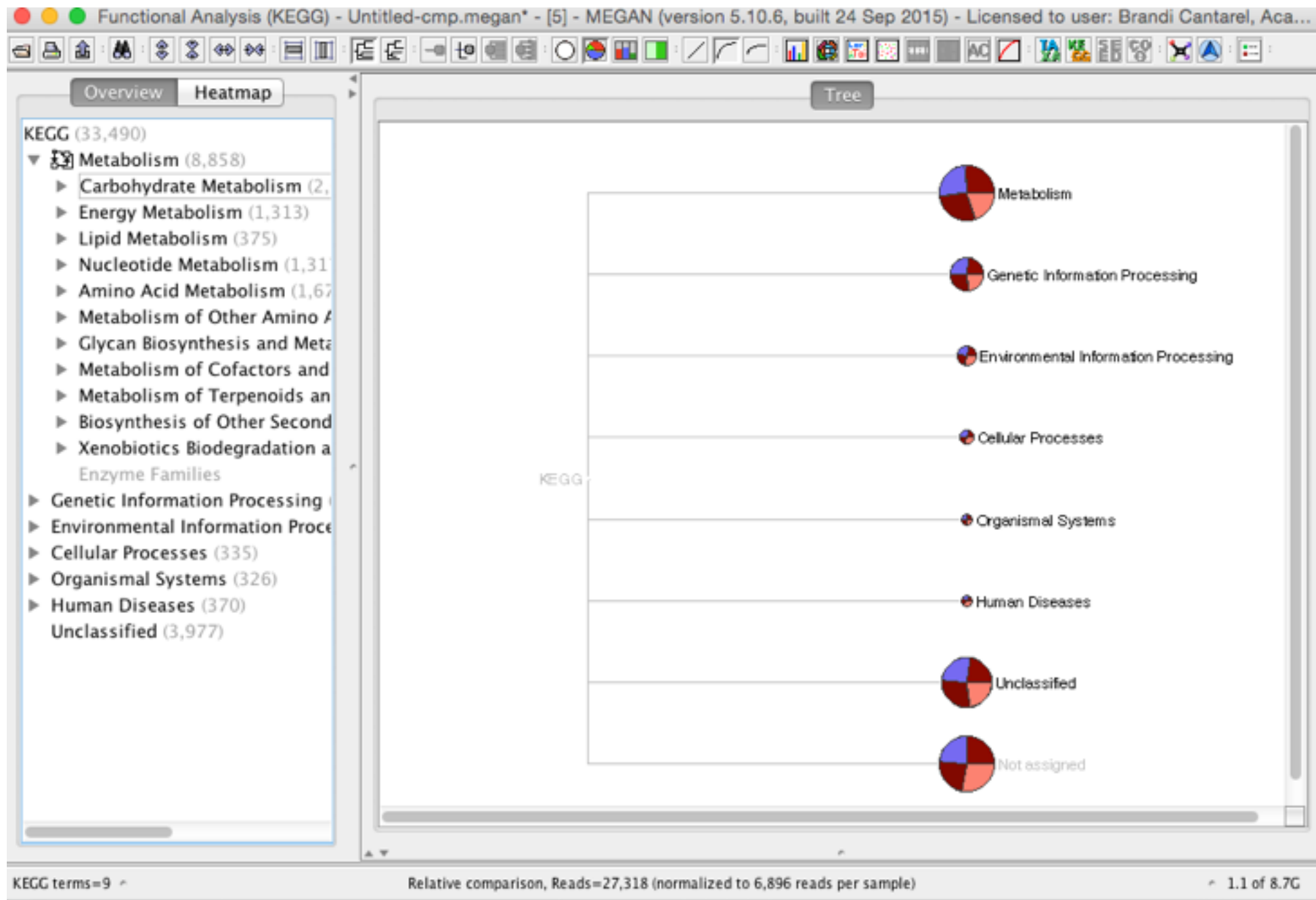


Select all files and select normalized counts

# 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?