Yeast from the brewmaster
Steps taken before practical
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???

Sequence Genome
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Add other yeast genomes
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*challenge*
Challenge
• Using a reduced set of protein sequences in FILES_Wed_challenge_fastas.tar.gz to determine what the yeast is

1) Call orthologs
2) Align and trim orthologs
3) Concatenate sequences
4) Infer putative species tree

Hint: outgroup taxa are

*Starmerella apicola*
*Starmerella bombicola*
*Wickerhamiella versatilis*
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Hint: You can extract a FASTA entry from a multi-FASTA file using samtools faidx function with the format:
Samtools faidx fasta.file fasta.entry

e.g. if I want to extract gene Brewery_genome_1 from multi-FASTA file Brewery_genome.fa I would execute the command,
samtools faidx Brewery_genome.fa Brewery_genome_1