

- Compile previous information of *Debaryomyces hansenii*.
 - Make a short resume of the information about the specie.
 - Put together all the information about the strains.
 - Information about the two references.
- Download, organize and take a look to all Mahesh data assemblies.
 - Compare the information of the assemblies for the different strains.
- Download reference genomes, annotation only found in reference 1, CBS 767.
- Mapping of assemblies to the reference genome.
 - Error when using Bowtie2 (terminate called after throwing an instance of
'std::bad_alloc' what(): std::bad_alloc Aborted
(core dumped) (ERR): bowtie2-align exited with
value 134
 - NUCMER: It works, but still needed to figure out how to visualize the
output/outputs.
- Mapping of Raw-data to the reference genome.
 - Bowtie2: all the Raw reads mapped to the reference genome CBS 767. Each
strain has two sets of reads AH and BC.
 - Percentage of overall alignment rate obtained
 - Coverage visualized in IGV
 - Find script/program that outputs more information about the
coverage, regions of interest...
- Future perspectives
 - SNP calling for the Raw data and/or assemblies (at least with the ones that seem
to be *Debaryomyces hansenii*)
 - Gene annotation, the only one published is from 2004, I think it would be good
to actualize that. We could also ask the lab that published the reference of MTCC
234 to send us the information that they have on this aspect.
 - Phylogeny of the strains.
 - ...