

Oliver

0.) Revise circularization script to cut (after circularization) at a distant point from circularized junction

- 1.) build snp tree for the first 4 from Harm's initial genomes
- 2.) Build consensus ancestral genomes for the first 4 from Harm's initial genomes
- 3.) Circularize and resequence
 - if 1 seems reasonably accurate then redo 1 and 2 on the output from point 3
- 4.) annotate

Ted

- 1.) Build a repeat track and indel track
 - 2.) work on dat Rakefile
- may need to parse delta or

Harm Suggested form:

Pipeline sketch



