

**Notes:**

Target = Sample + Target combination, each are tracked separately

Start

- Launch Mapping\_job for each sample

Mapping\_job  
1 per sample

- Flag targets which are finished by
  - NumMapped <= oldNumMapped
- Build Mapping results file (txt)
- Add SplitReads job before exiting

SplitReads\_job  
1 per sample

- Load mapping results file
- Iterate over targets
  - generate temp folder + fastq
- Add Assembly job
- Populate assemblies list
- Launch CheckFinished with list of assemblies

CheckFinished\_job  
1 per sample

Assembly\_job  
1 per target

- Start assembly and check that it finished
- Report assembly finished (or monitor job finished)

- Count incomplete assemblies, if == 0
  - Add Concat job
- Else add CheckFinished job

Concat\_job

- If Target is finished
  - call Finish job, pass target
- Else
  - Combine and rename contigs from all Targets, write to new targets.fasta
  - Add Mapping\_job

Finish\_job

- Rename and add contigs to Sample\_assemblies.fasta
- Add statistics to Sample\_statistics.tsv

