The folder PARALLEL\_LASTZ contains:

1. A GENOMES\_DB folder that contains:
   1. A subfolder TARGET-Genomes with the chromosomes of the ref. genome (target)
   2. A subfolder Genomes with the whole genomes that we want to align (query).
2. A folder with the name of the Query genome that contains:
   1. A bin folder with all the tools
   2. A conf folder with the substitution matrix, a QUERY.conf file with the name of the query and a TARGET.conf with the list of the chromosomes of the reference genome.
   3. A log and a runlog folders for keeping the log outputs.
   4. A wrapper script gen\_bsub.pl that runs with the following commands:

./gen\_bsub.pl <path to conf folder> <num of cores> <name of the query> <step1/step2> <name of target>

eg.

Fisrt step:

./gen\_bsub.pl conf/ 8 step1 dm6 step1 anoGam1

Second step:

./gen\_bsub.pl conf/ 8 step2 dm6 step1 anoGam1

The first step generates the files that pipeline needs to run and the second step runs the alignment.