Check FASTA files format and restructure their headers

Feed the FASTA files to NUCmer along with the genome identity

Build Circos's karyotype file from FASTA and NUCmer's output files

Generate links based on the karyotype and NUCmer's output files

Generate labels for bands based on FASTA files' headers

Filter links based on filter threshold

Generate histograms based on links, karyotype and NUCmer's output files

Merge links based on the Merge Threshold (MT)

Build configuration file for Circos

Run Circos to plot the diagram based on configuration files using karyotype, label, links and histogram files