# Commands used for Brisera genome alignment program

# https://github.com/bbengfort/brisera

#Program that team corrected in python code ‘convert\_fasta.py’\*/

# if not os.path.exists(tempout):  
# os.makedirs(tempout)

#

# still have error:

# File "/home/biotools/brisera-master/apps/convert\_fasta.py", line 49, in <module> raise Exception("Could not find partition file in %s!" % tempout)Exception: Could not find partition file in /tmp/fastaWWp3Re/output!

$ spark-submit --master local[\*] /home/biotools/brisera-master/apps/convert\_fasta.py /home/ajm/Staphdata/RefSeq/genome/ASM58453v1\_genomic.fasta /home/ajm/outputs/brisera/ASM58453v1\_genomic.ser

# also tried this command

$spark-submit --master local[\*] /home/biotools/brisera-master/apps/convert\_fasta.py /home/ajm/Staphdata/RefSeq/genome/ASM58453v1\_genomic.fasta ASM58453v1\_genomic.ser

# Developers' original command that team corrected:

# $ spark-submit --master local[\*] apps/convert\_fasta.py input.fa output.ser

# Py code where error exists

# tempdir = tempfile.mkdtemp(prefix="fasta")

# tempout = os.path.join(tempdir, "output")