**Gene assembly scripts.**

#!/bin/sh

#this script should search for reads matching sodium channels, create a seed file from MiSeq and HiSeq reads, and start a PRICE assembly of the sodium channel using these seeds

#these steps use blatq to search for reads matching the sodium channel

echo "$@"\_starting blatq search to pull seeds for PRICE

blatq -t=dna /data/jdumbacher/Pitohui\_Nav/BlastLibs/SCN4A-Corvus\_cornix-Genomic.fa /data/jdumbacher/Pitohui\_Nextera/Pitohui\_HiSeq\_data/Final\_Fastq/Pitohui157\_HiSeq\_ALLDATA.trimmed.fastq /data/jdumbacher/Pitohui\_Nav/BlastResults/SCN4A-Corvus\_cornix\_HiSeq\_ALLDATA\_matches.m8 -out=blast8

blatq -t=dna /data/jdumbacher/Pitohui\_Nav/BlastLibs/SCN4A-Corvus\_cornix-Genomic.fa /data/jdumbacher/Pitohui\_Nextera/Pitohui\_MiSeq\_data/Final\_BBMerged\_Trimmed\_Files/Pitohui157\_MiSeq\_ALLDATA\_trimmed.fastq /data/jdumbacher/Pitohui\_Nav/BlastResults/SCN4A-Corvus\_cornix\_MiSeq\_ALLDATA\_matches.m8 -out=blast8

echo "$@" Blatq done

# Step 2 exerpt reads by id:

echo "$@"Now starting to excerpt reads with blatq hits by ID

/data/jdumbacher/bin/excerptByIDs /data/jdumbacher/Pitohui\_Nav/BlastResults/SCN4A-Corvus\_cornix\_HiSeq\_ALLDATA\_matches.m8 /data/jdumbacher/Pitohui\_Nextera/Pitohui\_HiSeq\_data/Final\_Fastq/Pitohui157\_HiSeq\_ALLDATA.trimmed.fastq > /data/jdumbacher/Pitohui\_Nav/BlastResults/SCN4A-Corvus\_cornix\_HiSeq\_ALLDATA\_matches.fastq

/data/jdumbacher/bin/excerptByIDs /data/jdumbacher/Pitohui\_Nav/BlastResults/SCN4A-Corvus\_cornix\_MiSeq\_ALLDATA\_matches.m8 /data/jdumbacher/Pitohui\_Nextera/Pitohui\_MiSeq\_data/Final\_BBMerged\_Trimmed\_Files/Pitohui157\_MiSeq\_ALLDATA\_trimmed.fastq > /data/jdumbacher/Pitohui\_Nav/BlastResults/SCN4A-Corvus\_cornix\_MiSeq\_ALLDATA\_matches.fastq

echo "$@"done excerpting reads

cat /data/jdumbacher/Pitohui\_Nav/BlastResults/SCN4A-Corvus\_cornix\_HiSeq\_ALLDATA\_matches.fastq /data/jdumbacher/Pitohui\_Nav/BlastResults/SCN4A-Corvus\_cornix\_MiSeq\_ALLDATA\_matches.fastq > /data/jdumbacher/Pitohui\_Nav/BlastResults/SCN4A-Corvus\_cornix.seeds.fastq

echo "$@"number of seeds in seed file, /data/jdumbacher/Pitohui\_Nav/BlastResults/SCN4A-Corvus\_cornix.seeds.fastq

grep -c "@" /data/jdumbacher/Pitohui\_Nav/BlastResults/SCN4A-Corvus\_cornix.seeds.fastq

# for larger read sets, assemble initial reads using spades:

python /data/jdumbacher/SPAdes-3.9.0-Linux/bin/spades.py --careful -s /data/jdumbacher/Pitohui\_Nav/BlastResults/SCN4A-Corvus\_cornix.seeds.fastq -o /data/jdumbacher/Pitohui\_Nav/BlastResults/SCN4A-Corvus\_cornix.assembled-seeds

# Assemble using PRICE (For PRICE assemblies - use note for PRICE assemblies Labnotes 25 November 2014)

echo "$@"Now starting PRICE assembly using reads

PriceTI -fp /data/jdumbacher/Pitohui\_Nextera/Pitohui\_MiSeq\_data/Final\_BBMerged\_Trimmed\_Files/Pitohui157\_Run1\_BBUnmerged\_trimmed\_paired\_R1.fastq /data/jdumbacher/Pitohui\_Nextera/Pitohui\_MiSeq\_data/Final\_BBMerged\_Trimmed\_Files/Pitohui157\_Run1\_BBUnmerged\_trimmed\_paired\_R2.fastq 549 -fp /data/jdumbacher/Pitohui\_Nextera/Pitohui\_HiSeq\_data/Final\_Fastq/Pitohui157\_HiSeq\_PE\_trimmed\_R1.fastq /data/jdumbacher/Pitohui\_Nextera/Pitohui\_HiSeq\_data/Final\_Fastq/Pitohui157\_HiSeq\_PE\_trimmed\_R2.fastq 482 -icf /data/jdumbacher/Pitohui\_Nav/BlastResults/SCN4A-Corvus\_cornix.assembled-seeds/contigs.fasta 1 1 5 -mol 30 -mpi 90 -MPI 85 -nc 50 -a 10 -target 85 1 1 1 -o /data/jdumbacher/Pitohui\_Nav/PriceAssemblies/Pitohui\_SCN4A-from\_Corvus\_cornix.Ass-seeds.fa -o /data/jdumbacher/Pitohui\_Nav/PriceAssemblies/Pitohui\_SCN4A-from\_Corvus\_cornix.ass-seeds.priceq -maxHp 25 -logf /data/jdumbacher/Pitohui\_Nav/PriceAssemblies/Pitohui\_SCN4A-from\_Corvus\_cornix.ass-seeds.log 2> /data/jdumbacher/Pitohui\_Nav/PriceAssemblies/Pitohui\_SCN4A-from\_Corvus\_cornix.ass-seeds.errorlog