Script to download the *Salmonella* Agona reference genome:

|  |
| --- |
| mkdir referencecd referencewget https://raw.githubusercontent.com/CFSAN-Biostatistics/snp-pipeline/master/snppipeline/data/agonaInputs/reference/NC\_011149.fasta |

Script to generate 1000 mutated genomes – assumes you have downloaded SNP mutator:

|  |
| --- |
| #!/bin/bashmkdir -p replicatessnpmutator.py -r 1 -o summary.tsv -n 1000 reference/NC\_011149.fastamv \*.fasta replicates |

Script to generate simulated Illumina fastq files at 100x coverage – assumes software art installed:

|  |
| --- |
| #!/bin/bashfunction runart{ basefile=$1 inputFile=replicates/$basefile.fasta outputDir=artsamples/$basefile mkdir -p $outputDir outputFile=$outputDir/${basefile}\_ art\_illumina --noALN -i $inputFile -p -l 250 -ss MS -f 100 -m 500 -s 10 -rs 1 -o $outputFile}export -f runartseq 1 1000 | xargs -I @ -P 8 bash -c "runart NC\_011149\_mutated\_@" |

Script to generate simulated Illumina fastq files at 20x coverage – assumes the software art installed:

|  |
| --- |
| #!/bin/bashfunction runart{ basefile=$1 inputFile=replicates/$basefile.fasta outputDir=artsamples/$basefile mkdir -p $outputDir outputFile=$outputDir/${basefile}\_ art\_illumina --noALN -i $inputFile -p -l 250 -ss MS -f 20 -m 500 -s 10 -rs 1 -o $outputFile}export -f runartseq 1 1000 | xargs -I @ -P 8 bash -c "runart NC\_011149\_mutated\_@" |

Script to run the CFSAN SNP Pipeline – assumes CFSAN SNP Pipeline is installed along with Bowtie2 v2.2.2 , VarScan v2.3.9, and samtools v0.1.19:

|  |
| --- |
| mkdir snppipelineworkdircopy\_snppipeline\_data.py configurationFileecho 'Bowtie2Align\_ExtraParams="--reorder -q -X 547"' >> snppipeline.confrun\_snp\_pipeline.sh –m soft -c snppipeline.conf -o snppipelineworkdir -s artsamples NC\_011149.fasta |