Script to run FREGENE for Bovine-Neut replications:

#Run a 62,000 population for 750,000 generations with a FREGENE scaling factor of 30 (with further scaling by factor of 5 in the input files – only in files for first command below)
i=30
/usr/local/bin/fregene -i in_0_b_n.xml -p par_0_b_n.xml -recomb recomb_0_b_n.xml -o rin_1_b_n.xml -af posAf_1_b_n.txt -sd $i -scale 30.0 -hz homoz_n_1.txt > log_1_b_n.txt

#Reduce Ne to 17,000 and run for 29,800 generations. Remove scale factor of 5 with new input files, while maintaining the FREGENE scaling factor of 30.
let i=$i+1
/usr/local/bin/fregene -i rin_1_b_n.xml -p par_b_n.xml -gn 29800 -recomb recomb_b_n.xml -subout 1 34000 -o rin_2_b_n.xml -af posAf_2_b_n.txt -sd $i -hz homoz_n_2.txt > log_2_b_n.txt

#Reduce population size 10,000 and run for 1,000 generations
let i=$i+1
/usr/local/bin/fregene -i rin_2_b_n.xml -p par_b_n.xml -gn 1000 -recomb recomb_b_n.xml -subout 1 20000 -o rin_3_b_n.xml -af posAf_3_b_n.txt -sd $i -hz homoz_n_3.txt > log_3_b_n.txt

#Reduce population size to 7000 and run for 600 generations
let i=$i+1
/usr/local/bin/fregene -i rin_3_b_n.xml -p par_b_n.xml -gn 600 -recomb recomb_b_n.xml -subout 1 14000 -o rin_4_b_n.xml -af posAf_4_b_n.txt -sd $i -hz homoz_n_4.txt > log_4_b_n.txt

#Reduce population size to 3500 and run for 1,100 generations
let i=$i+1
/usr/local/bin/fregene -i rin_4_b_n.xml -p par_b_n.xml -gn 1100 -recomb recomb_b_n.xml -subout 1 7000 -o rin_5_b_n.xml -af posAf_5_b_n.txt -sd $i -hz homoz_n_5.txt > log_5_b_n.txt

#Unscale the population (FREGENE scaling factor of 30).
let i=$i+1
/usr/local/bin/fregene -i rin_5_b_n.xml -p par_b_n.xml -gn 0 -recomb recomb_b_n.xml -o rin_6_b_n.xml -af posAf_9_b_n.txt -scale_exp 30.0 1 -sd $i -hz homoz_n_9.txt > log_9_b_n.txt

#Reduce population size to 2500 and run for 200 generations
let i=$i+1
/usr/local/bin/fregene -i rin_6_b_n.xml -p par_b_n.xml -gn 200 -recomb recomb_b_n.xml -subout 1 5000 -o rin_7_b_n.xml -af posAf_6_b_n.txt -sd $i -hz homoz_n_6.txt > log_6_b_n.txt

#Reduce population size to 2000 and run for 300 generations
let i=$i+1
/usr/local/bin/fregene -i rin_7_b_n.xml -p par_b_n.xml -gn 300 -recomb recomb_b_n.xml -subout 1 4000 -o rin_8_b_n.xml -af posAf_7_b_n.txt -sd $i -hz homoz_n_7.txt > log_7_b_n.txt

#Reduce population size to 1500 and run for 130 generations
let i=$i+1
/usr/local/bin/fregene -i rin_8_b_n.xml -p par_b_n.xml -gn 130 -recomb recomb_b_n.xml -subout 1 3000 -o rin_9_b_n.xml -af posAf_8_b_n.txt -sd $i -hz homoz_n_8.txt > log_8_b_n.txt

```
#Reduce population size to 1000 and run for 6 generations
let i=$i+1
/usr/local/bin/fregene -i rin_9_b_n.xml -p par_b_n.xml -gn 6 -recomb recomb_b_n.xml
-subout 1 2000 -o rin_10_b_n.xml  -af posAf_10_b_n.txt -sd $i -hz homoz_n_10.txt > log_10_b_n.txt

#Reduce population size to 350 and run for 6 generations
let i=$i+1
/usr/local/bin/fregene -i rin_10_b_n.xml -p par_b_n.xml -gn 6 -recomb recomb_b_n.xml
-subout 1 700 -o rin_11_b_n.xml  -af posAf_11_b_n.txt -sd $i -hz homoz_n_11.txt > log_11_b_n.txt

#Reduce population size to 250 and run for 6 generations
let i=$i+1
/usr/local/bin/fregene -i rin_11_b_n.xml -p par_b_n.xml -gn 6 -recomb recomb_b_n.xml
-subout 1 500 -o rin_12_b_n.xml  -af posAf_12_b_n.txt -sd $i -hz homoz_n_12.txt > log_12_b_n.txt

#Reduce population size to 120 and run for 3 generations
let i=$i+1
/usr/local/bin/fregene -i rin_12_b_n.xml -p par_b_n.xml -gn 3 -recomb recomb_b_n.xml
-subout 1 240 -o rin_13_b_n.xml  -af posAf_13_b_n.txt -sd $i -hz homoz_n_13.txt > log_13_b_n.txt

#Reduce population size to 90 and run for 3 generations – but input files scaled to give ~5000 individuals
output
let i=$i+1
/usr/local/bin/fregene -i rin_13_b_n.xml -p par_S_b_n.xml -gn 168 -recomb recomb_S_b_n.xml -subout 1
10080 -o rin_14_b_n.xml  -af posAf_14_b_n.txt -sd $i -hz homoz_n_14.txt > log_14_b_n.txt

#Run sample and make a genotype file of 10,000.   Select final 5000 genotypes from this file for "0_Gen" after
discarding any individuals that are closely duplicated - see Materials & Methods)
let i=$i+1
/usr/local/bin/sample -i rin_14_b_n.xml -log output_b_n_Sample -og geno_b_n_Sample_1
-controls 10,000 -chromolength 50.0 -sd $i > log_1_b_n_Sample.txt

#Run population size 5040 for 10 more generations -  for "10_Gen"
let i=$i+1
/usr/local/bin/fregene -i rin_14_b_n.xml -p par_b_n.xml -gn 10 -recomb recomb_b_n.xml
-subout 1 4000 -o rin_15_b_n.xml  -af posAf
_15_b_n.txt -sd $i -hz homoz_15_b_n.txt > log_15_b_n.txt

#Run sample and make a genotype file of 2000 individuals  for  "10_Gen"
let i=$i+1/usr/local/bin/sample -i rin_15_b_n.xml -log output_b_n_Sample_10 -og geno_b_n_Sample_10 -
controls 2000 -chromolength 50.0 -sd $i  > log_b_n_Sample_10.txt
```

Parameter Input files for Bovine-Neut FREGENE simulations (as specified in above script)

par_0_b_n.xml
```
<?xml version='1.0' ?>
<!-- Parameter File --><HEAD>
<NO_GENER>160000</NO_GENER>
<MUTAT_RATE>4.69e-08</MUTAT_RATE>
<PROP_SEL>5.0e-04</PROP_SEL>
<SEL_COEF_POS>0.005</SEL_COEF_POS>
<SEL_COEF_SD_POS>0.05</SEL_COEF_SD_POS>
<SEL_COEF_NEG>-0.01</SEL_COEF_NEG>
<SEL_COEF_SD_NEG>0.005</SEL_COEF_SD_NEG>
<PROP_POS_SEL_COEF>0.0</PROP_POS_SEL_COEF>
<SEL_DOM_POS>0.5</SEL_DOM_POS>
<SEL_DOM_SD_POS>0.2</SEL_DOM_SD_POS>
<SEL_DOM_NEG>1.2</SEL_DOM_NEG>
<SEL_DOM_SD_NEG>0.2</SEL_DOM_SD_NEG>
<PROP_POS_SEL_DOM>0.8</PROP_POS_SEL_DOM>
<GROWTH_RATE>0.0</GROWTH_RATE>
<DELETION_INTERVAL>16000</DELETION_INTERVAL>
<PROP_SEL_LOCAL>0.0</PROP_SEL_LOCAL>
</HEAD>
```

par_b_n.xml
```
<?xml version='1.0' ?>
<!-- Parameter File --><HEAD>
<NO_GENER>800000</NO_GENER>
<MUTAT_RATE>9.38e-09</MUTAT_RATE>
<PROP_SEL>5.0e-04</PROP_SEL>
<SEL_COEF_POS>0.005</SEL_COEF_POS>
<SEL_COEF_SD_POS>0.05</SEL_COEF_SD_POS>
<SEL_COEF_NEG>-0.01</SEL_COEF_NEG>
<SEL_COEF_SD_NEG>0.005</SEL_COEF_SD_NEG>
<PROP_POS_SEL_COEF>0.0</PROP_POS_SEL_COEF>
<SEL_DOM_POS>0.5</SEL_DOM_POS>
<SEL_DOM_SD_POS>0.2</SEL_DOM_SD_POS>
<SEL_DOM_NEG>1.2</SEL_DOM_NEG>
<SEL_DOM_SD_NEG>0.2</SEL_DOM_SD_NEG>
<PROP_POS_SEL_DOM>0.8</PROP_POS_SEL_DOM>
<GROWTH_RATE>0.0</GROWTH_RATE>
<DELETION_INTERVAL>80000</DELETION_INTERVAL>
<PROP_SEL_LOCAL>0.5</PROP_SEL_LOCAL>
</HEAD>
```

par_S_b_n.xml
```
<?xml version='1.0' ?>
<!-- Parameter File --><HEAD>
<NO_GENER>168</NO_GENER>
<MUTAT_RATE>6.0357e-11</MUTAT_RATE>
```

```
<PROP_SEL>5.0e-04</PROP_SEL>
<SEL_COEF_POS>0.005</SEL_COEF_POS>
<SEL_COEF_SD_POS>0.05</SEL_COEF_SD_POS>
<SEL_COEF_NEG>-0.01</SEL_COEF_NEG>
<SEL_COEF_SD_NEG>0.005</SEL_COEF_SD_NEG>
<PROP_POS_SEL_COEF>0.0</PROP_POS_SEL_COEF>
<SEL_DOM_POS>0.5</SEL_DOM_POS>
<SEL_DOM_SD_POS>0.2</SEL_DOM_SD_POS>
<SEL_DOM_NEG>1.2</SEL_DOM_NEG>
<SEL_DOM_SD_NEG>0.2</SEL_DOM_SD_NEG>
<PROP_POS_SEL_DOM>0.8</PROP_POS_SEL_DOM>
<GROWTH_RATE>0.0</GROWTH_RATE>
<DELETION_INTERVAL>168</DELETION_INTERVAL>
<PROP_SEL_LOCAL>0.5</PROP_SEL_LOCAL>
</HEAD>
```

in_0_b_n.xml

```
<?xml version='1.0' ?>
<!-- This a Forward Data Simulation --><HEAD><DATE>Fri Jan 31 14:30:34 2012
</DATE>
<SIMULATION_FEATURES>
<SEGMENTS>24800</SEGMENTS>
<MAX_MUT_CHROMO>0</MAX_MUT_CHROMO>
<CHROMO_LENGTH>5.0</CHROMO_LENGTH>
<MAX_MATRIX_SIZE>1.25e+15</MAX_MATRIX_SIZE>
</SIMULATION_FEATURES>
</HEAD>
<DATA>0
</DATA>
```

recomb_0_b_n.xml

```
<?xml version='1.0' ?>
<!-- Recombination File --><HEAD>
<RECOM_RATE>5.0e-08</RECOM_RATE>
<PROP_RECOM_HS>0</PROP_RECOM_HS>
<GC_RATE>0</GC_RATE>
<GC_LENGTH>0</GC_LENGTH>
<HS_LENGTH>10</HS_LENGTH>
<HS_SPACING>50000</HS_SPACING>
<N_REGIONS>1</N_REGIONS>
<SUBS_PER_REGION>1</SUBS_PER_REGION>
<REGION_GAMMA_SCALE>0</REGION_GAMMA_SCALE>
<REGION_GAMMA_SHAPE>1</REGION_GAMMA_SHAPE>
<SUB_REGION_GAMMA_SHAPE>1</SUB_REGION_GAMMA_SHAPE>
<INTENSITY_GAMMA_SHAPE>1</INTENSITY_GAMMA_SHAPE>
<HS_SPACING_GAMMA_SHAPE>1</HS_SPACING_GAMMA_SHAPE>
<HS_COMB>1</HS_COMB>
</HEAD>
```

recomb_b_n.xml

```xml
<?xml version='1.0' ?>
<!-- Recombination File --><HEAD>
<RECOM_RATE>1.0e-08</RECOM_RATE>
<PROP_RECOM_HS>0</PROP_RECOM_HS>
<GC_RATE>0</GC_RATE>
<GC_LENGTH>0</GC_LENGTH>
<HS_LENGTH>10</HS_LENGTH>
<HS_SPACING>50000</HS_SPACING>
<N_REGIONS>1</N_REGIONS>
<SUBS_PER_REGION>1</SUBS_PER_REGION>
<REGION_GAMMA_SCALE>0</REGION_GAMMA_SCALE>
<REGION_GAMMA_SHAPE>1</REGION_GAMMA_SHAPE>
<SUB_REGION_GAMMA_SHAPE>1</SUB_REGION_GAMMA_SHAPE>
<INTENSITY_GAMMA_SHAPE>1</INTENSITY_GAMMA_SHAPE>
<HS_SPACING_GAMMA_SHAPE>1</HS_SPACING_GAMMA_SHAPE>
<HS_COMB>1</HS_COMB>
</HEAD>
```

recomb_S_b_n.xml

```xml
<?xml version='1.0' ?>
<!-- Recombination File --><HEAD>
<RECOM_RATE>1.7860e-10</RECOM_RATE>
<PROP_RECOM_HS>0</PROP_RECOM_HS>
<GC_RATE>0</GC_RATE>
<GC_LENGTH>0</GC_LENGTH>
<HS_LENGTH>10</HS_LENGTH>
<HS_SPACING>5000</HS_SPACING>
<N_REGIONS>1</N_REGIONS>
<SUBS_PER_REGION>1</SUBS_PER_REGION>
<REGION_GAMMA_SCALE>0</REGION_GAMMA_SCALE>
<REGION_GAMMA_SHAPE>1</REGION_GAMMA_SHAPE>
<SUB_REGION_GAMMA_SHAPE>1</SUB_REGION_GAMMA_SHAPE>
<INTENSITY_GAMMA_SHAPE>1</INTENSITY_GAMMA_SHAPE>
<HS_SPACING_GAMMA_SHAPE>1</HS_SPACING_GAMMA_SHAPE>
<HS_COMB>1</HS_COMB>
</HEAD>
```