

Script to run FREGENE for Const-Sel replications:

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#Run a const size population of 25,900 with a FREGENE scaling factor of 40  
i=20  
/usr/local/bin/fregene -SELECT -sel_LE 700000 -i in_c_s.xml -p par_c_s.xml -recomb recomb_c_s.xml -o  
rin_1_c_s.xml -af posAf_1_c_s.txt -sd $i -scale 40.0 -hz homoz_1_c_s.txt > log_1_c_s.txt  
  
#Unscale population size  
let i=$i+1  
/usr/local/bin/fregene -SELECT -sel_LE 700000 -i rin_1_c_s.xml -p par_c_s.xml -gn 0 -recomb recomb_c_s.xml -  
o rin_2_c_s.xml -sd $i -scale_exp 40.0 1 -af posAf_2_c_s.txt -hz homoz_2_c_s.txt > log_2_c_s.txt  
  
#Run sample and make a genotype (-og) file for "Gen_0"  
let i=$i+1  
/usr/local/bin/sample -i rin_2_c_s.xml -log output_c_s_Sample -og geno_c_s_Sample_1  
-controls 5000 -chromolength 50.0 -sd $i > log_1_c_s_Sample.txt  
  
#Run population for 10 more generations at full size  
let i=$i+3  
/usr/local/bin/fregene -SELECT -sel_LE 700000 -i rin_2_c_s.xml -p par_c_s.xml -gn 10  
-recomb recomb_c_s.xml -o rin_3_c_s.xml -sd $i -af posAf_3_c_s.txt -hz homoz_3_c_s.txt > log_3_c_s.txt  
  
#Run sample and make a genotype (-og) for "Gen_10"  
let i=$i+1  
/usr/local/bin/sample -i rin_3_c_s.xml -log output_c_s_Sample_3 -og geno_c_s_Sample_3  
-controls 2000 -chromolength 50.0 -sd $i > log_3_c_s_Sample.txt
```

Input files for Const-Sel FREGENE simulations

par_c_s.xml

```
<?xml version='1.0' ?>  
<!-- Parameter File --><HEAD>  
<NO_GENER>370000</NO_GENER>  
<MUTAT_RATE>9.38e-09</MUTAT_RATE>  
<PROP_SEL>1.0e-03</PROP_SEL>  
<SEL_COEF_POS>0.0</SEL_COEF_POS>  
<SEL_COEF_SD_POS>0.0</SEL_COEF_SD_POS>  
<SEL_COEF_NEG>-2.0e-04</SEL_COEF_NEG>  
<SEL_COEF_SD_NEG>0.0</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>0.0</SEL_DOM_SD_POS>  
<SEL_DOM_NEG>0.5</SEL_DOM_NEG>  
<SEL_DOM_SD_NEG>0.0</SEL_DOM_SD_NEG>  
<PROP_POS_SEL_DOM>1.0</PROP_POS_SEL_DOM>  
<GROWTH_RATE>0.0</GROWTH_RATE>  
<DELETION_INTERVAL>37000</DELETION_INTERVAL>  
<PROP_SEL_LOCAL>0.0</PROP_SEL_LOCAL>  
</HEAD>
```

in_c_s.xml

```
<?xml version='1.0' ?>
<!-- This a Forward Data Simulation --><HEAD><DATE>Fri March 6th 11:30:50 2009
</DATE>
<SIMULATION_FEATURES>
<SEGMENTS>51800</SEGMENTS>
<MAX_MUT_CHROMO>0</MAX_MUT_CHROMO>
<CHROMO_LENGTH>50.0</CHROMO_LENGTH>
<MAX_MATRIX_SIZE>1.25e+15</MAX_MATRIX_SIZE>
</SIMULATION_FEATURES>
</HEAD>
<DATA>0
</DATA>
```

recomb_c_s.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>
```