

```
In [1]: # Founders: real haplotype data (chlto10.200SNP)
# "Sample animals for sire and dam candidates" & "Dams and Sires": dam size = N of dams
# One Dam -> 1 male & 1 female (1 dam -> 2 offsprings)
# selection: increase
# 5 generation selection: increase
# heritability = 0.1
# Phenotypes : all animals in G0 to G4
# Genotypes : all progeny in G5 and all sires in each generation
# Change muAlpha = 0.2
# 10 chromosomes; 20 loci per chromosome = > 200 Loci (50 QTL & 150 Markers)
```

```
In [2]: include("/home/nicole/Jupyter/XSimSel.jl")
```

```
Out[2]: XSim
```

```
In [3]: using DataFrames
```

```
In [4]: using Distributions
```

```
In [5]: using(Gadfly)
```

Initialize XSim

```
In [6]: numChr      = 10
chrLength = 0.01
numLoci    = 20
nQTL       = 5
mutRate    = 0.0
locusInt   = chrLength/numLoci
mapPos     = collect(locusInt/2:locusInt:chrLength)
geneFreq   = fill(0.5,numLoci)
QTL = sample(1:numLoci,nQTL,replace=false)
qtlMarker  = fill(false,numLoci)
qtlMarker[QTL] = true
mu = 100                                     #  $\alpha \sim N(100,1)$ 
Va = nQTL*numChr*0.5*mu*mu                  #  $Va = nQTL * 2pq * \text{mean}(\alpha)^2$ 
qtlEffects= rand(Normal(mu/sqrt(Va), sqrt(1/Va)),numLoci*numChr) # Let  $\alpha \mu = 0.115$ 
XSim.init(numChr,numLoci,chrLength,geneFreq,mapPos,qtlMarker,qtlEffects,mutRate)
```

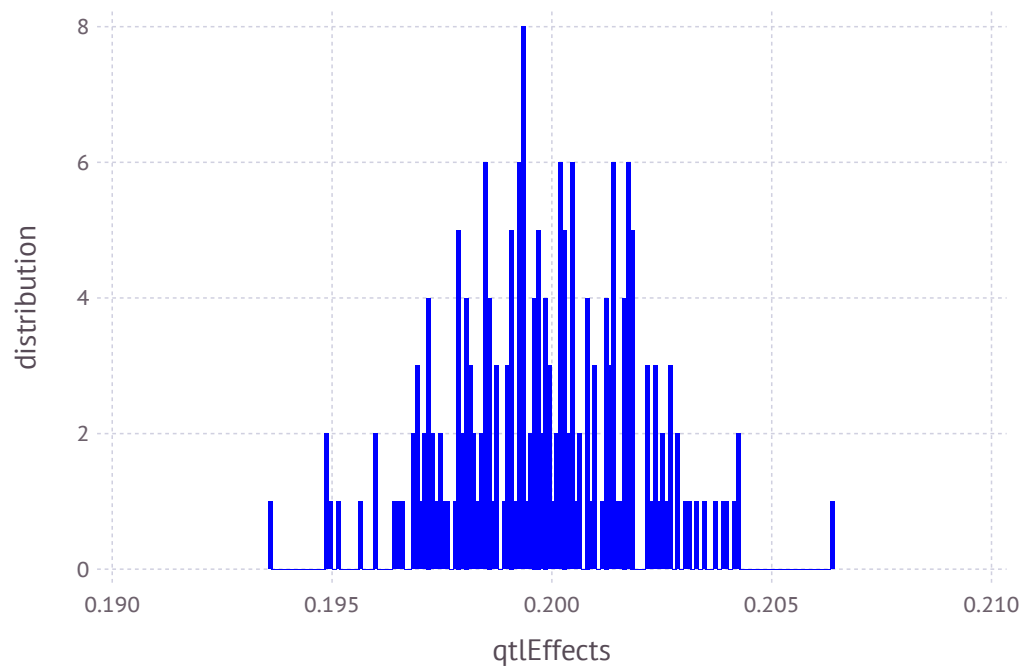
```
In [7]: qtlEffects
```

```
Out[7]: 200-element Array{Float64,1}:  
 0.201779  
 0.201652  
 0.199301  
 0.199022  
 0.199224  
 0.198763  
 0.198298  
 0.197873  
 0.202871  
 0.202701  
 0.200368  
 0.19836  
 0.19707  
 ⋮  
 0.197344  
 0.198441  
 0.196908  
 0.197155  
 0.200435  
 0.199718  
 0.19791  
 0.199728  
 0.199382  
 0.199581  
 0.197946  
 0.198503
```

```
In [8]: writedlm("qtlEffects",qtlEffects)
```

```
In [9]: plot(x=qtEffects, Geom.histogram, Guide.XLabel("qtEffects"), Guide.YLabel("distribution"), Theme(default
```

Out[9]:



```
In [10]: mean(qtEffects)
```

Out[10]: 0.19980190125607336

```
In [11]: var(qtEffects)
```

Out[11]: 4.32302413895192e-6

```
In [12]: # Base Population
gen=0
nGenBase    = 5
popSizeBase = 8000

# Sample 20 sire and 400 dams
popSizeSP = 8000

# Purbred Populations - mating
popSize = 8000
nGener  = 5
nSires  = 200
nDams   = 4000
npop    = 1
;
```

```

In [13]: # Animals with genotypes
posOFF0S = 1
posOFF0E = popSizeSP
posOFF1S = posOFF0E + 1
posOFF1E = posOFF0E + popSize
posOFF2S = posOFF1E + 1
posOFF2E = posOFF1E + popSize
posOFF3S = posOFF2E + 1
posOFF3E = posOFF2E + popSize
posOFF4S = posOFF3E + 1
posOFF4E = posOFF3E + popSize
posOFF5S = posOFF4E + 1
posOFF5E = posOFF4E + popSize
println("posOFF1S: ",posOFF1S,"; posOFF1E: ",posOFF1E)
println("posOFF2S: ",posOFF2S,"; posOFF2E: ",posOFF2E)
println("posOFF3S: ",posOFF3S,"; posOFF3E: ",posOFF3E)
println("posOFF4S: ",posOFF4S,"; posOFF4E: ",posOFF4E)
println("posOFF5S: ",posOFF5S,"; posOFF5E: ",posOFF5E)

# FileName :
PedAll = "PedAll.txt"           # pedigree file with all animals
PheAll = "PheAll.txt"          # phenotype file with all animals
GenAll = "GenAll.txt"          # genotype file with all animals

Gen = "Gen.txt"                 # genotype file with all progeny in G5 and all sires in each generation
Phe = "Phe.txt"                 # phenotype file with all animals in G1 to G4
QTL = "QTL.txt"                 # QTL with with all progeny in G5 and all sires in each generation
Mar = "Mar.txt"                 # Marker with with all progeny in G5 and all sires in each generation
GenNF = "GenNF.txt"             # remove fixed genes from genotype file
QTLNF = "QTLNF.txt"             # remove fixed genes from QTL file
MarNF = "MarNF.txt"             # remove fixed genes from Marker file
;

posOFF1S: 8001; posOFF1E: 16000
posOFF2S: 16001; posOFF2E: 24000
posOFF3S: 24001; posOFF3E: 32000
posOFF4S: 32001; posOFF4E: 40000
posOFF5S: 40001; posOFF5E: 48000

```

```
In [14]: fileName = "SS"
         pedText = fileName * ".ped"
         genText = fileName * ".gen"
         pheText = fileName * ".phe"
         ;
```

```
In [15]: ;rm $pedText $genText $pheText
```

```
rm: cannot remove 'SS.ped': No such file or directory
rm: cannot remove 'SS.gen': No such file or directory
rm: cannot remove 'SS.phe': No such file or directory
```

Sampling Founders

```
In [16]: sires = XSim.sampleFounders("/home/nicole/Jupyter/HERdata/data/Clean/newdata/ch1to10.200SNP.group1")
         dams  = XSim.sampleFounders("/home/nicole/Jupyter/HERdata/data/Clean/newdata/ch1to10.200SNP.group2");
```

```
Sampling 360 animals into base population.
Sampling 361 animals into base population.
```

Base population

```
In [17]: baseSires, baseDams, baseGen = XSim.sampleRan(popSizeBase, nGenBase, sires, dams, gen=gen);
```

```
Generation      1: sampling  4000 males and  4000 females
Generation      2: sampling  4000 males and  4000 females
Generation      3: sampling  4000 males and  4000 females
Generation      4: sampling  4000 males and  4000 females
Generation      5: sampling  4000 males and  4000 females
```

Sample animals for sire and dam candidates

```
In [18]: popSP = XSim.sampleRan(popSizeSP, 1, baseSires, baseDams, gen=baseGen, fileName=fileName);
```

```
Generation      6: sampling  4000 males and  4000 females
```

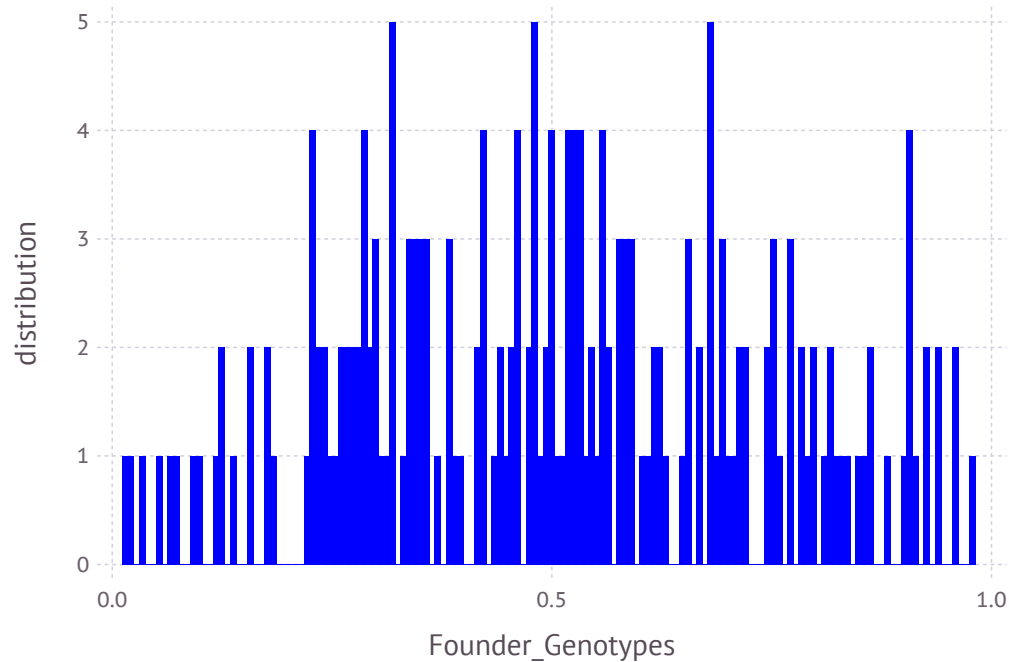
```
In [19]: gSPSire = XSim.getOurGenotypes(popSP[1])
gSPDam = XSim.getOurGenotypes(popSP[2])
gSP = [gSPSire;gSPSire];
```

```
In [20]: FCM = mean(gSP/2,1)
```

```
Out[20]: 1x200 Array{Float64,2}:
 0.06725  0.8355  0.288125  0.942  0.817625  ...  0.386625  0.904125  0.532375
```

```
In [21]: plot(x=FCM, Geom.histogram, Guide.XLabel("Founder_Genotypes"), Guide.YLabel("distribution"), Theme(default
```

```
Out[21]:
```



```
In [22]: V=var(gSP,1)
Mark=gSP[:,V.>0]
corMat=cor(Mark)
nRows =size(corMat,1)
LDMat =zeros(nRows-1,20);
```



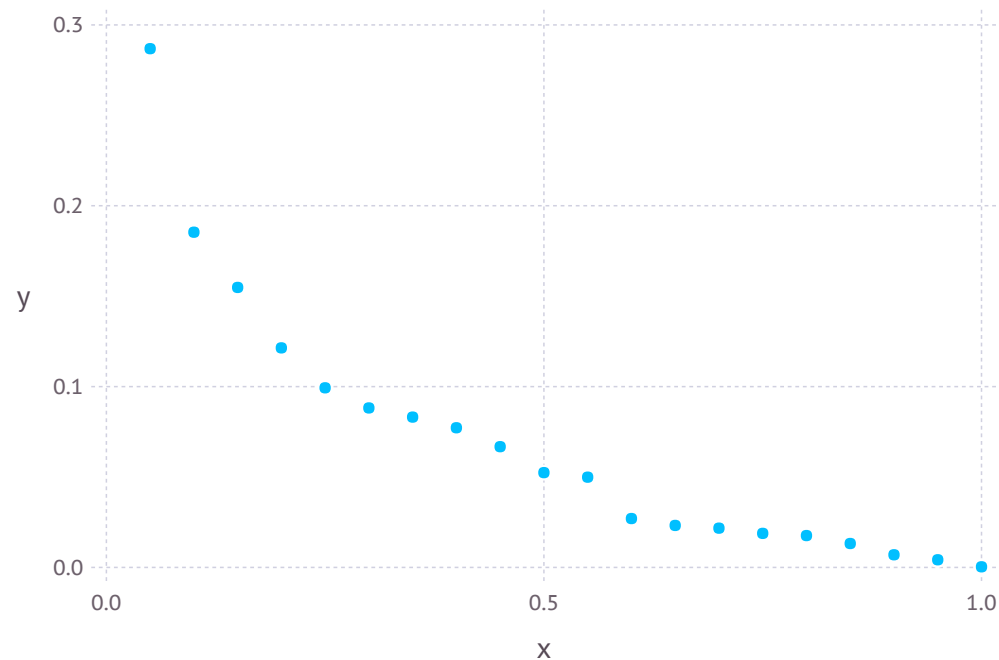
```
In [23]: for i=1:(nRows-20)
LDMat[i,:] = corMat[i,(i+1):(i+20)].^2
end
```

```
In [24]: y=mean(LDMat,1)
sort(y,2)
```

```
Out[24]: 1x20 Array{Float64,2}:
 0.000338771  0.00423232  0.0070215  ...  0.154833  0.18539  0.286848
```

```
In [25]: plot(x=(1:20)/20*1,y=y)
```

Out[25]:



```
In [26]: FCMstream = open("SNPCMF.txt", "w")
```

```
Out[26]: IOStream(<file SNPCMF.txt>)
```

```
In [27]: for i in 1:size(FCM,2)
          @printf(FCMstream, "%6.4f ", FCM[1,i])
        end
```

```
In [28]: close(FCMstream)
```

Selection - increase

```
In [29]: aSPSire = XSim.getOurGenVals(popSP[1])
          aSPDam = XSim.getOurGenVals(popSP[2])
          aSP = [aSPSire;aSPDam];
```

```
In [30]: mean(aSP)
```

```
Out[30]: 9.452028023464276
```

```
In [31]: varGen=var(aSP)
```

```
Out[31]: 0.8711064548172242
```

```
In [32]: XSim.common.varRes = 9*varGen    #heritability = 0.1
```

```
Out[32]: 7.839958093355017
```

```
In [33]: varRes = XSim.common.varRes
```

```
Out[33]: 7.839958093355017
```

```
In [34]: popRMP = XSim.sampleSelNoLap(nSires, nDams, nGener, popSP[1], popSP[2], gen=popSP[3], fileName=fileName, direc
```

```
Generation      7: sampling 4000 males and 4000 females
Generation      8: sampling 4000 males and 4000 females
Generation      9: sampling 4000 males and 4000 females
Generation     10: sampling 4000 males and 4000 females
Generation     11: sampling 4000 males and 4000 females
```

```
In [35]: ymRMP = XSim.getOurGenVals(popRMP[1])    # for males: pop[1]
         mean(ymRMP)
```

```
Out[35]: 11.195627531517506
```

```
In [36]: yfRMP = XSim.getOurGenVals(popRMP[2])    # for females: pop[2]
         mean(yfRMP)
```

```
Out[36]: 11.194031626267199
```

```
In [37]: amRMP = XSim.getOurGenVals(popRMP[1])
         var(amRMP)
```

```
Out[37]: 0.7971101621095362
```

```
In [38]: afRMP = XSim.getOurGenVals(popRMP[2])
         var(afRMP)
```

```
Out[38]: 0.8378297272839439
```

Pedigree: All animals

```
In [39]: PED = convert(Array,readtable(pedText,separator=' ',header=false))
```

```
Out[39]: 48000x3 Array{Int64,2}:  
  40722  34133  37664  
  40723  33080  38232  
  40724  36702  39968  
  40725  34112  37677  
  40726  35843  38722  
  40727  35681  36879  
  40728  33218  39116  
  40729  34223  38838  
  40730  36314  38913  
  40731  34588  38454  
  40732  33545  37696  
  40733  33888  37977  
  40734  35655  39897  
      ⋮  
  88710  73921  77196  
  88711  75575  79569  
  88712  74933  78920  
  88713  74591  77921  
  88714  75948  78168  
  88715  76224  80523  
  88716  75461  80334  
  88717  73586  79632  
  88718  75453  76924  
  88719  73454  80653  
  88720  73643  78835  
  88721  73747  79920
```

```
In [40]: PEDstream = open(PedAll, "w")
```

```
Out[40]: IOStream(<file PedAll.txt>)
```

```
In [41]: for i in 1:size(PED,1)  
          @printf(PEDstream, "%19d%19d%19d \n", PED[i,1], PED[i,2], PED[i,3])  
        end
```

```
In [42]: close(PEDstream)
```

Create matrix of "genotype" covariates for all animals

```
In [43]: nObs = countlines(pedText)
```

```
Out[43]: 48000
```

```
In [44]: nMarker = numChr*numLoci
```

```
Out[44]: 200
```

```
In [45]: GT = convert(Array,readtable(genText,separator=' ',header=false))
```

```
Out[45]: 48000x201 Array{Int64,2}:
```

```
40722  1  2  0  2  2  1  1  1  1  1  ...  2  0  1  2  0  2  1  1  1  0  2  2
40723  1  2  0  2  2  0  0  0  2  0      2  1  1  1  1  2  0  1  1  0  2  1
40724  0  2  1  2  1  0  0  0  2  0      1  1  2  1  1  1  1  1  1  1  2  1
40725  0  2  0  2  2  0  1  1  2  0      2  2  2  0  2  2  0  2  2  0  2  0
40726  0  1  1  1  1  0  1  1  1  1      2  1  1  1  2  2  0  1  1  1  2  0
40727  0  1  1  1  1  0  1  1  1  1  ...  0  0  2  2  0  0  2  0  0  2  2  2
40728  0  2  0  2  2  0  0  0  2  0      2  1  2  2  2  2  0  1  1  1  2  1
40729  0  2  0  2  2  1  1  1  1  1      1  1  2  1  1  1  1  1  1  1  2  1
40730  0  2  0  2  2  0  1  0  2  0      2  1  2  1  2  2  0  1  1  1  1  1
40731  0  2  0  2  2  1  1  1  1  1      2  2  2  1  2  2  0  1  1  1  2  0
40732  0  2  0  2  2  0  0  0  2  0  ...  2  2  2  1  2  2  0  1  1  1  2  0
40733  0  2  0  2  2  0  0  0  2  0      1  0  2  2  1  1  1  1  1  1  2  1
40734  0  2  0  2  2  1  1  1  1  1      2  1  1  1  1  2  0  1  1  0  2  1
      ⋮      ⋮      ⋮      ⋮      ⋮      ⋮      ⋮      ⋮      ⋮      ⋮
88710  0  1  1  1  1  0  1  1  1  1      2  0  1  2  2  2  0  0  0  2  1  1
88711  0  1  1  1  2  0  2  2  1  1      2  2  2  0  2  2  0  1  1  1  1  1
88712  0  1  1  2  2  1  1  1  1  1  ...  2  0  1  1  1  2  1  0  0  2  0  2
88713  0  1  1  2  2  1  1  1  1  1      2  0  1  2  1  2  0  0  0  1  1  2
88714  0  2  0  2  2  0  0  0  2  0      2  1  2  2  2  2  0  0  0  2  1  1
88715  1  2  0  2  2  1  1  1  1  1      1  0  2  2  2  1  1  1  1  1  2  1
88716  0  2  1  2  1  1  1  1  1  1      2  1  2  1  2  2  0  1  1  1  1  1
88717  0  2  1  2  1  0  0  0  2  0  ...  1  0  1  2  0  1  1  0  0  1  2  2
88718  0  2  0  2  2  0  1  0  2  0      2  1  2  2  2  2  0  0  0  1  1  1
88719  0  1  1  2  2  0  1  1  1  1      2  1  2  1  2  2  0  1  1  1  1  1
88720  0  2  0  2  2  0  1  0  2  0      2  1  1  1  1  1  1  1  1  1  2  1
88721  0  2  1  2  1  0  1  1  2  0      2  2  2  0  2  2  0  2  2  0  2  0
```

```
In [46]: allID = GT[:,1];
```

```
In [47]: GTM = GT[:,2:end];
```

Create marker file for all animals

```
In [48]: M = GTM      # maker file for Julia
```

```
Out[48]: 48000x200 Array{Int64,2}:
 1  2  0  2  2  1  1  1  1  1  1  1  ...  2  0  1  2  0  2  1  1  1  0  2  2
 1  2  0  2  2  0  0  0  2  0  0  1  0  ...  2  1  1  1  1  2  0  1  1  0  2  1
 0  2  1  2  1  0  0  0  2  0  0  2  1  ...  1  1  2  1  1  1  1  1  1  1  2  1
 0  2  0  2  2  0  1  1  2  0  0  2  2  ...  2  2  2  0  2  2  0  2  2  0  2  0
 0  1  1  1  1  0  1  1  1  1  1  1  2  ...  2  1  1  1  2  2  0  1  1  1  2  0
 0  1  1  1  1  0  1  1  1  1  1  0  1  ...  0  0  2  2  0  0  2  0  0  2  2  2
 0  2  0  2  2  0  0  0  2  0  0  2  2  ...  2  1  2  2  2  2  0  1  1  1  2  1
 0  2  0  2  2  1  1  1  1  1  1  1  2  ...  1  1  2  1  1  1  1  1  1  1  2  1
 0  2  0  2  2  0  1  0  2  0  0  0  0  ...  2  1  2  1  2  2  0  1  1  1  1  1
 0  2  0  2  2  1  1  1  1  1  1  1  2  ...  2  2  2  1  2  2  0  1  1  1  2  0
 0  2  0  2  2  0  0  0  2  0  0  1  1  ...  2  2  2  1  2  2  0  1  1  1  2  0
 0  2  0  2  2  0  0  0  2  0  0  2  2  ...  1  0  2  2  1  1  1  1  1  1  2  1
 0  2  0  2  2  1  1  1  1  1  1  1  2  ...  2  1  1  1  1  2  0  1  1  0  2  1
 ⋮          ⋮          ⋮          ⋮          ⋮
 0  1  1  1  1  0  1  1  1  1  1  0  1  ...  2  0  1  2  2  2  0  0  0  2  1  1
 0  1  1  1  2  0  2  2  1  1  1  0  0  ...  2  2  2  0  2  2  0  1  1  1  1  1
 0  1  1  2  2  1  1  1  1  1  1  0  1  ...  2  0  1  1  1  2  1  0  0  2  0  2
 0  1  1  2  2  1  1  1  1  1  1  1  2  ...  2  0  1  2  1  2  0  0  0  1  1  2
 0  2  0  2  2  0  0  0  2  0  0  0  0  ...  2  1  2  2  2  2  0  0  0  2  1  1
 1  2  0  2  2  1  1  1  1  1  1  1  2  ...  1  0  2  2  2  1  1  1  1  1  2  1
 0  2  1  2  1  1  1  1  1  1  1  1  1  ...  2  1  2  1  2  2  0  1  1  1  1  1
 0  2  1  2  1  0  0  0  2  0  0  1  1  ...  1  0  1  2  0  1  1  0  0  1  2  2
 0  2  0  2  2  0  1  0  2  0  0  1  1  ...  2  1  2  2  2  2  0  0  0  1  1  1
 0  1  1  2  2  0  1  1  1  1  1  0  0  ...  2  1  2  1  2  2  0  1  1  1  1  1
 0  2  0  2  2  0  1  0  2  0  0  2  2  ...  2  1  1  1  1  1  1  1  1  1  2  1
 0  2  1  2  1  0  1  1  2  0  0  2  1  ...  2  2  2  0  2  2  0  2  2  0  2  0
```

```
In [49]: Mstream = open(GenAll, "w")
```

```
Out[49]: IOStream(<file GenAll.txt>)
```

```
In [50]: for i in 1:size(M,1)
          @printf(Mstream, "%19d", allID[i])
          for j in 1:size(M,2)
              @printf(Mstream, "%3d", M[i,j])
          end
          @printf(Mstream, "\n")
        end
```

```
In [51]: close(Mstream)
```

Genotypes - all sires and all offsprings in G5

```
In [52]: AllSire = PED[posOFF1S:posOFF5E,2]
```

```
Out[52]: 40000-element Array{Int64,1}:
```

```
42423
44010
42537
43159
42112
42308
41678
42264
43911
41867
41678
42954
44099
⋮
73921
75575
74933
74591
75948
76224
75461
73586
75453
73454
73643
73747
```



```
In [53]: SireID = unique(AllSire)
```

```
Out[53]: 1000-element Array{Int64,1}:
```

```
42423
44010
42537
43159
42112
42308
41678
42264
43911
41867
42954
44099
43613
⋮
74589
73786
76483
74017
76412
74821
74756
74992
74683
74199
73404
76348
```

```
In [54]: OFF5 = PED[posOFF5S:posOFF5E,1]
```

```
Out[54]: 8000-element Array{Int64,1}:
```

```
80722
```

```
80723
```

```
80724
```

```
80725
```

```
80726
```

```
80727
```

```
80728
```

```
80729
```

```
80730
```

```
80731
```

```
80732
```

```
80733
```

```
80734
```

```
⋮
```

```
88710
```

```
88711
```

```
88712
```

```
88713
```

```
88714
```

```
88715
```

```
88716
```

```
88717
```

```
88718
```

```
88719
```

```
88720
```

```
88721
```

```
In [55]: SireOFF5ID = [SireID;OFF5]
```

```
Out[55]: 9000-element Array{Int64,1}:
 42423
 44010
 42537
 43159
 42112
 42308
 41678
 42264
 43911
 41867
 42954
 44099
 43613
      ⋮
 88710
 88711
 88712
 88713
 88714
 88715
 88716
 88717
 88718
 88719
 88720
 88721
```

```
In [56]: SOFF5ID= DataFrame()
         SOFF5ID[:ID] = SireOFF5ID;
```

```
In [57]: typeof(SOFF5ID)
```

```
Out[57]: DataFrames.DataFrame
```

```
In [58]: MT = readtable(GenAll,separator=' ',header=false);
```

```
In [59]: rename!(MT,:x1,:ID);
```

```
In [60]: GSOFF5 = join(SOFF5ID, MT, on = :ID, kind = :inner);
```

```
In [61]: size(GSOFF5)
```

```
Out[61]: (9000,201)
```

```
In [62]: GSOFF5Row = size(GSOFF5,1)
```

```
Out[62]: 9000
```

```
In [63]: GSOFF5Col = size(GSOFF5,2)
```

```
Out[63]: 201
```

```
In [64]: GSOFF5stream = open(Gen, "w")
```

```
Out[64]: IOStream(<file Gen.txt>)
```

```
In [65]: for i in 1:size(GSOFF5,1)
          for j in 1
              @printf(GSOFF5stream, "%19d", GSOF5[i,j])
          end
          for k in 2:size(GSOFF5,2)
              @printf(GSOFF5stream, "%3d", GSOF5[i,k])
          end
          @printf(GSOFF5stream, "\n")
        end
```

```
In [66]: close(GSOFF5stream)
```

Phenotypes - All animals

```
In [67]: PBV = convert(Array,readtable(pheText,separator=' ',header=false))
```

```
Out[67]: 48000x3 Array{Real,2}:
          40722  12.169  11.359
          40723   9.801   9.985
          40724  11.578  11.151
          40725  11.049   9.763
          40726  11.703  10.359
          40727   8.053   8.175
          40728   6.834   9.178
          40729   9.79   9.558
          40730  10.223  10.173
          40731   9.576  10.743
          40732  10.401   9.762
          40733  11.783  10.759
          40734   9.798  10.179
              ⋮
          88710   9.145  10.974
          88711  10.082  10.361
          88712   9.673  10.558
          88713  13.106  11.356
          88714  18.308  10.373
          88715   9.161  12.563
          88716  13.924  11.751
          88717   7.093  10.359
          88718   6.733  12.752
          88719   9.206  10.969
          88720   7.803  11.564
          88721  11.729  11.563
```

```
In [68]: PBVstream = open(PheAll, "w")
```

```
Out[68]: IOStream(<file PheAll.txt>)
```

```
In [69]: for i in 1:size(PBV,1)
          @printf(PBVstream, "%19d %10.3f %10.3f \n", PBV[i,1], PBV[i,2], PBV[i,3])
          end
```

```
In [70]: close(PBVstream )
```

Phenotypes - all animals from G0 to G4

```
In [71]: OFFG0toG4 = PED[posOFF0S:posOFF4E,1]
```

```
Out[71]: 40000-element Array{Int64,1}:
          40722
          40723
          40724
          40725
          40726
          40727
          40728
          40729
          40730
          40731
          40732
          40733
          40734
           ⋮
          80710
          80711
          80712
          80713
          80714
          80715
          80716
          80717
          80718
          80719
          80720
          80721
```

```
In [72]: OFFG0toG4ID= DataFrame()
          OFFG0toG4ID[:ID] = OFFG0toG4;
```

```
In [73]: typeof(OFFG0toG4ID)
```

```
Out[73]: DataFrames.DataFrame
```

```
In [74]: AllPBV= readtable(pheText,separator=' ',header=false);
```

```
In [75]: rename!(AllPBV,:x1,:ID)
         head(AllPBV);
```

```
In [76]: OFFG0toG4PBV = join(OFFG0toG4ID, AllPBV, on = :ID, kind = :inner);
```

```
In [77]: Row = size(OFFG0toG4PBV,1)
```

```
Out[77]: 40000
```

```
In [78]: Col = size(OFFG0toG4PBV,2)
```

```
Out[78]: 3
```

```
In [79]: Phestream = open(Phe, "w")
```

```
Out[79]: IOStream(<file Phe.txt>)
```

```
In [80]: for i in 1:size(OFFG0toG4PBV,1)
         @printf(Phestream, "%19d %10.3f %10.3f \n", OFFG0toG4PBV[i,1], OFFG0toG4PBV[i,2], OFFG0toG4PBV[i,3])
         end
```

```
In [81]: close(Phestream)
```

Get files with QTL only or Markers only

QTL file and Markers file

```
In [82]: QTLPos = XSim.common.G.qtl_index
```

```
Out[82]: 50-element Array{Int64,1}:
```

```
 1  
 2  
 6  
13  
18  
21  
22  
26  
33  
38  
41  
42  
46  
:  
153  
158  
161  
162  
166  
173  
178  
181  
182  
186  
193  
198
```



```
In [83]: k = size(M,2)
MarkerPos = deleteat!(collect(1:k),sort(QTLPos))
```

```
Out[83]: 150-element Array{Int64,1}:
 3
 4
 5
 7
 8
 9
10
11
12
14
15
16
17
 ⋮
187
188
189
190
191
192
194
195
196
197
199
200
```

Genotype codes: 0, 1, 2

```
In [84]: IDgen = convert(Array,readtable(Gen,separator=' ',header=false));
```

```
In [85]: onlyID = IDgen[:,1]
        QTLMarker = IDgen[:, 2:end]
```

```
Out[85]: 9000x200 Array{Int64,2}:
```

```
 1  2  0  2  2  1  1  1  1  1  1  1  ...  2  0  1  2  0  2  1  1  1  0  2  2
 0  1  1  1  1  0  1  1  1  1  1  1  2    2  1  1  1  2  2  0  1  1  1  2  0
 0  2  0  2  2  0  0  0  2  0  0  2  2    1  0  2  2  1  1  1  1  1  1  2  1
 0  2  0  2  2  0  0  0  2  0  0  2  2    2  1  2  2  1  2  0  0  0  1  1  1
 0  2  0  2  2  0  1  1  1  1  1  1  2    0  0  2  2  1  1  1  0  0  1  2  2
 0  2  1  2  1  1  1  1  1  1  0  1  1  ...  2  1  2  1  1  2  0  1  1  0  1  1
 0  2  0  2  2  1  1  1  1  1  1  1  2    2  1  1  2  1  1  1  0  0  1  2  2
 1  2  0  2  2  2  2  2  0  2  2  0  2    1  1  2  2  1  1  1  0  0  2  2  2
 0  2  1  2  1  0  0  0  2  0  0  2  1    2  1  2  1  2  1  1  1  1  1  2  1
 0  1  1  2  2  2  2  2  0  2  2  0  2    2  0  1  2  1  1  1  0  0  1  2  2
 0  2  0  2  2  0  1  1  2  0  0  2  2  ...  2  1  1  1  1  2  0  1  1  0  2  1
 0  2  0  2  2  1  2  2  1  1  1  1  2    2  2  2  1  2  2  0  1  1  0  2  0
 0  2  0  2  2  0  1  1  2  0  0  1  1    2  2  2  0  2  2  0  2  2  0  2  0
 ⋮          ⋮          ⋮          ⋮          ⋮          ⋮
 0  1  1  1  1  0  1  1  1  1  1  0  1    2  0  1  2  2  2  0  0  0  2  1  1
 0  1  1  1  2  0  2  2  1  1  1  0  0    2  2  2  0  2  2  0  1  1  1  1  1
 0  1  1  2  2  1  1  1  1  1  1  0  1  ...  2  0  1  1  1  2  1  0  0  2  0  2
 0  1  1  2  2  1  1  1  1  1  1  1  2    2  0  1  2  1  2  0  0  0  1  1  2
 0  2  0  2  2  0  0  0  2  0  0  0  0    2  1  2  2  2  2  0  0  0  2  1  1
 1  2  0  2  2  1  1  1  1  1  1  1  2    1  0  2  2  2  1  1  1  1  1  2  1
 0  2  1  2  1  1  1  1  1  1  1  1  1    2  1  2  1  2  2  0  1  1  1  1  1
 0  2  1  2  1  0  0  0  2  0  0  1  1  ...  1  0  1  2  0  1  1  0  0  1  2  2
 0  2  0  2  2  0  1  0  2  0  0  1  1    2  1  2  2  2  2  0  0  0  1  1  1
 0  1  1  2  2  0  1  1  1  1  1  0  0    2  1  2  1  2  2  0  1  1  1  1  1
 0  2  0  2  2  0  1  0  2  0  0  2  2    2  1  1  1  1  1  1  1  1  1  2  1
 0  2  1  2  1  0  1  1  2  0  0  2  1    2  2  2  0  2  2  0  2  2  0  2  0
```

```
In [86]: onlyQTL = QTLMarker[:,QTLPos]
```

```
Out[86]: 9000x50 Array{Int64,2}:
```

```
 1  2  1  1  0  1  1  0  1  1  1  1  2  ...  1  2  2  0  2  0  1  1  1  0  0  0
 0  1  0  2  1  2  1  0  1  2  1  1  1  ...  2  1  2  0  2  0  1  2  1  1  2  1
 0  2  0  2  1  2  1  0  1  2  2  0  0  ...  2  2  2  0  0  0  2  2  0  1  1  1
 0  2  0  2  1  2  2  0  2  2  2  0  1  ...  2  1  2  0  1  0  1  1  1  1  1  1
 0  2  0  2  1  1  0  0  1  1  0  2  2  ...  2  0  1  0  2  0  2  2  0  0  1  1
 0  2  1  1  0  2  2  0  2  2  1  2  2  ...  2  1  1  1  1  0  2  2  0  2  1  0
 0  2  1  2  1  2  1  1  2  1  2  1  2  ...  2  2  2  1  0  0  1  1  2  1  1  1
 1  2  2  2  0  2  2  1  1  2  0  2  1  ...  1  1  0  2  1  0  0  2  0  1  1  2
 0  2  0  1  2  1  1  0  2  1  0  2  2  ...  1  2  2  0  2  0  0  2  1  2  2  1
 0  1  2  2  0  2  1  0  1  2  1  1  2  ...  1  1  1  1  2  1  1  2  1  2  1  1
 0  2  0  2  1  2  0  0  1  2  2  1  1  ...  2  2  0  1  1  0  2  2  0  1  1  0
 0  2  1  2  1  2  0  0  0  2  2  0  0  ...  2  2  2  0  2  0  2  1  1  2  2  0
 0  2  0  1  1  1  2  0  2  2  1  1  0  ...  2  2  0  1  1  0  1  2  0  2  2  0
 ⋮          ⋮          ⋮          ⋮          ⋮          ⋮
 0  1  0  1  0  1  2  1  2  1  1  2  2  ...  1  1  1  1  1  0  2  2  2  1  2  2
 0  1  0  0  1  1  1  1  1  0  0  2  2  ...  2  2  2  0  1  0  1  1  1  1  2  1
 0  1  1  1  0  2  1  1  1  2  1  1  0  ...  2  2  1  1  1  0  1  2  1  0  1  2
 0  1  1  2  1  2  0  1  0  2  0  1  2  ...  2  1  2  0  2  0  2  2  0  1  1  1
 0  2  0  0  0  2  0  0  0  2  1  1  1  ...  1  1  2  1  0  0  2  2  0  2  2  2
 1  2  1  2  1  2  1  0  2  2  1  1  1  ...  2  1  2  0  0  0  2  2  1  1  2  1
 0  2  1  1  0  2  2  0  2  2  2  0  2  ...  2  2  2  0  2  0  0  2  1  2  2  1
 0  2  0  1  0  1  1  0  1  1  1  1  2  ...  1  2  0  0  2  0  2  2  0  0  0  1
 0  2  0  1  1  2  2  0  2  2  1  1  2  ...  1  2  2  0  0  1  1  1  2  2  2  1
 0  1  0  0  0  2  1  0  1  2  2  0  0  ...  2  1  1  1  1  0  1  2  1  2  2  1
 0  2  0  2  2  2  2  1  1  2  0  2  2  ...  2  2  0  2  1  0  0  2  1  1  1  1
 0  2  0  1  1  2  1  1  1  2  2  0  1  ...  2  0  2  0  2  0  1  2  0  2  2  0
```

```
In [87]: onlyMar = QTLMarker[:,MarkerPos];
```

```
In [88]: QTLstream = open(QTL, "w")
Marstream = open(Mar, "w");
```

```
In [89]: for i in 1:size(onlyID,1)
          @printf(QTLstream, "%19d", onlyID[i])
          for j in 1:size(onlyQTL,2)
              @printf(QTLstream, "%3d", onlyQTL[i,j])
          end
          @printf(QTLstream, "\n")
      end
```

```
In [90]: for i in 1:size(onlyID,1)
          @printf(Marstream, "%19d", onlyID[i])
          for j in 1:size(onlyMar,2)
              @printf(Marstream, "%3d", onlyMar[i,j])
          end
          @printf(Marstream, "\n")
      end
```

```
In [91]: close(QTLstream)
          close(Marstream)
```

Remove Fixed Gene from the panel

```
In [92]: VQM = var(QTLMarker,1)
          QMnoFixed = QTLMarker[:,VQM .> 0]
          VQ = var(onlyQTL,1)
          QnoFixed = onlyQTL[:,VQ .> 0]
          VM = var(onlyMar,1)
          MnoFixed = onlyMar[:,VM .> 0];
```

```
In [93]: GenNFstream = open(GenNF, "w")
          QTLNFstream = open(QTLNF, "w")
          MarNFstream = open(MarNF, "w");
```

```
In [94]: for i in 1:size(onlyID,1)
          @printf(GenNFstream, "%19d", onlyID[i])
          for j in 1:size(QMnoFixed,2)
              @printf(GenNFstream, "%3d", QMnoFixed[i,j])
          end
          @printf(GenNFstream, "\n")
      end
```

```
In [95]: for i in 1:size(onlyID,1)
          @printf(QTLNFstream, "%19d", onlyID[i])
          for j in 1:size(QnoFixed,2)
              @printf(QTLNFstream, "%3d", QnoFixed[i,j])
          end
          @printf(QTLNFstream, "\n")
      end
```

```
In [96]: for i in 1:size(onlyID,1)
          @printf(MarNFstream, "%19d", onlyID[i])
          for j in 1:size(MnoFixed,2)
              @printf(MarNFstream, "%3d", MnoFixed[i,j])
          end
          @printf(MarNFstream, "\n")
      end
```

```
In [97]: close(GenNFstream)
          close(QTLNFstream)
          close(MarNFstream)
```

Check heritability

```
In [98]: P = AllPBV[:,2]
          BV = AllPBV[:,3];
```

```
In [99]: VP = var(P)
          VBV = var(BV)
          H = VBV/VP
```

```
Out[99]: 0.14317890647778117
```

```
In [100]: cor=cor(P,BV)
```

WARNING: imported binding for cor overwritten in module Main

```
Out[100]: 0.3740538471781798
```

```
In [101]: QTLAll = M[:,QTLPos]
```

```
Out[101]: 48000x50 Array{Int64,2}:
```

```

 1  2  1  1  0  1  1  0  1  1  1  1  2  ...  1  2  2  0  2  0  1  1  1  0  0  0
 1  2  0  0  0  2  1  0  0  1  0  2  1  ...  1  1  1  1  1  0  2  2  0  1  1  0
 0  2  0  1  1  2  1  0  1  2  2  1  1  ...  2  1  2  0  1  0  2  2  0  1  1  1
 0  2  0  2  2  1  0  0  1  2  0  2  0  ...  1  2  2  0  1  1  1  2  0  2  2  0
 0  1  0  2  1  2  1  0  1  2  1  1  1  ...  2  1  2  0  2  0  1  2  1  1  2  1
 0  1  0  1  0  2  1  0  1  1  1  1  1  ...  1  1  2  0  1  0  1  2  0  0  0  2
 0  2  0  2  2  1  0  0  0  1  1  1  0  ...  1  1  0  1  0  0  1  2  0  2  2  1
 0  2  1  2  1  1  0  0  0  1  1  1  1  ...  1  2  2  1  0  1  1  2  0  1  1  1
 0  2  0  0  0  2  1  0  1  2  1  1  1  ...  2  1  2  0  1  0  0  2  1  2  2  1
 0  2  1  2  1  2  0  1  0  2  1  1  2  ...  1  1  2  0  1  2  1  2  0  2  2  1
 0  2  0  1  0  1  1  1  0  1  2  0  1  ...  1  2  1  0  1  0  2  2  0  2  2  1
 0  2  0  2  1  2  1  0  1  2  2  0  0  ...  2  2  2  0  0  0  2  2  0  1  1  1
 0  2  1  2  1  1  0  0  0  1  0  2  1  ...  0  2  2  0  2  0  2  2  1  1  1  0
 ⋮          ⋮          ⋮          ⋮          ⋮          ⋮
 0  1  0  1  0  1  2  1  2  1  1  2  2  ...  1  1  1  1  1  0  2  2  2  1  2  2
 0  1  0  0  1  1  1  1  1  0  0  2  2  ...  2  2  2  0  1  0  1  1  1  1  2  1
 0  1  1  1  0  2  1  1  1  2  1  1  0  ...  2  2  1  1  1  0  1  2  1  0  1  2
 0  1  1  2  1  2  0  1  0  2  0  1  2  ...  2  1  2  0  2  0  2  2  0  1  1  1
 0  2  0  0  0  2  0  0  0  2  1  1  1  ...  1  1  2  1  0  0  2  2  0  2  2  2
 1  2  1  2  1  2  1  0  2  2  1  1  1  ...  2  1  2  0  0  0  2  2  1  1  2  1
 0  2  1  1  0  2  2  0  2  2  2  0  2  ...  2  2  2  0  2  0  0  2  1  2  2  1
 0  2  0  1  0  1  1  0  1  1  1  1  2  ...  1  2  0  0  2  0  2  2  0  0  0  1
 0  2  0  1  1  2  2  0  2  2  1  1  2  ...  1  2  2  0  0  1  1  1  2  2  2  1
 0  1  0  0  0  2  1  0  1  2  2  0  0  ...  2  1  1  1  1  0  1  2  1  2  2  1
 0  2  0  2  2  2  2  1  1  2  0  2  2  ...  2  2  0  2  1  0  0  2  1  1  1  1
 0  2  0  1  1  2  1  1  1  2  2  0  1  ...  2  0  2  0  2  0  1  2  0  2  2  0

```

```
In [102]: QTL=qtEffects[QTLPos]
```

```
Out[102]: 50-element Array{Float64,1}:
```

```
0.201779  
0.201652  
0.198763  
0.19707  
0.197193  
0.199313  
0.199271  
0.198483  
0.199378  
0.199365  
0.199877  
0.203093  
0.197218  
:  
0.199114  
0.202658  
0.203063  
0.19862  
0.199992  
0.19927  
0.201623  
0.201832  
0.198531  
0.204223  
0.200435  
0.199581
```

```
In [103]: EAlpha=QTLAll*QTLo
```

```
Out[103]: 48000-element Array{Float64,1}:
 11.4148
 10.0088
 11.1998
  9.83233
 10.3948
  8.20405
  9.20403
  9.6107
 10.2218
 10.7969
  9.81656
 10.8104
 10.2166
  :
 10.9933
 10.405
 10.6128
 11.4002
 10.4117
 12.6076
 11.8096
 10.401
 12.8122
 11.0029
 11.5826
 11.5817
```

```
In [104]: meanEAlphaG0=mean(EAlpha[1:8000])    # our mu_g
```

```
Out[104]: 9.488768740333251
```

```
In [105]: meanEAlphaG1=mean(EAlpha[8001:16000])
```

```
Out[105]: 10.149502704338898
```

```
In [106]: meanEAlphaG2=mean(EAlpha[16001:24000])
```

```
Out[106]: 10.42919780220928
```



```
In [107]: meanEAlphaG3=mean(EAlpha[24001:32000])
```

```
Out[107]: 10.6852057309698
```

```
In [108]: meanEAlphaG4=mean(EAlpha[32001:40000])
```

```
Out[108]: 10.95602415864258
```

```
In [109]: meanEAlphaG5=mean(EAlpha[40001:48000])
```

```
Out[109]: 11.238249218937293
```

```
In [110]: EAlphaG=onlyQTL*QTLo
```

```
Out[110]: 9000-element Array{Float64,1}:
```

```
11.4148
10.3948
10.8104
10.9951
11.195
11.2077
12.6021
11.2007
11.6117
12.0018
10.4073
11.2159
10.6067
⋮
10.9933
10.405
10.6128
11.4002
10.4117
12.6076
11.8096
10.401
12.8122
11.0029
11.5826
11.5817
```

```
In [111]: meanEAlphaG=mean(EAlphaG)
```

```
Out[111]: 11.214941664924627
```

```
In [112]: meanBreedingValueSelected=meanEAlphaG-meanEAlphaG0    # Legarra mu_g
```

```
Out[112]: 1.726172924591376
```

```
In [113]: meanEAlphaS0=mean(EAlphaG[1:200])
```

```
Out[113]: 10.805048689655164
```

```
In [114]: meanBreedingValueSelectedG0=meanEAlphaS0-meanEAlphaG0
```

```
Out[114]: 1.3162799493219133
```

```
In [115]: meanEAlphaS1=mean(EAlphaG[201:400])
```

```
Out[115]: 10.679284464273355
```

```
In [116]: meanBreedingValueSelectedG1=meanEAlphaS1-meanEAlphaG0
```

```
Out[116]: 1.1905157239401039
```

```
In [117]: meanEAlphaS2=mean(EAlphaG[401:600])
```

```
Out[117]: 10.957080472440587
```

```
In [118]: meanBreedingValueSelectedG2=meanEAlphaS2-meanEAlphaG0
```

```
Out[118]: 1.4683117321073365
```

```
In [119]: meanEAlphaS3=mean(EAlphaG[601:800])
```

```
Out[119]: 11.203544607788853
```

```
In [120]: meanBreedingValueSelectedG3=meanEAlphaS3-meanEAlphaG0
```

```
Out[120]: 1.714775867455602
```

```
In [121]: meanEAlphaS4=mean(EAlphaG[801:1000])
```

```
Out[121]: 11.497447929958703
```

```
In [122]: meanBreedingValueSelectedG4=meanEAlphaS4-meanEAlphaG0
```

```
Out[122]: 2.008679189625452
```

```
In [123]: meanEAlphaS5=mean(EAlphaG[1001:9000])
```

```
Out[123]: 11.238249218937293
```

```
In [124]: meanBreedingValueSelectedG5=meanEAlphaS5-meanEAlphaG0
```

```
Out[124]: 1.7494804786040419
```