In [1]:
```
include("/home/nicole/Jupyter/SSBRJ/src/SSBR.jl")
using SSBR
```

In [2]:
```
function getPos(ped,IDs)
    posAi = Array(Int64,size(IDs,1))
    for (i,id) = enumerate(IDs[:,1])
        posAi[i] = ped.idMap[id].seqID
    end
    return posAi
end
```

Out[2]:
```
getPos (generic function with 1 method)
```

In [3]:
```
; cd Data/0.5a0/M/1
```

```
/home/nicole/Jupyter/JG3/Data/0.5a0/M/1
```

In [4]:
```
;ls
```

```
Correlation.G5.M.C*.txt
Correlation.G5.M.JC*.txt
Correlation.G5.M.JC.txt
Correlation.G5.M.N.txt
G0.Genotype.ID
G0.ID
G0.noGenotype.ID
G1.Genotype.ID
G1.ID
G1.noGenotype.ID
G2.Genotype.ID
G2.ID
G2.noGenotype.ID
G3.Genotype.ID
G3.ID
G3.noGenotype.ID
G4.Genotype.ID
G4.ID
G4.noGenotype.ID
G5.Genotype.ID
G5.ID
G5.noGenotype.ID
MarNF.txt
MarNFCenter.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.M.C*.txt
Regression.G5.M.JC*.txt
Regression.G5.M.JC.txt
Regression.G5.M.N.txt
all.ID
alphaEstimatesJC
alphaEstimatesLeggaraC
alphaEstimatesLeggaraJC
alphaEstimatesN
epsiEstimatesJC
epsiEstimatesLeggaraC
epsiEstimatesLeggaraJC
epsiEstimatesN
genotype.ID
noGenotype.ID
sim.bv
sim.phenotype
```

In [5]:
```
;awk '{print $1}' PedAll.txt | sort -b > all.ID
```

In [6]:
```
;awk '{print $1}' MarNF.txt | sort -b > genotype.ID
```

In [7]:
```
;join -v1 all.ID genotype.ID > noGenotype.ID
```

In [8]:
```
;awk '{print $1,$2}' Phe.txt > sim.phenotype
```

In [9]:
```
;awk '{print $1,$3}' PheAll.txt > sim.bv
```

In [10]:
```
; awk 'NR >=1 && NR <=8000 {print $1}' PedAll.txt | sort -b > G0.ID
```

In [11]:
```
; awk 'NR >=8001 && NR <=16000 {print $1}' PedAll.txt | sort -b > G1.ID
```

In [12]:
```
; awk 'NR >=16001 && NR <=24000 {print $1}' PedAll.txt | sort -b > G2.ID
```

In [13]:
```
; awk 'NR >=24001 && NR <=32000 {print $1}' PedAll.txt | sort -b > G3.ID
```

In [14]:
```
; awk 'NR >=32001 && NR <=40000 {print $1}' PedAll.txt | sort -b > G4.ID
```

In [15]:
```
; awk 'NR >=40001 && NR <=48000 {print $1}' PedAll.txt | sort -b > G5.ID
```

In [16]:
```
;join G0.ID genotype.ID > G0.Genotype.ID
```

In [17]:
```
;join G1.ID genotype.ID > G1.Genotype.ID
```

In [18]:
```
;join G2.ID genotype.ID > G2.Genotype.ID
```

In [19]:
```
;join G3.ID genotype.ID > G3.Genotype.ID
```

In [20]:
```
;join G4.ID genotype.ID > G4.Genotype.ID
```

In [21]:
```
;join G5.ID genotype.ID > G5.Genotype.ID
```

In [22]:
```
;join -v1 G0.ID genotype.ID > G0.noGenotype.ID
```

In [23]:
```
;join -v1 G1.ID genotype.ID > G1.noGenotype.ID
```

In [24]:
```
;join -v1 G2.ID genotype.ID > G2.noGenotype.ID
```

In [25]:
```
;join -v1 G3.ID genotype.ID > G3.noGenotype.ID
```

In [26]:
```
;join -v1 G4.ID genotype.ID > G4.noGenotype.ID
```

In [27]:
```
;join -v1 G5.ID genotype.ID > G5.noGenotype.ID
```

In [28]:
```
;wc G0.Genotype.ID;wc G1.Genotype.ID;wc G2.Genotype.ID;wc
G3.Genotype.ID;wc G4.Genotype.ID;wc G5.Genotype.ID
```

```
 200  200 1200 G0.Genotype.ID
 200  200 1200 G1.Genotype.ID
 200  200 1200 G2.Genotype.ID
 200  200 1200 G3.Genotype.ID
 200  200 1200 G4.Genotype.ID
8000  8000 48000 G5.Genotype.ID
```

In [29]:
```
;wc G0.noGenotype.ID;wc G1.noGenotype.ID;wc G2.noGenotype.ID;wc G3.noGen
otype.ID;wc G4.noGenotype.ID;wc G5.noGenotype.ID
```

```
 7800  7800 46800 G0.noGenotype.ID
 7800  7800 46800 G1.noGenotype.ID
 7800  7800 46800 G2.noGenotype.ID
 7800  7800 46800 G3.noGenotype.ID
 7800  7800 46800 G4.noGenotype.ID
0 0 0 G5.noGenotype.ID
```

In [30]:
```
ped,A_Mats,numSSBayes = calc_Ai("PedAll.txt","genotype.ID",calculateInbr
eeding=false)
nothing
df     = read_genotypes("MarNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped);                                    #
 without centering
y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes)
J_Vecs = make_JVecs(numSSBayes,A_Mats)
Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
X_Mats, W_Mats = make_XWMats(J_Vecs,Z_Mats,M_Mats,numSSBayes)          #
 with J
nothing
```

In [31]:
```
vRes   = 1.408
vG     = 1.408
nIter  = 50000
@time aHat1,alphaHat,betaHat,epsiHat =
ssGibbs(M_Mats,y_Vecs,J_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRe
s,vG,nIter, outFreq=5000);
nothing
```

```
This is iteration 5000
This is iteration 10000
This is iteration 15000
This is iteration 20000
This is iteration 25000
This is iteration 30000
This is iteration 35000
This is iteration 40000
This is iteration 45000
This is iteration 50000
2500.736366 seconds (23.05 G allocations: 724.026 GB, 7.43% gc time)
```

In [32]:
```
betaHat
```

Out[32]:
```
2-element Array{Float64,1}:
  0.575173
 -3.3671
```

In [33]:
```
mu  = betaHat[1]
mug = betaHat[2]
```

Out[33]:
```
-3.3671023158860893
```

In [34]:
```
(mu+mug)/2
```

Out[34]:
```
-1.3959644560229802
```

In [35]:
```
alphaHat
```

Out[35]:
```
150-element Array{Float64,1}:
  0.0381026
 -0.0147576
 -0.065776
  0.11922
  0.0112622
 -0.179808
  0.115181
 -0.0495392
 -0.0361855
 -0.0443527
  0.066742
 -0.0709246
 -0.0257367
  ⋮
  0.0213895
 -0.0796487
 -0.312875
 -0.14382
  0.0142084
  0.0647867
 -0.00291889
 -0.0230031
  0.298449
  0.102393
 -0.246672
  0.144838
```

In [36]:
```
writedlm("alphaEstimatesJ",alphaHat)
```

In [37]:
```
epsiHat
```

Out[37]:
```
45950-element Array{Float64,1}:
  0.75303
 -0.121834
  0.104639
 -0.205233
  0.233565
 -0.363265
  0.298461
 -0.269063
  0.797938
 -0.918827
  0.00686965
 -0.212839
 -0.848108
  ⋮
  0.0434788
  0.187655
  0.30525
  0.257805
  1.30781
  0.425541
  0.0711354
 -0.372893
  0.332058
 -0.189128
 -0.0224529
  0.117178
```

In [38]:
```
writedlm("epsiEstimatesJ",epsiHat)
```

In [39]:
```
using DataFrames
```

In [40]:
```
df = readtable("sim.bv", eltypes =[UTF8String, Float64], separator = '
',header=false)
a  = Array(Float64,numSSBayes.num_ped)
for (i,ID) in enumerate(df[:,1])
    j = ped.idMap[ID].seqID
    a[j] = df[i,2]
end
```

In [41]:
```
IDs = readtable("all.ID", eltypes =[UTF8String], separator = '
',header=false)
posAi = getPos(ped,IDs)
cor1 = cor(a[posAi],aHat1[posAi])[1,1]
reg1 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - all.ID : correlation = %6.3f\n", cor1 ) # w
ith epsilon
@printf("SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =
%6.3f\n", reg1)
JCAll = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation =  0.903
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.985
```

Out[41]:
```
0.9031367905747063
```

In [42]:
```
TBV = a[posAi]
mean(TBV)
```

Out[42]:
```
2.642914354166667
```

In [43]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[43]:
```
2.0631410889059754
```

In [44]:
```
IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',he
ader=false)
posAi = getPos(ped,IDs)
cor2 = cor(a[posAi],aHat1[posAi])[1,1]
reg2 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - genotype.ID : correlation = %6.3f\n", cor2
) # with epsilon
@printf("SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =
%6.3f\n", reg2)
JCAll = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation =  0.830
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  0.918
```

Out[44]:
```
0.8300915982194037
```

In [45]:
```
TBV = a[posAi]
mean(TBV)
```

Out[45]:
```
4.108706222222223
```

In [46]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[46]:
```
3.5157749731829075
```

In [47]:
```
IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = '
',header=false)
posAi = getPos(ped,IDs)
cor3 = cor(a[posAi],aHat1[posAi])[1,1]
reg3 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - noGenotype.ID : correlation = %6.3f\n", cor
3 ) # with epsilon
@printf("SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV
 = %6.3f\n", reg3)
JCAll = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation =  0.879
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.983
```

Out[47]:
```
0.8787864731362638
```

In [48]:
```
TBV = a[posAi]
mean(TBV)
```

Out[48]:
```
2.3046546923076923
```

In [49]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[49]:
```
1.727917884842068
```

In [50]:
```
IDs = readtable("G0.ID", eltypes =[UTF8String], separator = ' ',header=f
alse)
posAi = getPos(ped,IDs)
cor4 = cor(a[posAi],aHat1[posAi])[1,1]
reg4 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G0.ID : correlation = %6.3f\n", cor4 ) # wi
th epsilon
@printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =
%6.3f\n", reg4)
JCAll = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation =  0.793
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  1.084
```

Out[50]:
```
0.7932263048950755
```

In [51]:
```
TBV = a[posAi]
G0TBV=mean(TBV)
```

Out[51]:
```
0.8388541249999999
```

In [52]:
```
GEBV = aHat1[posAi]
G0GEBV=mean(GEBV)
```

Out[52]:
```
0.1725335290611448
```

In [53]:
```
IDs = readtable("G1.ID", eltypes =[UTF8String], separator = ' ',header=f
alse)
posAi = getPos(ped,IDs)
cor4 = cor(a[posAi],aHat1[posAi])[1,1]
reg4 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G1.ID : correlation = %6.3f\n", cor4 ) # wi
th epsilon
@printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =
%6.3f\n", reg4)
JCAll = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =  0.773
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.007
```

Out[53]:
```
0.772773175927165
```

In [54]:
```
TBV = a[posAi]
G1TBV=mean(TBV)
```

Out[54]:
```
1.7074885
```

In [55]:
```
GEBV = aHat1[posAi]
G1GEBV=mean(GEBV)
```

Out[55]:
```
1.1674933676459747
```

In [56]:
```
IDs = readtable("G2.ID", eltypes =[UTF8String], separator = ' ',header=f
alse)
posAi = getPos(ped,IDs)
cor5 = cor(a[posAi],aHat1[posAi])[1,1]
reg5 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G2.ID : correlation = %6.3f\n", cor5 ) # wi
th epsilon
@printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =
%6.3f\n", reg5)
JCAll = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =  0.744
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.965
```

Out[56]:
```
0.7444039544740254
```

In [57]:
```
TBV = a[posAi]
G2TBV=mean(TBV)
```

Out[57]:
```
2.43677575
```

In [58]:
```
GEBV = aHat1[posAi]
G2GEBV=mean(GEBV)
```

Out[58]:
```
1.8887250347171443
```

In [59]:
```
IDs = readtable("G3.ID", eltypes =[UTF8String], separator = ' ',header=f
alse)
posAi = getPos(ped,IDs)
cor6 = cor(a[posAi],aHat1[posAi])[1,1]
reg6 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G3.ID : correlation = %6.3f\n", cor6 ) # wi
th epsilon
@printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =
%6.3f\n", reg6)
JCAll = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation =  0.735
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.964
```

Out[59]:
```
0.7353756000232886
```

In [60]:
```
TBV = a[posAi]
G3TBV=mean(TBV)
```

Out[60]:
```
3.0633003750000003
```

In [61]:
```
GEBV = aHat1[posAi]
G3GEBV=mean(GEBV)
```

Out[61]:
```
2.5230754684019954
```

In [62]:
```
IDs = readtable("G4.ID", eltypes =[UTF8String], separator = ' ',header=f
alse)
posAi = getPos(ped,IDs)
cor7 = cor(a[posAi],aHat1[posAi])[1,1]
reg7 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G4.ID : correlation = %6.3f\n", cor7 ) # wi
th epsilon
@printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =
%6.3f\n", reg7)
JCAll = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =  0.740
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.955
```

Out[62]:
```
0.7402464764805735
```

In [63]:
```
TBV = a[posAi]
G4TBV=mean(TBV)
```

Out[63]:
```
3.6475862500000003
```

In [64]:
```
GEBV = aHat1[posAi]
G4GEBV=mean(GEBV)
```

Out[64]:
```
3.0652239769216085
```

In [65]:
```
IDs = readtable("G5.ID", eltypes =[UTF8String], separator = ' ',header=f
alse)
posAi = getPos(ped,IDs)
cor8 = cor(a[posAi],aHat1[posAi])[1,1]
reg8 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G5.ID : correlation = %6.3f\n", cor8 ) # wi
th epsilon
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =
%6.3f\n", reg8)
JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =  0.810
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.887
```

Out[65]:
```
0.8101540377162266
```

In [66]:
```
writedlm("Correlation.G5.M.J.txt",cor13)
```

```
LoadError: UndefVarError: cor13 not defined
while loading In[66], in expression starting on line 1
```

In [67]:
```
writedlm("Regression.G5.M.J.txt",reg13)
```

```
LoadError: UndefVarError: reg13 not defined
while loading In[67], in expression starting on line 1
```

In [68]:
```
TBV = a[posAi]
G5TBV=mean(TBV)
```

Out[68]:
```
4.163481125000001
```

In [69]:
```
GEBV = aHat1[posAi]
G5GEBV=mean(GEBV)
```

Out[69]:
```
3.5617951566879844
```

In [70]:
```
reg8 = linreg(aHat1[posAi], a[posAi])
```

Out[70]:
```
2-element Array{Float64,1}:
 1.00447
 0.886916
```

In [71]:
```
VarGEBV=var(aHat1[posAi])
```

Out[71]:
```
0.6016009758967009
```

In [72]:
```
VarTBV=var(a[posAi])
```

Out[72]:
```
0.7210049007563287
```

In [73]:
```
Cov=cov(aHat1[posAi], a[posAi])
```

Out[73]:
```
0.5335694739577045
```

In [74]:
```
b=Cov/VarGEBV
```

Out[74]: 0.8869159049524582

In [75]:
```
IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = '
',header=false)
posAi = getPos(ped,IDs)
cor9 = cor(a[posAi],aHat1[posAi])[1,1]
reg9 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G0.Genotype.ID : correlation = %6.3f\n", co
r9 ) # with epsilon
@printf("SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV
 = %6.3f\n", reg9)
JCAll = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation =  0.834
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.908
```

Out[75]: 0.833788933475526

In [76]:
```
TBV = a[posAi]
mean(TBV)
```

Out[76]: 2.558755

In [77]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[77]: 2.2732186795398523

In [78]:
```
IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = '
',header=false)
posAi = getPos(ped,IDs)
cor9 = cor(a[posAi],aHat1[posAi])[1,1]
reg9 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G1.Genotype.ID : correlation = %6.3f\n", co
r9 ) # with epsilon
@printf("SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV
 = %6.3f\n", reg9)
JCAll = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation =  0.875
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.915
```

Out[78]: 0.8754098992688917

In [79]:
```
TBV = a[posAi]
mean(TBV)
```

Out[79]: 3.1442850000000004

In [80]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[80]: 2.6751649370336468

In [81]:
```
IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = '
',header=false)
posAi = getPos(ped,IDs)
cor10 = cor(a[posAi],aHat1[posAi])[1,1]
reg10 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G2.Genotype.ID : correlation = %6.3f\n", co
r10 ) # with epsilon
@printf("SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV
 = %6.3f\n", reg10)
JCAll = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation =  0.847
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.910
```

Out[81]:
```
0.8472020977086319
```

In [82]:
```
TBV = a[posAi]
mean(TBV)
```

Out[82]:
```
3.7104500000000002
```

In [83]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[83]:
```
3.186781946901502
```

In [84]:
```
IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = '
',header=false)
posAi = getPos(ped,IDs)
cor11 = cor(a[posAi],aHat1[posAi])[1,1]
reg11 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G3.Genotype.ID : correlation = %6.3f\n", co
r11 ) # with epsilon
@printf("SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV
 = %6.3f\n", reg11)
JCAll = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation =  0.822
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.986
```

Out[84]:
```
0.8216557281627168
```

In [85]:
```
TBV = a[posAi]
mean(TBV)
```

Out[85]:
```
4.21913
```

In [86]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[86]:
```
3.601005727512127
```

In [87]:
```
IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = '
',header=false)
posAi = getPos(ped,IDs)
cor12 = cor(a[posAi],aHat1[posAi])[1,1]
reg12 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G4.Genotype.ID : correlation = %6.3f\n", co
r12 ) # with epsilon
@printf("SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV
 = %6.3f\n", reg12)
JCAll = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation =  0.713
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.712
```

Out[87]:
```
0.7132747186518585
```

In [88]:
```
TBV = a[posAi]
mean(TBV)
```

Out[88]:
```
4.719915
```

In [89]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[89]:
```
4.0018962347243106
```

In [90]:
```
IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = '
',header=false)
posAi = getPos(ped,IDs)
cor13 = cor(a[posAi],aHat1[posAi])[1,1]
reg13 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G5.Genotype.ID : correlation = %6.3f\n", co
r13 ) # with epsilon
@printf("SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV
 = %6.3f\n", reg13)
JCAll = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation =  0.810
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.887
```

Out[90]:
```
0.8101540377162266
```

In [91]:
```
TBVG5Gall = a[posAi]
TBVG5G=mean(TBVG5Gall)
```

Out[91]:
```
4.163481125000001
```

In [92]:
```
GEBVG5Gall = aHat1[posAi]
GEBVG5G=mean(GEBVG5Gall)
```

Out[92]:
```
3.5617951566879844
```

In [93]:
```
IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = '
 ',header=false)
posAi = getPos(ped,IDs)
cor14 = cor(a[posAi],aHat1[posAi])[1,1]
reg14 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G0.noGenotype.ID : correlation = %6.3f\n",
cor14 ) # with epsilon
@printf("SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEB
V = %6.3f\n", reg14)
JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.784
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.1
36
```

Out[93]:
```
0.7840216862598142
```

In [94]:
```
TBV = a[posAi]
mean(TBV)
```

Out[94]:
```
0.7947541025641025
```

In [95]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[95]:
```
0.11866980725399845
```

In [96]:
```
IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = '
 ',header=false)
posAi = getPos(ped,IDs)
cor14 = cor(a[posAi],aHat1[posAi])[1,1]
reg14 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G1.noGenotype.ID : correlation = %6.3f\n",
cor14 ) # with epsilon
@printf("SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEB
V = %6.3f\n", reg14)
JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.759
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.0
14
```

Out[96]:
```
0.7586038594191356
```

In [97]:
```
TBV = a[posAi]
mean(TBV)
```

Out[97]:
```
1.6706475641025644
```

In [98]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[98]:
```
1.12883512227706
```

In [99]:
```
IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = '
 ',header=false)
posAi = getPos(ped,IDs)
cor15 = cor(a[posAi],aHat1[posAi])[1,1]
reg15 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G2.noGenotype.ID : correlation = %6.3f\n",
cor15 ) # with epsilon
@printf("SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEB
V = %6.3f\n", reg15)
JCAll = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.730
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.9
65
```

Out[99]:
```
0.7298612732785874
```

In [100]:
```
TBV = a[posAi]
mean(TBV)
```

Out[100]:
```
2.4041174358974358
```

In [101]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[101]:
```
1.8554415241483142
```

In [102]:
```
IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = '
 ',header=false)
posAi = getPos(ped,IDs)
cor16 = cor(a[posAi],aHat1[posAi])[1,1]
reg16 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G3.noGenotype.ID : correlation = %6.3f\n",
cor16 ) # with epsilon
@printf("SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEB
V = %6.3f\n", reg16)
JCAll = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.722
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.9
57
```

Out[102]:
```
0.7224465374299034
```

In [103]:
```
TBV = a[posAi]
mean(TBV)
```

Out[103]:
```
3.033663717948718
```

In [104]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[104]:
```
2.4954362309889153
```

In [105]:
```
IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = '
 ',header=false)
posAi = getPos(ped,IDs)
cor17 = cor(a[posAi],aHat1[posAi])[1,1]
reg17 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G4.noGenotype.ID : correlation = %6.3f\n",
cor17 ) # with epsilon
@printf("SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEB
V = %6.3f\n", reg17)
JCAll = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation =  0.730
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.9
51
```

Out[105]:
```
0.730388299241449
```

In [106]:
```
TBV = a[posAi]
mean(TBV)
```

Out[106]:
```
3.6200906410256413
```

In [107]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[107]:
```
3.041206739542052
```

In [108]:
```
numSSBayes
```

Out[108]:
```
SSBR.NumSSBayes(54950,45950,9000,40000,39000,1000,150)
```

In [109]:
```
J_Vecs.J1
```

Out[109]:
```
45950x1 Array{Float64,2}:
 -0.167188
 -0.00117096
 -0.0471935
 -0.925122
 -0.674094
 -0.501695
 -0.00234167
 -0.751907
 -0.75191
 -0.809791
 -0.00116448
 -0.751918
 -0.96261
  ⋮
 -0.943867
 -0.962573
 -0.168957
 -0.756756
 -0.752337
 -0.187793
 -0.975023
 -0.748392
 -0.888052
 -0.884964
 -0.00351546
 -0.00117515
```

In [110]:
```
sortrows(J_Vecs.J1[end-8000:end,:])
```

Out[110]:
```
8001x1 Array{Float64,2}:
 -0.98556
 -0.983607
 -0.982758
 -0.982664
 -0.981588
 -0.981374
 -0.981221
 -0.981142
 -0.980883
 -0.980671
 -0.979584
 -0.979441
 -0.97908
  ⋮
  5.57058e-17
  5.57176e-17
  5.57792e-17
  5.5891e-17
  5.59092e-17
  5.795e-17
  6.00216e-17
  7.15228e-17
  7.22383e-17
  7.46619e-17
  8.88923e-17
  1.18284e-16
```

In [111]:
```
J1 = sortrows(J_Vecs.J1)
```

Out[111]:
```
45950x1 Array{Float64,2}:
 -0.998128
 -0.989112
 -0.986218
 -0.986069
 -0.98556
 -0.985539
 -0.985398
 -0.985287
 -0.984751
 -0.983664
 -0.983657
 -0.983607
 -0.983579
  ⋮
  7.22383e-17
  7.40727e-17
  7.42191e-17
  7.46619e-17
  7.52197e-17
  8.88923e-17
  8.92435e-17
  8.94813e-17
  1.18284e-16
  1.22329e-16
  1.44477e-16
  1.47425e-16
```

In [112]:
```
J1[J1 .< 0.0,:]
```

Out[112]:
```
43902x1 Array{Float64,2}:
 -0.998128
 -0.989112
 -0.986218
 -0.986069
 -0.98556
 -0.985539
 -0.985398
 -0.985287
 -0.984751
 -0.983664
 -0.983657
 -0.983607
 -0.983579
  ⋮
 -7.21238e-36
 -7.2121e-36
 -7.20816e-36
 -7.20371e-36
 -7.18073e-36
 -2.1823e-51
 -3.19403e-65
 -2.57004e-65
 -5.46188e-67
 -2.73094e-67
 -1.79614e-67
 -1.78856e-67
```

In [113]:
```
J1[J1 .> 0.0,:]
```

Out[113]:
```
1371x1 Array{Float64,2}:
 6.06391e-83
 8.05497e-52
 8.08909e-52
 1.60053e-51
 1.60147e-51
 1.60241e-51
 1.60567e-51
 1.60617e-51
 1.60859e-51
 1.61099e-51
 1.61782e-51
 2.21192e-51
 2.45981e-51
 ⋮
 7.22383e-17
 7.40727e-17
 7.42191e-17
 7.46619e-17
 7.52197e-17
 8.88923e-17
 8.92435e-17
 8.94813e-17
 1.18284e-16
 1.22329e-16
 1.44477e-16
 1.47425e-16
```

In [114]:
```
G = convert(Array,readtable("MarNF.txt", separator = ' ',header=false));
```

In [115]:
```
GAll=mean(G[:,2:end],1)
```

Out[115]:
```
1x150 Array{Float64,2}:
 0.0895556  1.83011  0.411333  …  0.427778  1.16178  1.85289  1.57467
```

In [116]:
```
GG0=mean(G[1:200,2:end],1)
```

Out[116]:
```
1x150 Array{Float64,2}:
 0.125  1.77  0.46  1.925  0.115  0.42  …  1.215  0.62  0.875  1.865
 1.29
```

In [117]:
```
GG1=mean(G[201:400,2:end],1)
```

Out[117]:
```
1x150 Array{Float64,2}:
 0.08  1.715  0.53  1.935  0.155  0.465  …  1.095  0.52  1.015  1.875
 1.43
```

In [118]:
```
GG2=mean(G[401:600,2:end],1)
```

Out[118]:
```
1x150 Array{Float64,2}:
 0.095  1.805  0.46  1.95  0.155  0.385  …  1.015  0.48  1.09  1.825
 1.515
```

In [119]:
```
GG3=mean(G[601:800,2:end],1)
```

Out[119]:
```
1x150 Array{Float64,2}:
 0.085  1.865  0.365  1.975  0.12  0.29  …  0.96  0.405  1.175  1.85
 1.585
```

In [120]:
```
GG4=mean(G[801:1000,2:end],1)
```

Out[120]:
```
1x150 Array{Float64,2}:
 0.09  1.87  0.375  1.97  0.105  0.265  …  0.825  0.375  1.255  1.87
 1.655
```

In [121]:
```
GG5=mean(G[1001:9000,2:end],1)
```

Out[121]:
```
1x150 Array{Float64,2}:
 0.088875  1.83325  0.408  1.96075  …  0.42125  1.17175  1.85238  1.584
62
```

In [122]:
```
writedlm("meanOfSNPMAll",GAll)
```

In [123]:
```
writedlm("meanOfSNPMG0",GG0)
```

In [124]:
```
writedlm("meanOfSNPMG1",GG1)
```

In [125]:
```
writedlm("meanOfSNPMG2",GG2)
```

In [126]:
```
writedlm("meanOfSNPMG3",GG3)
```

In [127]:
```
writedlm("meanOfSNPMG4",GG4)
```

In [128]:
```
writedlm("meanOfSNPMG5",GG5)
```