```
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/G/5
```

```
/home/nicole/Jupyter/JG3/Data/0.5a0/G/5
```

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

```
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
GenNF.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.G.JC.txt
all.ID
genotype.ID
noGenotype.ID
sim.bv
sim.phenotype
```

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

```
In [6]:  ;awk '{print $1}' GenNF.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 (
```

```
  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.noGenotype`

```
  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",calculateInbreedin
nothing
df       = read_genotypes("GenNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped);                              # witl
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)    # witl
nothing
```

In [31]:
```
vRes    = 0.767
vG      = 0.767
nIter   = 50000
@time aHat1,alphaHat,betaHat,epsiHat =
ssGibbs(M_Mats,y_Vecs,J_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG
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
2561.062461 seconds (23.06 G allocations: 724.034 GB, 7.48% gc time)
```

In [32]: `betaHat`

Out[32]:
```
2-element Array{Float64,1}:
 3.44936
 1.71373
```

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

Out[33]: `1.7137277340364698`

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

Out[34]: `2.5815432912859375`

In [35]: `alphaHat`

Out[35]: 200-element Array{Float64,1}:
    -0.0425742
    -0.0596723
     0.154755
     0.0172183
    -0.0292608
     0.0494062
     0.0738062
     0.11415
    -0.0619655
     0.0666274
     0.035622
     0.0455178
    -0.0237473
     ⋮
    -0.0423371
     0.00115417
     0.00470132
    -0.0459525
     0.0413223
    -0.0452329
     0.0340837
     0.0538881
     0.0203544
    -0.00593078
    -0.0270205
     0.0227784

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

In [37]:
```julia
using DataFrames
```

In [38]:
```julia
df = readtable("sim.bv", eltypes =[UTF8String, Float64], separator = ' ',hea
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 [39]:
```julia
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 ) # with
@printf("SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV = %6.3f\n",
JCAll = cor1
```

         SSBRJC from Gibbs - all.ID : correlation = 0.913
         SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.966

Out[39]: 0.9130190947198547

In [40]:
```
TBV = a[posAi]
mean(TBV)
```

Out[40]: 4.957202791666667

In [41]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[41]: 1.513448143632928

In [42]:
```
IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=
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 ) # u
@printf("SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV = %6.3:
JCAll = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation =   0.983
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =   1.032
```

Out[42]: 0.9834417264419717

In [43]:
```
TBV = a[posAi]
mean(TBV)
```

Out[43]: 6.157122333333334

In [44]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[44]: 2.7565771986494703

In [45]:
```
IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',heade
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", cor3 ) ;
@printf("SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV = %6
JCAll = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation =   0.872
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =   0.958
```

Out[45]: 0.8715814366596255

In [46]:
```
TBV = a[posAi]
mean(TBV)
```

Out[46]: 4.680298282051282

In [47]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[47]: 1.2265722078598795

```
In [48]: IDs = readtable("G0.ID", eltypes =[UTF8String], separator = ' ',header=false
         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 ) # with e
         @printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", re
         JCAll = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation =  0.717
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.900
```

Out[48]: 0.7166281815473606

```
In [49]: TBV = a[posAi]
         G0TBV=mean(TBV)
```

Out[49]: 3.6482481250000003

```
In [50]: GEBV = aHat1[posAi]
         G0GEBV=mean(GEBV)
```

Out[50]: 0.11945692776209785

```
In [51]: IDs = readtable("G1.ID", eltypes =[UTF8String], separator = ' ',header=false
         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 ) # with e
         @printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", re
         JCAll = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =  0.773
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.982
```

Out[51]: 0.7726418322263895

```
In [52]: TBV = a[posAi]
         G1TBV=mean(TBV)
```

Out[52]: 4.197937250000001

```
In [53]: GEBV = aHat1[posAi]
         G1GEBV=mean(GEBV)
```

Out[53]: 0.7468037276511887

In [54]:
```
IDs = readtable("G2.ID", eltypes =[UTF8String], separator = ' ',header=false
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 ) # with ep
@printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =  0.771
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.995
```

Out[54]: 0.7706579427234367

In [55]:
```
TBV = a[posAi]
G2TBV=mean(TBV)
```

Out[55]: 4.739230875

In [56]:
```
GEBV = aHat1[posAi]
G2GEBV=mean(GEBV)
```

Out[56]: 1.307042937292494

In [57]:
```
IDs = readtable("G3.ID", eltypes =[UTF8String], separator = ' ',header=false
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 ) # with ep
@printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation =  0.768
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.004
```

Out[57]: 0.7683851721872921

In [58]:
```
TBV = a[posAi]
G3TBV=mean(TBV)
```

Out[58]: 5.237892250000001

In [59]:
```
GEBV = aHat1[posAi]
G3GEBV=mean(GEBV)
```

Out[59]: 1.810953259894896

In [60]:
```
IDs = readtable("G4.ID", eltypes =[UTF8String], separator = ' ',header=false
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 ) # with ej
@printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =  0.770
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.973
```

Out[60]: 0.7703037123218243

In [61]:
```
TBV = a[posAi]
G4TBV=mean(TBV)
```

Out[61]: 5.710383875

In [62]:
```
GEBV = aHat1[posAi]
G4GEBV=mean(GEBV)
```

Out[62]: 2.2894764239094276

In [63]:
```
IDs = readtable("G5.ID", eltypes =[UTF8String], separator = ' ',header=false
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 ) # with ej
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =  0.981
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.030
```

Out[63]: 0.9811708190169526

In [64]:
```
TBV = a[posAi]
G5TBV=mean(TBV)
```

Out[64]: 6.209524375

In [65]:
```
GEBV = aHat1[posAi]
G5GEBV=mean(GEBV)
```

Out[65]: 2.8069555852874637

In [66]:
```
IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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", cor9 )
@printf("SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = %6
JCAll = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation =  0.976
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.036
```

Out[66]: 0.9760925967702443

In [67]:
```
TBV = a[posAi]
mean(TBV)
```

Out[67]: 4.735164999999999

In [68]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[68]: 1.3927941375091544

In [69]:
```
IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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", cor9 )
@printf("SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = %6
JCAll = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation =  0.981
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.039
```

Out[69]: 0.9810733281254298

In [70]:
```
TBV = a[posAi]
mean(TBV)
```

Out[70]: 5.295249999999995

In [71]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[71]: 1.9281736831152052

In [72]:
```
IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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", cor10
@printf("SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = %6
JCAll = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation =  0.980
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.044
```

Out[72]: 0.9801133664009926

In [73]:
```
TBV = a[posAi]
mean(TBV)
```

Out[73]: 5.739855

In [74]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[74]: 2.3487736531400216

In [75]:
```
IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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", cor11
@printf("SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = %6
JCAll = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation =  0.976
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.035
```

Out[75]: 0.9759494900089349

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

Out[76]: 6.20947

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

Out[77]: 2.8099673692382923

In [78]:
```
IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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", cor12
@printf("SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = %6
JCAll = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation =  0.970
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.021
```

Out[78]: 0.9697091094757274

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

Out[79]: 6.709115

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

Out[80]: 3.2880416847249534

In [81]:
```
IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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", cor13
@printf("SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = %6
JCAll = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation =  0.981
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.030
```

Out[81]: 0.9811708190169526

In [82]:
```
writedlm("Correlation.G5.G.J.txt",cor13)
```

In [83]:
```
writedlm("Regression.G5.G.J.txt",reg13)
```

In [84]:
```
TBVG5Gall = a[posAi]
TBVG5G=mean(TBVG5Gall)
```

Out[84]: 6.209524375

In [85]:
```
GEBVG5Gall = aHat1[posAi]
GEBVG5G=mean(GEBVG5Gall)
```

Out[85]: 2.8069555852874637

```
In [86]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
         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
         @printf("SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = !
         JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.699
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.902
```

Out[86]: 0.6988578367064423

```
In [87]: TBV = a[posAi]
         mean(TBV)
```

Out[87]: 3.6203784615384613

```
In [88]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[88]: 0.08680725571730154

```
In [89]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
         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
         @printf("SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = !
         JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.756
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.985
```

Out[89]: 0.7558096288183523

```
In [90]: TBV = a[posAi]
         mean(TBV)
```

Out[90]: 4.169783717948718

```
In [91]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[91]: 0.7165121903315985

In [92]:
```
IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
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", cor1!
@printf("SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = !
JCAll = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.754
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.997
```

Out[92]: 0.7543409636246182

In [93]:
```
TBV = a[posAi]
mean(TBV)
```

Out[93]: 4.713573846153845

In [94]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[94]: 1.2803318932964034

In [95]:
```
IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
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", cor1(
@printf("SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = !
JCAll = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.753
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.005
```

Out[95]: 0.7533226991115092

In [96]:
```
TBV = a[posAi]
mean(TBV)
```

Out[96]: 5.212980000000001

In [97]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[97]: 1.7853375135014757

In [98]:
```julia
IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
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
@printf("SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = %
JCAll = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation =  0.753
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.970
```

Out[98]: 0.7533973771822602

In [99]:
```julia
TBV = a[posAi]
mean(TBV)
```

Out[99]: 5.684775384615386

In [100]:
```julia
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[100]: 2.263872186452619

In [101]:
```julia
IDs = readtable("G5.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
posAi = getPos(ped,IDs)
cor18 = cor(a[posAi],aHat1[posAi])[1,1]
reg18 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G5.noGenotype.ID : correlation = %6.3f\n", cor18
@printf("SSBRJC from Gibbs - G5.noGenotype.ID : regression of TBV on GEBV = %
JCAll = cor17
```

```
LoadError: BoundsError: attempt to access 0-element Array{UInt8,1}
  at index [1]
while loading In[101], in expression starting on line 1

 [inlined code] from /home/nicole/.julia/v0.4/DataFrames/src/dataframe/i
o.jl:167
 in readnrows! at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.j
l:222
 in readtable! at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.j
l:774
 in readtable at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:
862
 in readtable at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:
956
```

In [102]:
```julia
TBVG5NGall = a[posAi]
TBVG5NG=mean(TBVG5NGall)
```

Out[102]: 5.684775384615386

In [103]:
```julia
GEBVG5NGall = aHat1[posAi]
GEBVG5NG=mean(GEBVG5NGall)
```

Out[103]: 2.263872186452619

```
In [104]:   numSSBayes
```

Out[104]:   SSBR.NumSSBayes(54924,45924,9000,40000,39000,1000,200)

```
In [105]:   J_Vecs.J1
```

Out[105]:   45924x1 Array{Float64,2}:
             -0.00234055
             -0.500667
             -0.897156
             -0.522889
             -0.501754
             -0.0122695
             -0.825927
             -0.751907
             -0.768559
              0.0
             -0.75555
             -0.962581
             -0.545309
              ⋮
             -0.943999
             -0.962573
              1.30003e-19
             -0.822729
             -0.75248
             -0.838053
             -0.0501533
             -0.966121
             -0.504111
             -0.887714
             -0.878378
             -0.00235249

```
In [106]:   sortrows(J_Vecs.J1[end-8000:end,:])
```

Out[106]: 8001x1 Array{Float64,2}:
           -0.984954
           -0.984489
           -0.984394
           -0.982634
           -0.981548
           -0.981238
           -0.981167
           -0.981142
           -0.981142
           -0.980901
           -0.980893
           -0.980805
           -0.98078
            ⋮
            5.55925e-17
            5.56171e-17
            5.58448e-17
            5.60069e-17
            5.64132e-17
            5.70208e-17
            5.83156e-17
            6.07471e-17
            6.08578e-17
            6.62914e-17
            6.66168e-17
            7.44469e-17

```
In [107]: J1 = sortrows(J_Vecs.J1)
```

Out[107]: 45924x1 Array{Float64,2}:
          −0.989812
          −0.987653
          −0.986861
          −0.986797
          −0.98561
          −0.98559
          −0.985305
          −0.985289
          −0.984954
          −0.98495
          −0.984499
          −0.984489
          −0.984394
           ⋮
           7.41469e−17
           7.44469e−17
           8.57318e−17
           8.88581e−17
           8.89405e−17
           8.91914e−17
           8.93206e−17
           1.07468e−16
           1.10173e−16
           1.11047e−16
           1.1138e−16
           1.11899e−16

In [108]: `J1[J1 .< 0.0,:]`

Out[108]: 43918x1 Array{Float64,2}:
          -0.989812
          -0.987653
          -0.986861
          -0.986797
          -0.98561
          -0.98559
          -0.985305
          -0.985289
          -0.984954
          -0.98495
          -0.984499
          -0.984489
          -0.984394
           ⋮
          -1.08312e-35
          -1.08228e-35
          -1.08217e-35
          -8.72663e-36
          -7.2166e-36
          -7.2166e-36
          -7.2166e-36
          -7.2166e-36
          -7.20827e-36
          -5.41087e-36
          -2.54007e-65
          -5.32825e-67

```
In [109]: J1[J1 .> 0.0,:]
```

```
Out[109]: 1311x1 Array{Float64,2}:
           1.20145e-51
           1.60056e-51
           1.60241e-51
           1.60241e-51
           2.39963e-51
           3.20106e-51
           4.79926e-51
           4.81291e-51
           1.83882e-50
           6.88311e-50
           1.14395e-49
           2.28789e-49
           2.58203e-49
           ⋮
           7.41469e-17
           7.44469e-17
           8.57318e-17
           8.88581e-17
           8.89405e-17
           8.91914e-17
           8.93206e-17
           1.07468e-16
           1.10173e-16
           1.11047e-16
           1.1138e-16
           1.11899e-16
```

```
In [110]: G = convert(Array,readtable("GenNF.txt", separator = ' ',header=false));
```

```
In [111]: GAll=mean(G[:,2:end],1)
```

```
Out[111]: 1x200 Array{Float64,2}:
           0.137333  1.08967  1.11756  1.727  1.47956  …  0.356444  1.83711  0.5834
          44
```

```
In [112]: GG0=mean(G[1:200,2:end],1)
```

```
Out[112]: 1x200 Array{Float64,2}:
           0.115  1.535  0.72  1.845  1.6  0.385  …  1.035  1.025  0.54  1.785  0.8
          65
```

```
In [113]: GG1=mean(G[201:400,2:end],1)
```

```
Out[113]: 1x200 Array{Float64,2}:
           0.15  1.36  0.84  1.77  1.555  0.42  …  0.3  1.11  1.11  0.495  1.81  0.
          735
```

```
In [114]: GG2=mean(G[401:600,2:end],1)
```

```
Out[114]: 1x200 Array{Float64,2}:
           0.155  1.24  0.985  1.78  1.525  0.47  …  1.325  1.32  0.375  1.81  0.62
```

```
In [115]: GG3=mean(G[601:800,2:end],1)
```

```
Out[115]: 1x200 Array{Float64,2}:
           0.145   1.05   1.18   1.715   1.445   …   0.21   1.34   1.33   0.34   1.835   0.62
```

```
In [116]: GG4=mean(G[801:1000,2:end],1)
```

```
Out[116]: 1x200 Array{Float64,2}:
           0.125   0.935   1.245   1.695   1.435   …   0.245   1.48   1.48   0.3   1.86   0.47
```

```
In [117]: GG5=mean(G[1001:9000,2:end],1)
```

```
Out[117]: 1x200 Array{Float64,2}:
           0.13725   1.07288   1.133   1.72275   …   1.35838   0.34975   1.83925   0.573625
```

```
In [118]: writedlm("meanOfSNPGAll",GAll)
```

```
In [119]: writedlm("meanOfSNPGG0",GG0)
```

```
In [120]: writedlm("meanOfSNPGG1",GG1)
```

```
In [121]: writedlm("meanOfSNPGG2",GG2)
```

```
In [122]: writedlm("meanOfSNPGG3",GG3)
```

```
In [123]: writedlm("meanOfSNPGG4",GG4)
```

```
In [124]: writedlm("meanOfSNPGG5",GG5)
```