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/0.5/G/10
```

/home/nicole/Jupyter/JG3/Data/0.5/G/10

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

Correlation.G5.G.JC.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

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",calculateInbreedi
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   = 0.583
vG   = 0.583
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
4395.219836 seconds (23.06 G allocations: 724.143 GB, 7.04% gc time)
```

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

Out[32]: ```
2-element Array{Float64,1}:
 8.35299
 4.27292
```

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

Out[33]: `4.2729168439383285`

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

Out[34]: `6.312951069150653`

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

```
Out[35]: 200-element Array{Float64,1}:
           0.0111745
           0.0991469
          -0.0221103
           0.0693139
          -0.00454865
           0.0985917
           0.0936005
           0.0854724
          -0.0216301
           0.00852411
           0.0279112
           0.0341564
           0.0175278
           ⋮
           0.0145097
          -0.00907921
           0.0394817
          -0.0291146
           0.00434893
          -0.0376225
           0.157162
           0.0970946
           0.0531627
           0.0085332
          -0.0233372
           0.0115932
```

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

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

```
In [38]: df = readtable("sim.bv", eltypes =[UTF8String, Float64], separator = ' ',head
         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]: 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 =  0.919
         SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.982
```

```
Out[39]: 0.9194391279101742
```

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

Out[40]: 9.817296166666667

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

Out[41]: 1.4691152358766664

```
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 =  0.978
          SSBRJC from Gibbs – genotype.ID  : regression of TBV on GEBV =  1.087
```

Out[42]: 0.978375571077224

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

Out[43]: 10.99899311111111

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

Out[44]: 2.6586378056806046

```
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 =  0.880
          SSBRJC from Gibbs – noGenotype.ID  : regression of TBV on GEBV =  0.964
```

Out[45]: 0.8798363459429129

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

Out[46]: 9.544596871794871

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

Out[47]: 1.1946100274603728

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 =  0.681
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.812
```

Out[48]: 0.681357270628408

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

Out[49]: 8.537600375

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

Out[50]: 0.1142575175347203

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 =  0.774
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.970
```

Out[51]: 0.7744475105451991

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

Out[52]: 9.044070624999998

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

Out[53]: 0.7105060484796188

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 ej
@printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =  0.768
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.017
```

Out[54]: 0.7675398269519222

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

Out[55]: 9.610254000000001

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

Out[56]: 1.2849684899400728

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 ej
@printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation =  0.780
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.058
```

Out[57]: 0.7804071198042223

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

Out[58]: 10.094816125000001

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

Out[59]: 1.7696454986287458

```
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 e_
         @printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", re
         JCAll = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =  0.793
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.067
```

Out[60]: 0.7929363914160042

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

Out[61]: 10.564574125

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

Out[62]: 2.22772675262081

```
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 e_
         @printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", re
         JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =  0.975
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.086
```

Out[63]: 0.9751574950345381

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

Out[64]: 11.052461749999999

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

Out[65]: 2.70758710805603

```
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 =  0.971
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.057
```

Out[66]: 0.9713232543378344

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

Out[67]: 9.537889999999999

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

Out[68]: 1.3219826283654266

```
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 =  0.962
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.056
```

Out[69]: 0.9620157890684267

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

Out[70]: 10.16994

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

Out[71]: 1.9015650603283323

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 =  0.977
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.091
```

Out[72]: 0.9773651959311391

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

Out[73]: 10.58867

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

Out[74]: 2.287055378021668

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 =  0.971
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.081
```

Out[75]: 0.9710100932560057

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

Out[76]: 11.03682

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

Out[77]: 2.6852779901911252

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 =  0.953
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.061
```

Out[78]: 0.9526693576499553

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

Out[79]: 11.5229

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

Out[80]: 3.1393358764794437

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 =  0.975
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.086
```

Out[81]: 0.9751574950345381

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]: 11.052461749999999

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

Out[85]: 2.70758710805603

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", cor1
@printf("SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 
JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.658
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.806
```

Out[86]: 0.6577597759330326

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

Out[87]: 8.511951923076923

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

Out[88]: 0.08329020700059964

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", cor1
@printf("SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 
JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.754
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.971
```

Out[89]: 0.7540932408085322

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

Out[90]: 9.01520217948718

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

Out[91]: 0.6799660738168313

```
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 =  0.749
         SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.020
```

Out[92]: 0.7492194170325511

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

Out[93]: 9.585166410256411

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

Out[94]: 1.2592739543482374

```
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 =  0.765
         SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.060
```

Out[95]: 0.7654742497166092

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

Out[96]: 10.07066217948718

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

Out[97]: 1.7461677424348385

In [98]:
```
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 =   0.779
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =   1.068
```

Out[98]: 0.7793983386233698

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

Out[99]: 10.540001666666667

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

Out[100]: 2.2043521597013584

In [101]:
```
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]:
```
TBVG5NGall = a[posAi]
TBVG5NG=mean(TBVG5NGall)
```

Out[102]: 10.540001666666667

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

Out[103]: 2.2043521597013584

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

Out[104]: SSBR.NumSSBayes(54932,45932,9000,40000,39000,1000,200)

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

Out[105]: 45932x1 Array{Float64,2}:
          -0.00117028
           0.0
          -0.897397
          -0.504674
          -0.501177
          -0.00234399
          -0.752046
          -0.753565
          -0.752047
           1.49432e-18
          -0.751765
          -0.975067
          -0.543029
           ⋮
          -0.965907
          -0.00117096
          -0.756882
          -0.751902
          -0.768544
           1.99782e-18
          -0.963525
          -0.537651
          -0.887654
          -0.879173
          -0.00351084
          -0.0241544

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

Out[106]: 8001x1 Array{Float64,2}:
           -0.985316
           -0.983749
           -0.98286
           -0.98127
           -0.981231
           -0.981152
           -0.981143
           -0.981092
           -0.980863
           -0.980849
           -0.980809
           -0.980475
           -0.979826
            ⋮
            5.55355e-17
            5.55837e-17
            5.55842e-17
            5.56411e-17
            5.56488e-17
            5.5714e-17
            5.57303e-17
            5.5942e-17
            5.71723e-17
            6.07752e-17
            6.66221e-17
            7.12178e-17

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

Out[107]: 45932x1 Array{Float64,2}:
          −0.999967
          −0.987231
          −0.986975
          −0.986214
          −0.98601
          −0.985787
          −0.985511
          −0.985316
          −0.985246
          −0.985205
          −0.983749
          −0.983608
          −0.983471
            ⋮
           6.52796e−17
           6.53185e−17
           6.66221e−17
           7.12178e−17
           7.14e−17
           7.3991e−17
           8.73907e−17
           8.88254e−17
           8.90717e−17
           1.02696e−16
           1.11298e−16
           1.16024e−16

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

Out[108]: 43949x1 Array{Float64,2}:
          -0.999967
          -0.987231
          -0.986975
          -0.986214
          -0.98601
          -0.985787
          -0.985511
          -0.985316
          -0.985246
          -0.985205
          -0.983749
          -0.983608
          -0.983471
           ⋮
          -7.22083e-36
          -7.22083e-36
          -7.22083e-36
          -7.22083e-36
          -7.2166e-36
          -7.2166e-36
          -7.20809e-36
          -7.16816e-36
          -5.41404e-36
          -1.78007e-67
          -1.78007e-67
          -8.90036e-68

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

```
Out[109]: 1281x1 Array{Float64,2}:
            1.97628e-83
            8.01673e-52
            8.01673e-52
            1.59165e-51
            1.60052e-51
            1.60241e-51
            1.60335e-51
            1.60335e-51
            1.60335e-51
            1.60335e-51
            2.1823e-51
            6.41485e-51
            1.24261e-50
            ⋮
            6.52796e-17
            6.53185e-17
            6.66221e-17
            7.12178e-17
            7.14e-17
            7.3991e-17
            8.73907e-17
            8.88254e-17
            8.90717e-17
            1.02696e-16
            1.11298e-16
            1.16024e-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}:
           0.296111  1.646  0.518556  1.89822  1.73978  …  0.481778  1.84222  0.694
          222
```

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

```
Out[112]: 1x200 Array{Float64,2}:
           0.185  1.71  0.545  1.905  1.65  0.35  …  0.97  0.975  0.615  1.81  0.92
```

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

```
Out[113]: 1x200 Array{Float64,2}:
           0.18  1.675  0.555  1.915  1.68  0.495  …  1.115  1.115  0.565  1.825
           0.835
```

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

```
Out[114]: 1x200 Array{Float64,2}:
           0.285  1.585  0.57  1.86  1.7  0.63  …  1.185  1.185  0.54  1.825  0.705
```

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

Out[115]: 1x200 Array{Float64,2}:
  0.285 1.645 0.55 1.88 1.69 0.75 … 1.275 1.27 0.43 1.825 0.655

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

Out[116]: 1x200 Array{Float64,2}:
  0.36 1.65 0.49 1.91 1.79 0.885 … 1.295 1.29 0.44 1.86 0.625

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

Out[117]: 1x200 Array{Float64,2}:
  0.30075 1.64512 0.515625 1.89875 … 1.22175 0.47725 1.84387 0.687
  5

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)`