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/3
```

/home/nicole/Jupyter/JG3/Data/0.5/G/3

In [4]:
```
;ls
```
```
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
GenNF.txt
PedAll.txt
Phe.txt
PheAll.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 G
          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);                              # wit
          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)    # wit
          nothing
```

```
In [31]:  vRes    = 0.664
          vG      = 0.664
          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
          4985.820784 seconds (23.03 G allocations: 723.234 GB, 6.46% gc time)
```

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

```
Out[32]:  2-element Array{Float64,1}:
           9.66531
           4.89981
```

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

```
Out[33]:  4.899809798881774
```

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

```
Out[34]:  7.282561109225061
```

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

```
Out[35]: 200-element Array{Float64,1}:
            0.191052
            0.116351
           -0.0449499
            0.0251194
           -0.0183794
            0.0340892
            0.0503745
            0.110249
           -0.0833239
            0.0771736
            0.0356513
            0.0254111
           -0.00829003
            ⋮
            0.0338892
            0.172897
            0.0256029
           -0.0461473
            0.0190415
            0.0171178
            0.022544
           -0.0336253
           -0.0332683
           -0.0315067
            0.117384
           -0.0435583
```

```
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 =  0.914
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.978
```

```
Out[39]: 0.9135147924181873
```

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

Out[40]: 11.135083416666665

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

Out[41]: 1.4742781846191155

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 =  1.075
```

Out[42]: 0.9779463253405684

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

Out[43]: 12.273038222222223

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

Out[44]: 2.6235445720067245

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 =  0.874
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.963
```

Out[45]: 0.8741178559863835

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

Out[46]: 10.872478461538462

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

Out[47]: 1.2090628644527448

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 =  0.702
SSBRJC from Gibbs – G0.ID : regression of TBV on GEBV =  0.866
```

Out[48]: 0.7016636895928543

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

Out[49]: 9.84533075

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

Out[50]: 0.12099632669398629

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 =  0.778
SSBRJC from Gibbs – G1.ID : regression of TBV on GEBV =  0.979
```

Out[51]: 0.7782015386874239

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

Out[52]: 10.40474075

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

Out[53]: 0.7585918617630153

```
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 =   0.758
         SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.993
```

Out[54]: 0.7579358186427834

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

Out[55]: 10.945704874999999

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

Out[56]: 1.297437270001161

```
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 =   0.752
         SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.999
```

Out[57]: 0.7520449884264485

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

Out[58]: 11.422414125000001

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

Out[59]: 1.7768554469673787

```
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 =  0.770
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.993
```

Out[60]: 0.7697355098354678

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

Out[61]: 11.871169375

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

Out[62]: 2.2247881579973843

```
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 =  1.071
```

Out[63]: 0.974956740743285

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

Out[64]: 12.321140625

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

Out[65]: 2.66700004429177

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 =  0.975
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.087
```

Out[66]: 0.9745322580345741

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

Out[67]: 10.961675

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

Out[68]: 1.4287553919878753

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 =  0.974
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.094
```

Out[69]: 0.9735584300471738

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

Out[70]: 11.464300000000001

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

Out[71]: 1.8939951093500258

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 =  0.971
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.072
```

Out[72]: 0.9713677896749272

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

Out[73]: 11.912560000000003

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

Out[74]: 2.293268196521497

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 =  1.058
```

Out[75]: 0.9760666970443803

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

Out[76]: 12.34098

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

Out[77]: 2.7013925571440676

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 =  0.967
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.070
```

Out[78]: 0.9668184880034842

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

Out[79]: 12.761580000000002

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

Out[80]: 3.0620927136283513

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 =  1.071
```

Out[81]: 0.974956740743285

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]: 12.321140625

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

Out[85]: 2.66700004429177

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 =  0.678
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.863
```

Out[86]: 0.6778155755292825

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

Out[87]: 9.81670653846154

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

Out[88]: 0.08746404296850196

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 =  0.761
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.982
```

Out[89]: 0.7610279377740317

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

Out[90]: 10.377572564102563

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

Out[91]: 0.7294789579787331

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", cor15
@printf("SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 9
JCAll = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =   0.741
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =   0.994
```

Out[92]: 0.7409155787572157

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

Out[93]: 10.92091371794872

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

Out[94]: 1.271903143680127

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", cor16
@printf("SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 9
JCAll = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =   0.735
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =   0.998
```

Out[95]: 0.7347466804992641

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

Out[96]: 11.398861153846154

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

Out[97]: 1.7531493672192584

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 =  0.754
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.987
```

Out[98]: 0.7540131497896552

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

Out[99]: 11.848338333333334

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

Out[100]: 2.2033188104171026

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]: 11.848338333333334

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

Out[103]: 2.2033188104171026

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

Out[104]: SSBR.NumSSBayes(54866,45866,9000,40000,39000,1000,200)

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

Out[105]: 45866x1 Array{Float64,2}:
           0.0
          -0.00117302
          -0.887723
          -0.504384
          -0.501755
          -1.21757e-64
          -0.757182
          -0.752189
          -0.752047
          -0.00117102
          -0.972845
          -0.501755
          -0.945121
           ⋮
          -0.957917
          -0.962595
          -0.777018
          -0.802518
          -0.81379
          -0.00117302
          -0.962551
          -0.504094
          -0.887588
          -0.913356
          -0.00117096
          -0.00058548

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

Out[106]: 8001x1 Array{Float64,2}:
          -0.984926
          -0.983886
          -0.982583
          -0.981896
          -0.981718
          -0.981265
          -0.98111
          -0.981026
          -0.98102
          -0.980888
          -0.980687
          -0.980459
          -0.979645
           ⋮
           5.56333e-17
           5.56717e-17
           5.58164e-17
           5.58897e-17
           5.59488e-17
           5.60308e-17
           5.68502e-17
           5.86245e-17
           5.8916e-17
           6.66984e-17
           9.72087e-17
           1.07645e-16

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

Out[107]: 45866x1 Array{Float64,2}:
          -0.999514
          -0.989317
          -0.98626
          -0.985919
          -0.985309
          -0.985285
          -0.984926
          -0.984854
          -0.984306
          -0.984196
          -0.984131
          -0.983886
          -0.983656
           ⋮
           7.07401e-17
           7.2845e-17
           7.33351e-17
           8.29252e-17
           8.89268e-17
           8.89663e-17
           8.89737e-17
           9.40272e-17
           9.72087e-17
           9.73518e-17
           1.07645e-16
           1.17135e-16

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

Out[108]: 43894x1 Array{Float64,2}:
          -0.999514
          -0.989317
          -0.98626
          -0.985919
          -0.985309
          -0.985285
          -0.984926
          -0.984854
          -0.984306
          -0.984196
          -0.984131
          -0.983886
          -0.983656
           ⋮
          -1.26309e-35
          -1.25967e-35
          -1.08297e-35
          -7.2166e-36
          -7.21238e-36
          -7.20818e-36
          -7.20816e-36
          -4.91411e-36
          -1.21757e-64
          -7.63876e-65
          -6.08783e-65
          -7.00015e-66

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

```
Out[109]: 1293x1 Array{Float64,2}:
           1.60053e-51
           1.60241e-51
           2.1823e-51
           2.79703e-51
           2.80462e-51
           3.17934e-51
           3.20482e-51
           4.80488e-51
           9.97839e-51
           1.99568e-50
           3.15259e-50
           6.30517e-50
           6.63481e-50
           ⋮
           7.07401e-17
           7.2845e-17
           7.33351e-17
           8.29252e-17
           8.89268e-17
           8.89663e-17
           8.89737e-17
           9.40272e-17
           9.72087e-17
           9.73518e-17
           1.07645e-16
           1.17135e-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}:
           0.478667  1.53011  0.622889  1.861  1.64889  …  0.455444  1.96233  0.618
          556
```

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

```
Out[112]: 1x200 Array{Float64,2}:
           0.23  1.59  0.62  1.855  1.625  …  0.34  0.99  0.99  0.57  1.905  0.86
```

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

```
Out[113]: 1x200 Array{Float64,2}:
           0.315  1.55  0.635  1.86  1.645  …  0.305  1.08  1.08  0.525  1.9  0.78
```

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

```
Out[114]: 1x200 Array{Float64,2}:
           0.375  1.535  0.625  1.885  1.66  0.55  …  1.22  1.22  0.51  1.945  0.63
          5
```

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

```
Out[115]: 1x200 Array{Float64,2}:
          0.47  1.56  0.595  1.89  1.675  0.595  …  1.275  1.265  0.41  1.97  0.59
```

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

```
Out[116]: 1x200 Array{Float64,2}:
          0.59  1.5  0.635  1.84  1.65  0.635  …  1.335  1.335  0.4  1.995  0.535
```

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

```
Out[117]: 1x200 Array{Float64,2}:
          0.489  1.528  0.623  1.86038  1.64863  …  1.2435  0.452  1.96475  0.6108
          75
```

```
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)
```