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

In [2]:
```julia
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/0.1/G/5
```

/home/nicole/Jupyter/JG3/Data/0.1/G/5

In [4]:
```
;ls
```
```
G5.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.C.txt
Regression.G5.G.JC.txt
Regression.G5.G.N.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",calculateInbreedir
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    = 0.872
vG      = 7.848
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
2571.237159 seconds (23.03 G allocations: 723.345 GB, 7.61% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
 10.7678
  1.01221
```

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

Out[33]:
```
1.0122076354672356
```

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

Out[34]:
```
5.889999296362729
```

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

```
Out[35]:  200-element Array{Float64,1}:
            0.0849117
           -0.155909
           -0.122056
           -0.0583542
            0.127469
           -0.0169071
            0.181112
            0.0162971
            0.0347508
           -0.0254972
            0.174318
            0.222008
           -0.0538696
            ⋮
           -0.0362037
           -0.163786
            0.191437
           -0.0923639
            0.1085
            0.0977481
            0.113486
           -0.215013
           -0.0530285
           -0.0547601
           -0.051285
            0.0354394
```

```
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 =  0.527
          SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.251
```

```
Out[39]:  0.5273876018008098
```

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

Out[40]: 12.021351125

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

Out[41]: 1.5181759771972374

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 ) # 
@printf("SSBRJC from Gibbs – genotype.ID  : regression of TBV on GEBV = %6.3:
JCAll = cor2
```

```
SSBRJC from Gibbs – genotype.ID : correlation =  0.868
SSBRJC from Gibbs – genotype.ID  : regression of TBV on GEBV =  0.837
```

Out[42]: 0.8676803265275926

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

Out[43]: 12.704885333333333

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

Out[44]: 3.534953389264149

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 =  0.433
SSBRJC from Gibbs – noGenotype.ID  : regression of TBV on GEBV =  0.206
```

Out[45]: 0.43304800195097953

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

Out[46]: 11.863612461538462

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

Out[47]: 1.052765805181796

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", r
JCAll = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation =  0.698
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.527
```

Out[48]: 0.6980392657388472

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

Out[49]: 11.057711750000003

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

Out[50]: 0.20033796401715184

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", r
JCAll = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =  0.337
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.133
```

Out[51]: 0.3373594832128307

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

Out[52]: 11.6935705

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

Out[53]: 0.9046632584475078

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

```
SSBRJC from Gibbs - G2.ID : correlation =   0.343
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.136
```

Out[54]: 0.3426375521339989

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

Out[55]: 11.94432025

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

Out[56]: 1.167153579535252

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

```
SSBRJC from Gibbs - G3.ID : correlation =   0.352
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.144
```

Out[57]: 0.3522815243187441

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

Out[58]: 12.217771250000002

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

Out[59]: 1.4346714204897923

```
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 =  0.355
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.138
```

Out[60]: 0.3553079807073736

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

Out[61]: 12.489685875

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

Out[62]: 1.8364337697580104

```
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 =  0.863
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.838
```

Out[63]: 0.8632338304895611

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

Out[64]: 12.725047124999998

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

Out[65]: 3.565795870935709

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 =  0.865
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.808
```

Out[66]: 0.8646989133399843

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

Out[67]: 12.315005000000001

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

Out[68]: 2.8957778717694214

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 =  0.886
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.860
```

Out[69]: 0.8858672498226426

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

Out[70]: 12.191195000000002

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

Out[71]: 2.9055984904328738

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 =  0.915
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.922
```

Out[72]: 0.9151716020128363

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

Out[73]: 12.469374999999998

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

Out[74]: 3.178210888341202

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 =  0.904
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.852
```

Out[75]: 0.904355818681636

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

Out[76]: 12.78123

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

Out[77]: 3.561523159186793

In [78]:
```julia
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 =  0.853
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.837
```

Out[78]: 0.8533112157309997

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

Out[79]: 12.961149999999998

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

Out[80]: 3.899957269728044

In [81]:
```julia
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 =  0.863
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.838
```

Out[81]: 0.8632338304895611

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

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

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

Out[84]: 12.725047124999998

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

Out[85]: 3.565795870935709

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 = 9
JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.678
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.533
```

Out[86]: 0.6781441639241305

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

Out[87]: 11.025473461538466

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

Out[88]: 0.13122412022863214

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 = 9
JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.325
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.127
```

Out[89]: 0.3252685550727795

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

Out[90]: 11.680810897435897

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

Out[91]: 0.8533572268581394

```
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 =  0.329
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.130
```

Out[92]: 0.3293343573381887

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

Out[93]: 11.930857307692309

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

Out[94]: 1.1155880075145868

```
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 =  0.339
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.138
```

Out[95]: 0.33905126241875705

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

Out[96]: 12.20332358974359

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

Out[97]: 1.3801367605232024

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 =   0.345
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =   0.134
```

Out[98]: 0.34494175657115295

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

Out[99]: 12.477597051282052

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

Out[100]: 1.7835229107844195

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]: 12.477597051282052

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

Out[103]: 1.7835229107844195

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

Out[104]:   SSBR.NumSSBayes(54874,45874,9000,40000,39000,1000,200)

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

Out[105]:   45874x1 Array{Float64,2}:
             -0.0047014
             -0.00117044
              1.30251e-19
             -0.887698
             -0.503513
             -0.501756
              6.58913e-19
             -0.751902
             -0.752624
             -0.813763
             -0.00233986
             -0.772642
             -0.96566
              ⋮
             -0.975
             -0.313741
             -0.756583
             -0.752192
             -0.752049
             -0.00204996
             -0.962595
             -0.669084
             -0.887704
             -0.879097
              1.29925e-19
             -0.107678

```

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

Out[106]: 8001x1 Array{Float64,2}:
     -0.985395
     -0.982364
     -0.981598
     -0.981442
     -0.981293
     -0.981282
     -0.981033
     -0.980984
     -0.980901
     -0.980898
     -0.980513
     -0.979544
     -0.979535
      ⋮
      5.5465e-17
      5.54705e-17
      5.54875e-17
      5.55112e-17
      5.55843e-17
      5.56006e-17
      5.58119e-17
      5.58201e-17
      6.09915e-17
      6.77188e-17
      7.4291e-17
      7.44698e-17

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

```
Out[107]: 45874x1 Array{Float64,2}:
          -0.999675
          -0.987323
          -0.986174
          -0.985395
          -0.985332
          -0.984131
          -0.98413
          -0.982808
          -0.982653
          -0.982593
          -0.982364
          -0.982323
          -0.981637
           ⋮
           6.77188e-17
           7.393e-17
           7.4291e-17
           7.44698e-17
           8.3077e-17
           8.77235e-17
           8.87952e-17
           8.88495e-17
           1.04174e-16
           1.05731e-16
           1.07411e-16
           1.11144e-16
```

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

```
Out[108]: 43825x1 Array{Float64,2}:
           -0.999675
           -0.987323
           -0.986174
           -0.985395
           -0.985332
           -0.984131
           -0.98413
           -0.982808
           -0.982653
           -0.982593
           -0.982364
           -0.982323
           -0.981637
            ⋮
           -5.41167e-36
           -5.4077e-36
           -7.63874e-65
           -7.60646e-65
           -7.60646e-65
           -3.81937e-65
           -3.80323e-65
           -2.90722e-65
           -2.59338e-65
           -6.99614e-66
           -9.01683e-67
           -1.78007e-67
```

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

Out[109]: 1366x1 Array{Float64,2}:
          8.44487e-81
          5.45576e-52
          8.01673e-52
          1.60053e-51
          1.60139e-51
          1.60335e-51
          1.60617e-51
          1.60806e-51
          1.60854e-51
          2.8066e-51
          3.19312e-51
          3.20105e-51
          3.20294e-51
          ⋮
          6.77188e-17
          7.393e-17
          7.4291e-17
          7.44698e-17
          8.3077e-17
          8.77235e-17
          8.87952e-17
          8.88495e-17
          1.04174e-16
          1.05731e-16
          1.07411e-16
          1.11144e-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}:
          0.196556 1.54756 0.642 1.88611 1.68633 … 0.842222 1.79767 1.1075
          6

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

Out[112]: 1x200 Array{Float64,2}:
          0.225 1.665 0.57 1.93 1.69 0.35 … 0.845 0.84 0.75 1.83 1.065

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

Out[113]: 1x200 Array{Float64,2}:
          0.19 1.61 0.59 1.885 1.68 0.305 … 0.505 0.77 0.765 0.78 1.78
          1.1

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

Out[114]: 1x200 Array{Float64,2}:
          0.215 1.61 0.58 1.9 1.695 0.29 … 0.84 0.84 0.735 1.825 1.01

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

```
Out[115]: 1x200 Array{Float64,2}:
           0.215  1.525  0.645  1.9  1.71  0.33  …  0.5  0.76  0.76  0.8  1.785  1.
          125
```

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

```
Out[116]: 1x200 Array{Float64,2}:
           0.2  1.53  0.65  1.87  1.68  0.29  0.885  …  0.71  0.71  0.905  1.79  1.
          15
```

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

```
Out[117]: 1x200 Array{Float64,2}:
           0.195  1.5425  0.646375  1.88475  …  0.74725  0.84825  1.79713  1.10975
```

```
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)
```