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]:
```julia
; cd Data/0.1/G/7
```

/home/nicole/Jupyter/JG3/Data/0.1/G/7

In [4]:
```julia
;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]:
```julia
;awk '{print $1}' PedAll.txt | sort -b > all.ID
```

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

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

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

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

In [10]:
```julia
; 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);   # with
y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes)
J_Vecs = make_JVecs(numSSBayes,A_Mats)
Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
X_Mats, W_Mats = make_XWMats(J_Vecs,Z_Mats,M_Mats,numSSBayes)   # with
nothing
```

In [31]: ```
vRes   = 0.823
vG   = 7.410
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
2502.806572 seconds (23.03 G allocations: 723.400 GB, 7.72% gc time)
```

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

Out[32]: ```
2-element Array{Float64,1}:
 9.14087
 4.42319
```

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

Out[33]: 4.423193683471432

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

Out[34]: 6.782031277921189

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

Out[35]: 
```
200-element Array{Float64,1}:
 -0.197185
 -0.00925315
  0.180315
  0.00803967
  0.152051
  0.033048
  0.0579341
  0.118578
 -0.227981
  0.0909243
 -0.196441
  0.063709
  0.025401
  ⋮
 -0.127348
  0.129845
  0.14187
  0.0744269
  0.100795
 -0.018986
  0.0377355
 -0.129854
 -0.293996
 -0.106034
  0.107125
  0.105439
```

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

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

In [38]: 
```
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]: 
```
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 =  0.530
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.252
```

Out[39]: 0.5303670460030795

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

Out[40]: 10.374861416666667

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

Out[41]: 1.5032763689730824

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

```
SSBRJC from Gibbs – genotype.ID : correlation =   0.870
SSBRJC from Gibbs – genotype.ID  : regression of TBV on GEBV =   0.815
```

Out[42]: 0.8702031347589383

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

Out[43]: 11.072055888888888

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

Out[44]: 3.5114024154315358

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 =   0.427
SSBRJC from Gibbs – noGenotype.ID  : regression of TBV on GEBV =   0.203
```

Out[45]: 0.42716745903260406

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

Out[46]: 10.213970384615385

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

Out[47]: 1.0398626659442085

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 =   0.692
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =   0.514
```

Out[48]: 0.6915114679033688

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

Out[49]: 9.430121124999998

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

Out[50]: 0.20449965104296758

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 =   0.333
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =   0.129
```

Out[51]: 0.33321578282914605

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

Out[52]: 10.039424624999999

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

Out[53]: 0.8580426094643314

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 =   0.353
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.139
```

Out[54]: 0.35333727886221156

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

Out[55]: 10.300734250000001

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

Out[56]: 1.188312644937387

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 =   0.329
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.130
```

Out[57]: 0.3294744835885137

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

Out[58]: 10.567823500000001

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

Out[59]: 1.4307655269915676

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", r
JCAll = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =  0.329
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.133
```

Out[60]: 0.32915220199691064

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

Out[61]: 10.815741125

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

Out[62]: 1.7941804136048012

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", r
JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =  0.868
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.814
```

Out[63]: 0.86831636427885

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

Out[64]: 11.095323875000002

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

Out[65]: 3.543857367797439

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 =  0.854
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.818
```

Out[66]: 0.8539360520881469

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

Out[67]: 10.636680000000002

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

Out[68]: 2.8446661174750596

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 =  0.910
```

Out[69]: 0.885810006497384

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

Out[70]: 10.58951

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

Out[71]: 2.9337336575914437

```
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 =  0.878
         SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.893
```

Out[72]: 0.8779576548256596

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

Out[73]: 10.818140000000001

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

Out[74]: 3.170663517621658

```
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 =  0.889
         SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.901
```

Out[75]: 0.8885205663488589

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

Out[76]: 11.036305000000002

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

Out[77]: 3.3876949438280803

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 =  0.824
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.801
```

Out[78]: 0.8241472613270109

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

Out[79]: 11.348925

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

Out[80]: 3.9220557460053116

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 =  0.868
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.814
```

Out[81]: 0.86831636427885

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]: 11.095323875000002

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

Out[85]: 3.543857367797439

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 =  0.672
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.519
```

Out[86]: 0.6720461522838765

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

Out[87]: 9.399183717948718

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

Out[88]: 0.13680307498060626

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 =  0.320
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.124
```

Out[89]: 0.3196823850390766

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

Out[90]: 10.02531987179487

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

Out[91]: 0.8048197620764567

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 =  0.342
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.134
```

Out[92]: 0.3417096604947595

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

Out[93]: 10.287467435897435

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

Out[94]: 1.1374831353813804

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 =  0.317
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.125
```

Out[95]: 0.31739824037785636

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

Out[96]: 10.555811153846154

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

Out[97]: 1.3805878496367852

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 =  0.316
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.128
```

Out[98]: 0.31611431691097386

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

Out[99]: 10.802069743589744

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

Out[100]: 1.739619507645814

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]: 10.802069743589744

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

Out[103]: 1.739619507645814

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

Out[104]: SSBR.NumSSBayes(54878,45878,9000,40000,39000,1000,200)

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

Out[105]: 45878x1 Array{Float64,2}:
          -0.0121991
          -0.00205168
          -0.00117096
          -0.887713
          -0.503521
          -0.501175
          -0.813764
          -0.751902
           0.0
          -0.755539
          -0.962595
          -0.543665
          -0.943801
           ⋮
          -0.962529
          -0.00233133
          -0.769921
          -0.772491
          -0.772497
          -0.00907231
          -0.963442
          -0.503824
          -0.925081
          -0.91875
           7.59745e-19
          -0.250332

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

Out[106]: 8001x1 Array{Float64,2}:
            −0.985313
            −0.982631
            −0.982551
            −0.981658
            −0.981208
            −0.980864
            −0.980511
            −0.980025
            −0.979414
            −0.979268
            −0.979003
            −0.978971
            −0.978947
             ⋮
             5.54868e−17
             5.54868e−17
             5.55112e−17
             5.55112e−17
             5.55112e−17
             5.69453e−17
             5.70543e−17
             5.8333e−17
             6.37497e−17
             7.3328e−17
             7.42307e−17
             7.46336e−17

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

Out[107]: 45878x1 Array{Float64,2}:
          -0.988738
          -0.986089
          -0.985607
          -0.985582
          -0.98553
          -0.98553
          -0.985313
          -0.984285
          -0.983856
          -0.983591
          -0.982955
          -0.982631
          -0.982551
           ⋮
           6.10733e-17
           6.37497e-17
           6.61749e-17
           6.62723e-17
           6.66898e-17
           6.86565e-17
           7.3328e-17
           7.42307e-17
           7.46336e-17
           7.49056e-17
           1.00288e-16
           1.11142e-16

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

```
Out[108]: 43879x1 Array{Float64,2}:
          -0.988738
          -0.986089
          -0.985607
          -0.985582
          -0.98553
          -0.98553
          -0.985313
          -0.984285
          -0.983856
          -0.983591
          -0.982955
          -0.982631
          -0.982551
           ⋮
          -7.25056e-36
          -7.24658e-36
          -7.2166e-36
          -7.2166e-36
          -6.62379e-36
          -5.41403e-36
          -1.39667e-49
          -7.23748e-67
          -1.78642e-67
          -1.78642e-67
          -1.77903e-67
          -1.63289e-67
```

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

```
Out[109]: 1315x1 Array{Float64,2}:
           7.35388e-52
           7.35388e-52
           8.01204e-52
           8.04532e-52
           8.04532e-52
           8.04974e-52
           1.20216e-51
           1.47078e-51
           1.60241e-51
           1.60906e-51
           1.60995e-51
           1.86453e-51
           2.38016e-51
           ⋮
           6.10733e-17
           6.37497e-17
           6.61749e-17
           6.62723e-17
           6.66898e-17
           6.86565e-17
           7.3328e-17
           7.42307e-17
           7.46336e-17
           7.49056e-17
           1.00288e-16
           1.11142e-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}:
           0.141556  1.57567  0.684889  1.90856  1.62  …  0.834889  1.83644  1.1385
          6
```

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

```
Out[112]: 1x200 Array{Float64,2}:
           0.15  1.655  0.6  1.91  1.63  0.41  0.795  …  0.795  0.78  0.78  1.845
           1.06
```

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

```
Out[113]: 1x200 Array{Float64,2}:
           0.17  1.655  0.635  1.915  1.59  0.33  …  0.745  0.74  0.77  1.78  1.11
```

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

```
Out[114]: 1x200 Array{Float64,2}:
           0.12  1.6  0.685  1.91  1.605  0.425  …  0.675  0.66  0.85  1.805  1.19
```

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

Out[115]: 1x200 Array{Float64,2}:
 0.155 1.58 0.685 1.925 1.625 0.46 … 0.665 0.655 0.87 1.825 1.
155

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

Out[116]: 1x200 Array{Float64,2}:
 0.13 1.53 0.72 1.9 1.625 0.49 0.94 … 0.68 0.66 0.84 1.855 1.
12

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

Out[117]: 1x200 Array{Float64,2}:
 0.141125 1.57212 0.687375 1.90813 … 0.667375 0.8365 1.83825 1.14

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)`