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/1
```

/home/nicole/Jupyter/JG3/Data/0.1/G/1

In [4]:
```julia
;ls
```
```
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
Regression.G5.G.PBLUP.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 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);                              # 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   = 7.831
vG     = 0.870
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
2516.777600 seconds (23.05 G allocations: 723.772 GB, 7.64% gc time)
```

In [32]: `betaHat`

Out[32]:
```
2-element Array{Float64,1}:
  10.0327
   3.73563
```

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

Out[33]: `3.7356344637882906`

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

Out[34]: `6.884191277089196`

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

```
Out[35]:  200-element Array{Float64,1}:
             0.0569885
            -0.000414735
            -0.037553
             0.0387705
             0.114206
             0.00763704
             0.0682531
             0.0439253
            -0.026662
             0.0258139
             0.0467378
             0.00265621
            -0.0696929
             ⋮
            -0.00171933
            -0.0222688
             0.0792191
            -0.034097
             0.0544055
             0.040138
            -0.02336
             0.0881024
             0.0886312
             0.00953565
             0.0285189
            -0.0239293
```

```
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 =  0.761
          SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.998
```

```
Out[39]:  0.7610030094453861
```

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

Out[40]: 11.285119854166668

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

Out[41]: 1.2501215850108067

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

```
SSBRJC from Gibbs - genotype.ID : correlation =   0.943
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =   1.201
```

Out[42]: 0.943425209338538

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

Out[43]: 11.993996777777777

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

Out[44]: 1.9972610578375933

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 =   0.687
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =   0.968
```

Out[45]: 0.6869699533138781

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

Out[46]: 11.121532871794871

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

Out[47]: 1.0777047835892406

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 ej
@printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation =  0.538
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  1.325
```

Out[48]: 0.5376412332252114

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

Out[49]: 10.310185249999998

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

Out[50]: 0.1127825255609822

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 ej
@printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =  0.535
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.119
```

Out[51]: 0.5351644113778504

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

Out[52]: 10.942740625000003

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

Out[53]: 0.8700393416849501

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 =  0.585
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.133
```

Out[54]: 0.5851494706811932

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

Out[55]: 11.215667624999998

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

Out[56]: 1.229528951528861

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 =  0.599
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.088
```

Out[57]: 0.599246903366855

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

Out[58]: 11.4849005

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

Out[59]: 1.5093324331087277

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 =  0.676
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.150
```

Out[60]: 0.6759947846905204

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

Out[61]: 11.742411499999998

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

Out[62]: 1.7646248668918603

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 =  0.943
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.204
```

Out[63]: 0.94275283593586

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

Out[64]: 12.014813624999999

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

Out[65]: 2.014421391289459

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 =  0.906
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.139
```

Out[66]: 0.9063641291750677

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

Out[67]: 11.595910000000002

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

Out[68]: 1.6478892870494317

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 =  0.944
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.197
```

Out[69]: 0.9441979506758927

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

Out[70]: 11.474039999999995

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

Out[71]: 1.5933202556222668

```
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 =   0.950
         SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =   1.156
```

Out[72]: 0.9499458520676198

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

Out[73]: 11.749784999999997

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

Out[74]: 1.8005700276721623

```
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 =   0.946
         SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =   1.139
```

Out[75]: 0.9457976894622587

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

Out[76]: 12.014095000000003

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

Out[77]: 2.0183187121024804

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 =  0.944
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.209
```

Out[78]: 0.9436972330850345

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

Out[79]: 12.30348

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

Out[80]: 2.239793668666996

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 =  0.943
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.204
```

Out[81]: 0.94275283593586

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]: 12.014813624999999

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

Out[85]: 2.014421391289459

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 =   0.527
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =   1.734
```

Out[86]: 0.5271015572153277

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

Out[87]: 10.277217948717947

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

Out[88]: 0.07342081372794503

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 =   0.519
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =   1.147
```

Out[89]: 0.5186729057978687

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

Out[90]: 10.929117564102565

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

Out[91]: 0.851493677225019

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 = '
JCAll = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.569
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.140
```

Out[92]: 0.5690451139534165

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

Out[93]: 11.201972307692307

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

Out[94]: 1.214886872653392

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 = '
JCAll = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.584
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.087
```

Out[95]: 0.58438294361734

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

Out[96]: 11.471331410256408

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

Out[97]: 1.4962815028781185

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 =  0.664
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.147
```

Out[98]: 0.6643416573953235

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

Out[99]: 11.728025128205127

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

Out[100]: 1.7524410514617281

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]: 11.728025128205127

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

Out[103]: 1.7524410514617281

In [104]: `numSSBayes`

Out[104]: SSBR.NumSSBayes(54905,45905,9000,40000,39000,1000,200)

In [105]: `J_Vecs.J1`

Out[105]: 45905x1 Array{Float64,2}:
          -0.0520833
          -0.00321427
           5.35868e-18
          -0.914299
          -0.503805
          -0.514155
           0.0
          -0.7519
          -0.753712
          -0.834642
          -0.00117786
          -0.751756
          -0.962529
           ⋮
          -0.945493
          -0.962568
          -0.00087456
          -0.779413
          -0.751902
          -0.751902
           2.60165e-19
          -0.962594
          -0.503517
          -0.913826
          -0.878375
          -0.00175559

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

Out[106]: 8001x1 Array{Float64,2}:
          -0.986037
          -0.985903
          -0.985634
          -0.985288
          -0.983758
          -0.98206
          -0.981313
          -0.981263
          -0.98126
          -0.981251
          -0.981251
          -0.981241
          -0.980905
           ⋮
           5.21789e-17
           5.52068e-17
           5.54624e-17
           5.55385e-17
           5.55842e-17
           5.55843e-17
           5.57135e-17
           5.57706e-17
           5.62247e-17
           5.70597e-17
           6.6105e-17
           6.61774e-17

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

Out[107]: 45905x1 Array{Float64,2}:
          −0.987503
          −0.986037
          −0.986007
          −0.985991
          −0.985903
          −0.985634
          −0.985614
          −0.985579
          −0.985507
          −0.985288
          −0.985284
          −0.985085
          −0.984751
            ⋮
           6.02079e−17
           6.07214e−17
           6.0938e−17
           6.3236e−17
           6.6105e−17
           6.61774e−17
           6.63649e−17
           6.65614e−17
           6.66877e−17
           8.88178e−17
           1.06976e−16
           1.14306e−16

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

```
Out[108]: 43957x1 Array{Float64,2}:
          -0.987503
          -0.986037
          -0.986007
          -0.985991
          -0.985903
          -0.985634
          -0.985614
          -0.985579
          -0.985507
          -0.985288
          -0.985284
          -0.985085
          -0.984751
           ⋮
          -1.08217e-35
          -1.0817e-35
          -7.22085e-36
          -7.22081e-36
          -7.21871e-36
          -7.2166e-36
          -7.21238e-36
          -7.21237e-36
          -7.21237e-36
          -5.41087e-36
          -2.55363e-65
          -5.29562e-67
```

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

Out[109]: 1235x1 Array{Float64,2}:
          8.01438e-52
          1.60147e-51
          1.60241e-51
          1.60288e-51
          1.60335e-51
          1.60339e-51
          2.38494e-51
          3.20482e-51
          3.20678e-51
          3.20678e-51
          4.76987e-51
          4.80829e-51
          4.80958e-51
          ⋮
          6.02079e-17
          6.07214e-17
          6.0938e-17
          6.3236e-17
          6.6105e-17
          6.61774e-17
          6.63649e-17
          6.65614e-17
          6.66877e-17
          8.88178e-17
          1.06976e-16
          1.14306e-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}:
          0.262889 1.56067 0.546222 1.94511 … 1.103 0.507222 1.836 0.75377
          8

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

Out[112]: 1x200 Array{Float64,2}:
          0.245 1.595 0.56 1.92 1.795 0.29 … 1.08 1.08 0.565 1.855 0.79
          5

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

Out[113]: 1x200 Array{Float64,2}:
          0.215 1.595 0.545 1.935 1.815 … 0.29 0.97 0.97 0.57 1.83 0.88

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

Out[114]: 1x200 Array{Float64,2}:
          0.25 1.57 0.56 1.905 1.8 0.3 0.96 … 1.115 1.115 0.47 1.81 0.
          775

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

Out[115]: 1x200 Array{Float64,2}:
 0.27 1.615 0.485 1.95 1.885 0.31 … 1.055 1.055 0.575 1.845 0.
785

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

Out[116]: 1x200 Array{Float64,2}:
 0.275 1.515 0.575 1.95 1.895 0.285 … 1.18 1.18 0.46 1.84 0.69
5

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

Out[117]: 1x200 Array{Float64,2}:
 0.264375 1.5585 0.546375 1.94675 … 1.10587 0.504625 1.836 0.7497
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)`