```
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/0.5a0/G/7
```

```
/home/nicole/Jupyter/JG3/Data/0.5a0/G/7
```

```
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   = 0.738
vG   = 0.738
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
4487.234714 seconds (23.04 G allocations: 723.496 GB, 6.98% gc time)
```

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

Out[32]: ```
2-element Array{Float64,1}:
 1.0346
 0.112542
```

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

Out[33]: `0.11254201392789563`

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

Out[34]: `0.5735688235476113`

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

```
Out[35]:  200-element Array{Float64,1}:
          -0.0199801
           0.0758227
           0.00836915
           0.12666
           0.0367841
          -0.00452854
          -0.117228
          -0.116203
           0.014664
          -0.00786798
           0.00602477
           0.0446092
          -0.0577932
           ⋮
           0.00119946
           0.00474795
           0.00758726
          -0.010047
           0.014987
           0.0173641
           0.00301294
           0.0179465
           0.0272529
          -0.00903069
           0.0134341
           0.0415515
```

```
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=fals
          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 =  0.920
          SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.977
```

```
Out[39]:  0.9195726612778852
```

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

Out[40]: 2.6270850208333334

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

Out[41]: 1.5968287381105468

```
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 =   1.069
```

Out[42]: 0.9778737783065585

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

Out[43]: 3.8989498888888887

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

Out[44]: 2.8865568471889707

```
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 =   0.881
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =   0.963
```

Out[45]: 0.8810162254378276

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

Out[46]: 2.3335777435897436

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

Out[47]: 1.2991991744770641

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

```
SSBRJC from Gibbs - G0.ID : correlation =   0.720
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =   0.883
```

Out[48]: 0.7203171558979928

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

Out[49]: 1.242720875

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

Out[50]: 0.1246989688906886

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

```
SSBRJC from Gibbs - G1.ID : correlation =   0.772
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =   0.973
```

Out[51]: 0.7721700340422956

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

Out[52]: 1.806066625

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

Out[53]: 0.7841055916372143

```
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 =  0.772
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.006
```

Out[54]: 0.7717046426421428

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

Out[55]: 2.3675376249999998

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

Out[56]: 1.3680892233266004

```
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 =  0.774
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.010
```

Out[57]: 0.7744520491313601

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

Out[58]: 2.9335720000000003

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

Out[59]: 1.9304353353391157

```
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 =   0.769
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =   1.007
```

Out[60]: 0.7693445566148841

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

Out[61]: 3.4565102499999996

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

Out[62]: 2.4350380295192524

```
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 =   1.065
```

Out[63]: 0.9746993709967

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

Out[64]: 3.9561027499999994

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

Out[65]: 2.938605279950408

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 =  0.974
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.064
```

Out[66]: 0.973891829959792

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

Out[67]: 2.353905

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

Out[68]: 1.4842363254096662

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 =  0.967
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.062
```

Out[69]: 0.9672224943914844

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

Out[70]: 2.9259999999999997

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

Out[71]: 2.0041692635602835

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 =  0.967
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.036
```

Out[72]: 0.9667133038685266

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

Out[73]: 3.5142349999999998

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

Out[74]: 2.5325685810145906

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 =  0.962
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.038
```

Out[75]: 0.961840531687107

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

Out[76]: 3.953035

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

Out[77]: 2.9303177576860384

In [78]:
```
IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
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 =  0.968
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.052
```

Out[78]: 0.968052102438322

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

Out[79]: 4.46146

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

Out[80]: 3.399554997816754

In [81]:
```
IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
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 =  1.065
```

Out[81]: 0.9746993709967

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]: 3.9561027499999994

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

Out[85]: 2.938605279950408

```
In [86]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
         posAi = getPos(ped,IDs)
         cor14 = cor(a[posAi],aHat1[posAi])[1,1]
         reg14 = linreg(aHat1[posAi], a[posAi])[2,1]
         @printf("SSBRJC from Gibbs - G0.noGenotype.ID : correlation = %6.3f\n", cor1
         @printf("SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 9
         JCAll = cor14
```

         SSBRJC from Gibbs - G0.noGenotype.ID : correlation = 0.701
         SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.886

Out[86]: 0.7005437881560566

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

Out[87]: 1.2142289743589743

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

Out[88]: 0.08983903667225326

```
In [89]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
         posAi = getPos(ped,IDs)
         cor14 = cor(a[posAi],aHat1[posAi])[1,1]
         reg14 = linreg(aHat1[posAi], a[posAi])[2,1]
         @printf("SSBRJC from Gibbs - G1.noGenotype.ID : correlation = %6.3f\n", cor1
         @printf("SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 9
         JCAll = cor14
```

         SSBRJC from Gibbs - G1.noGenotype.ID : correlation = 0.755
         SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.977

Out[89]: 0.7551627257077512

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

Out[90]: 1.7773503846153844

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

Out[91]: 0.752821907741751

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 =  0.753
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.007
```

Out[92]: 0.7529588015528312

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

Out[93]: 2.338135128205128

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

Out[94]: 1.3382307782576772

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 =  0.760
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.009
```

Out[95]: 0.7595385168938626

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

Out[96]: 2.907431923076923

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

Out[97]: 1.9047973245097072

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 =  0.752
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.003
```

Out[98]: 0.7518897024270211

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

Out[99]: 3.4307423076923076

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

Out[100]: 2.410306825203932

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]: 3.4307423076923076

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

Out[103]: 2.410306825203932

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

```
Out[104]:  SSBR.NumSSBayes(54885,45885,9000,40000,39000,1000,200)
```

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

```
Out[105]:  45885x1 Array{Float64,2}:
            -0.166518
            -0.0015779
            -0.00117302
            -0.924647
            -0.503804
            -0.502046
            -0.00116954
            -0.813923
            -0.751899
            -0.751902
            -0.026875
            -0.971965
            -0.548897
              ⋮
            -0.972696
            -0.00116959
            -0.756478
            -0.751906
            -0.753278
            -0.00231669
            -0.965455
            -0.507176
            -0.888786
            -0.878366
            -0.00224735
            -0.0011811
```

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

```
Out[106]: 8001x1 Array{Float64,2}:
          -0.988862
          -0.985588
          -0.981364
          -0.981296
          -0.981241
          -0.981142
          -0.980905
          -0.980877
          -0.980876
          -0.980855
          -0.980791
          -0.980502
          -0.979913
           ⋮
           5.54868e-17
           5.54896e-17
           5.55601e-17
           5.56092e-17
           5.56329e-17
           5.56412e-17
           5.56735e-17
           5.56903e-17
           5.57142e-17
           5.63755e-17
           5.66456e-17
           1.001e-16
```

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

Out[107]: 45885x1 Array{Float64,2}:
          -0.990515
          -0.988862
          -0.986904
          -0.985937
          -0.985772
          -0.98563
          -0.985588
          -0.985585
          -0.985577
          -0.985568
          -0.985522
          -0.985411
          -0.985291
           ⋮
           6.28015e-17
           6.28015e-17
           6.66725e-17
           7.05189e-17
           7.40958e-17
           7.41458e-17
           7.43712e-17
           7.70326e-17
           8.89475e-17
           1.001e-16
           1.0697e-16
           1.11088e-16

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

```
Out[108]: 43889x1 Array{Float64,2}:
           -0.990515
           -0.988862
           -0.986904
           -0.985937
           -0.985772
           -0.98563
           -0.985588
           -0.985585
           -0.985577
           -0.985568
           -0.985522
           -0.985411
           -0.985291
            ⋮
           -1.25934e-35
           -1.15288e-35
           -7.22719e-36
           -7.21871e-36
           -7.2166e-36
           -7.2166e-36
           -2.59644e-65
           -7.1781e-66
           -2.56107e-66
           -3.40781e-67
           -1.77903e-67
           -8.89515e-68
```

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

```
Out[109]: 1241x1 Array{Float64,2}:
           1.97512e-83
           8.01203e-52
           1.53474e-51
           1.60241e-51
           1.60288e-51
           1.60476e-51
           2.5599e-51
           3.06949e-51
           3.20571e-51
           4.91957e-51
           9.69951e-51
           1.1534e-50
           2.30681e-50
           ⋮
           6.28015e-17
           6.28015e-17
           6.66725e-17
           7.05189e-17
           7.40958e-17
           7.41458e-17
           7.43712e-17
           7.70326e-17
           8.89475e-17
           1.001e-16
           1.0697e-16
           1.11088e-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}:
           0.151556  1.90956  0.253778  1.99011  1.81044  …  0.860444  1.84244  1.4
          6089
```

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

```
Out[112]: 1x200 Array{Float64,2}:
           0.11  1.795  0.405  1.965  1.77  0.22  …  0.715  0.72  0.82  1.83  1.18
```

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

```
Out[113]: 1x200 Array{Float64,2}:
           0.11  1.855  0.38  1.985  1.74  0.18  …  0.65  0.6  0.6  0.86  1.835  1.
          355
```

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

```
Out[114]: 1x200 Array{Float64,2}:
           0.135  1.91  0.325  1.995  1.755  0.14  …  0.58  0.58  0.795  1.865  1.3
          9
```

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

Out[115]: 1x200 Array{Float64,2}:
 0.17 1.9 0.24 1.99 1.83 0.11 0.215 … 0.58 0.58 0.805 1.885
 1.445

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

Out[116]: 1x200 Array{Float64,2}:
 0.15 1.95 0.205 2.0 1.825 0.085 … 0.7 0.48 0.48 0.88 1.825
 1.54

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

Out[117]: 1x200 Array{Float64,2}:
 0.153625 1.913 0.246625 1.9905 … 0.534 0.864 1.84175 1.47075

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)`