

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

```
In [2]: function getPos(ped,IDs)  
        posAi = Array{Int64,1}(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/M/1  
  
/home/nicole/Jupyter/JG3/Data/0.5a0/M/1
```

```
In [4]: ;ls
```

```
Correlation.G5.M.JC.txt
Correlation.G5.M.N.txt
G0.Genotype.ID
G0.ID
G0.noGenotype.ID
G1.Genotype.ID
G1.ID
G1.noGenotype.ID
G2.Genotype.ID
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
MarNF.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.M.JC.txt
Regression.G5.M.N.txt
all.ID
alphaEstimatesJC
alphaEstimatesN
epsiEstimatesJC
epsiEstimatesN
genotype.ID
noGenotype.ID
sim.bv
sim.phenotype
```

```
In [5]: using DataFrames
```

```
In [6]: MarNF = convert(Array,readtable("MarNF.txt",separator=' ',header=false))
```

```
Out[6]: 9000x151 Array{Int64,2}:
```

```
40750 0 2 0 2 0 0 2 0 1 1 ... 2 0 0 1 0 2 0 1 0 1 2 2
40758 0 2 0 2 0 0 2 0 0 0 ... 2 1 1 2 1 2 1 2 0 0 2 1
40774 0 1 1 2 0 1 1 1 1 2 ... 1 1 1 2 1 1 2 2 1 1 2 0
40788 0 2 1 2 0 0 2 0 2 1 ... 2 1 1 1 0 2 1 0 0 2 2 2
40797 0 2 0 2 0 0 2 0 1 1 ... 2 2 2 2 2 0 2 2 2 0 2 0
40802 0 2 1 2 0 0 2 0 2 1 ... 1 1 1 2 1 1 1 2 1 0 1 1
40809 0 2 1 2 0 0 2 0 1 0 ... 2 1 0 1 0 2 1 0 0 1 2 2
40842 0 1 2 1 0 1 1 1 1 0 ... 2 0 0 0 0 2 0 0 0 2 2 2
40855 2 2 0 2 0 1 1 1 1 0 ... 2 1 1 1 1 1 1 1 1 1 2 1
40880 0 2 1 2 0 0 2 0 2 1 ... 1 0 0 1 0 2 1 1 0 2 2 1
40936 0 1 1 2 1 2 0 2 0 2 ... 2 0 0 1 0 2 0 0 0 1 2 2
40999 0 2 0 2 0 0 2 0 2 2 ... 2 0 0 1 0 2 1 2 0 1 2 1
41000 0 2 0 2 0 0 2 0 2 2 ... 2 0 0 1 0 2 0 1 0 1 2 2
      ⋮           ⋮           ⋮ ⋮           ⋮           ⋮
88710 0 2 1 2 0 0 2 0 1 0 ... 2 1 0 1 1 2 2 2 1 1 2 1
88711 0 2 0 2 0 0 2 0 1 1 ... 2 0 0 0 0 2 0 0 0 2 2 2
88712 0 2 0 2 0 0 2 0 0 0 ... 2 1 0 1 1 2 2 2 1 1 2 1
88713 0 2 0 2 0 0 2 0 1 1 ... 2 1 0 1 1 2 1 1 0 2 2 2
88714 0 2 0 2 0 0 2 0 1 1 ... 2 0 0 0 0 2 0 0 0 2 2 2
88715 0 2 0 2 0 0 2 0 0 0 ... 2 1 1 2 2 0 2 2 2 0 2 0
88716 0 2 0 2 0 0 2 0 2 2 ... 2 0 0 0 0 2 0 0 0 2 2 2
88717 0 2 0 2 0 0 2 0 1 1 ... 2 0 0 1 1 2 1 1 0 1 2 2
88718 0 2 0 2 0 0 2 0 0 0 ... 2 1 1 2 2 1 1 1 1 1 2 1
88719 0 2 0 2 0 0 2 0 0 0 ... 2 1 0 1 1 2 2 2 1 1 2 1
88720 0 2 0 2 0 0 2 0 0 0 ... 2 1 1 2 1 1 2 2 2 0 2 1
88721 0 2 0 2 0 0 2 0 1 1 ... 2 0 0 1 0 2 1 1 1 1 2 1
```

```
In [7]: MID = MarNF[:,1]
        M = MarNF[:,2:end]
```

```
Out[7]: 9000x150 Array{Int64,2}:
```

```
 0  2  0  2  0  0  2  0  1  1  1  1  1  ...  2  0  0  1  0  2  0  1  0  1  2  2
 0  2  0  2  0  0  2  0  0  0  2  0  0  ...  2  1  1  2  1  2  1  2  0  0  2  1
 0  1  1  2  0  1  1  1  1  2  0  2  1  ...  1  1  1  2  1  1  2  2  1  1  2  0
 0  2  1  2  0  0  2  0  2  1  1  1  2  ...  2  1  1  1  0  2  1  0  0  2  2  2
 0  2  0  2  0  0  2  0  1  1  1  1  1  ...  2  2  2  2  2  0  2  2  2  0  2  0
 0  2  1  2  0  0  2  0  2  1  1  1  1  ...  1  1  1  2  1  1  1  2  1  0  1  1
 0  2  1  2  0  0  2  0  1  0  2  1  0  ...  2  1  0  1  0  2  1  0  0  1  2  2
 0  1  2  1  0  1  1  1  1  0  2  0  1  ...  2  0  0  0  0  2  0  0  0  2  2  2
 2  2  0  2  0  1  1  1  1  0  1  2  0  ...  2  1  1  1  1  1  1  1  1  1  2  1
 0  2  1  2  0  0  2  0  2  1  1  1  2  ...  1  0  0  1  0  2  1  1  0  2  2  1
 0  1  1  2  1  2  0  2  0  2  1  1  0  ...  2  0  0  1  0  2  0  0  0  1  2  2
 0  2  0  2  0  0  2  0  2  2  0  2  1  ...  2  0  0  1  0  2  1  2  0  1  2  1
 0  2  0  2  0  0  2  0  2  2  0  2  1  ...  2  0  0  1  0  2  0  1  0  1  2  2
 ⋮          ⋮          ⋮          ⋮          ⋮          ⋮
 0  2  1  2  0  0  2  0  1  0  2  1  1  ...  2  1  0  1  1  2  2  2  1  1  2  1
 0  2  0  2  0  0  2  0  1  1  1  1  1  ...  2  0  0  0  0  2  0  0  0  2  2  2
 0  2  0  2  0  0  2  0  0  0  2  0  0  ...  2  1  0  1  1  2  2  2  1  1  2  1
 0  2  0  2  0  0  2  0  1  1  1  1  1  ...  2  1  0  1  1  2  1  1  0  2  2  2
 0  2  0  2  0  0  2  0  1  1  1  1  1  ...  2  0  0  0  0  2  0  0  0  2  2  2
 0  2  0  2  0  0  2  0  0  0  2  0  0  ...  2  1  1  2  2  0  2  2  2  0  2  0
 0  2  0  2  0  0  2  0  2  2  0  2  2  ...  2  0  0  0  0  2  0  0  0  2  2  2
 0  2  0  2  0  0  2  0  1  1  1  1  1  ...  2  0  0  1  1  2  1  1  0  1  2  2
 0  2  0  2  0  0  2  0  0  0  2  0  0  ...  2  1  1  2  2  1  1  1  1  1  2  1
 0  2  0  2  0  0  2  0  0  0  2  1  0  ...  2  1  0  1  1  2  2  2  1  1  2  1
 0  2  0  2  0  0  2  0  0  0  2  0  0  ...  2  1  1  2  1  1  2  2  2  0  2  1
 0  2  0  2  0  0  2  0  1  1  1  1  1  ...  2  0  0  1  0  2  1  1  1  1  2  1
```

```
In [8]: MC = M - ones(size(M,1))*mean(M,1)
```

```
Out[8]: 9000x150 Array{Float64,2}:
```

```
-0.0895556  0.169889 -0.411333 ... -0.161778  0.147111  0.425333
-0.0895556  0.169889 -0.411333    -1.16178  0.147111 -0.574667
-0.0895556 -0.830111  0.588667    -0.161778  0.147111 -1.57467
-0.0895556  0.169889  0.588667     0.838222  0.147111  0.425333
-0.0895556  0.169889 -0.411333    -1.16178  0.147111 -1.57467
-0.0895556  0.169889  0.588667 ... -1.16178 -0.852889 -0.574667
-0.0895556  0.169889  0.588667    -0.161778  0.147111  0.425333
-0.0895556 -0.830111  1.58867     0.838222  0.147111  0.425333
 1.91044    0.169889 -0.411333    -0.161778  0.147111 -0.574667
-0.0895556  0.169889  0.588667     0.838222  0.147111 -0.574667
-0.0895556 -0.830111  0.588667 ... -0.161778  0.147111  0.425333
-0.0895556  0.169889 -0.411333    -0.161778  0.147111 -0.574667
-0.0895556  0.169889 -0.411333    -0.161778  0.147111  0.425333
⋮
-0.0895556  0.169889  0.588667    -0.161778  0.147111 -0.574667
-0.0895556  0.169889 -0.411333     0.838222  0.147111  0.425333
-0.0895556  0.169889 -0.411333 ... -0.161778  0.147111 -0.574667
-0.0895556  0.169889 -0.411333     0.838222  0.147111  0.425333
-0.0895556  0.169889 -0.411333     0.838222  0.147111  0.425333
-0.0895556  0.169889 -0.411333    -1.16178  0.147111 -1.57467
-0.0895556  0.169889 -0.411333     0.838222  0.147111  0.425333
-0.0895556  0.169889 -0.411333 ... -0.161778  0.147111  0.425333
-0.0895556  0.169889 -0.411333    -0.161778  0.147111 -0.574667
-0.0895556  0.169889 -0.411333    -0.161778  0.147111 -0.574667
-0.0895556  0.169889 -0.411333    -1.16178  0.147111 -0.574667
-0.0895556  0.169889 -0.411333    -0.161778  0.147111 -0.574667
```

```
In [9]: mean(MC,1)
```

```
Out[9]: 1x150 Array{Float64,2}:
```

```
-1.15463e-17 -5.84224e-17 2.36848e-17 ... -7.45083e-17 4.26326e-17
```

```
In [10]: MCstream=open("MarNFCenter.txt","w")
```

```
Out[10]: IOStream(<file MarNFCenter.txt>)
```

```
In [11]: for i in 1:size(MID,1)
        @printf(MCstream, "%19d", MID[i])
        for j in 1:size(MC,2)
            @printf(MCstream, "%10.6f", MC[i,j])
        end
        @printf(MCstream, "\n")
    end
```

```
In [12]: close(MCstream)
```

```
In [13]: ;awk '{print $1}' PedAll.txt | sort -b > all.ID
```

```
In [14]: ;awk '{print $1}' MarNFCenter.txt | sort -b > genotype.ID
```

```
In [15]: ;join -v1 all.ID genotype.ID > noGenotype.ID
```

```
In [16]: ;awk '{print $1,$2}' Phe.txt > sim.phenotype
```

```
In [17]: ;awk '{print $1,$3}' PheAll.txt > sim.bv
```

```
In [18]: ; awk 'NR >=1 && NR <=8000 {print $1}' PedAll.txt | sort -b > G0.ID
```

```
In [19]: ; awk 'NR >=8001 && NR <=16000 {print $1}' PedAll.txt | sort -b > G1.ID
```

```
In [20]: ; awk 'NR >=16001 && NR <=24000 {print $1}' PedAll.txt | sort -b > G2.ID
```

```
In [21]: ; awk 'NR >=24001 && NR <=32000 {print $1}' PedAll.txt | sort -b > G3.ID
```

```
In [22]: ; awk 'NR >=32001 && NR <=40000 {print $1}' PedAll.txt | sort -b > G4.ID
```

```
In [23]: ; awk 'NR >=40001 && NR <=48000 {print $1}' PedAll.txt | sort -b > G5.ID
```

```
In [24]: ;join G0.ID genotype.ID > G0.Genotype.ID
```

```
In [25]: ;join G1.ID genotype.ID > G1.Genotype.ID
```

```
In [26]: ;join G2.ID genotype.ID > G2.Genotype.ID
```

```
In [27]: ;join G3.ID genotype.ID > G3.Genotype.ID
```

```
In [28]: ;join G4.ID genotype.ID > G4.Genotype.ID
```

```
In [29]: ;join G5.ID genotype.ID > G5.Genotype.ID
```

```
In [30]: ;join -v1 G0.ID genotype.ID > G0.noGenotype.ID
```

```
In [31]: ;join -v1 G1.ID genotype.ID > G1.noGenotype.ID
```

```
In [32]: ;join -v1 G2.ID genotype.ID > G2.noGenotype.ID
```

```
In [33]: ;join -v1 G3.ID genotype.ID > G3.noGenotype.ID
```

```
In [34]: ;join -v1 G4.ID genotype.ID > G4.noGenotype.ID
```

```
In [35]: ;join -v1 G5.ID genotype.ID > G5.noGenotype.ID
```

```
In [36]: ;wc G0.Genotype.ID;wc G1.Genotype.ID;wc G2.Genotype.ID;wc G3.Genotype.ID;wc G4.Genotype.ID;wc G5.Genotype
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 [37]: ;wc G0.noGenotype.ID;wc G1.noGenotype.ID;wc G2.noGenotype.ID;wc G3.noGenotype.ID;wc G4.noGenotype.ID;wc G
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 [38]: ped,A_Mats,numSSBayes = calc_Ai("PedAll.txt","genotype.ID",calculateInbreeding=false)
nothing
df      = read_genotypes("MarNFCenter.txt",numSSBayes)  # genotype file - centered already
M_Mats = make_MMats(df,A_Mats,ped);                    # M file centered already
y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes);
Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
X_Mats, W_Mats = make_XWMats(Z_Mats,M_Mats,numSSBayes)      # no J
nothing
```

```
In [39]: vRes    = 1.408
vG       = 1.408
nIter    = 50000
@time aHat1,alphaHat,betaHat,epsiHat =
ssGibbs(M_Mats,y_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG,nIter, outFreq=5000);
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
2375.484860 seconds (23.05 G allocations: 724.011 GB, 7.69% gc time)
```

```
In [40]: betaHat
```

```
Out[40]: 1-element Array{Float64,1}:
 2.96505
```



```
In [41]: alphaHat
```

```
Out[41]: 150-element Array{Float64,1}:
```

```
-0.0530023  
-0.0981605  
-0.145427  
0.151411  
0.0481839  
-0.188031  
0.013137  
0.0580835  
0.116121  
-0.0440243  
0.179097  
-0.0634289  
-0.0349498  
:  
0.0142942  
-0.0151714  
-0.220969  
-0.0806118  
-0.000742773  
0.113757  
-0.062971  
0.0316935  
0.205751  
0.0748191  
-0.195264  
0.00474758
```

```
In [42]: writedlm("alphaEstimatesLeggaraC",alphaHat)
```

```
In [43]: epsiHat
```

```
Out[43]: 45950-element Array{Float64,1}:
```

```
-0.101632  
-1.01088  
-1.38181  
-0.101895  
0.0778912  
-1.07165  
-1.3304  
-0.440627  
0.302108  
-1.20975  
-0.43107  
-0.431904  
-0.631954  
:  
0.314096  
0.446706  
-0.577686  
0.109359  
1.0006  
0.249532  
0.282345  
-0.275145  
0.281369  
-0.058551  
-1.57139  
-1.62839
```

```
In [44]: writedlm("epsiEstimatesLeggaraC",epsiHat)
```

```
In [45]: df = readtable("sim.bv", eltypes =[UTF8String, Float64], separator = ' ',header=false)  
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 [46]: 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 epsilon
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n", reg1)
JCA11 = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.842
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 1.403
```

```
Out[46]: 0.8422315652765249
```

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

```
Out[47]: -0.5189976830851024
```

```
In [48]: IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = %6.3f\n", reg2)
JCA11 = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.718
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.229
```

```
Out[48]: 0.7184507375014973
```

```
In [49]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[49]: 4.1907034063607777e-7
```

```
In [50]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg3)
JCA11 = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.850
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 1.292
```

```
Out[50]: 0.8495411245414473
```

```
In [51]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[51]: -0.6387664758902047
```

```
In [52]: 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 epsilon
@printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", reg4)
JCA11 = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation = 0.781
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 1.152
```

```
Out[52]: 0.7813674935449508
```

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

```
Out[53]: -1.4516551957843196
```

```
In [54]: 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 epsilon
@printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", reg4)
JCA11 = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation = 0.761
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 1.077
```

```
Out[54]: 0.7611803216032326
```

```
In [55]: GEBV = aHat1[posAi]
G1GEBV=mean(GEBV)
```

```
Out[55]: -1.0984940921682491
```

```
In [56]: 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 epsilon
@printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", reg5)
JCA11 = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation = 0.722
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.023
```

```
Out[56]: 0.7216761058685163
```

```
In [57]: GEBV = aHat1[posAi]
G2GEBV=mean(GEBV)
```

```
Out[57]: -0.6111407278117709
```

```
In [58]: 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 epsilon
@printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", reg6)
JCall = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation = 0.705
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.015
```

```
Out[58]: 0.7049116931046682
```

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

```
Out[59]: -0.1409564270946421
```

```
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 epsilon
@printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", reg7)
JCall = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation = 0.687
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.022
```

```
Out[60]: 0.6873938445090874
```

```
In [61]: GEBV = aHat1[posAi]
G4GEBV=mean(GEBV)
```

```
Out[61]: 0.1700406906736679
```

```
In [62]: 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 epsilon
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", reg8)
JCA11 = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation = 0.700
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.162
```

```
Out[62]: 0.7003576020359029
```

```
In [63]: GEBV = aHat1[posAi]
G5GEBV=mean(GEBV)
```

```
Out[63]: 0.01821965367469936
```

```
In [64]: GEBVG5G1=G5GEBV-G1GEBV
```

```
Out[64]: 1.1167137458429486
```

```
In [65]: GEBVG1G5=[G1GEBV;G2GEBV;G3GEBV;G4GEBV;G5GEBV]
```

```
Out[65]: 5-element Array{Float64,1}:
-1.09849
-0.611141
-0.140956
0.170041
0.0182197
```

```
In [66]: reg8 = linreg(aHat1[posAi], a[posAi])
```

```
Out[66]: 2-element Array{Float64,1}:
4.14232
1.16159
```

```
In [67]: VarGEBV=var(aHat1[posAi])
```

```
Out[67]: 0.26210493818528086
```

```
In [68]: VarTBV=var(a[posAi])
```

```
Out[68]: 0.7210049007563287
```

```
In [69]: Cov=cov(aHat1[posAi], a[posAi])
```

```
Out[69]: 0.3044574159824124
```

```
In [70]: b=Cov/VarGEBV
```

```
Out[70]: 1.1615859590069713
```

```
In [71]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg9)
JCA11 = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.779
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.251
```

```
Out[71]: 0.7790331142507083
```

```
In [72]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[72]: -0.6120561723374073
```

```
In [73]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg9)
JCA11 = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.788
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.206
```

```
Out[73]: 0.7878369290754262
```



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

```
Out[74]: -0.3516120275179383
```

```
In [75]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @printf("SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg10)
         JCA11 = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation =  0.730
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.193
```

```
Out[75]: 0.7304341857510817
```

```
In [76]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[76]: -0.0732552454687148
```

```
In [77]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @printf("SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg11)
         JCA11 = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation =  0.718
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.221
```

```
Out[77]: 0.718216419373934
```

```
In [78]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[78]: 0.13191233301820587
```

```
In [79]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg12)
JCA11 = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.643
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.889
```

```
Out[79]: 0.6430846908410701
```

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

```
Out[80]: 0.17624382348320844
```

```
In [81]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg13)
JCA11 = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.700
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.162
```

```
Out[81]: 0.7003576020359029
```

```
In [82]: writedlm("Correlation.G5.M.C*.txt",cor13)
```

```
In [83]: writedlm("Regression.G5.M.C*.txt",reg13)
```

```
In [84]: GEBVG5Gall = aHat1[posAi]
GEBVG5G=mean(GEBVG5Gall)
```

```
Out[84]: 0.01821965367469936
```

```
In [85]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg14)
JCA11 = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.774
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.125
```

```
Out[85]: 0.7743106849388752
```

```
In [86]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[86]: -1.4731833758727022
```

```
In [87]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg14)
JCA11 = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.754
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.054
```

```
Out[87]: 0.7537781118823741
```

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

```
Out[88]: -1.1176449143387701
```

```
In [89]: IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg15)
JCA11 = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.717
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.001
```

```
Out[89]: 0.7171769591980182
```

```
In [90]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[90]: -0.6249326632564646
```

```
In [91]: IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg16)
JCA11 = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.707
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.999
```

```
Out[91]: 0.7069436128976945
```

```
In [92]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[92]: -0.14795306196933045
```

```
In [93]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg17)
JCall = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation =  0.700
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.023
```

```
Out[93]: 0.7003105502846821
```

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

```
Out[94]: 0.16988163598624373
```

```
In [95]: numSSBayes
```

```
Out[95]: SSBR.NumSSBayes(54950,45950,9000,40000,39000,1000,150)
```