In [1]:
```julia
include("/home/nicole/Jupyter/SSBRnoJ/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/0.3/G/2
```

/home/nicole/Jupyter/JG3/Data/0.3/G/2

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

Correlation.G5.G.J.txt
Correlation.G5.G.JC.txt
Correlation.G5.G.PBLUP.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

```
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 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 [29]:
```
;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 [30]:
```
ped,A_Mats,numSSBayes = calc_Ai("PedAll.txt","genotype.ID",calculateInbreeding=false)
nothing
df      = read_genotypes("GenNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped,center=true);                    # with centering
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 [31]:
```
vG      = 0.731
vRes    = 1.706
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
2479.954453 seconds (23.06 G allocations: 724.155 GB, 7.43% gc time)
```

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

Out[32]:
```
1-element Array{Float64,1}:
 12.2173
```

In [33]:
```
using DataFrames
```

In [34]:
```
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 [35]:
```
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)
JCAll = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation =  0.857
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.989
```

Out[35]: 0.8568567436843337

In [36]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[36]: 0.13224472801675563

In [37]:
```
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)
JCAll = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation =  0.938
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.117
```

Out[37]: 0.9379404473458274

In [38]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[38]: 1.0281220851792365

In [39]:
```
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)
JCAll = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation =  0.808
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.969
```

Out[39]: 0.8083279429324747

In [40]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[40]: -0.07449620055920134

In [41]:
```
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)
JCAll = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation =  0.690
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  1.148
```

Out[41]: 0.6896548692711091

In [42]:
```
GEBV = aHat1[posAi]
G1GEBV=mean(GEBV)
```

Out[42]: -1.0780967809541548

In [43]:
```
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)
JCAll = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =  0.685
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.007
```

Out[43]: 0.6850293930851707

In [44]:
```
GEBV = aHat1[posAi]
G1GEBV=mean(GEBV)
```

Out[44]: -0.3926723173021774

In [45]:
```
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)
JCAll = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =  0.676
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.992
```

Out[45]: 0.6761584978914771

In [46]:
```
GEBV = aHat1[posAi]
G2GEBV=mean(GEBV)
```

Out[46]: 0.0577406766323755

In [47]:
```
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 =  0.666
SSBRJC from Gibbs – G3.ID : regression of TBV on GEBV =  0.993
```

Out[47]: 0.6655591835880451

In [48]:
```
GEBV = aHat1[posAi]
G3GEBV=mean(GEBV)
```

Out[48]: 0.4184059604918812

In [49]:
```
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 =  0.695
SSBRJC from Gibbs – G4.ID : regression of TBV on GEBV =  1.015
```

Out[49]: 0.6948461573841903

In [50]:
```
GEBV = aHat1[posAi]
G4GEBV=mean(GEBV)
```

Out[50]: 0.7327401884851374

In [51]:
```
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)
JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =  0.934
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.115
```

Out[51]: 0.9338038731346935

In [52]:
```
GEBV = aHat1[posAi]
G5GEBV=mean(GEBV)
```

Out[52]: 1.0553506407474724

In [53]:
```
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)
JCAll = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation =  0.940
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.047
```

Out[53]: 0.9400389009510088

In [54]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[54]: 0.3188080607127937

In [55]:
```
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)
JCAll = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation =  0.936
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.080
```

Out[55]: 0.9361629048435645

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

Out[56]: 0.5428044712134167

In [57]:
```
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)
JCAll = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation =  0.938
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.106
```

Out[57]: 0.93847550301213

In [58]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[58]: 0.8078041946110062

In [59]:
```
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)
JCAll = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation =  0.933
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.087
```

Out[59]: 0.9330499740929016

In [60]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[60]: 1.0416498715354607

In [61]:
```
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)
JCAll = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation =  0.926
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.118
```

Out[61]: 0.9263542844376513

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

Out[62]: 1.3404016050940757

In [63]:
```
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)
JCAll = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation =  0.934
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.115
```

Out[63]: 0.9338038731346935

In [64]:
```
writedlm("Correlation.G5.G.C.txt",cor13)
```

In [65]:
```
writedlm("Regression.G5.G.C.txt",reg13)
```

In [66]:
```
GEBVG5Gall = aHat1[posAi]
GEBVG5G=mean(GEBVG5Gall)
```

Out[66]: 1.0553506407474724

In [67]:
```
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)
JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.672
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.227
```

Out[67]: 0.6722861347366013

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

Out[68]: -1.1139148538174102

In [69]:
```
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)
JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.668
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.016
```

Out[69]: 0.6684062898059506

In [70]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[70]: -0.41665890162309005

In [71]:
```
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)
JCAll = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.659
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.988
```

Out[71]: 0.6594354149627717

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

Out[72]: 0.038508278735487546

In [73]:
```
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)
JCAll = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.651
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.987
```

Out[73]: 0.6505018803071381

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

Out[74]: 0.40242534738819963

In [75]:
```
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 =  0.681
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.007
```

Out[75]: 0.6812382556291628

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

Out[76]: 0.7171591265208057

In [77]:
```
numSSBayes
```

Out[77]: SSBR.NumSSBayes(54934,45934,9000,40000,39000,1000,200)