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]:
```
; cd Data/0.5/G/50QTL
```

/home/nicole/Jupyter/JG3/Data/0.5/G/50QTL

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

GenNF.txt
PedAll.txt
Phe.txt
PheAll.txt

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)
J_Vecs = make_JVecs(numSSBayes,A_Mats)
Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
X_Mats, W_Mats = make_XWMats(J_Vecs,Z_Mats,M_Mats,numSSBayes)        # with J
nothing
```

In [31]:
```
vRes    = 0.668
vG      = 0.668
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,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
4956.904947 seconds (23.05 G allocations: 723.785 GB, 6.97% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
 14.0489
  4.49117
```

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 =  0.915
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.968
```

Out[35]: 0.9148357711064404

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

Out[36]: -2.6560286123389445

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 =  0.980
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.082
```

Out[37]: 0.9798929610052075

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

Out[38]: -1.4936252448025082

```
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 =  0.877
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.952
```

Out[39]: 0.8767440924729033

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

Out[40]: -2.924275543308891

```
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 =  0.710
         SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.854
```

Out[41]: 0.709657446045942

```
In [42]: GEBV = aHat1[posAi]
         G0GEBV=mean(GEBV)
```

Out[42]: -4.01839480240412

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 =  0.779
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.989
```

Out[43]: 0.7794076373978222

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

Out[44]: -3.397267553254392

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 =  0.770
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.989
```

Out[45]: 0.7695930418856333

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

Out[46]: -2.8449655371210993

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 =   0.770
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =   0.995
```

Out[47]: 0.7699406121106825

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

Out[48]: -2.341391482794613

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 =   0.789
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =   1.007
```

Out[49]: 0.7891255466562688

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

Out[50]: -1.8846615833488458

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 =  0.977
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.081
```

Out[51]: 0.9773288484091962

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

Out[52]: -1.4494907151105982

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 =  0.974
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.097
```

Out[53]: 0.97388811482882

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

Out[54]: -2.7394771590796063

```
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 =  0.979
         SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.043
```

Out[55]: 0.9792150839457098

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

Out[56]: -2.24051648218705

```
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 =  0.972
         SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.059
```

Out[57]: 0.9723804990091306

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

Out[58]: -1.7859814881920952

```
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 =  0.976
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.065
```

Out[59]: 0.9758731544196928

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

Out[60]: -1.4122598125681065

```
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 =  0.962
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.070
```

Out[61]: 0.9615659245809142

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

Out[62]: -1.0552724696620845

```
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 =  0.977
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.081
```

Out[63]: 0.9773288484091962

```
In [64]: TBVG5Gall = a[posAi]
         TBVG5G=mean(TBVG5Gall)
```

Out[64]: 12.573878249999998

```
In [65]: GEBVG5Gall = aHat1[posAi]
         GEBVG5G=mean(GEBVG5Gall)
```

Out[65]: -1.4494907151105982

```
In [66]: 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 =  0.690
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.855
```

Out[66]: 0.6901729453567725

```
In [67]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[67]: -4.051187562489364

In [68]:
```
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 =  0.762
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.993
```

Out[68]: 0.7622780105346335

In [69]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[69]: -3.4269278371279133

In [70]:
```
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 =  0.752
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.989
```

Out[70]: 0.7517105034997498

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

Out[71]: -2.8721189742731252

In [72]:
```
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 =  0.754
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.992
```

Out[72]: 0.75354484988484

In [73]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[73]: -2.36521537177478

In [74]:
```
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 =  0.777
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.005
```

Out[74]: 0.7773727581443894

In [75]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[75]: -1.9059279708792758

In [76]:
```
numSSBayes
```

Out[76]: SSBR.NumSSBayes(54906,45906,9000,40000,39000,1000,200)

```
In [77]:   J1 = sortrows(J_Vecs.J1)
```

```
Out[77]:  45906x1 Array{Float64,2}:
           -0.999676
           -0.997643
           -0.988757
           -0.987284
           -0.985823
           -0.985587
           -0.985551
           -0.985066
           -0.984633
           -0.984498
           -0.984346
           -0.984273
           -0.984156
              ⋮
            6.08279e-17
            6.14904e-17
            6.60531e-17
            6.67238e-17
            6.67549e-17
            7.5108e-17
            8.07893e-17
            8.88438e-17
            9.974e-17
            1.0006e-16
            1.10761e-16
            1.10949e-16
```

```
In [78]: J1[J1 .< 0.0,:]
```

```
Out[78]: 43936x1 Array{Float64,2}:
          -0.999676
          -0.997643
          -0.988757
          -0.987284
          -0.985823
          -0.985587
          -0.985551
          -0.985066
          -0.984633
          -0.984498
          -0.984346
          -0.984273
          -0.984156
             ⋮
          -7.21871e-36
          -7.20816e-36
          -7.20816e-36
          -7.20812e-36
          -7.20812e-36
          -7.20395e-36
          -7.05053e-36
          -4.91411e-36
          -2.5921e-65
          -5.33294e-67
          -2.66647e-67
          -1.78216e-67
```

```
In [79]: J1[J1 .> 0.0,:]

Out[79]: 1264x1 Array{Float64,2}:
          8.00262e-52
          8.02614e-52
          1.60052e-51
          1.60476e-51
          1.60523e-51
          1.60523e-51
          2.40174e-51
          3.19885e-51
          3.20388e-51
          3.20953e-51
          4.53675e-51
          4.80349e-51
          6.42512e-51
          ⋮
          6.08279e-17
          6.14904e-17
          6.60531e-17
          6.67238e-17
          6.67549e-17
          7.5108e-17
          8.07893e-17
          8.88438e-17
          9.974e-17
          1.0006e-16
          1.10761e-16
          1.10949e-16
```