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/10
```

/home/nicole/Jupyter/JG3/Data/0.5a0/G/10

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

```
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
G5.noGenotype.ID
GenNF.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.G.PBLUP.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",calculateInbreedin
         nothing
         df     = read_genotypes("GenNF.txt",numSSBayes)
         M_Mats = make_MMats(df,A_Mats,ped,center=true);                  # with
         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
         nothing
```

```
In [31]: vRes   = 0.460
         vG     = 0.460
         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
       2555.498608 seconds (23.06 G allocations: 724.102 GB, 7.51% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          5.81827
          1.64285
```

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

In [34]:
```
df = readtable("sim.bv", eltypes =[UTF8String, Float64], separator = ' ',head
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
@printf("SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV = %6.3f\n",
JCAll = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation =  0.910
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.947
```

Out[35]: 0.9096473479319694

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

Out[36]: -0.9078722279538987

In [37]:
```
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 =  0.982
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.030
```

Out[37]: 0.9823137312752407

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

Out[38]: 0.10556971544249082

In [39]:
```
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 =  0.867
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.934
```

Out[39]: 0.8666358276033275

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

Out[40]: −1.1417434456607576

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

```
SSBRJC from Gibbs - G0.ID : correlation =  0.634
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.717
```

Out[41]: 0.6343444223996542

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

Out[42]: −2.0341856246581567

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

```
SSBRJC from Gibbs - G1.ID : correlation =  0.779
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.972
```

Out[43]: 0.7785581854265996

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

Out[44]: −1.5557735174712843

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 e
@printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", r
JCAll = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =  0.764
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.988
```

Out[45]: 0.7642294296711255

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

Out[46]: -1.0758067031328282

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 e
@printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation =   0.766
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.983
```

Out[47]: 0.7660845656859318

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

Out[48]: -0.6700169654464937

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 e
@printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =   0.780
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.979
```

Out[49]: 0.7796752551323727

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

Out[50]: -0.25828945485512106

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 e
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =   0.979
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.029
```

Out[51]: 0.9794934668879882

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

Out[52]: 0.14683889784049217

In [53]:
```
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 =   0.984
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =   1.046
```

Out[53]: 0.983599163563904

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

Out[54]: -1.0459087998861325

In [55]:
```
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 =   0.976
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =   1.017
```

Out[55]: 0.9760330083175025

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

Out[56]: -0.5441137774947732

In [57]:
```
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 =   0.978
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =   1.015
```

Out[57]: 0.9776904987214403

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

Out[58]: -0.23101039326177875

In [59]:
```
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 =   0.971
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =   0.995
```

Out[59]: 0.9713641571233127

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

Out[60]: 0.16761201961086772

In [61]:
```
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 =   0.972
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =   1.025
```

Out[61]: 0.9720178881660148

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

Out[62]: 0.5305022323242168

In [63]:
```
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 =   0.979
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =   1.029
```

Out[63]: 0.9794934668879882

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

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

In [66]:
```
TBVG5Gall = a[posAi]
TBVG5G=mean(TBVG5Gall)
```

Out[66]: 5.911964

In [67]:
```
GEBVG5Gall = aHat1[posAi]
GEBVG5G=mean(GEBVG5Gall)
```

Out[67]: 0.14683889784049217

In [68]:
```
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 = 
JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =   0.610
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =   0.704
```

Out[68]: 0.610252621712907

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

Out[69]: -2.059526056062567

In [70]:
```
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 = 
JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =   0.760
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =   0.974
```

Out[70]: 0.7599495197105519

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

Out[71]: -1.5817135108040155

In [72]:
```
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 = 9
JCAll = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.748
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.991
```

Out[72]: 0.7478425919097834

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

Out[73]: -1.097468146975676

In [74]:
```
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 = 9
JCAll = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.749
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.985
```

Out[74]: 0.7494182377031193

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

Out[75]: -0.6914946317300158

In [76]:
```
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 = 9
JCAll = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation =  0.764
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.978
```

Out[76]: 0.7641337843707041

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

Out[77]: -0.27851488273151437

```
In [78]:  numSSBayes
```

Out[78]: SSBR.NumSSBayes(54929,45929,9000,40000,39000,1000,200)

```
In [79]:  J1 = sortrows(J_Vecs.J1)
```

Out[79]: 45929x1 Array{Float64,2}:
          −0.999204
          −0.99309
          −0.989635
          −0.989354
          −0.986951
          −0.985619
          −0.985586
          −0.985568
          −0.98548
          −0.985301
          −0.984423
          −0.98427
          −0.98317
           ⋮
           7.41993e−17
           7.42088e−17
           7.65502e−17
           7.85836e−17
           8.88438e−17
           8.88468e−17
           8.90394e−17
           8.90569e−17
           1.10945e−16
           1.11217e−16
           1.21753e−16
           1.2328e−16

```
In [80]: J1[J1 .< 0.0,:]
```

Out[80]: 43854x1 Array{Float64,2}:
         -0.999204
         -0.99309
         -0.989635
         -0.989354
         -0.986951
         -0.985619
         -0.985586
         -0.985568
         -0.98548
         -0.985301
         -0.984423
         -0.98427
         -0.98317
          ⋮
         -1.12625e-35
         -1.10536e-35
         -7.23354e-36
         -7.22508e-36
         -7.2166e-36
         -7.19638e-36
         -7.19638e-36
         -4.91411e-36
         -7.61803e-65
         -2.53068e-66
         -1.43549e-66
         -8.89359e-67