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/Q/1
```

/home/nicole/Jupyter/JG3/Data/0.5/Q/1

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

PedAll.txt
Phe.txt
PheAll.txt
QTLNF.txt

In [5]:
```
;awk '{print $1}' PedAll.txt | sort -b > all.ID
```

In [6]:
```
;awk '{print $1}' QTLNF.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("QTLNF.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
4094.589663 seconds (22.98 G allocations: 722.689 GB, 8.03% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
 16.1151
  7.80469
```

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 =  0.917
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.965
```

Out[35]: 0.9166480047083984

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

Out[36]: -4.721008633121645

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 =  0.994
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.074
```

Out[37]: 0.9943240264426597

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

Out[38]: -3.553392258782622

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 =  0.878
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.951
```

Out[39]: 0.877593056113813

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

Out[40]: -4.990458565661421

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 =  0.855
```

Out[41]: 0.7103928993776527

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

Out[42]: -6.081787316915463

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 =  0.781
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.985
```

Out[43]: 0.7808049650904414

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

Out[44]: -5.470321054738566

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 =  0.771
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.988
```

Out[45]: 0.7709307988693541

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

Out[46]: -4.912472055941913

```
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 =  0.772
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.994
```

Out[47]: 0.7722522896983929

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

Out[48]: -4.4071904243602535

```
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 =  0.793
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.006
```

Out[49]: 0.7929292927679071

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

Out[50]: -3.945597097922986

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 =  0.994
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.074
```

Out[51]: 0.9936934381057226

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

Out[52]: -3.5086838488506937

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 =  0.992
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.077
```

Out[53]: 0.9920095765500103

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

Out[54]: -4.831777679148007

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 =  0.993
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.049
```

Out[55]: 0.9928181689736062

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

Out[56]: -4.302631677554441

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 =  0.991
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.064
```

Out[57]: 0.991179497888628

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

Out[58]: -3.847244314799222

```
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 =  0.991
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.067
```

Out[59]: 0.9908142289522173

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

Out[60]: -3.463253516418321

```
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 =  0.990
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.075
```

Out[61]: 0.9898369969346134

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

Out[62]: -3.1103905032702563

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 =  0.994
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.074
```

Out[63]: 0.9936934381057226

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

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

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

Out[66]: -3.5086838488506937

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

Out[67]: 0.6903155006661795

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

Out[68]: -6.113838846088987

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 =  0.764
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.989
```

Out[69]: 0.7635602150787062

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

Out[70]: -5.500261807999697

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 =  0.753
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.988
```

Out[71]: 0.752807466420016

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

Out[72]: -4.9397855877660835

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 =  0.756
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.992
```

Out[73]: 0.7557148350458793

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

Out[74]: -4.431393934820304

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 =  0.781
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =   1.004
```

Out[75]: 0.780970545089229

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

Out[76]: -3.9670126516320297

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

Out[77]: SSBR.NumSSBayes(54906,45906,9000,40000,39000,1000,50)

```
In [78]: J1 = sortrows(J_Vecs.J1)
```

Out[78]: 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 [79]: J1[J1 .< 0.0,:]
```

Out[79]: 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 [80]: J1[J1 .> 0.0,:]
```

Out[80]: 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