

```
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/0.5/Q/3  
  
/home/nicole/Jupyter/JG3/Data/0.5/Q/3
```

```
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.ID
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 G5.noGenotype.ID
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",calculateInbreedingCoefficients)
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 W_Mats
nothing
```

```
In [31]: vRes    = 0.664
         vG      = 0.664
         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
         3541.087727 seconds (22.96 G allocations: 722.137 GB, 8.37% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          15.9406
           7.91945
```

```
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",
         JCall = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.915
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.975
```

```
Out[35]: 0.915344334913003
```

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

```
Out[36]: -4.798620295214217
```

```
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 ) # v
@printf("SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = %6.3f\n", reg2)
JCA11 = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.994
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.070
```

```
Out[37]: 0.9939418237917104
```

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

```
Out[38]: -3.6381278357223734
```

```
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 ) # v
@printf("SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg3)
JCA11 = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.875
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.962
```

```
Out[39]: 0.8748784616121538
```

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

```
Out[40]: -5.066426247404642
```

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

```
SSBRJC from Gibbs - G0.ID : correlation = 0.702
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.867
```

```
Out[41]: 0.7023738888212686
```

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

```
Out[42]: -6.153469969935416
```

```
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", re
JCA11 = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation = 0.780
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.978
```

```
Out[43]: 0.7802437629814768
```

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

```
Out[44]: -5.518523453374597
```

```
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", re
JCA11 = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation = 0.760
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 0.990
```

```
Out[45]: 0.7596650269870883
```

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

```
Out[46]: -4.980199574757531
```

```
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
JCA11 = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation = 0.754
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 0.995
```

```
Out[47]: 0.7536824613118476
```

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

```
Out[48]: -4.497364594094779
```

```
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
JCA11 = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation = 0.774
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 0.991
```

```
Out[49]: 0.7737235915599152
```

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

```
Out[50]: -4.0486545195500145
```

```
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
JCA11 = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation = 0.993
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.069
```

```
Out[51]: 0.9932297855970482
```

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

```
Out[52]: -3.593509659572962
```

```
In [53]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
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.
JCA11 = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.992
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.070
```

```
Out[53]: 0.9919298354784355
```

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

```
Out[54]: -4.85516324893034
```

```
In [55]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=10,
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 = %6.3f\n", reg9 )
JCA11 = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.992
```

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

```
Out[55]: 0.9918515499493847
```

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

```
Out[56]: -4.386942463184474
```

```
In [57]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=10,
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 = %6.3f\n", reg10 )
JCA11 = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation = 0.991
```

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

```
Out[57]: 0.9907323445866221
```

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

```
Out[58]: -3.976500502253542
```

```
In [59]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=10,
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 = %6.3f\n", reg11 )
JCA11 = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation = 0.991
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.059
```

```
Out[59]: 0.9910080690936177
```

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

```
Out[60]: -3.5720794677535843
```

```
In [61]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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 = %6.3f\n", reg12 )
JCall = cor12
```

SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.990

SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.060

Out[61]: 0.9903465169214613

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

Out[62]: -3.1846805424663605

```
In [63]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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 = %6.3f\n", reg13 )
JCall = cor13
```

SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.993

SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.069

Out[63]: 0.9932297855970482

```
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]: -3.593509659572962

```
In [67]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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 )
@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 = 0.678

SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.863

Out[67]: 0.6781378402701661


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

```
Out[68]: -6.186759885858624
```

```
In [69]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
         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)
         @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 = 0.763
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.981
```

```
Out[69]: 0.7628557419961008
```

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

```
Out[70]: -5.54753835055896
```

```
In [71]: IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
         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 = %6.3f\n", reg15)
         JCall = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation = 0.742
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 0.991
```

```
Out[71]: 0.7424406281627366
```

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

```
Out[72]: -5.0059354484114795
```

```
In [73]: IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
         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 = %6.3f\n", reg16)
         JCall = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation = 0.736
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 0.994
```

```
Out[73]: 0.736218670540499
```

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

```
Out[74]: -4.521089853744553
```

```
In [75]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
         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 = %6.3f\n", reg17)
         JCall = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation = 0.758
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.986
```

```
Out[75]: 0.7577234806302149
```

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

```
Out[76]: -4.070807698449595
```

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

```
Out[77]: SSBR.NumSSBayes(54866,45866,9000,40000,39000,1000,50)
```

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

```
Out[78]: 45866x1 Array{Float64,2}:
         -0.999514
         -0.989317
         -0.98626
         -0.985919
         -0.985309
         -0.985285
         -0.984926
         -0.984854
         -0.984306
         -0.984196
         -0.984131
         -0.983886
         -0.983656
         ⋮
         7.07401e-17
         7.2845e-17
         7.33351e-17
         8.29252e-17
         8.89268e-17
         8.89663e-17
         8.89737e-17
         9.40272e-17
         9.72087e-17
         9.73518e-17
         1.07645e-16
         1.17135e-16
```

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

```
Out[79]: 43894x1 Array{Float64,2}:  
  -0.999514  
  -0.989317  
  -0.98626  
  -0.985919  
  -0.985309  
  -0.985285  
  -0.984926  
  -0.984854  
  -0.984306  
  -0.984196  
  -0.984131  
  -0.983886  
  -0.983656  
  ⋮  
 -1.26309e-35  
 -1.25967e-35  
 -1.08297e-35  
 -7.2166e-36  
 -7.21238e-36  
 -7.20818e-36  
 -7.20816e-36  
 -4.91411e-36  
 -1.21757e-64  
 -7.63876e-65  
 -6.08783e-65  
 -7.00015e-66
```

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

```
Out[80]: 1293x1 Array{Float64,2}:  
 1.60053e-51  
 1.60241e-51  
 2.1823e-51  
 2.79703e-51  
 2.80462e-51  
 3.17934e-51  
 3.20482e-51  
 4.80488e-51  
 9.97839e-51  
 1.99568e-50  
 3.15259e-50  
 6.30517e-50  
 6.63481e-50  
 ⋮  
 7.07401e-17  
 7.2845e-17  
 7.33351e-17  
 8.29252e-17  
 8.89268e-17  
 8.89663e-17  
 8.89737e-17  
 9.40272e-17  
 9.72087e-17  
 9.73518e-17  
 1.07645e-16  
 1.17135e-16
```