

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

```
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.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("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 W_Mats
nothing
```

```
In [31]: vRes    = 0.583
         vG      = 0.583
         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
2557.988401 seconds (23.06 G allocations: 724.143 GB, 7.53% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          12.5071
           4.53894
```

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

```
In [34]: df = readtable("sim.bv", eltypes=[UTF8String, Float64], separator = ' ', header=1,
          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 correlation
          @printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n",
          JCall = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.919
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.982
```

```
Out[35]: 0.9194939259017888
```

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

```
Out[36]: -2.6850478063234955
```

```
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 ) # 1
@printf("SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = %6.3f\n", reg2)
JCA11 = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.979
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.086
```

```
Out[37]: 0.978719021846793
```

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

```
Out[38]: -1.4954117715130086
```

```
In [39]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=
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 = %6.3f\n", reg3)
JCA11 = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.880
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.964
```

```
Out[39]: 0.8798688072466349
```

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

```
Out[40]: -2.9595791989720697
```

```
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", reg4)
JCA11 = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation = 0.681
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.813
```

```
Out[41]: 0.6813927913714942
```

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

```
Out[42]: -4.039738454942906
```

```
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
JCA11 = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation = 0.774
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.970
```

```
Out[43]: 0.7744654962988496
```

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

```
Out[44]: -3.444035947175071
```

```
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
JCA11 = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation = 0.768
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.018
```

```
Out[45]: 0.7676340869354882
```

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

```
Out[46]: -2.869225529889193
```

```
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", r
JCA11 = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation = 0.780
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.058
```

```
Out[47]: 0.780462991075949
```

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

```
Out[48]: -2.3845873617979985
```

```
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", r
JCA11 = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =  0.793
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.067
```

```
Out[49]: 0.7930383502475454
```

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

```
Out[50]: -1.9262799757277467
```

```
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", r
JCA11 = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =  0.976
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.085
```

```
Out[51]: 0.9755537334718162
```

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

```
Out[52]: -1.4464195684080585
```

```
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 =  0.972
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.056
```

```
Out[53]: 0.9718294358822032
```

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

```
Out[54]: -2.8337899727480216
```

```
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 = 0.963
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.057
```

```
Out[55]: 0.9626068756734297
```

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

```
Out[56]: -2.252495639331686
```

```
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 = 0.978
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.091
```

```
Out[57]: 0.9778619053263707
```

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

```
Out[58]: -1.867323696241035
```

```
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 = 0.971
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.081
```

```
Out[59]: 0.9711597750738814
```

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

```
Out[60]: -1.468643826028863
```

```
In [61]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=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)
JCA11 = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.953
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.061
```

```
Out[61]: 0.9534549659719445
```

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

```
Out[62]: -1.0144938474134317
```

```
In [63]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=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)
JCA11 = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.976
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.085
```

```
Out[63]: 0.9755537334718162
```

```
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]: 11.052461749999999
```

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

```
Out[67]: -1.4464195684080585
```



```
In [68]: 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)
JCA11 = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation = 0.658
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.806
```

```
Out[68]: 0.6577865316177075
```

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

```
Out[69]: -4.070660210896621
```

```
In [70]: 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)
JCA11 = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation = 0.754
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.971
```

```
Out[70]: 0.7541051522866555
```

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

```
Out[71]: -3.4745882627607987
```

```
In [72]: 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)
JCA11 = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation = 0.749
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.020
```

```
Out[72]: 0.749311944524489
```

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

```
Out[73]: -2.894915320495556
```

```
In [74]: 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 = 0.766
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.060
```

```
Out[74]: 0.7655322079899659
```

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

```
Out[75]: -2.408073093484386
```

```
In [76]: 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 = 0.779
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.068
```

```
Out[76]: 0.7794977837745634
```

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

```
Out[77]: -1.9496591072229852
```

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

```
Out[78]: SSBR.NumSSBayes(54932,45932,9000,40000,39000,1000,200)
```

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

```
Out[79]: 45932x1 Array{Float64,2}:  
  -0.999967  
  -0.987231  
  -0.986975  
  -0.986214  
  -0.98601  
  -0.985787  
  -0.985511  
  -0.985316  
  -0.985246  
  -0.985205  
  -0.983749  
  -0.983608  
  -0.983471  
  ⋮  
  6.52796e-17  
  6.53185e-17  
  6.66221e-17  
  7.12178e-17  
  7.14e-17  
  7.3991e-17  
  8.73907e-17  
  8.88254e-17  
  8.90717e-17  
  1.02696e-16  
  1.11298e-16  
  1.16024e-16
```

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

```
Out[80]: 43949x1 Array{Float64,2}:  
  -0.999967  
  -0.987231  
  -0.986975  
  -0.986214  
  -0.98601  
  -0.985787  
  -0.985511  
  -0.985316  
  -0.985246  
  -0.985205  
  -0.983749  
  -0.983608  
  -0.983471  
  ⋮  
  -7.22083e-36  
  -7.22083e-36  
  -7.22083e-36  
  -7.22083e-36  
  -7.2166e-36  
  -7.2166e-36  
  -7.20809e-36  
  -7.16816e-36  
  -5.41404e-36  
  -1.78007e-67  
  -1.78007e-67  
  -8.90036e-68
```