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/2
```

/home/nicole/Jupyter/JG3/Data/0.5a0/G/2

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 (
```
```
 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    = 0.323
vG      = 0.323
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
2490.148243 seconds (23.07 G allocations: 724.446 GB, 7.51% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
 3.92482
 0.618027
```

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

In [34]:
```
df = readtable("sim.bv", eltypes =[UTF8String, Float64], separator = ' ',hea
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 =  0.904
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.949
```

Out[35]:
```
0.9041988761586703
```

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

Out[36]:
```
-0.2824397997897779
```

```
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 ) # 
         @printf("SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV = %6.3:
         JCAll = cor2
```

```
         SSBRJC from Gibbs - genotype.ID : correlation =  0.981
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.119
```

Out[37]: 0.9812784808842219

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

Out[38]: 0.5901645876645978

```
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 =  0.857
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.912
```

Out[39]: 0.8565294053772358

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

Out[40]: -0.48381004304848

```
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 =  0.575
         SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.585
```

Out[41]: 0.5749295511500818

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

Out[42]: -1.2673463252792363

```
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
          JCAll = cor4
```

```
          SSBRJC from Gibbs - G1.ID : correlation =   0.774
          SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =   0.953
```

Out[43]: 0.7744846436726577

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

Out[44]: -0.8340944280095338

```
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
          JCAll = cor5
```

```
          SSBRJC from Gibbs - G2.ID : correlation =   0.785
          SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =   1.022
```

Out[45]: 0.7845141876732502

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

Out[46]: -0.42172428053917793

```
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 =   0.775
          SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =   1.046
```

Out[47]: 0.775272826323911

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

Out[48]: -0.07984044999069712

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
JCAll = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =  0.792
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.058
```

Out[49]: 0.7919359933344579

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

Out[50]: 0.2825593196178959

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
JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =  0.979
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.116
```

Out[51]: 0.978526436822004

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

Out[52]: 0.6258073654620816

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 =  0.980
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.142
```

Out[53]: 0.9796052881771797

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

Out[54]: -0.37882762059129826

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 =  1.109
```

Out[55]: 0.9760035370189121

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

Out[56]: 0.03831322546312863

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 =  0.975
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.076
```

Out[57]: 0.9753953264111516

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

Out[58]: 0.2855321905822103

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 =  0.975
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.091
```

Out[59]: 0.9753681495864669

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

Out[60]: 0.640066060065744

In [61]:
```
IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
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 =  0.962
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.087
```

Out[61]: 0.9623418182052793

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

Out[62]: 0.9400279709038503

In [63]:
```
IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
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 =  1.116
```

Out[63]: 0.978526436822004

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]: 4.55633275

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

Out[67]: 0.6258073654620816

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", cor14
@printf("SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 9
JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =   0.549
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =   0.567
```

Out[68]: 0.5491534278518209

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

Out[69]: -1.2901288561686708

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", cor14
@printf("SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 9
JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =   0.755
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =   0.951
```

Out[70]: 0.7545905993922073

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

Out[71]: -0.8564638550216533

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 =   0.769
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =   1.023
```

Out[72]: 0.7693761113438087

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

Out[73]: -0.43985906184998275

```
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 =  0.758
         SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.045
```

Out[74]: 0.7576376693064029

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

Out[75]: -0.09829959127419559

```
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 =  0.778
         SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.056
```

Out[76]: 0.7779739541725793

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

Out[77]: 0.26570114907210224

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

Out[78]: SSBR.NumSSBayes(54954,45954,9000,40000,39000,1000,200)

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

Out[79]: 45954x1 Array{Float64,2}:
    −0.990207
    −0.987007
    −0.985912
    −0.985806
    −0.985626
    −0.985577
    −0.985452
    −0.985448
    −0.98531
    −0.985263
    −0.984879
    −0.98461
    −0.984436
     ⋮
     5.6874e−17
     6.32693e−17
     6.33331e−17
     6.6688e−17
     7.0995e−17
     7.41042e−17
     7.42296e−17
     7.52177e−17
     7.52508e−17
     8.53373e−17
     8.54678e−17
     8.89738e−17

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

Out[80]: 43889x1 Array{Float64,2}:
         -0.990207
         -0.987007
         -0.985912
         -0.985806
         -0.985626
         -0.985577
         -0.985452
         -0.985448
         -0.98531
         -0.985263
         -0.984879
         -0.98461
         -0.984436
           ⋮
         -7.2166e-36
         -7.2166e-36
         -7.2166e-36
         -7.2166e-36
         -7.21238e-36
         -7.21237e-36
         -7.17242e-36
         -6.64565e-36
         -5.93075e-36
         -5.78073e-36
         -5.45576e-52
         -1.36439e-65