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/7
```

/home/nicole/Jupyter/JG3/Data/0.5a0/G/7

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",calculateInbreedi
         nothing
         df     = read_genotypes("GenNF.txt",numSSBayes)
         M_Mats = make_MMats(df,A_Mats,ped,center=true);                    # wit
         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)      # wit
         nothing
```

In [31]:
```
vRes    = 0.738
vG      = 0.738
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
4506.471211 seconds (23.04 G allocations: 723.496 GB, 7.07% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
 2.70103
 0.357906
```

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 =  0.920
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.977
```

Out[35]:
```
0.9195713202856867
```

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

Out[36]:
```
-0.06959158313351357
```

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

```
         SSBRJC from Gibbs - genotype.ID : correlation =  0.978
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.069
```

Out[37]: 0.9779556346303911

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

Out[38]: 1.220245666235018

```
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 =  0.881
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.963
```

Out[39]: 0.8809978873117448

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

Out[40]: -0.36724633298779

```
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", re
         JCAll = cor4
```

```
         SSBRJC from Gibbs - G0.ID : correlation =  0.720
         SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.883
```

Out[41]: 0.7202117494074363

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

Out[42]: -1.5416239916443533

```
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 =   0.772
         SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =   0.973
```

Out[43]: 0.7721541286412721

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

Out[44]: -0.8824036954764579

```
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 =   0.772
         SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =   1.006
```

Out[45]: 0.7717283051645624

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

Out[46]: -0.2984752432557108

```
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 =   0.774
         SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =   1.010
```

Out[47]: 0.7744201823670491

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

Out[48]: 0.2640482814585804

```
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 =  0.769
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.007
```

Out[49]: 0.7692760283320568

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

Out[50]: 0.7685913508295794

```
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 =  0.975
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.064
```

Out[51]: 0.9747944374222911

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

Out[52]: 1.2723137992872813

```
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 =  0.974
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.064
```

Out[53]: 0.9742171166350532

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

Out[54]: -0.18256832014774563

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 =  0.967
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.062
```

Out[55]: 0.9674035580897423

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

Out[56]: 0.3373662853858738

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 =  0.966
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.036
```

Out[57]: 0.9664984377585616

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

Out[58]: 0.866251561702096

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 =  0.962
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.038
```

Out[59]: 0.9620311802682153

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

Out[60]: 1.2639089793484575

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 =  0.968
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.051
```

Out[61]: 0.9681351037227014

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

Out[62]: 1.733544502795874

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 =  0.975
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.064
```

Out[63]: 0.9747944374222911

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]: 3.9561027499999994

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

Out[67]: 1.2723137992872813

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 = %
JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =   0.700
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =   0.886
```

Out[68]: 0.7004191119294636

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

Out[69]: -1.5764715729647791

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 = %
JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =   0.755
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =   0.977
```

Out[70]: 0.7551394120689068

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

Out[71]: -0.9136798488319022

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 = %
JCAll = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =   0.753
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =   1.007
```

Out[72]: 0.7529891164349606

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

Out[73]: -0.3283400331264238

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", cor1(
@printf("SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = !
JCAll = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.760
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.009
```

Out[74]: 0.7595011714093455

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

Out[75]: 0.23841082766653227

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", cor1'
@printf("SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = !
JCAll = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation =  0.752
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.003
```

Out[76]: 0.7518118956578482

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

Out[77]: 0.7438489623176231

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

Out[78]: SSBR.NumSSBayes(54885,45885,9000,40000,39000,1000,200)

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

Out[79]: 45885x1 Array{Float64,2}:
 -0.990515
 -0.988862
 -0.986904
 -0.985937
 -0.985772
 -0.98563
 -0.985588
 -0.985585
 -0.985577
 -0.985568
 -0.985522
 -0.985411
 -0.985291
   ⋮
  6.28015e-17
  6.28015e-17
  6.66725e-17
  7.05189e-17
  7.40958e-17
  7.41458e-17
  7.43712e-17
  7.70326e-17
  8.89475e-17
  1.001e-16
  1.0697e-16
  1.11088e-16

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

Out[80]: 43889x1 Array{Float64,2}:
         −0.990515
         −0.988862
         −0.986904
         −0.985937
         −0.985772
         −0.98563
         −0.985588
         −0.985585
         −0.985577
         −0.985568
         −0.985522
         −0.985411
         −0.985291
            ⋮
         −1.25934e−35
         −1.15288e−35
         −7.22719e−36
         −7.21871e−36
         −7.2166e−36
         −7.2166e−36
         −2.59644e−65
         −7.1781e−66
         −2.56107e−66
         −3.40781e−67
         −1.77903e−67
         −8.89515e−68