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]:
```julia
; cd Data/0.5/G/7
```

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

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

GenNF.txt
PedAll.txt
Phe.txt
PheAll.txt

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

In [6]:
```julia
;awk '{print $1}' GenNF.txt | sort -b > genotype.ID
```

In [7]:
```julia
;join -v1 all.ID genotype.ID > noGenotype.ID
```

In [8]:
```julia
;awk '{print $1,$2}' Phe.txt > sim.phenotype
```

In [9]:
```julia
;awk '{print $1,$3}' PheAll.txt > sim.bv
```

In [10]:
```julia
; awk 'NR >=1 && NR <=8000 {print $1}' PedAll.txt | sort -b > G0.ID
```

In [11]:
```julia
; awk 'NR >=8001 && NR <=16000 {print $1}' PedAll.txt | sort -b > G1.ID
```

In [12]:
```julia
; awk 'NR >=16001 && NR <=24000 {print $1}' PedAll.txt | sort -b > G2.ID
```

In [13]:
```julia
; awk 'NR >=24001 && NR <=32000 {print $1}' PedAll.txt | sort -b > G3.ID
```

In [14]:
```julia
; awk 'NR >=32001 && NR <=40000 {print $1}' PedAll.txt | sort -b > G4.ID
```

In [15]:
```julia
; awk 'NR >=40001 && NR <=48000 {print $1}' PedAll.txt | sort -b > G5.ID
```

In [16]:
```julia
;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 G
```
```
 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   = 0.711
         vG     = 0.711
         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
5167.100924 seconds (23.05 G allocations: 723.936 GB, 6.23% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          13.99
           4.67149
```

```
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 =  0.916
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.976
```

```
Out[35]: 0.915664225698805
```

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

```
Out[36]: -2.7630672098664957
```

```
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 = %6.3:
         JCAll = cor2
```

```
         SSBRJC from Gibbs - genotype.ID : correlation =  0.978
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.076
```

Out[37]: 0.9777048685572935

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

Out[38]: -1.547057770204538

```
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 =  0.877
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.962
```

Out[39]: 0.8770431514076494

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

Out[40]: -3.043684772865409

```
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 ej
         @printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", re
         JCAll = cor4
```

```
         SSBRJC from Gibbs - G0.ID : correlation =  0.712
         SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.885
```

Out[41]: 0.7124005770020589

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

Out[42]: -4.1687361010146695

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 ej
@printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =   0.779
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =   0.996
```

Out[43]: 0.7792806740405422

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

Out[44]: -3.5265138186218974

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 ej
@printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =   0.781
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =   1.022
```

Out[45]: 0.7805060942314663

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

Out[46]: -2.994584511950136

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 ej
@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 =   1.017
```

Out[47]: 0.775399014599305

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

Out[48]: -2.4271582142022505

```
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 =  0.783
          SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.017
```

Out[49]: 0.7831303735603942

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

Out[50]: -1.9623119903976671

```
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 =  1.074
```

Out[51]: 0.9749207173600163

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

Out[52]: -1.4990986230123504

```
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 =  1.060
```

Out[53]: 0.9743625948907203

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

Out[54]: -2.8359561884558118

```
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 =   0.975
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =   1.080
```

Out[55]: 0.9748585721571006

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

Out[56]: -2.429903907167214

```
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]: 0.9751778853243681

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

Out[58]: -1.8285934390229281

```
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 =   0.968
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =   1.062
```

Out[59]: 0.9678877937686048

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

Out[60]: -1.4899572457793873

In [61]:
```
IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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 =  0.954
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.090
```

Out[61]: 0.9540122752789227

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

Out[62]: -1.0692439582848587

In [63]:
```
IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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 =  1.074
```

Out[63]: 0.9749207173600163

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]: 12.462021125

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

Out[67]: -1.4990986230123504

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 =  0.692
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.889
```

Out[68]: 0.6916341191079611

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

Out[69]: -4.202909944926434

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 =  0.765
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.001
```

Out[70]: 0.7651887145388565

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

Out[71]: -3.55463202147971

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 =  0.762
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.025
```

Out[72]: 0.7622305433391583

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

Out[73]: -3.0244817189482704

```
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 =  0.761
         SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.017
```

Out[74]: 0.7614377416368033

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

Out[75]: -2.4511890082643752

```
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 =  0.770
         SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.014
```

Out[76]: 0.770209927420175

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

Out[77]: -1.985211170708252

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

Out[78]: SSBR.NumSSBayes(54917,45917,9000,40000,39000,1000,200)

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

Out[79]: 45917x1 Array{Float64,2}:
         -0.986868
         -0.985718
         -0.985549
         -0.985507
         -0.985337
         -0.98531
         -0.98449
         -0.983869
         -0.983768
         -0.983758
         -0.983587
         -0.983232
         -0.982671
          ⋮
          7.40483e-17
          7.42043e-17
          7.42098e-17
          7.4361e-17
          8.51031e-17
          8.51031e-17
          8.61278e-17
          8.89559e-17
          1.02969e-16
          1.11022e-16
          1.11095e-16
          1.11274e-16

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

Out[80]: 43998x1 Array{Float64,2}:
          −0.986868
          −0.985718
          −0.985549
          −0.985507
          −0.985337
          −0.98531
          −0.98449
          −0.983869
          −0.983768
          −0.983758
          −0.983587
          −0.983232
          −0.982671
           ⋮
          −7.34107e−36
          −7.23782e−36
          −7.2166e−36
          −7.2166e−36
          −7.21449e−36
          −7.00015e−66
          −3.56334e−67
          −3.55597e−67
          −1.78167e−67
          −1.77903e−67
          −1.77799e−67
          −8.89515e−68