```
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/6
```

```
/home/nicole/Jupyter/JG3/Data/0.5a0/G/6
```

```
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   = 0.262
vG     = 0.262
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
2741.164003 seconds (23.05 G allocations: 723.923 GB, 7.34% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
 4.78493
 1.3489
```

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 =  0.889
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.916
```

Out[35]:
```
0.8889696219111853
```

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

Out[36]:
```
-0.7630571516346379
```

```
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 =  1.074
```

Out[37]: 0.9780244420957661

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

Out[38]: -0.03877617863836052

```
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 =  0.838
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.885
```

Out[39]: 0.838459033049399

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

Out[40]: -0.9301989146337788

```
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 =  0.545
         SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.533
```

Out[41]: 0.5450208074291613

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

Out[42]: -1.5594598350637299

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 e₁
@printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =   0.765
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.936
```

Out[43]: 0.7647120351671746

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

Out[44]: -1.2280684194291849

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 e₁
@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 =  0.994
```

Out[45]: 0.7721525290547819

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

Out[46]: -0.8890226373101932

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 e₁
@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 =  0.998
```

Out[47]: 0.7740078437827679

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

Out[48]: -0.5982913338312303

```
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 ep
         @printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", re
         JCAll = cor7
```

```
         SSBRJC from Gibbs - G4.ID : correlation =  0.778
         SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.981
```

Out[49]: 0.7779091133676712

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

Out[50]: -0.29549183967006537

```
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 ep
         @printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", re
         JCAll = cor8
```

```
         SSBRJC from Gibbs - G5.ID : correlation =  0.974
         SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.069
```

Out[51]: 0.9741460087059728

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

Out[52]: -0.008008844503423419

```
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 =  1.113
```

Out[53]: 0.9799381089747038

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

Out[54]: -0.8769268843151741

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 =  0.978
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.090
```

Out[55]: 0.9779415460648819

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

Out[56]: -0.5040828573577197

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 =  0.978
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.100
```

Out[57]: 0.9779832485200544

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

Out[58]: -0.28096102535216033

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 =  0.971
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.030
```

Out[59]: 0.9710027485382055

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

Out[60]: 0.012291602910019923

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 =  0.955
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.044
```

Out[61]: 0.9548466436466649

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

Out[62]: 0.22510490552574655

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 =  0.974
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.069
```

Out[63]: 0.9741460087059728

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]: 4.740360375

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

Out[67]: -0.008008844503423419

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 =   0.523
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =   0.517
```

Out[68]: 0.5233408571949613

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

Out[69]: -1.5769606799547182

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 =   0.747
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =   0.935
```

Out[70]: 0.7472317706196263

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

Out[71]: -1.2466321517899916

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 =   0.757
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =   0.995
```

Out[72]: 0.7573719283732679

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

Out[73]: -0.9046139606937327

```
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 = 9
         JCAll = cor16
```

```
         SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.758
         SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.998
```

Out[74]: 0.758135309546859

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

Out[75]: -0.6139473065681854

```
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 =  0.765
         SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.979
```

Out[76]: 0.7649474739746969

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

Out[77]: -0.3088404741622657

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

Out[78]: SSBR.NumSSBayes(54916,45916,9000,40000,39000,1000,200)

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

Out[79]: 45916x1 Array{Float64,2}:
         −0.988548
         −0.986981
         −0.986553
         −0.985968
         −0.98556
         −0.985416
         −0.985321
         −0.985276
         −0.984341
         −0.984239
         −0.983132
         −0.982628
         −0.981694
          ⋮
          6.66038e−17
          6.95754e−17
          7.11282e−17
          7.11548e−17
          7.17203e−17
          7.29782e−17
          7.43911e−17
          7.92991e−17
          8.60319e−17
          8.91038e−17
          1.11144e−16
          1.11714e−16

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

Out[80]: 43939x1 Array{Float64,2}:
           −0.988548
           −0.986981
           −0.986553
           −0.985968
           −0.98556
           −0.985416
           −0.985321
           −0.985276
           −0.984341
           −0.984239
           −0.983132
           −0.982628
           −0.981694
              ⋮
           −7.31545e−36
           −7.24235e−36
           −7.22085e−36
           −7.2166e−36
           −7.21449e−36
           −7.21238e−36
           −7.20815e−36
           −5.41087e−36
           −7.16595e−66
           −2.03618e−66
           −3.51359e−67
           −1.77903e−67