Debug SynSurr

Height

```
# read in the data
pheno <- readRDS("Data/Old/height_imputed.rds")

# read in the genetic data
G <- BEDMatrix::BEDMatrix(path = "Data/allchromosome.bed", simple_names = TRUE)

# a random SNP
i <- sample(1:ncol(G), size = 1)
print(i)
```

```
## [1] 80090
```

```
g <- as.numeric(G[as.character(pheno$f.eid), i]) # snp i
length(g)
```

```
## [1] 349474
```

```
g_complete <- g[!is.na(g)]
length(g_complete)
```

```
## [1] 348952
```

```
X.cov <- cbind(
  g_complete,
  (pheno %>%
    select(
      f.21022.0.0, f.22001.0.0,
      starts_with("PC")
    ))[!is.na(g), ]
)
dim(X.cov)
```

```
## [1] 348952     13
```

```
colnames(X.cov)
```

```
##  [1] "g_complete"  "f.21022.0.0" "f.22001.0.0" "PC1"         "PC2"
##  [6] "PC3"         "PC4"         "PC5"         "PC6"         "PC7"
## [11] "PC8"         "PC9"         "PC10"
```

```
X.cov <- scale(X.cov)
X.cov <- cbind(X.cov, rep(1, nrow(X.cov))) # append intercept
X.cov[, 1] <- g_complete # dont scale G
X.cov[, 3] <- pheno$f.22001.0.0[!is.na(g)] # dont scale sex


# Check Imputed Linear
```

```r
summary(lm(pheno$int[!is.na(g)] ~ pheno$imputed_linear[!is.na(g)]))
```

```
##
## Call:
## lm(formula = pheno$int[!is.na(g)] ~ pheno$imputed_linear[!is.na(g)])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.6233 -0.4839  0.0051  0.4950  4.2172
##
## Coefficients:
##                                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)                     0.031622   0.001834   17.24   <2e-16 ***
## pheno$imputed_linear[!is.na(g)] 0.634012   0.001843  344.09   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7661 on 174432 degrees of freedom
##   (174518 observations deleted due to missingness)
## Multiple R-squared:  0.4043, Adjusted R-squared:  0.4043
## F-statistic: 1.184e+05 on 1 and 174432 DF,  p-value: < 2.2e-16
```

```r
summary(lm(pheno$int[!is.na(g)] ~ pheno$imputed_linear[!is.na(g)] + X.cov))
```

```
##
## Call:
## lm(formula = pheno$int[!is.na(g)] ~ pheno$imputed_linear[!is.na(g)] +
##     X.cov)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.6764 -0.4523  0.0090  0.4622  4.2250
##
## Coefficients: (1 not defined because of singularities)
##                                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)                     -0.592928   0.007191 -82.454  < 2e-16 ***
## pheno$imputed_linear[!is.na(g)]  0.023674   0.009117   2.597  0.00942 **
## X.covg_complete                  0.006088   0.011429   0.533  0.59425
## X.covf.21022.0.0                -0.121237   0.005458 -22.212  < 2e-16 ***
## X.covf.22001.0.0                 1.358391   0.015199  89.377  < 2e-16 ***
## X.covPC1                        -0.009708   0.001867  -5.200 2.00e-07 ***
## X.covPC2                         0.040440   0.009516   4.250 2.14e-05 ***
## X.covPC3                         0.040122   0.009564   4.195 2.73e-05 ***
## X.covPC4                        -0.009431   0.001746  -5.400 6.68e-08 ***
## X.covPC5                        -0.034020   0.003638  -9.351  < 2e-16 ***
## X.covPC6                         0.034168   0.003129  10.918  < 2e-16 ***
## X.covPC7                         0.015272   0.002519   6.062 1.35e-09 ***
## X.covPC8                        -0.004934   0.001746  -2.825  0.00472 **
## X.covPC9                        -0.012215   0.001724  -7.084 1.41e-12 ***
## X.covPC10                        0.023987   0.001815  13.216  < 2e-16 ***
## X.cov                                 NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Residual standard error: 0.6974 on 174419 degrees of freedom
##   (174518 observations deleted due to missingness)
## Multiple R-squared:  0.5065, Adjusted R-squared:  0.5064
## F-statistic: 1.278e+04 on 14 and 174419 DF,  p-value: < 2.2e-16
```

```
# Check Permuted Outcome
permuted <- sample(pheno$yhat[!is.na(g)])
summary(lm(pheno$int[!is.na(g)] ~ permuted))
```

```
##
## Call:
## lm(formula = pheno$int[!is.na(g)] ~ permuted)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.2170 -0.6495 -0.0258  0.6265  4.3369
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.0316020  0.0023768  13.296   <2e-16 ***
## permuted    -0.0004946  0.0023797  -0.208    0.835
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9927 on 174432 degrees of freedom
##   (174518 observations deleted due to missingness)
## Multiple R-squared:  2.477e-07,  Adjusted R-squared:  -5.485e-06
## F-statistic: 0.0432 on 1 and 174432 DF,  p-value: 0.8353
```

```
summary(lm(pheno$int[!is.na(g)] ~ permuted + X.cov))
```

```
##
## Call:
## lm(formula = pheno$int[!is.na(g)] ~ permuted + X.cov)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.6746 -0.4523  0.0092  0.4628  4.2276
##
## Coefficients: (1 not defined because of singularities)
##                    Estimate Std. Error  t value Pr(>|t|)
## (Intercept)      -0.610629   0.002285 -267.230  < 2e-16 ***
## permuted         -0.000728   0.001672   -0.435  0.66326
## X.covg_complete   0.006094   0.011429    0.533  0.59388
## X.covf.21022.0.0 -0.134733   0.001669  -80.706  < 2e-16 ***
## X.covf.22001.0.0  1.396883   0.003352  416.744  < 2e-16 ***
## X.covPC1         -0.009712   0.001867   -5.202 1.98e-07 ***
## X.covPC2          0.040445   0.009516    4.250 2.14e-05 ***
## X.covPC3          0.040132   0.009565    4.196 2.72e-05 ***
## X.covPC4         -0.009420   0.001747   -5.394 6.91e-08 ***
## X.covPC5         -0.034007   0.003638   -9.347  < 2e-16 ***
## X.covPC6          0.034155   0.003129   10.914  < 2e-16 ***
## X.covPC7          0.015262   0.002519    6.058 1.38e-09 ***
## X.covPC8         -0.004918   0.001746   -2.816  0.00486 **
## X.covPC9         -0.012215   0.001724   -7.084 1.40e-12 ***
```

```
## X.covPC10         0.023993   0.001815   13.219  < 2e-16 ***
## X.cov                   NA         NA       NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6974 on 174419 degrees of freedom
##   (174518 observations deleted due to missingness)
## Multiple R-squared:  0.5064, Adjusted R-squared:  0.5064
## F-statistic: 1.278e+04 on 14 and 174419 DF,  p-value: < 2.2e-16
```

```
# SynSurr with linear regression
SurrogateRegression::FitBNR(
  t = pheno$int[!is.na(g)],
  s = pheno$imputed_linear[!is.na(g)],
  X = X.cov
)@Regression.tab %>%
  filter(Outcome == "Target" & Coefficient == "g_complete")
```

```
##   Outcome Coefficient       Point         SE          L          U         p
## 1  Target  g_complete 0.006084183 0.01142932 -0.01631687 0.02848524 0.5944967
```

```
# SynSurr with permuted outcome
SurrogateRegression::FitBNR(
  t = pheno$int[!is.na(g)],
  s = permuted,
  X = X.cov
)@Regression.tab %>%
  filter(Outcome == "Target" & Coefficient == "g_complete")
```

```
##   Outcome Coefficient       Point         SE          L          U         p
## 1  Target  g_complete 0.006092206 0.01142943 -0.01630906 0.02849347 0.5940142
```

```
# Check Random Forest
summary(lm(pheno$int[!is.na(g)] ~ pheno$yhat[!is.na(g)]))
```

```
##
## Call:
## lm(formula = pheno$int[!is.na(g)] ~ pheno$yhat[!is.na(g)])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.7688 -0.3827  0.0041  0.3867  3.8867
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)             0.030378   0.001449   20.97   <2e-16 ***
## pheno$yhat[!is.na(g)] 0.786886   0.001449  543.10   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6051 on 174432 degrees of freedom
##   (174518 observations deleted due to missingness)
## Multiple R-squared:  0.6284, Adjusted R-squared:  0.6284
## F-statistic: 2.95e+05 on 1 and 174432 DF,  p-value: < 2.2e-16
```

```
summary(lm(pheno$int[!is.na(g)] ~ pheno$yhat[!is.na(g)] + X.cov))
```

```
##
## Call:
## lm(formula = pheno$int[!is.na(g)] ~ pheno$yhat[!is.na(g)] + X.cov)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.0360 -0.3810  0.0018  0.3858  3.8452
##
## Coefficients: (1 not defined because of singularities)
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)            -0.1567443  0.0026089 -60.081  < 2e-16 ***
## pheno$yhat[!is.na(g)]   0.6247245  0.0024016 260.133  < 2e-16 ***
## X.covg_complete         0.0117659  0.0097014   1.213  0.22521
## X.covf.21022.0.0       -0.0165224  0.0014881 -11.103  < 2e-16 ***
## X.covf.22001.0.0        0.4071163  0.0047510  85.691  < 2e-16 ***
## X.covPC1               -0.0076005  0.0015848  -4.796 1.62e-06 ***
## X.covPC2                0.0400338  0.0080775   4.956 7.20e-07 ***
## X.covPC3                0.0427403  0.0081185   5.265 1.41e-07 ***
## X.covPC4               -0.0044529  0.0014826  -3.003  0.00267 **
## X.covPC5               -0.0332783  0.0030883 -10.776  < 2e-16 ***
## X.covPC6                0.0282792  0.0026564  10.646  < 2e-16 ***
## X.covPC7                0.0142599  0.0021383   6.669 2.59e-11 ***
## X.covPC8                0.0006603  0.0014825   0.445  0.65603
## X.covPC9               -0.0102524  0.0014636  -7.005 2.48e-12 ***
## X.covPC10               0.0212806  0.0015406  13.813  < 2e-16 ***
## X.cov                         NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.592 on 174419 degrees of freedom
##   (174518 observations deleted due to missingness)
## Multiple R-squared:  0.6444, Adjusted R-squared:  0.6444
## F-statistic: 2.258e+04 on 14 and 174419 DF,  p-value: < 2.2e-16
```

```
# SynSurr with permuted outcome
SurrogateRegression::FitBNR(
  t = pheno$int[!is.na(g)],
  s = pheno$yhat[!is.na(g)],
  X = X.cov
)@Regression.tab %>%
  filter(Outcome == "Target" & Coefficient == "g_complete")
```

```
##   Outcome Coefficient       Point         SE           L          U        p
## 1  Target  g_complete 0.009045909 0.01060138 -0.01173241 0.02982423 0.393506
```

FEV1

```
# read in the data
pheno <- readRDS("Data/Old/fev1_imputed.rds")

# a random SNP
i <- sample(1:ncol(G), size = 1)
print(i)
```

```
## [1] 237238
```

```
g <- as.numeric(G[as.character(pheno$f.eid), i]) # snp i
length(g)
```

```
## [1] 260878
```

```
g_complete <- g[!is.na(g)]
length(g_complete)
```

```
## [1] 260520
```

```
X.cov <- cbind(
  g_complete,
  (pheno %>%
    select(
      f.21022.0.0, f.22001.0.0,
      starts_with("PC")
    ))[!is.na(g), ]
)
dim(X.cov)
```

```
## [1] 260520     13
```

```
colnames(X.cov)
```

```
##  [1] "g_complete"  "f.21022.0.0" "f.22001.0.0" "PC1"         "PC2"
##  [6] "PC3"         "PC4"         "PC5"         "PC6"         "PC7"
## [11] "PC8"         "PC9"         "PC10"
```

```
X.cov <- scale(X.cov)
X.cov <- cbind(X.cov, rep(1, nrow(X.cov))) # append intercept
X.cov[, 1] <- g_complete # dont scale G
X.cov[, 3] <- pheno$f.22001.0.0[!is.na(g)] # dont scale sex


# Check Imputed Linear
summary(lm(pheno$int[!is.na(g)] ~ pheno$imputed_linear[!is.na(g)]))
```

```
##
## Call:
## lm(formula = pheno$int[!is.na(g)] ~ pheno$imputed_linear[!is.na(g)])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.5507 -0.4229  0.0487  0.4734  4.0110
##
## Coefficients:
##                                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)                     0.006575   0.002044   3.217  0.00129 **
## pheno$imputed_linear[!is.na(g)] 0.678302   0.002053 330.452  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7371 on 130101 degrees of freedom
##   (130417 observations deleted due to missingness)
## Multiple R-squared:  0.4563, Adjusted R-squared:  0.4563
## F-statistic: 1.092e+05 on 1 and 130101 DF,  p-value: < 2.2e-16
```

```r
summary(lm(pheno$int[!is.na(g)] ~ pheno$imputed_linear[!is.na(g)] + X.cov))
```

```
##
## Call:
## lm(formula = pheno$int[!is.na(g)] ~ pheno$imputed_linear[!is.na(g)] +
##     X.cov)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.6246 -0.4125  0.0523  0.4698  4.1348
##
## Coefficients: (1 not defined because of singularities)
##                                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)                     -0.505444   0.009125 -55.388  < 2e-16 ***
## pheno$imputed_linear[!is.na(g)]  0.045399   0.011629   3.904 9.47e-05 ***
## X.covg_complete                  0.006072   0.007292   0.833 0.405041
## X.covf.21022.0.0                -0.344822   0.007079 -48.712  < 2e-16 ***
## X.covf.22001.0.0                 1.098329   0.019072  57.587  < 2e-16 ***
## X.covPC1                        -0.008445   0.002253  -3.748 0.000178 ***
## X.covPC2                         0.009106   0.011496   0.792 0.428298
## X.covPC3                         0.025713   0.011547   2.227 0.025957 *
## X.covPC4                        -0.004263   0.002113  -2.017 0.043658 *
## X.covPC5                        -0.002496   0.004392  -0.568 0.569823
## X.covPC6                         0.012292   0.003782   3.250 0.001152 **
## X.covPC7                        -0.002115   0.003040  -0.696 0.486559
## X.covPC8                         0.003843   0.002105   1.826 0.067869 .
## X.covPC9                        -0.004517   0.002086  -2.165 0.030370 *
## X.covPC10                        0.006275   0.002187   2.869 0.004116 **
## X.cov                                 NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.727 on 130088 degrees of freedom
##   (130417 observations deleted due to missingness)
## Multiple R-squared:  0.4712, Adjusted R-squared:  0.4712
## F-statistic:  8281 on 14 and 130088 DF,  p-value: < 2.2e-16
```

```r
# Check Permuted Outcome
permuted <- sample(pheno$yhat[!is.na(g)])
summary(lm(pheno$int[!is.na(g)] ~ permuted))
```

```
##
## Call:
## lm(formula = pheno$int[!is.na(g)] ~ permuted)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.5176 -0.6786  0.0068  0.6752  4.2015
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.005339   0.002773   1.925   0.0542 .
## permuted    0.001505   0.002782   0.541   0.5885
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9997 on 130101 degrees of freedom
##   (130417 observations deleted due to missingness)
## Multiple R-squared:  2.25e-06,   Adjusted R-squared:  -5.437e-06
## F-statistic: 0.2927 on 1 and 130101 DF,  p-value: 0.5885
```

```
summary(lm(pheno$int[!is.na(g)] ~ permuted + X.cov))
```

```
##
## Call:
## lm(formula = pheno$int[!is.na(g)] ~ permuted + X.cov)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.6312 -0.4128  0.0523  0.4705  4.1400
##
## Coefficients: (1 not defined because of singularities)
##                    Estimate Std. Error  t value Pr(>|t|)
## (Intercept)      -0.539369   0.002815 -191.638  < 2e-16 ***
## permuted          0.001288   0.002023    0.637 0.524285
## X.covg_complete   0.006058   0.007293    0.831 0.406133
## X.covf.21022.0.0 -0.371312   0.002018 -183.995  < 2e-16 ***
## X.covf.22001.0.0  1.171091   0.004042  289.725  < 2e-16 ***
## X.covPC1         -0.008469   0.002253   -3.759 0.000171 ***
## X.covPC2          0.009041   0.011496    0.786 0.431625
## X.covPC3          0.025695   0.011547    2.225 0.026069 *
## X.covPC4         -0.004230   0.002113   -2.002 0.045318 *
## X.covPC5         -0.002497   0.004392   -0.568 0.569713
## X.covPC6          0.012280   0.003782    3.247 0.001166 **
## X.covPC7         -0.002120   0.003040   -0.697 0.485569
## X.covPC8          0.003864   0.002105    1.836 0.066390 .
## X.covPC9         -0.004521   0.002086   -2.167 0.030232 *
## X.covPC10         0.006311   0.002187    2.885 0.003911 **
## X.cov                   NA         NA       NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.727 on 130088 degrees of freedom
##   (130417 observations deleted due to missingness)
## Multiple R-squared:  0.4712, Adjusted R-squared:  0.4711
## F-statistic:  8279 on 14 and 130088 DF,  p-value: < 2.2e-16
```

```
# SynSurr with linear regression
SurrogateRegression::FitBNR(
  t = pheno$int[!is.na(g)],
  s = pheno$imputed_linear[!is.na(g)],
  X = X.cov
)@Regression.tab %>%
  filter(Outcome == "Target" & Coefficient == "g_complete")
```

```
##   Outcome Coefficient       Point          SE           L          U         p
## 1  Target  g_complete 0.006090789 0.007292399 -0.008202051 0.02038363 0.4035915
```

```
# SynSurr with permuted outcome
SurrogateRegression::FitBNR(
```

```
  t = pheno$int[!is.na(g)],
  s = permuted,
  X = X.cov
)@Regression.tab %>%
  filter(Outcome == "Target" & Coefficient == "g_complete")
```

```
##   Outcome Coefficient       Point          SE           L          U         p
## 1  Target  g_complete 0.006062352 0.007292605 -0.008230891 0.02035559 0.4058034
```

```
# Check Random Forest
summary(lm(pheno$int[!is.na(g)] ~ pheno$yhat[!is.na(g)]))
```

```
##
## Call:
## lm(formula = pheno$int[!is.na(g)] ~ pheno$yhat[!is.na(g)])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.5834 -0.3711  0.0520  0.4286  3.9049
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)            -0.019363   0.001857  -10.43   <2e-16 ***
## pheno$yhat[!is.na(g)]  0.746796   0.001867  399.99   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6695 on 130101 degrees of freedom
##   (130417 observations deleted due to missingness)
## Multiple R-squared:  0.5515, Adjusted R-squared:  0.5515
## F-statistic: 1.6e+05 on 1 and 130101 DF,  p-value: < 2.2e-16
```

```
summary(lm(pheno$int[!is.na(g)] ~ pheno$yhat[!is.na(g)] + X.cov))
```

```
##
## Call:
## lm(formula = pheno$int[!is.na(g)] ~ pheno$yhat[!is.na(g)] + X.cov)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.6466 -0.3655  0.0539  0.4269  3.9712
##
## Coefficients: (1 not defined because of singularities)
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)            -0.1398885  0.0035896 -38.971  < 2e-16 ***
## pheno$yhat[!is.na(g)]  0.6081498  0.0038103 159.608  < 2e-16 ***
## X.covg_complete         0.0055445  0.0066688   0.831  0.40575
## X.covf.21022.0.0       -0.0864192  0.0025674 -33.660  < 2e-16 ***
## X.covf.22001.0.0        0.2683327  0.0067568  39.713  < 2e-16 ***
## X.covPC1               -0.0040390  0.0020606  -1.960  0.04999 *
## X.covPC2               -0.0005140  0.0105131  -0.049  0.96101
## X.covPC3                0.0148520  0.0105599   1.406  0.15959
## X.covPC4               -0.0016075  0.0019324  -0.832  0.40549
## X.covPC5                0.0101239  0.0040174   2.520  0.01174 *
## X.covPC6               -0.0011034  0.0034595  -0.319  0.74976
```

```
## X.covPC7              -0.0088513  0.0027806  -3.183  0.00146 **
## X.covPC8               0.0049813  0.0019246   2.588  0.00965 **
## X.covPC9              -0.0002562  0.0019080  -0.134  0.89319
## X.covPC10             -0.0034675  0.0020010  -1.733  0.08312 .
## X.cov                        NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6648 on 130088 degrees of freedom
##   (130417 observations deleted due to missingness)
## Multiple R-squared:  0.5578, Adjusted R-squared:  0.5577
## F-statistic: 1.172e+04 on 14 and 130088 DF,  p-value: < 2.2e-16
```

```
# SynSurr with permuted outcome
SurrogateRegression::FitBNR(
  t = pheno$int[!is.na(g)],
  s = pheno$yhat[!is.na(g)],
  X = X.cov
)@Regression.tab %>%
  filter(Outcome == "Target" & Coefficient == "g_complete")
```

```
##   Outcome Coefficient      Point         SE           L          U         p
## 1  Target  g_complete 0.00406326 0.00699338 -0.009643513 0.01777003 0.5612302
```