

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] 16556

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] 347963

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] 347963      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
## -4.6233 -0.4840  0.0054  0.4953  4.2175
##
## Coefficients:
##                                Estimate Std. Error t value Pr(>|t|)
## (Intercept)                   0.031476   0.001837   17.13   <2e-16 ***
## pheno$imputed_linear[!is.na(g)] 0.634144   0.001846  343.60   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7662 on 173919 degrees of freedom
## (174042 observations deleted due to missingness)
## Multiple R-squared:  0.4043, Adjusted R-squared:  0.4043
## F-statistic: 1.181e+05 on 1 and 173919 DF,  p-value: < 2.2e-16
summary(lm(pheno$int[!is.na(g)] ~ pheno$imputed_linear[!is.na(g)] + X.cov - 1))
```

```
##
## Call:
## lm(formula = pheno$int[!is.na(g)] ~ pheno$imputed_linear[!is.na(g)] +
##      X.cov - 1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.6778 -0.4523  0.0093  0.4621  4.2247
##
## Coefficients:
##                                Estimate Std. Error t value Pr(>|t|)
## pheno$imputed_linear[!is.na(g)] 0.023328   0.009130   2.555  0.01062 *
## X.covg_complete                 -0.012095   0.007801  -1.551  0.12101
## X.covf.21022.0.0                -0.121560   0.005466 -22.240 < 2e-16 ***
## X.covf.22001.0.0                 1.359125   0.015221  89.295 < 2e-16 ***
## X.covPC1                        -0.009465   0.001870  -5.061 4.17e-07 ***
## X.covPC2                         0.040751   0.009532   4.275 1.91e-05 ***
## X.covPC3                         0.040441   0.009581   4.221 2.43e-05 ***
## X.covPC4                        -0.009565   0.001749  -5.468 4.56e-08 ***
## X.covPC5                        -0.034080   0.003644  -9.353 < 2e-16 ***
## X.covPC6                         0.034384   0.003134  10.970 < 2e-16 ***
## X.covPC7                         0.015172   0.002523   6.012 1.83e-09 ***
## X.covPC8                        -0.004987   0.001749  -2.851 0.00436 **
## X.covPC9                        -0.012269   0.001727  -7.105 1.21e-12 ***
## X.covPC10                       0.023856   0.001818  13.125 < 2e-16 ***
## X.cov                           -0.592720   0.007207 -82.245 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6975 on 173906 degrees of freedom
```

```

## (174042 observations deleted due to missingness)
## Multiple R-squared: 0.507, Adjusted R-squared: 0.5069
## F-statistic: 1.192e+04 on 15 and 173906 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
## -4.2178 -0.6495 -0.0257  0.6270  4.3373
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.0315235  0.0023805  13.242  <2e-16 ***
## permuted    0.0006865  0.0023832   0.288    0.773
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9928 on 173919 degrees of freedom
## (174042 observations deleted due to missingness)
## Multiple R-squared: 4.771e-07, Adjusted R-squared: -5.273e-06
## F-statistic: 0.08298 on 1 and 173919 DF, p-value: 0.7733

summary(lm(pheno$int[!is.na(g)] ~ permuted + X.cov - 1))

##
## Call:
## lm(formula = pheno$int[!is.na(g)] ~ permuted + X.cov - 1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.6779 -0.4524  0.0094  0.4626  4.2269
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## permuted          1.597e-05  1.674e-03   0.010  0.9924
## X.covg_complete -1.210e-02  7.801e-03  -1.551  0.1208
## X.covf.21022.0.0 -1.349e-01  1.672e-03 -80.651 < 2e-16 ***
## X.covf.22001.0.0  1.397e+00  3.357e-03 416.131 < 2e-16 ***
## X.covPC1         -9.472e-03  1.870e-03  -5.065 4.09e-07 ***
## X.covPC2          4.077e-02  9.532e-03   4.277 1.90e-05 ***
## X.covPC3          4.046e-02  9.581e-03   4.223 2.41e-05 ***
## X.covPC4         -9.552e-03  1.749e-03  -5.460 4.76e-08 ***
## X.covPC5         -3.406e-02  3.644e-03  -9.347 < 2e-16 ***
## X.covPC6          3.437e-02  3.134e-03  10.965 < 2e-16 ***
## X.covPC7          1.516e-02  2.524e-03   6.006 1.90e-09 ***
## X.covPC8         -4.969e-03  1.749e-03  -2.841  0.0045 **
## X.covPC9         -1.227e-02  1.727e-03  -7.105 1.21e-12 ***
## X.covPC10         2.386e-02  1.818e-03  13.125 < 2e-16 ***
## X.cov            -6.102e-01  2.305e-03 -264.700 < 2e-16 ***

```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6975 on 173906 degrees of freedom
## (174042 observations deleted due to missingness)
## Multiple R-squared:  0.5069, Adjusted R-squared:  0.5069
## F-statistic: 1.192e+04 on 15 and 173906 DF,  p-value: < 2.2e-16

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

##      Outcome Coefficient      Point      SE      L      U      p
## 1 Target g_complete -0.01210227 0.007800633 -0.02739123 0.003186693 0.1207947

round(fit@Covariance, digits = 3)

##           Target Surrogate
## Target      0.486      0.001
## Surrogate   0.001      0.033

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

##      Outcome Coefficient      Point      SE      L      U      p
## 1 Target g_complete -0.01210124 0.007800706 -0.02739035 0.003187858 0.1208295

round(fit@Covariance, digits = 3)

##           Target Surrogate
## Target      0.486      0.000
## Surrogate   0.000      0.999

# 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
## -3.7687 -0.3827  0.0042  0.3867  3.8866
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.030294   0.001451  20.88  <2e-16 ***
```

```
## pheno$yhat[!is.na(g)] 0.786765 0.001451 542.28 <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6052 on 173919 degrees of freedom
## (174042 observations deleted due to missingness)
## Multiple R-squared: 0.6284, Adjusted R-squared: 0.6284
## F-statistic: 2.941e+05 on 1 and 173919 DF, p-value: < 2.2e-16
summary(lm(pheno$int[!is.na(g)] ~ pheno$yhat[!is.na(g)] + X.cov - 1))

##
## Call:
## lm(formula = pheno$int[!is.na(g)] ~ pheno$yhat[!is.na(g)] + X.cov -
## 1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.0374 -0.3810  0.0017  0.3858  3.8452
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## pheno$yhat[!is.na(g)] 0.624574   0.002405 259.727 < 2e-16 ***
## X.covg_complete      -0.007882   0.006621  -1.190 0.23391
## X.covf.21022.0.0     -0.016605   0.001491 -11.140 < 2e-16 ***
## X.covf.22001.0.0      0.407277   0.004758  85.589 < 2e-16 ***
## X.covPC1             -0.007379   0.001587  -4.648 3.35e-06 ***
## X.covPC2              0.040244   0.008091   4.974 6.58e-07 ***
## X.covPC3              0.043039   0.008133   5.292 1.21e-07 ***
## X.covPC4             -0.004511   0.001485  -3.038 0.00238 **
## X.covPC5             -0.033297   0.003093 -10.765 < 2e-16 ***
## X.covPC6              0.028349   0.002661  10.655 < 2e-16 ***
## X.covPC7              0.014151   0.002142   6.606 3.95e-11 ***
## X.covPC8              0.000594   0.001485   0.400 0.68917
## X.covPC9             -0.010346   0.001466  -7.058 1.70e-12 ***
## X.covPC10            0.021190   0.001543  13.733 < 2e-16 ***
## X.cov                -0.156298   0.002623 -59.579 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5921 on 173906 degrees of freedom
## (174042 observations deleted due to missingness)
## Multiple R-squared: 0.6447, Adjusted R-squared: 0.6447
## F-statistic: 2.104e+04 on 15 and 173906 DF, p-value: < 2.2e-16

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

## Outcome Coefficient      Point      SE      L      U      p
```

```
## 1 Target g_complete -0.0109346 0.007239333 -0.02512343 0.003254235 0.1309305
```

```
round(fitCovariance, digits = 3)
```

```
##           Target Surrogate
## Target    0.486    0.217
## Surrogate 0.217    0.348
```

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] 227726
```

```
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] 259115
```

```
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] 259115      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
## -4.5521 -0.4217  0.0489  0.4729  4.0097
##
## Coefficients:
##                                Estimate Std. Error t value Pr(>|t|)
## (Intercept)                   0.007854   0.002046   3.838 0.000124 ***
## pheno$imputed_linear[!is.na(g)] 0.678376   0.002055 330.031 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7362 on 129395 degrees of freedom
## (129718 observations deleted due to missingness)
## Multiple R-squared:  0.457, Adjusted R-squared:  0.457
## F-statistic: 1.089e+05 on 1 and 129395 DF, p-value: < 2.2e-16
summary(lm(pheno$int[!is.na(g)] ~ pheno$imputed_linear[!is.na(g)] + X.cov - 1))

##
## Call:
## lm(formula = pheno$int[!is.na(g)] ~ pheno$imputed_linear[!is.na(g)] +
##     X.cov - 1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.6276 -0.4124  0.0521  0.4691  4.1337
##
## Coefficients:
##                                Estimate Std. Error t value Pr(>|t|)
## pheno$imputed_linear[!is.na(g)]  0.0466177   0.0116441   4.004 6.24e-05 ***
## X.covg_complete                  -0.0006753   0.0033446  -0.202 0.839983
## X.covf.21022.0.0                 -0.3440172   0.0070885 -48.532 < 2e-16 ***
## X.covf.22001.0.0                  1.0966825   0.0190971  57.427 < 2e-16 ***
## X.covPC1                         -0.0084091   0.0022562  -3.727 0.000194 ***
## X.covPC2                          0.0067245   0.0115141   0.584 0.559206
## X.covPC3                          0.0233773   0.0115652   2.021 0.043246 *
## X.covPC4                         -0.0039817   0.0021156  -1.882 0.059827 .
## X.covPC5                         -0.0018332   0.0043962  -0.417 0.676685
## X.covPC6                          0.0112614   0.0037868   2.974 0.002942 **
## X.covPC7                         -0.0021534   0.0030439  -0.707 0.479284
## X.covPC8                          0.0036785   0.0021081   1.745 0.080995 .
## X.covPC9                         -0.0045530   0.0020898  -2.179 0.029360 *
## X.covPC10                        0.0059514   0.0021897   2.718 0.006571 **
## X.cov                            -0.5025367   0.0092526 -54.313 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.726 on 129382 degrees of freedom
## (129718 observations deleted due to missingness)
## Multiple R-squared:  0.4719, Adjusted R-squared:  0.4719
## F-statistic: 7709 on 15 and 129382 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
## -4.5194 -0.6798  0.0062  0.6742  4.1989
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.007086   0.002779   2.550   0.0108 *
## permuted    -0.001345   0.002782  -0.483   0.6288
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.999 on 129395 degrees of freedom
## (129718 observations deleted due to missingness)
## Multiple R-squared:  1.806e-06, Adjusted R-squared:  -5.922e-06
## F-statistic: 0.2337 on 1 and 129395 DF,  p-value: 0.6288
```

```
summary(lm(pheno$int[!is.na(g)] ~ permuted + X.cov - 1))
```

```
##
## Call:
## lm(formula = pheno$int[!is.na(g)] ~ permuted + X.cov - 1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.6349 -0.4126  0.0520  0.4700  4.1412
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## permuted        -0.0011767   0.0020222  -0.582 0.560645
## X.covg_complete  -0.0007315   0.0033447  -0.219 0.826873
## X.covf.21022.0.0 -0.3712149   0.0020209 -183.685 < 2e-16 ***
## X.covf.22001.0.0  1.1714066   0.0040476  289.408 < 2e-16 ***
## X.covPC1         -0.0084277   0.0022564  -3.735 0.000188 ***
## X.covPC2          0.0066977   0.0115149   0.582 0.560800
## X.covPC3          0.0234051   0.0115659   2.024 0.043011 *
## X.covPC4         -0.0039559   0.0021157  -1.870 0.061517 .
## X.covPC5         -0.0018561   0.0043965  -0.422 0.672891
## X.covPC6          0.0112576   0.0037871   2.973 0.002953 **
## X.covPC7         -0.0021513   0.0030441  -0.707 0.479753
## X.covPC8          0.0036979   0.0021082   1.754 0.079421 .
## X.covPC9         -0.0045673   0.0020899  -2.185 0.028864 *
## X.covPC10         0.0059872   0.0021899   2.734 0.006257 **
## X.cov            -0.5372665   0.0031947 -168.175 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```



```
## Residual standard error: 0.7261 on 129382 degrees of freedom
## (129718 observations deleted due to missingness)
## Multiple R-squared: 0.4719, Adjusted R-squared: 0.4718
## F-statistic: 7707 on 15 and 129382 DF, p-value: < 2.2e-16

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

## Outcome Coefficient Point SE L U
## 1 Target g_complete -0.0007134113 0.003344629 -0.007268763 0.005841941
## p
## 1 0.8310925

round(fit@Covariance, digits = 3)

## Target Surrogate
## Target 0.527 0.001
## Surrogate 0.001 0.030

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

## Outcome Coefficient Point SE L U
## 1 Target g_complete -0.0007337736 0.003344731 -0.007289325 0.005821778
## p
## 1 0.8263525

round(fit@Covariance, digits = 3)

## Target Surrogate
## Target 0.527 -0.001
## Surrogate -0.001 0.992

# 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
## -4.5842 -0.3712 0.0518 0.4279 3.9038
##
## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)          -0.01832    0.00186  -9.851   <2e-16 ***
## pheno$yhat[!is.na(g)] 0.74659    0.00187 399.313   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6687 on 129395 degrees of freedom
## (129718 observations deleted due to missingness)
## Multiple R-squared:  0.552, Adjusted R-squared:  0.552
## F-statistic: 1.595e+05 on 1 and 129395 DF, p-value: < 2.2e-16
summary(lm(pheno$int[!is.na(g)] ~ pheno$yhat[!is.na(g)] + X.cov - 1))

##
## Call:
## lm(formula = pheno$int[!is.na(g)] ~ pheno$yhat[!is.na(g)] + X.cov -
##     1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.6487 -0.3656  0.0536  0.4264  3.9707
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## pheno$yhat[!is.na(g)] 6.074e-01  3.817e-03 159.152 < 2e-16 ***
## X.covg_complete       2.358e-05  3.059e-03   0.008 0.99385
## X.covf.21022.0.0     -8.659e-02  2.572e-03 -33.672 < 2e-16 ***
## X.covf.22001.0.0      2.696e-01  6.768e-03  39.825 < 2e-16 ***
## X.covPC1              -3.971e-03  2.064e-03  -1.924 0.05431 .
## X.covPC2              -1.705e-03  1.053e-02  -0.162 0.87138
## X.covPC3               1.376e-02  1.058e-02   1.301 0.19342
## X.covPC4              -1.275e-03  1.935e-03  -0.659 0.50997
## X.covPC5               1.065e-02  4.021e-03   2.648 0.00809 **
## X.covPC6              -2.033e-03  3.464e-03  -0.587 0.55723
## X.covPC7              -9.121e-03  2.784e-03  -3.276 0.00105 **
## X.covPC8               4.923e-03  1.928e-03   2.553 0.01067 *
## X.covPC9              -3.215e-04  1.911e-03  -0.168 0.86644
## X.covPC10             -3.705e-03  2.004e-03  -1.849 0.06444 .
## X.cov                 -1.389e-01  3.847e-03 -36.114 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.664 on 129382 degrees of freedom
## (129718 observations deleted due to missingness)
## Multiple R-squared:  0.5583, Adjusted R-squared:  0.5583
## F-statistic: 1.09e+04 on 15 and 129382 DF, p-value: < 2.2e-16

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

```
## Outcome Coefficient      Point      SE      L      U
## 1 Target g_complete -0.001926588 0.003205199 -0.008208662 0.004355486
##      p
## 1 0.5477852
```

```
round(fit@Covariance, digits = 3)
```

```
##      Target Surrogate
## Target    0.527    0.142
## Surrogate 0.142    0.234
```