New way of creating and standardizing phenotype data with variance partitioning

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Variance partitioning

$V_P = V_G + V_E + V_{GE} + Cov_{GE}$

In a reciprocal transplant experiment, there are g genotypes transplanted into e environmental patches, for a total of $g * e = n_{GE}$ genotype-environment combinations.

g is levels of genotypes for $i = 1, 2...g$ e is levels of environments for $j = 1, 2...e$

Assuming the equal sample sizes r $(1, 2, ...k)$ within each genotype-environment combination, could partitioning the variance be as simple as:

$V_G = re \sum_{i=1}^{g} (\bar{y_i} - \bar{y})^2$

$V_E = rg \sum_{j=1}^{e} (\bar{y_j} - \bar{y})^2$

$V_{GE} = r \sum_{i=1}^{g} \sum_{j=1}^{e} (\bar{y_{ij}} - \bar{y_i} - \bar{y_j} + \bar{y})^2$

$V_{Cov_{GE}} = \frac{ger}{(\sum_{i=1}^{g} \sum_{j=1}^{e} I_{ij})} \sum_{i=1}^{g} \sum_{j=1}^{e} (\bar{y_i} - \bar{y})(\bar{y_j} - \bar{y}) I$

- I is an indicator variable that is 1 when the genotype i originated from environment j and 0 otherwise
- basically, each summation needs to count the same number of times to be comparable as a SS on the same scale.
- If we have a 2x2 reciprocal transplant, we have 2 of 4 treatment combinations that count toward the sum (and 2 that do not). If we have a 4x4 reciprocal transplat, we have 4 of 16 reciprocal transplants that count toward the sum (and 12 that do not). If we have 8 genotypes in 2 environments (4 from each env), then we have 4 genotypes that count toward the cov and (4 that do not). The ones that that count make this SS not
- We can get this SS to a comparable amount to the other SS by multiplying by the factor at the beginning of the equation.

$V_{error} = \sum_{i=1}^{g} \sum_{j=1}^{e} \sum_{k=1}^{r} (y_{ijk} - \bar{y}_{ij})^2$

Some evidence that this is behaving as expected:

- if you set beta1 = 1 and beta2 = 1 and int = 0, with little error, you get equal amounts of variance explained for G, E, and CovGE for n pops
- if you set beta1 = 1 and beta2 = 0.1 and int = 0, you get more variance explained for V_E, a little bit for V_G, and a decent amount for cov_GE
- if you set beta1 = 0.1 and beta2 = 1 and int = 0, you get the same pattern as above but V_E and V_G switched
- if you set beta1 or beta2 negative and the other positive, you get negative covGE
- try adding noise and see if outputs make sense
  - Adding noise can sometimes "create" some CovGE when there are enough pops and beta1=0 or beta2=0
  - But for most part seems to work (?)

Effect size

$$Cov_{GE} = \frac{1}{\sum_{i=1}^{g}\sum_{j=1}^{e}(I)-1}\frac{\sum_{i=1}^{g}\sum_{j=1}^{e}(\bar{y}_i-\bar{y})(\bar{y}_j-\bar{y})I}{max(\sigma_{\bar{y}_i},\sigma_{\bar{y}_j})}$$

$$G \times E = \frac{1}{ge}\sum_{i=1}^{g}\sum_{j=1}^{e}|(\bar{y_{ij}} - \bar{y_i} - \bar{y_j} + \bar{y})|$$

Step 1: create true phenotype data without error

```
beta1 = -1 # the amount the phenotype changes across 1 value of the environment (i.e., the slope). This

n_genotypes = 10 # the number of genotypes collected from different locations
n = 10 # sample size
beta2 = 1 # the amount the phenotype changes from one genotype to the next. This is essitially the incr

scale = 0.01 # the scale for sd_noise within pops compared to sd_means among pops
# I'll let you explore the space, but I think the upper would be scale = 1
# I'd start with scale = 1 and scale = 1/2 and see what that looks like

sd_int = 0#n_genotypes # sd of the interaction terms that will be drawn
    #  beta1 <- 1
    #  beta2 <- 1

    # Generate data

    n_environments = n_genotypes # the number of common garden environments that the genotypes are grow

    ## Create levels of genotypes and environments ####
    G = rep(1:n_genotypes, each=n*n_genotypes) # '0' n times, '1' n times
    E = rep(1:n_environments,times=n*n_genotypes) # '0'x50, '1'x50, '0'x50, '1'x50
    #set.seed(97)


    ## Create interaction effect for each level of both factors ####
    # In this case we assume the GxE interactions are a
    # normally distributed random variable with a mean of 0
    # As the sd increases, so does the GxE among treatments
    if(sd_int == 0){
      int = 0
    }else{
    int <- rnorm(n_genotypes * n_environments, 0, sd=sd_int)
    }
    # no GxE

     # this sd determines the amount of GxE
    int_df <- data.frame(expand.grid(G=1:n_genotypes, E=1:n_environments),
                         int)

    ### Create the model dataframe ####
    model_df <- data.frame(G, E)
    model_df$GE_factor <- paste0("G",model_df$G, "E", model_df$E)
    model_df <- merge(model_df, int_df)
    model_df <- model_df[order(model_df$G, model_df$E),]
    dim(model_df)
```

```
## [1] 1000    4
```

```
    head(model_df, 30)
```

```
##    G E GE_factor int
## 1  1 1      G1E1   0
## 2  1 1      G1E1   0
## 3  1 1      G1E1   0
## 4  1 1      G1E1   0
## 5  1 1      G1E1   0
## 6  1 1      G1E1   0
## 7  1 1      G1E1   0
## 8  1 1      G1E1   0
## 9  1 1      G1E1   0
## 10 1 1      G1E1   0
## 21 1 2      G1E2   0
## 22 1 2      G1E2   0
## 23 1 2      G1E2   0
## 24 1 2      G1E2   0
## 25 1 2      G1E2   0
## 26 1 2      G1E2   0
## 27 1 2      G1E2   0
## 28 1 2      G1E2   0
## 29 1 2      G1E2   0
## 30 1 2      G1E2   0
## 31 1 3      G1E3   0
## 32 1 3      G1E3   0
## 33 1 3      G1E3   0
## 34 1 3      G1E3   0
## 35 1 3      G1E3   0
## 36 1 3      G1E3   0
## 37 1 3      G1E3   0
## 38 1 3      G1E3   0
## 39 1 3      G1E3   0
## 40 1 3      G1E3   0
```

```
    # Generate phenotype data using the regression equation ####
    model_df$GE_true = beta1*model_df$E + beta2*model_df$G + model_df$int

    G_true <- data.frame(G=1:n_genotypes, G_true=tapply(model_df$GE_true, model_df$G, mean))
    E_true <- data.frame(E=1:n_genotypes , E_true=tapply(model_df$GE_true, model_df$E, mean))

    model_df1 <- merge(model_df,G_true)
    model_df2 <- merge(model_df1,E_true)
    model_df <- model_df2

    model_df$mean_true <- mean(model_df$GE_true)

    model_df$int_true <- model_df$mean_true + model_df$GE_true -
                         model_df$G_true -   model_df$E_true
    head(model_df)
```

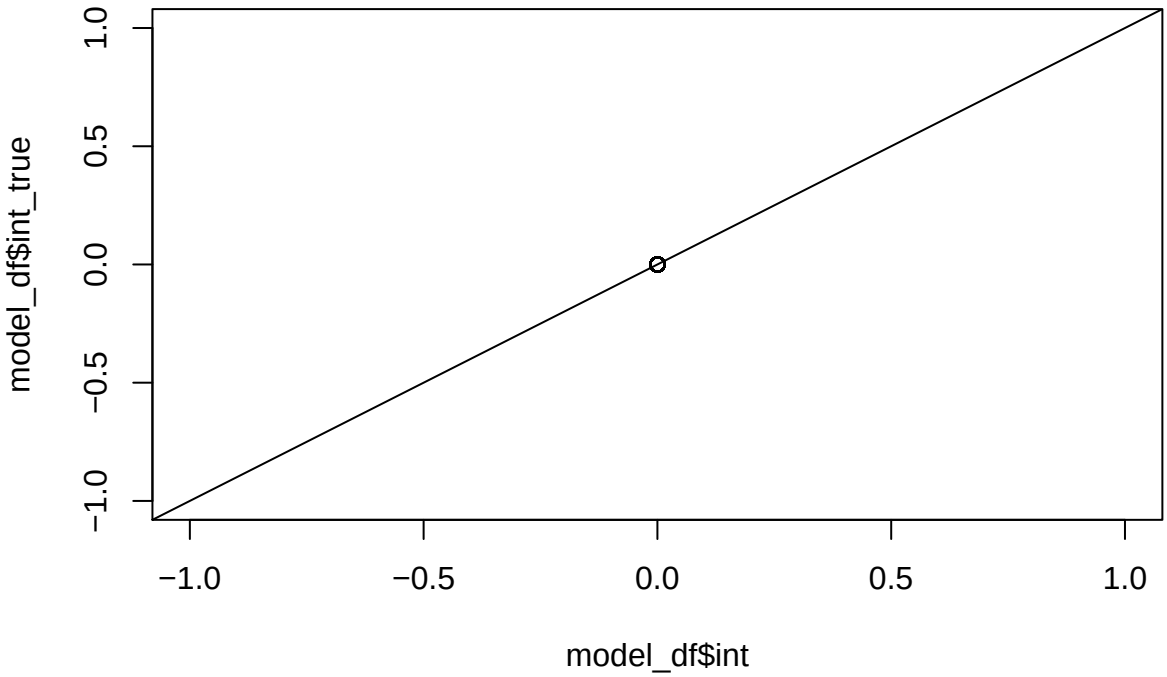
```
##   E G GE_factor int GE_true G_true E_true mean_true int_true
## 1 1 1      G1E1   0       0   -4.5    4.5         0        0
```

```
## 2 1 1      G1E1   0       0   -4.5    4.5         0        0
## 3 1 1      G1E1   0       0   -4.5    4.5         0        0
## 4 1 1      G1E1   0       0   -4.5    4.5         0        0
## 5 1 1      G1E1   0       0   -4.5    4.5         0        0
## 6 1 1      G1E1   0       0   -4.5    4.5         0        0
```

```
    tail(model_df)
```

```
##       E  G GE_factor int GE_true G_true E_true mean_true int_true
## 995  10 10    G10E10   0       0    4.5   -4.5         0        0
## 996  10 10    G10E10   0       0    4.5   -4.5         0        0
## 997  10 10    G10E10   0       0    4.5   -4.5         0        0
## 998  10 10    G10E10   0       0    4.5   -4.5         0        0
## 999  10 10    G10E10   0       0    4.5   -4.5         0        0
## 1000 10 10    G10E10   0       0    4.5   -4.5         0        0
```

```
    par(mfrow=c(1,1))
    plot(model_df$int, model_df$int_true)
    abline(0,1)
```



Note that the way we add "int" to create phenotypic variation is not the same way that the actual interaction is calculated from the data. Our simulations create an interaction, but as we create an interaction we also change the G-means and E-means, and so the calculated interaction is a bit different.

Step 2: standardize true phenotype data

```
GE_true_means <- tapply(model_df$GE_true, model_df$GE_factor, mean)

model_df$GE_stn_true <- (model_df$GE_true - mean(GE_true_means))/sd(GE_true_means)

GE_stn_true_means <- tapply(model_df$GE_stn_true, model_df$GE_factor, mean)

    G_stn_true <- data.frame(G=1:n_genotypes, G_stn_true=tapply(model_df$GE_stn_true, model_df$G, mean))
```

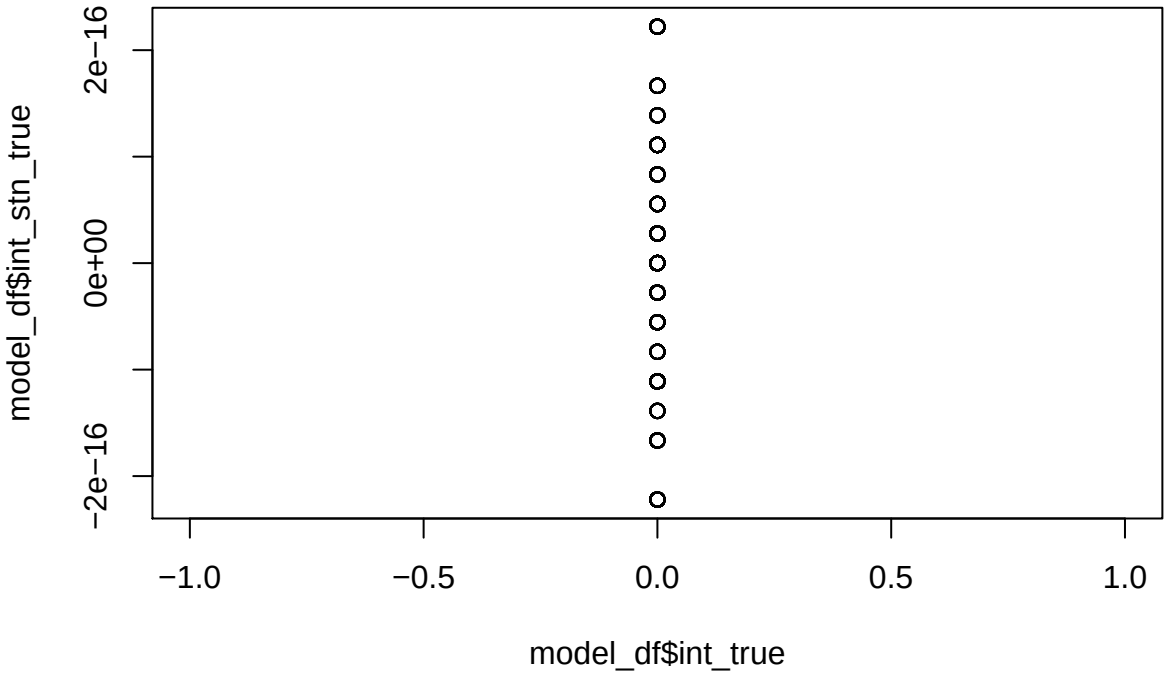
```
    E_stn_true <- data.frame(E=1:n_genotypes , E_stn_true=tapply(model_df$GE_stn_true, model_df$E, mean)

    model_df1 <- merge(model_df,G_stn_true)
    model_df2 <- merge(model_df1,E_stn_true)
    model_df <- model_df2

    model_df$mean_stn_true <- mean(model_df$GE_stn_true)

    model_df$int_stn_true <- model_df$mean_stn_true + model_df$GE_stn_true -
                        model_df$G_stn_true -   model_df$E_stn_true
    head(model_df)
```

```
##   E G GE_factor int GE_true G_true E_true mean_true int_true GE_stn_true
## 1 1 1      G1E1   0       0   -4.5    4.5         0        0           0
## 2 1 1      G1E1   0       0   -4.5    4.5         0        0           0
## 3 1 1      G1E1   0       0   -4.5    4.5         0        0           0
## 4 1 1      G1E1   0       0   -4.5    4.5         0        0           0
## 5 1 1      G1E1   0       0   -4.5    4.5         0        0           0
## 6 1 1      G1E1   0       0   -4.5    4.5         0        0           0
##   G_stn_true E_stn_true mean_stn_true int_stn_true
## 1   -1.10227    1.10227             0            0
## 2   -1.10227    1.10227             0            0
## 3   -1.10227    1.10227             0            0
## 4   -1.10227    1.10227             0            0
## 5   -1.10227    1.10227             0            0
## 6   -1.10227    1.10227             0            0
```

```
    tail(model_df)
```

```
##       E G GE_factor int GE_true G_true E_true mean_true int_true GE_stn_true
## 995  10 9     G9E10   0      -1    3.5   -4.5         0        0  -0.2449490
## 996  10 7     G7E10   0      -3    1.5   -4.5         0        0  -0.7348469
## 997  10 6     G6E10   0      -4    0.5   -4.5         0        0  -0.9797959
## 998  10 3     G3E10   0      -7   -2.5   -4.5         0        0  -1.7146428
## 999  10 8     G8E10   0      -2    2.5   -4.5         0        0  -0.4898979
## 1000 10 6     G6E10   0      -4    0.5   -4.5         0        0  -0.9797959
##      G_stn_true E_stn_true mean_stn_true int_stn_true
## 995   0.8573214   -1.10227             0 0.000000e+00
## 996   0.3674235   -1.10227             0 2.220446e-16
## 997   0.1224745   -1.10227             0 0.000000e+00
## 998  -0.6123724   -1.10227             0 0.000000e+00
## 999   0.6123724   -1.10227             0 0.000000e+00
## 1000  0.1224745   -1.10227             0 0.000000e+00
```

```
    par(mfrow=c(1,1))
    plot(model_df$int_true, model_df$int_stn_true)
```




```
      # awesome
```

Step 3: add error to stnd phenotype data

scaled to the variation in the phenotype means

```
sd(GE_stn_true_means)
```

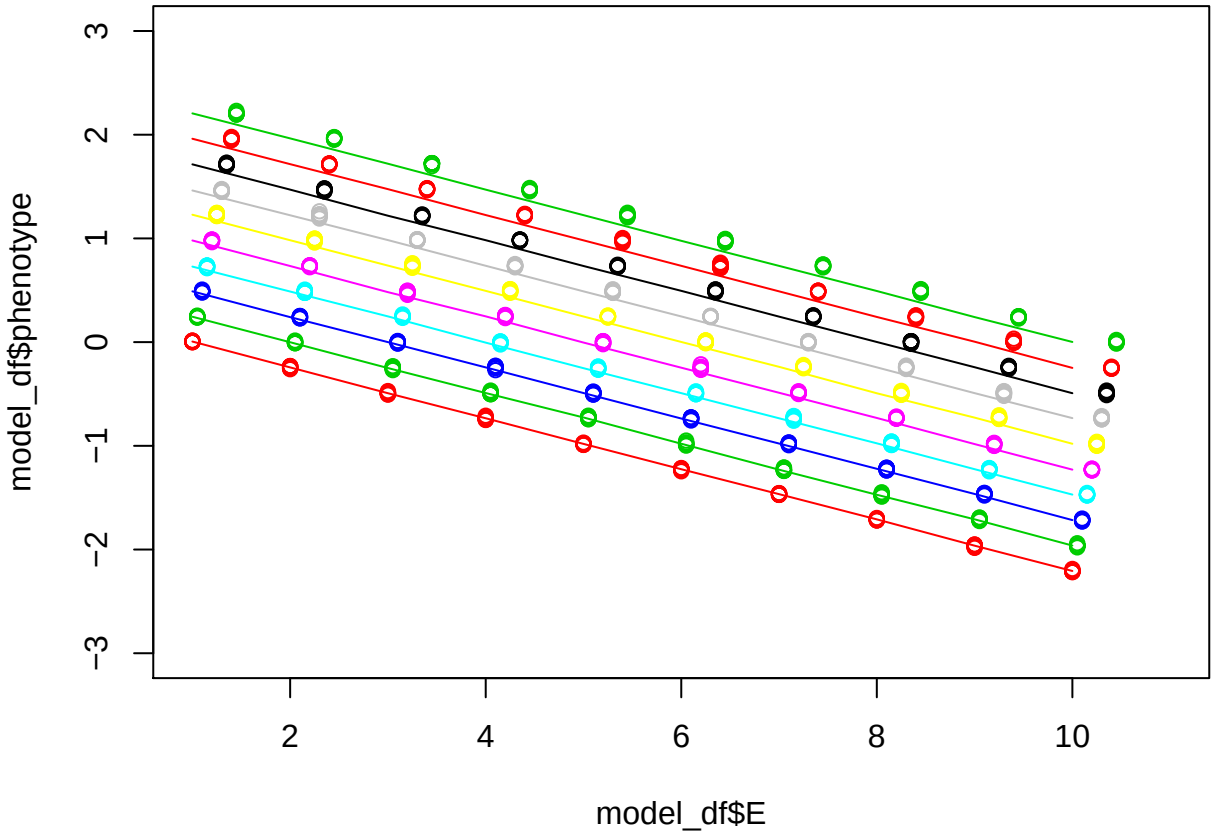
```
## [1] 1
```

```
# I guess this will always be 1 because we standardize.
sd_noise <- sd(as.numeric(GE_stn_true_means))*scale
model_df$e = rnorm(n*n_genotypes*n_environments, 0, sd=sd_noise) # Random noise

model_df$phenotype <- model_df$GE_stn_true + model_df$e
head(model_df)
```

```
##   E G GE_factor int GE_true G_true E_true mean_true int_true GE_stn_true
## 1 1 1      G1E1   0       0   -4.5    4.5         0        0           0
## 2 1 1      G1E1   0       0   -4.5    4.5         0        0           0
## 3 1 1      G1E1   0       0   -4.5    4.5         0        0           0
## 4 1 1      G1E1   0       0   -4.5    4.5         0        0           0
## 5 1 1      G1E1   0       0   -4.5    4.5         0        0           0
## 6 1 1      G1E1   0       0   -4.5    4.5         0        0           0
##   G_stn_true E_stn_true mean_stn_true int_stn_true           e    phenotype
## 1   -1.10227    1.10227             0            0 0.0137900743 0.0137900743
## 2   -1.10227    1.10227             0            0 0.0134055721 0.0134055721
## 3   -1.10227    1.10227             0            0 0.0030803668 0.0030803668
## 4   -1.10227    1.10227             0            0 0.0001205224 0.0001205224
## 5   -1.10227    1.10227             0            0 0.0083358383 0.0083358383
## 6   -1.10227    1.10227             0            0 0.0016980784 0.0016980784
```

Step 4: plot the pattern so we can see what it looks like

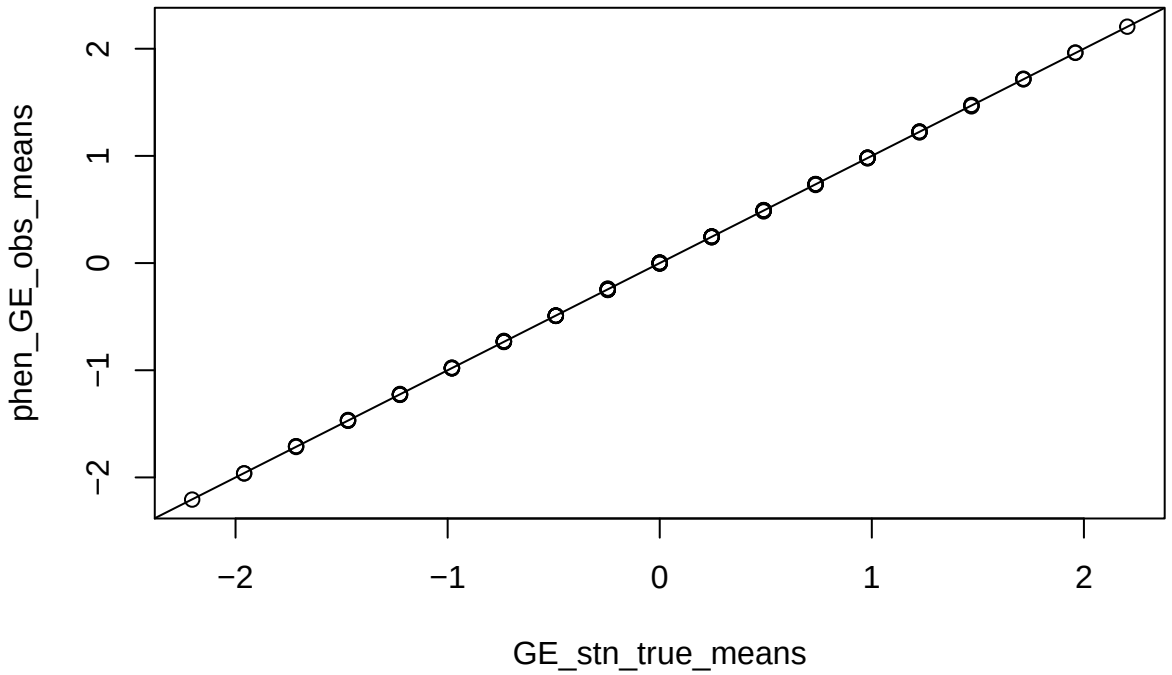
```
par(mfrow=c(1,1), mar=c(4,4,1,1))
 plot(model_df$phenotype~model_df$E, col=0, xlim=c(1,n_genotypes+1), ylim=c(-3,3))
 for (m in 1:n_genotypes){
   x <- model_df$E[model_df$G==m]+0.05*(m-1)
   points(model_df$phenotype[model_df$G==m]~x, col=m+1)
   p_means <- tapply(model_df$phenotype[model_df$G==m],model_df$E[model_df$G==m], mean)
   points(p_means~as.numeric(names(p_means)),
          col=m+1, type="l")
 }
```



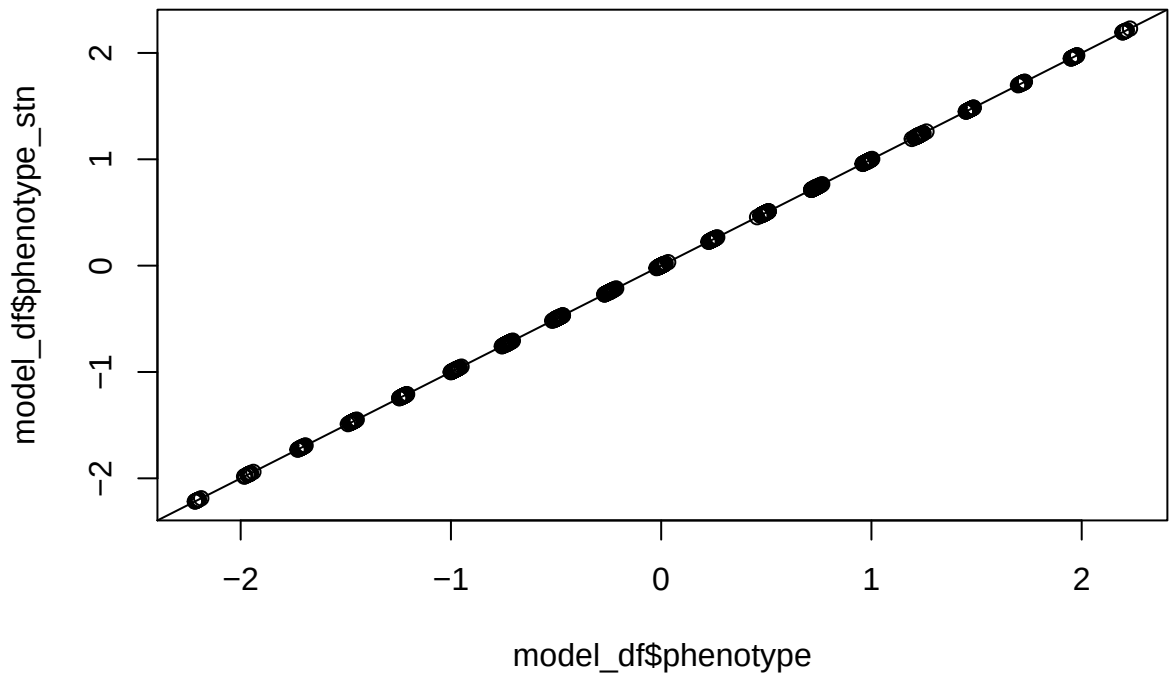
Step 5: pretend we start with noisy simulated data

Go through the steps we will go through in the study

```
# Step A: standardize by mean(GE_means) and sd(GE_means)
phen_GE_obs_means <- tapply(model_df$phenotype, model_df$GE_factor, mean)

plot(GE_stn_true_means, phen_GE_obs_means) #sanity check
abline(0,1)
```

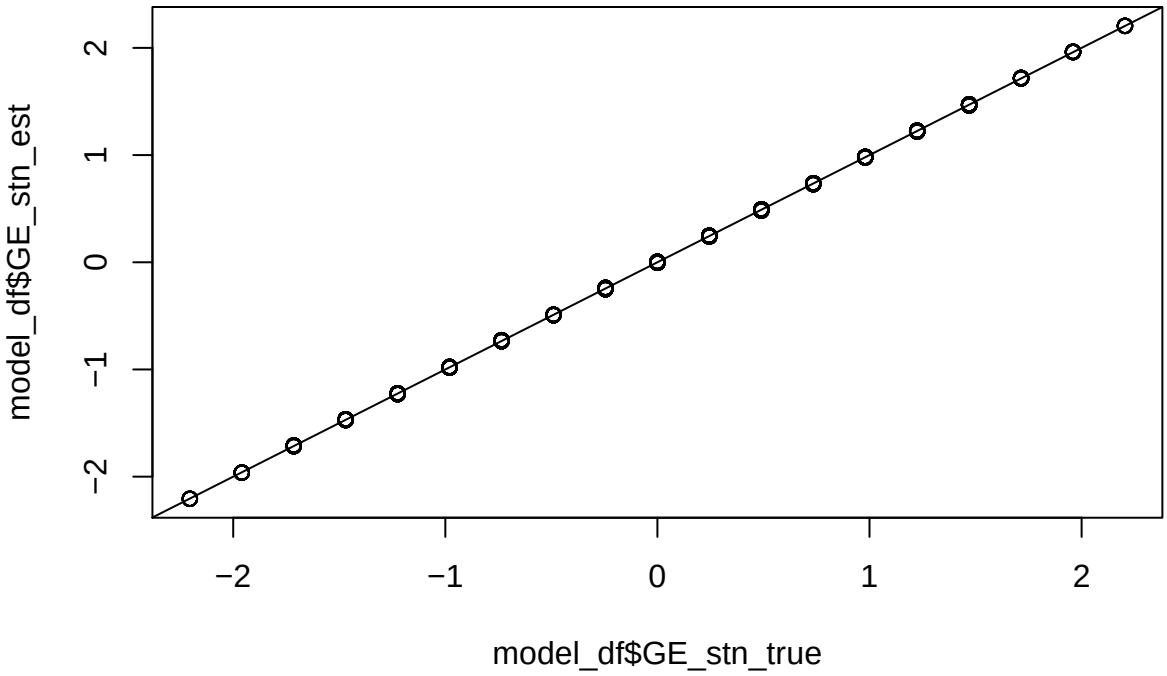



```
model_df$phenotype_stn <- (model_df$phenotype-mean(phen_GE_obs_means))/sd(phen_GE_obs_means)

plot(model_df$phenotype, model_df$phenotype_stn)
abline(0,1)
```




```
# Step B: calculate observed G_means and E_means and interaction
    G_stn_est <- data.frame(G=1:n_genotypes, G_stn_est=tapply(model_df$phenotype_stn, model_df$G, mean))
    E_stn_est <- data.frame(E=1:n_genotypes , E_stn_est=tapply(model_df$phenotype_stn, model_df$E, mean)

    GE_stn_est_means <- tapply(model_df$phenotype_stn, model_df$GE_factor, mean)
    GE_stn_est_means_df <- data.frame(GE_factor=names(GE_stn_est_means) , GE_stn_est=GE_stn_est_means)
```

```
model_df1 <- merge(model_df,G_stn_est)
model_df2 <- merge(model_df1,E_stn_est)
model_df3 <- merge(model_df2, GE_stn_est_means_df)
model_df <- model_df3

plot(model_df$GE_stn_true, model_df$GE_stn_est)
abline(0,1) # looks good
```




```
model_df$mean_stn_est <- mean(model_df$phenotype_stn)

# Calculate interaction
model_df$int_stn_est <- model_df$mean_stn_est + model_df$GE_stn_est -
                    model_df$G_stn_est -   model_df$E_stn_est
```

Step 6: Compare true values to estimated values

```
head(model_df)
```

```
##   GE_factor E  G int GE_true G_true E_true mean_true int_true GE_stn_true
## 1     G10E1 1 10   0       9    4.5    4.5         0        0    2.204541
## 2     G10E1 1 10   0       9    4.5    4.5         0        0    2.204541
## 3     G10E1 1 10   0       9    4.5    4.5         0        0    2.204541
## 4     G10E1 1 10   0       9    4.5    4.5         0        0    2.204541
## 5     G10E1 1 10   0       9    4.5    4.5         0        0    2.204541
## 6     G10E1 1 10   0       9    4.5    4.5         0        0    2.204541
##   G_stn_true E_stn_true mean_stn_true int_stn_true             e phenotype
## 1    1.10227    1.10227             0            0  0.0251070399  2.229648
## 2    1.10227    1.10227             0            0  0.0100089224  2.214550
## 3    1.10227    1.10227             0            0 -0.0040215584  2.200519
## 4    1.10227    1.10227             0            0 -0.0088955574  2.195645
## 5    1.10227    1.10227             0            0  0.0024205489  2.206961
```

```
## 6    1.10227    1.10227             0            0 -0.0002390923  2.204302
##   phenotype_stn G_stn_est E_stn_est GE_stn_est mean_stn_est  int_stn_est
## 1      2.228813  1.102784  1.101539   2.204857 1.212113e-18 0.0005341392
## 2      2.213718  1.102784  1.101539   2.204857 1.212113e-18 0.0005341392
## 3      2.199691  1.102784  1.101539   2.204857 1.212113e-18 0.0005341392
## 4      2.194818  1.102784  1.101539   2.204857 1.212113e-18 0.0005341392
## 5      2.206132  1.102784  1.101539   2.204857 1.212113e-18 0.0005341392
## 6      2.203473  1.102784  1.101539   2.204857 1.212113e-18 0.0005341392
```

```
(true_int <- mean(abs(model_df$int_stn_true)))
```

```
## [1] 5.440093e-17
```

```
(obs_int <- mean(abs(model_df$int_stn_est)))
```

```
## [1] 0.002285848
```

New step 6.5: make ANOVA table with CovGE

Here, I didn't write loops to calculate the equations, so the code will look different from the equations.

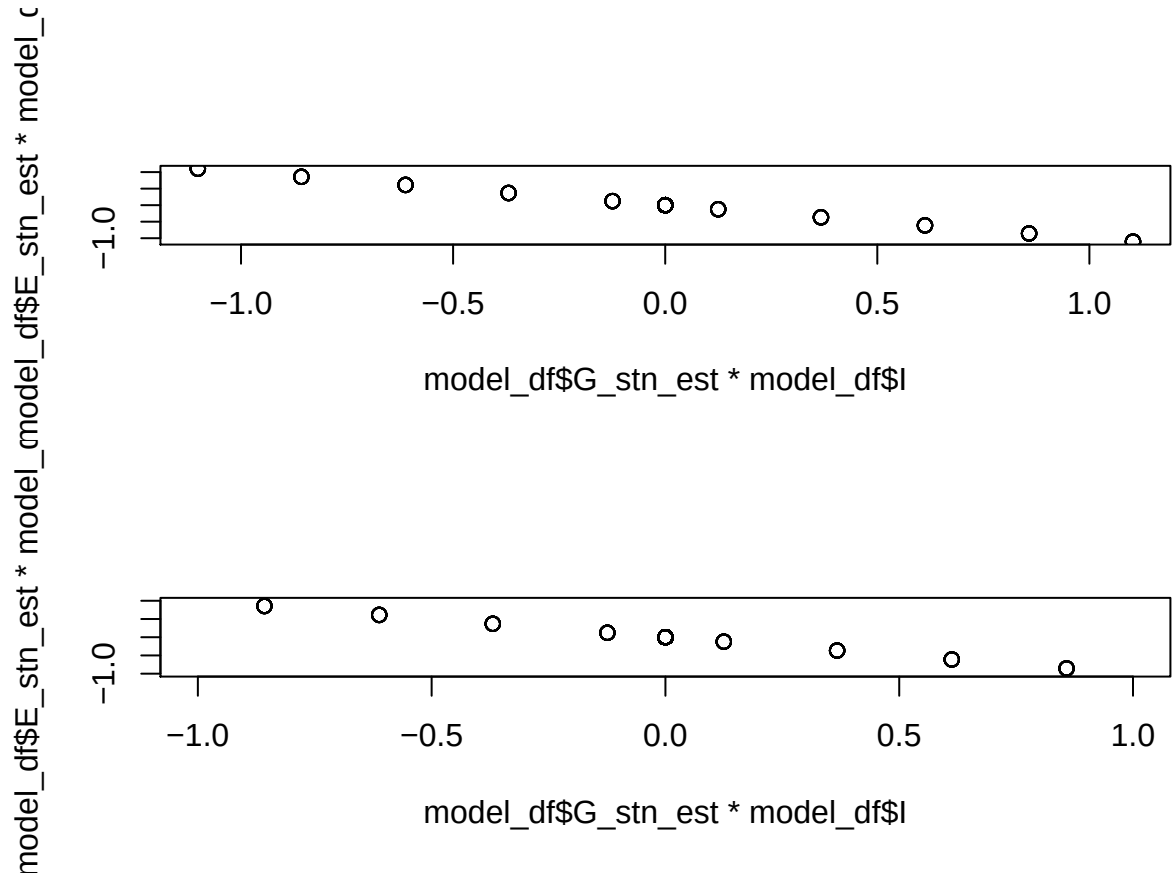
TO DO: check to code the loops as written in the equations and make sure it gives the same answer as what I calculated here

```
head(model_df)
```

```
##   GE_factor E  G int GE_true G_true E_true mean_true int_true GE_stn_true
## 1     G10E1 1 10   0       9    4.5    4.5         0        0    2.204541
## 2     G10E1 1 10   0       9    4.5    4.5         0        0    2.204541
## 3     G10E1 1 10   0       9    4.5    4.5         0        0    2.204541
## 4     G10E1 1 10   0       9    4.5    4.5         0        0    2.204541
## 5     G10E1 1 10   0       9    4.5    4.5         0        0    2.204541
## 6     G10E1 1 10   0       9    4.5    4.5         0        0    2.204541
##   G_stn_true E_stn_true mean_stn_true int_stn_true             e phenotype
## 1    1.10227    1.10227             0            0  0.0251070399  2.229648
## 2    1.10227    1.10227             0            0  0.0100089224  2.214550
## 3    1.10227    1.10227             0            0 -0.0040215584  2.200519
## 4    1.10227    1.10227             0            0 -0.0088955574  2.195645
## 5    1.10227    1.10227             0            0  0.0024205489  2.206961
## 6    1.10227    1.10227             0            0 -0.0002390923  2.204302
##   phenotype_stn G_stn_est E_stn_est GE_stn_est mean_stn_est  int_stn_est
## 1      2.228813  1.102784  1.101539   2.204857 1.212113e-18 0.0005341392
## 2      2.213718  1.102784  1.101539   2.204857 1.212113e-18 0.0005341392
## 3      2.199691  1.102784  1.101539   2.204857 1.212113e-18 0.0005341392
## 4      2.194818  1.102784  1.101539   2.204857 1.212113e-18 0.0005341392
## 5      2.206132  1.102784  1.101539   2.204857 1.212113e-18 0.0005341392
## 6      2.203473  1.102784  1.101539   2.204857 1.212113e-18 0.0005341392
```

```
V_G_SS = sum((model_df$G_stn_est-model_df$mean_stn_est)^2)
V_E_SS = sum((model_df$E_stn_est-model_df$mean_stn_est)^2)
V_GE_SS = sum(model_df$int_stn_est^2)
V_error = sum((model_df$phenotype_stn - model_df$GE_stn_est)^2)

model_df$I = model_df$E==model_df$G

# Covariance pattern (ignore the 0,0 points)
par(mfrow=c(2,1))
```

```
plot(model_df$G_stn_est*model_df$I, model_df$E_stn_est*model_df$I)
plot(model_df$G_stn_est*model_df$I, model_df$E_stn_est*model_df$I, xlim=c(-1,1), ylim=c(-1,1))
```




```
V_Cov_GE <-  nrow(model_df)/sum(model_df$I)*
  sum((model_df$G_stn_est-model_df$mean_stn_est)*(model_df$E_stn_est-model_df$mean_stn_est)*model_df$I)

SS <- round(rbind(V_G_SS, V_E_SS, V_GE_SS, V_Cov_GE, V_error),2)
omega2 <- round(abs(SS)/sum(abs(SS)),2)
data.frame(SS, abs(SS), omega2)
```

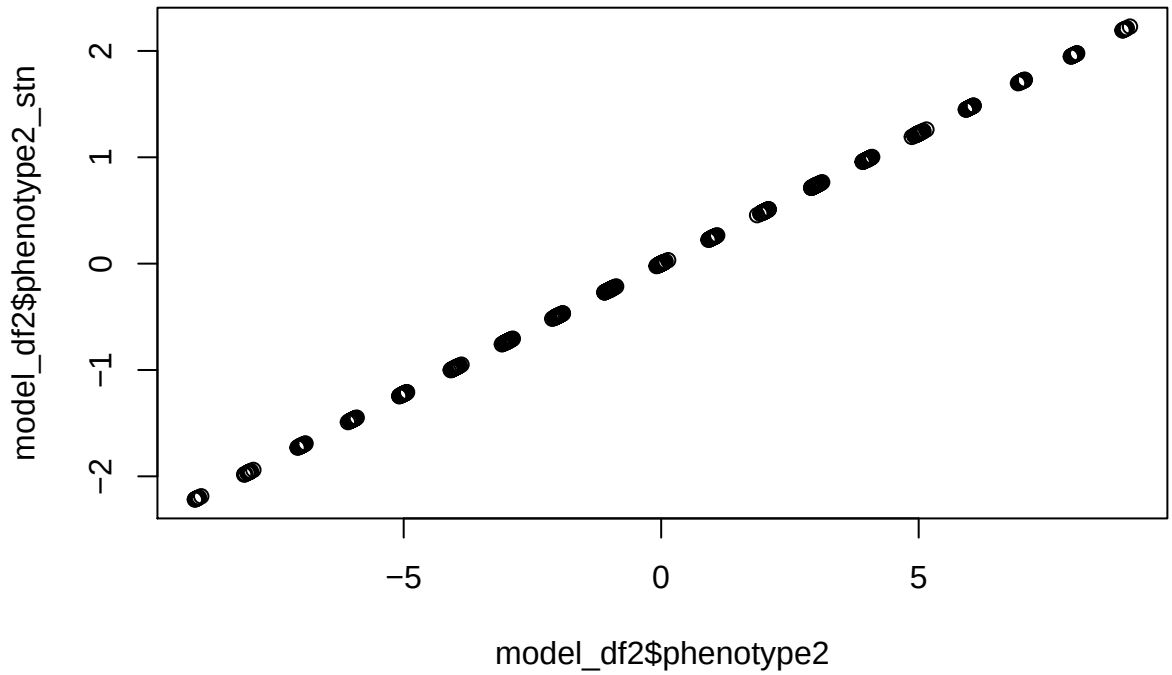
```
##                SS abs.SS. omega2
## V_G_SS     495.33  495.33   0.33
## V_E_SS     494.66  494.66   0.33
## V_GE_SS      0.01    0.01   0.00
## V_Cov_GE -494.99  494.99   0.33
## V_error      0.09    0.09   0.00
```

Step 7: pretend we start with noisy empirical data

Let's back transform the noisy data, then go through the steps and see what happens

```
# what we did to standardize: model_df$GE_stn_true <- (model_df$GE_true - mean(GE_true_means))/sd(GE_tr
model_df2 <- model_df[,1:3]
model_df2$phenotype2 <- model_df$phenotype*sd(GE_true_means)+mean(GE_true_means) #backtransform
```

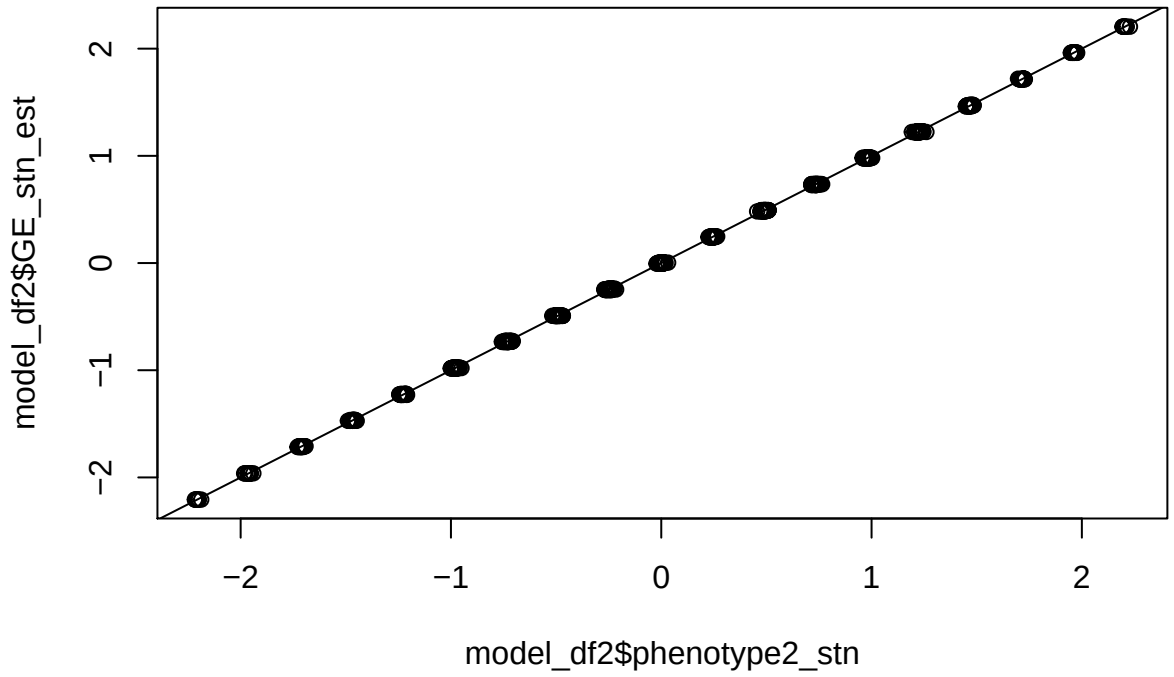
```r
# Step A: standardize by mean(GE_means) and sd(GE_means)
phen_GE_obs_means <- tapply(model_df2$phenotype2, model_df2$GE_factor, mean)

model_df2$phenotype2_stn <- (model_df2$phenotype2-mean(phen_GE_obs_means))/sd(phen_GE_obs_means)

plot(model_df2$phenotype2, model_df2$phenotype2_stn) # straight line check
```




```r
# Step B: calculate observed G_means and E_means and interaction
    G_stn_est <- data.frame(G=1:n_genotypes, G_stn_est=tapply(model_df2$phenotype2_stn, model_df2$G, mea
    E_stn_est <- data.frame(E=1:n_genotypes , E_stn_est=tapply(model_df2$phenotype2_stn, model_df2$E, me

    GE_stn_est_means <- tapply(model_df2$phenotype2_stn, model_df2$GE_factor, mean)
    GE_stn_est_means_df <- data.frame(GE_factor=names(GE_stn_est_means) , GE_stn_est=GE_stn_est_means)

    model_dfa <- merge(model_df2,G_stn_est)
    model_dfb <- merge(model_dfa,E_stn_est)
    model_dfc <- merge(model_dfb, GE_stn_est_means_df)
    head(model_dfc)
```

```
##   GE_factor E  G phenotype2 phenotype2_stn G_stn_est E_stn_est GE_stn_est
## 1     G10E1 1 10   8.983582       2.199691  1.102784  1.101539   2.204857
## 2     G10E1 1 10   9.102499       2.228813  1.102784  1.101539   2.204857
## 3     G10E1 1 10   9.040861       2.213718  1.102784  1.101539   2.204857
## 4     G10E1 1 10   8.974309       2.197420  1.102784  1.101539   2.204857
## 5     G10E1 1 10   8.957046       2.193193  1.102784  1.101539   2.204857
## 6     G10E1 1 10   8.997669       2.203141  1.102784  1.101539   2.204857
```

```r
    model_df2 <- model_dfc

    plot(model_df2$phenotype2_stn, model_df2$GE_stn_est)
    abline(0,1) # looks good
```




```
    model_df2$mean_stn_est <- mean(model_df2$phenotype2_stn)

    # Calculate interaction
    model_df2$int_stn_est <- model_df2$mean_stn_est + model_df2$GE_stn_est -
                         model_df2$G_stn_est -   model_df2$E_stn_est
```

Step 8: Compare true values to estimated values

```
head(model_df)
```

```
##   GE_factor E  G int GE_true G_true E_true mean_true int_true GE_stn_true
## 1     G10E1 1 10   0       9    4.5    4.5         0        0    2.204541
## 2     G10E1 1 10   0       9    4.5    4.5         0        0    2.204541
## 3     G10E1 1 10   0       9    4.5    4.5         0        0    2.204541
## 4     G10E1 1 10   0       9    4.5    4.5         0        0    2.204541
## 5     G10E1 1 10   0       9    4.5    4.5         0        0    2.204541
## 6     G10E1 1 10   0       9    4.5    4.5         0        0    2.204541
##   G_stn_true E_stn_true mean_stn_true int_stn_true             e phenotype
## 1    1.10227    1.10227             0            0  0.0251070399  2.229648
## 2    1.10227    1.10227             0            0  0.0100089224  2.214550
## 3    1.10227    1.10227             0            0 -0.0040215584  2.200519
## 4    1.10227    1.10227             0            0 -0.0088955574  2.195645
## 5    1.10227    1.10227             0            0  0.0024205489  2.206961
## 6    1.10227    1.10227             0            0 -0.0002390923  2.204302
##   phenotype_stn G_stn_est E_stn_est GE_stn_est mean_stn_est  int_stn_est     I
## 1      2.228813  1.102784  1.101539   2.204857 1.212113e-18 0.0005341392 FALSE
## 2      2.213718  1.102784  1.101539   2.204857 1.212113e-18 0.0005341392 FALSE
## 3      2.199691  1.102784  1.101539   2.204857 1.212113e-18 0.0005341392 FALSE
## 4      2.194818  1.102784  1.101539   2.204857 1.212113e-18 0.0005341392 FALSE
## 5      2.206132  1.102784  1.101539   2.204857 1.212113e-18 0.0005341392 FALSE
## 6      2.203473  1.102784  1.101539   2.204857 1.212113e-18 0.0005341392 FALSE
```

```r
(true_int <- mean(abs(model_df$int_stn_true)))
```

```
## [1] 5.440093e-17
```

```r
# Although we call this "true_int", when int=0 this should be 0
# note this is a shortcut that only works with equal sample sizes

(obs_int_sim <- mean(abs(model_df$int_stn_est)))
```

```
## [1] 0.002285848
```

```r
# when int=0, this will increase as the within-population mean gets less accurate

(obs_int_emp <- mean(abs(model_df2$int_stn_est)))
```

```
## [1] 0.002285848
```

Drop the mic.