9. Appendices

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Generating Data and Models

The data generating model used was from Appendix 3 of Bowden et al (ref); the relevant section describing their model is reproduced below:

"...

$$U_i = \sum_{j=1}^{J} \phi_j G_{ij} + \epsilon_i^U \tag{1}$$

$$X_i = \sum_{j=1}^{J} \gamma_j G_{ij} + U_i + \epsilon_i^X \tag{2}$$

$$Y_i = \sum_{j=1}^{J} \alpha_j G_{ij} + \beta X_i + U_i + \epsilon_i^Y \tag{3}$$

for participants indexed by $i = 1, ..., N$, and genetic instruments indexed by $j = 1, ..., J$.

The error terms ϵ_i^U, ϵ_i^X and ϵ_i^Y were each drawn independently from standard normal distributions. The genetic effects on the exposure j are drawn from a uniform distribution between 0.03 and 0.1. Pleiotropic effects α_j and ϕ_j were set to zero if the genetic instrument was a valid instrumental variable. Otherwise (with probability 0.1, 0.2, or 0.3):

1. In Scenario 1 (balanced pleiotropy, InSIDE satisfied), the α_j parameter was drawn from a uniform distribution between −0.2 and 0.2.

2. In Scenario 2 (directional pleiotropy, InSIDE satisfied), the α_j parameter was drawn from a uniform distribution between 0 and 0.2.

3. In Scenario 3 (directional pleiotropy, InSIDE not satisfied), the ϕ_j parameter was drawn from a uniform distribution between −0.2 and 0.2.

The causal effect of the exposure on the outcome was either $\beta X = 0$ (null causal effect) or $\beta X = 0.1$ (positive causal effect). A total of 10 000 simulated datasets were generated for sample sizes of N = 10 000 and 20 [sic] participants. Only the summary data, that is genetic associations with the exposure and with the outcome and their standard errors as estimated by univariate regression on the genetic instruments in turn, were used by the analysis methods. In the two-sample setting, data were generated on 2N participants, and genetic associations with the exposure were estimated in the first N participants, and genetic associations with the outcome in the second N participants."[1]

To reproduce this model, code was written in R to generate the relevant participant level data. First, a function (`simulate_MR_data`) was written which included parameters specified by Bowden et al, and also to allow testing of data simulation:

```r
# Define function to create data generating model
# Arguments/default values based on Bowden et al
simulate_MR_data <- function(n_participants = as.integer(),
                             n_instruments = as.integer(),
                             n_datasets = as.integer(),
                             prop_invalid = 0.1,
                             causal_effect = TRUE,
                             balanced_pleio = TRUE,
                             InSIDE_satisfied = TRUE,
                             rand_error = TRUE,      # remove random errors, for testing
                             two_sample = TRUE,      # 1- or 2-sample MR toggle, for testing
                             beta_val = 0.1,         # size of causal effect
                             allele_freq_min = 0.01, # frequency of effect allele
                             allele_freq_max = 0.99,
                             gamma_min = 0.03,       # size of pleiotropic effects on exposure
                             gamma_max = 0.1,
                             alpha_min = -0.2,       # size of pleiotropic effects on outcome
                             alpha_max = 0.2,
                             phi_min = -0.2,         # size of additional pleiotropic effects
                             phi_max = 0.2){         # when InSIDE not satisfied



  # Initialise blank lists to receive datasets for
  # each of:
  #     U (vector: unmeasured confounding exposures per participant),
  #     X (vector: exposure:outcome associations estimated per participant)
  #     Y (vector: gene:outcome association estimated per participant),
  #     G (Matrices: Genotype data)
  #
  #     gamma (vector: pleiotropic effects of each instrument on exposure)
  #     alpha (vector: pleiotropic effects of each instrument on outcome)
  #     phi (vector: additional pleiotropic effects of each instrument when InSIDE
  #     assumption not satisfied)
  U_list <- list()
  X_list <- list()
  Y_list <- list()
  G_X_list <- list()
  G_Y_list <- list()

  gamma_list <- list()
  alpha_list <- list()
  phi_list <- list()
  beta_list <- list()
  #prop_invalid_list <- list()

  n_participants_list <- list()
  n_instruments_list <- list()
  n_datasets_list <- list()
  prop_invalid_list <- list()
  causal_effect_list <- list()
  balanced_pleio_list <- list()
  InSIDE_satisfied_list <- list()
  rand_error_list <- list()
  two_sample_list <- list()
  beta_val_list <- list()
  allele_freq_min_list <- list()
  allele_freq_max_list <- list()
  gamma_min_list <- list()
  gamma_max_list <- list()
  alpha_min_list <- list()
  alpha_max_list <- list()
```

```r
phi_min_list <- list()
phi_max_list <- list()


# --- Assign features common to all datasets --- #

beta <- if_else(causal_effect == TRUE, # size of causal effect
                beta_val,
                0)

# create vector of participant indices for 1st n participants
# i.e. participants used for estimating gene:exposure coefficient
sample_1_ref <- 1:n_participants


# Default is to estimate gene:outcome coefficient from different sample
# to gene:exposure coefficient (i.e. simulating 2-sample MR)
# two_sample == FALSE toggles to single sample for testing simulation

ifelse(two_sample == FALSE,
       sample_2_ref <- sample_1_ref, # 1 sample MR
       sample_2_ref <- (n_participants+1):(2*n_participants)) # 2 sample MR

# --- Create separate datasets --- #

# Create N datasets by simulating genotype matrices with
# 1 row per participant, 1 column per genetic instrument
# Use these to estimate U, X + Y

for(n in 1:n_datasets){

  # Create error terms for U, X + Y per participant,
  # each drawn from standard normal distribution
  # unless random error turned off (for testing)

  ifelse(rand_error == TRUE,
         U_epsilon_vect <- rnorm(n = 2 * n_participants),
         U_epsilon_vect <- rep(0, 2 * n_participants))

  ifelse(rand_error == TRUE,
         X_epsilon_vect <- rnorm(n = n_participants),
         X_epsilon_vect <- rep(0, n_participants))

  ifelse(rand_error == TRUE,
         Y_epsilon_vect <- rnorm(n = n_participants),
         Y_epsilon_vect <- rep(0, n_participants))


  # --- Create matrix of genotypes --- #

  # 0 = reference, i.e. zero effect alleles,
  # 1 = 1 effect allele, 2 = 2 effect alleles
  # Probability of effect allele set per dataset
  # for each instrument, default value set at
  # random between 0.01-0.99 (i.e. both effect +
  # reference are common alleles)
  allele_freq_vect <- runif(n = n_instruments,
                            min = allele_freq_min,
                            max = allele_freq_max)



  # Assign genotypes by sampling from binomial distribution
  # twice (as two alleles) per participant with probability
  # equal to frequency of effect allele
  # Create twice as many genotypes as participants in sample
  # to simulate 2 sample MR, i.e. first half used to estimate
  # Gene:Exposure, second half used to estimate Gene:Outcome


  # Matrix where columns are instruments, rows are participants
  # Values 0, 1 or 2
  G_mat <- matrix(rbinom(n = 2 * n_participants * n_instruments,
                         size = 2,
                         prob = rep(allele_freq_vect, 2 * n_participants)),
                  nrow = 2 * n_participants,
                  ncol = n_instruments,
                  byrow = TRUE)


  # --- Set characteristics for each genetic instrument --- #

  # Set which instruments invalid, 0 = valid, 1 = invalid
  invalid_instrument_vect <- rbinom(n = n_instruments,
                                    size = 1,
                                    prob = prop_invalid)


  # Set genetic effects of each instrument on the exposure,
  # drawn from uniform distribution, min/max as per Bowden
  # et al
  gamma_vect <- runif(n = n_instruments,
                      min = gamma_min,
                      max = gamma_max)


  # Set pleiotropic effects on outcome, Scenarios and
  # min/max from Bowden et al
  alpha_vect <- double() # Pleiotropic effects of instruments on outcome
  phi_vect <- double() # Pleiotropic effects of confounders on outcome

  for(j in 1:n_instruments){
    ifelse(invalid_instrument_vect[j] == 0, # alpha = 0 if valid
           alpha_vect[j] <- 0,
           ifelse(balanced_pleio == TRUE,
                    alpha_vect[j] <- runif(n = n_instruments, # balanced
                                           min = alpha_min,
                                           max = alpha_max),
                    alpha_vect[j] <- runif(n = n_instruments, # directional
                                           min = 0,
                                           max = alpha_max)
             )
    )

    # Assign default phi = 0 unless directional pleiotropy &
    # InSIDE assumption not satisfied & genetic instrument invalid
    if(balanced_pleio == FALSE & InSIDE_satisfied == FALSE){
      ifelse(invalid_instrument_vect[j] == 0,
             phi_vect[j] <- 0,
             phi_vect[j] <- runif(n = 1,
                                  min = phi_min,
                                  max = phi_max)
      )

    }
    else{
      phi_vect[j] <- 0
    }
  }


  # --- Combine Gene matrix/parameters to recreate model --- #

  # Create vectors of estimates for U, X and Y per individual,
  # i.e. Ui, Xi and Yi. Uses matrix inner product operator " %*%"
  # https://stackoverflow.com/questions/22060515/the-r-operator
  # http://matrixmultiplication.xyz/


  Ui_vect <-  G_mat %*% phi_vect + U_epsilon_vect

  Xi_vect <-  G_mat[sample_1_ref, ] %*% gamma_vect +
    Ui_vect[sample_1_ref, ] +
    X_epsilon_vect

  Yi_vect <-  G_mat[sample_2_ref, ] %*% alpha_vect +
    beta * Xi_vect +
    Ui_vect[sample_2_ref, ] +
    Y_epsilon_vect


  # Add vectors of estimates from this dataset to lists of
  # estimates from all datasets
  U_list[[n]] <- Ui_vect

  X_list[[n]] <- Xi_vect

  Y_list[[n]] <- Yi_vect
```

```r
  G_X_list[[n]] <- G_mat[sample_1_ref, ]

  G_Y_list[[n]] <- G_mat[sample_2_ref, ]


  # Include actual parameters used in simulation for testing
  alpha_list[[n]] <- alpha_vect

  gamma_list[[n]] <- gamma_vect

  phi_list[[n]] <- phi_vect

  beta_list[[n]] <- beta

  #prop_invalid_list[[n]] <- prop_invalid


  n_participants_list[[n]] <- n_participants
  n_instruments_list[[n]] <- n_instruments
  n_datasets_list[[n]] <- n_datasets
  prop_invalid_list[[n]] <- prop_invalid
  causal_effect_list[[n]] <- causal_effect
  balanced_pleio_list[[n]] <- balanced_pleio
  InSIDE_satisfied_list[[n]] <- InSIDE_satisfied
  rand_error_list[[n]] <- rand_error
  two_sample_list[[n]] <- two_sample
  beta_val_list[[n]] <- beta_val
  allele_freq_min_list[[n]] <- allele_freq_min
  allele_freq_max_list[[n]] <- allele_freq_max
  gamma_min_list[[n]] <- gamma_min
  gamma_max_list[[n]] <- gamma_max
  alpha_min_list[[n]] <- alpha_min
  alpha_max_list[[n]] <- alpha_max
  phi_min_list[[n]] <- phi_min
  phi_max_list[[n]] <- phi_max

}

#     U (vector: unmeasured confounding exposures per participant),
#     X (vector: exposure:outcome associations estimated per participant)
#     Y (vector: gene:outcome association estimated per participant)


# --- Combine all outputs to return --- #

combined_list <- list(U = U_list,         # Estimates
                      X = X_list,
                      Y = Y_list,
                      G_X = G_X_list,     # Genotypes of 1st sample
                      G_Y = G_Y_list,     # Genotypes of 2nd sample

                      alpha = alpha_list, # Actual values for validating simulation
                      gamma = gamma_list,
                            phi = phi_list,
                            #beta = beta_list,
                            #prop_invalid = prop_invalid_list,

                            n_participants = n_participants_list, # Inputs
                            n_instruments = n_instruments_list,
                            n_datasets = n_datasets_list,
                            prop_invalid = prop_invalid_list,
                            causal_effect = causal_effect_list,
                            balanced_pleio = balanced_pleio_list,
                            InSIDE_satisfied = InSIDE_satisfied_list,
                            rand_error = rand_error_list,
                            two_sample = two_sample_list,
                            beta_val = beta_val_list,
                            allele_freq_min = allele_freq_min_list,
                            allele_freq_max = allele_freq_max_list,
                            gamma_min = gamma_min_list,
                            gamma_max = gamma_max_list,
                            alpha_min = alpha_min_list,
                            alpha_max = alpha_max_list,
                            phi_min = phi_min_list,
                            phi_max = phi_max_list
  )

  return(combined_list)
}
```

This initial simulation function generated data in the following format:

```
# Check data produced in expected format
set.seed(1701)
test_data_sim <- simulate_MR_data(n_participants = 1000,
                                  n_instruments = 25,
                                  n_datasets = 2,
                                  prop_invalid = 0.3,
                                  rand_error = FALSE,
                                  causal_effect = TRUE,
                                  balanced_pleio = TRUE,
                                  InSIDE_satisfied = TRUE)

str(test_data_sim)
```

```
## List of 26
##  $ U               :List of 2
##   ..$ : num [1:2000, 1] 0 0 0 0 0 0 0 0 0 0 ...
##   ..$ : num [1:2000, 1] 0 0 0 0 0 0 0 0 0 0 ...
##  $ X               :List of 2
##   ..$ : num [1:1000, 1] 1.12 1.59 1.76 1.49 1.56 ...
##   ..$ : num [1:1000, 1] 1.84 1.7 1.6 1.66 1.5 ...
##  $ Y               :List of 2
##   ..$ : num [1:1000, 1] -0.24 -0.311 -0.393 -0.227 -0.1 ...
##   ..$ : num [1:1000, 1] -0.872 -0.901 -0.772 -0.999 -0.477 ...
##  $ G_X             :List of 2
##   ..$ : int [1:1000, 1:25] 0 1 1 1 1 0 0 0 0 0 ...
##   ..$ : int [1:1000, 1:25] 1 2 1 2 2 2 2 2 2 2 ...
##  $ G_Y            :List of 2
##   ..$ : int [1:1000, 1:25] 0 1 1 0 1 0 0 0 0 0 ...
##   ..$ : int [1:1000, 1:25] 2 2 2 2 1 2 1 1 2 1 ...
##  $ alpha          :List of 2
##   ..$ : num [1:25] -0.106 0 -0.121 0 0 ...
##   ..$ : num [1:25] 0 0 -0.0786 0 0 ...
##  $ gamma          :List of 2
##   ..$ : num [1:25] 0.0902 0.0878 0.08 0.0832 0.084 ...
##   ..$ : num [1:25] 0.0374 0.0721 0.0975 0.085 0.0322 ...
##  $ phi            :List of 2
##   ..$ : num [1:25] 0 0 0 0 0 0 0 0 0 0 ...
##   ..$ : num [1:25] 0 0 0 0 0 0 0 0 0 0 ...
##  $ n_participants  :List of 2
##   ..$ : num 1000
##   ..$ : num 1000
##  $ n_instruments   :List of 2
##   ..$ : num 25
##   ..$ : num 25
##  $ n_datasets      :List of 2
##   ..$ : num 2
##   ..$ : num 2
##  $ prop_invalid    :List of 2
##   ..$ : num 0.3
##   ..$ : num 0.3
##  $ causal_effect   :List of 2
##   ..$ : logi TRUE
##   ..$ : logi TRUE
##  $ balanced_pleio  :List of 2
##   ..$ : logi TRUE
##   ..$ : logi TRUE
##  $ InSIDE_satisfied:List of 2
##   ..$ : logi TRUE
##   ..$ : logi TRUE
##  $ rand_error      :List of 2
##   ..$ : logi FALSE
##   ..$ : logi FALSE
##  $ two_sample      :List of 2
##   ..$ : logi TRUE
##   ..$ : logi TRUE
##  $ beta_val        :List of 2
##   ..$ : num 0.1
##   ..$ : num 0.1
##  $ allele_freq_min :List of 2
##   ..$ : num 0.01
##   ..$ : num 0.01
##  $ allele_freq_max :List of 2
##   ..$ : num 0.99
##   ..$ : num 0.99
##  $ gamma_min       :List of 2
##   ..$ : num 0.03
##   ..$ : num 0.03
##  $ gamma_max       :List of 2
##   ..$ : num 0.1
##   ..$ : num 0.1
##  $ alpha_min       :List of 2
##   ..$ : num -0.2
##   ..$ : num -0.2
##  $ alpha_max       :List of 2
##   ..$ : num 0.2
##   ..$ : num 0.2
##  $ phi_min         :List of 2
##   ..$ : num -0.2
##   ..$ : num -0.2
##  $ phi_max         :List of 2
##   ..$ : num 0.2
##   ..$ : num 0.2
```

A function (`extract_models`) was then written to create linear models from each dataset generated as per Bowden et al:

```
# Create plotting tibble with Mean/SD X + Y grouped by
# Dataset + instrument
extract_models <- function(sim){

  output_list <- list()

  # Create linear models per dataset to get coefficients
  # for gene:exposure association (coeff_G_X) and gene:outcome
  # association (coeff_G_Y)
  for(dataset in 1:length(sim$X)){

    X <- sim$X[[dataset]]
    Y <- sim$Y[[dataset]]
    Instruments_X <- sim$G_X[[dataset]]
    Instruments_Y <- sim$G_Y[[dataset]]

    alpha <- sim$alpha[[dataset]]
    gamma <- sim$gamma[[dataset]]
    phi <- sim$phi[[dataset]]
    beta <- sim$beta_val[[dataset]]
    prop_invalid <- sim$prop_invalid[[dataset]]


    # Model for gene:exposure
    X_lm <- lm(X ~ 0 + Instruments_X)
    coeff_G_X_vect <- coef(summary(X_lm))[1:(ncol(Instruments_X)), 1]
    SE_coeff_G_X_vect <- coef(summary(X_lm))[1:(ncol(Instruments_X)), 2]

    # Model for gene:outcome
    Y_lm <- lm(Y ~ 0 + Instruments_Y)
    coeff_G_Y_vect <- coef(summary(Y_lm))[1:(ncol(Instruments_Y)), 1]
    SE_coeff_G_Y_vect <- coef(summary(Y_lm))[1:(ncol(Instruments_Y)), 2]

    output_list[[dataset]] <- as_tibble(list(dataset = dataset,
                                         Instrument = c(1:ncol(Instruments_X)),
                                         coeff_G_X = coeff_G_X_vect,
                                                      coeff_G_X_SE = SE_coeff_G_X_vect,
                                                      gamma = gamma,
                                                      coeff_G_Y = coeff_G_Y_vect,
                                                      coeff_G_Y_SE = SE_coeff_G_Y_vect,
                                                      alpha = alpha,
                                                      phi = phi,
                                                      beta = beta,
                                                      prop_invalid = prop_invalid),
                                                .name_repair = "unique")
  }

  return(output_list)

}
```

These models generated estimates of the coefficient of gene:exposure association (`coeff_G_X`), coefficient of gene:outcome association (`coeff_G_Y`), and the relevant standard errors of these estimates. The values of parameters inputted were also returned to aid in further testing of data/model generation, i.e. actual gene:exposure associations (`gamma`), pleiotropic effects of invalid instruments (`alpha`), additional pleiotropic effects when InSIDE assumption not satified (`phi`), causal effect of exposure on outcome (`beta`) and the proportion of invalid genetic instruments with pleiotropic effects on the outcome (`prop_invalid`).

```
test_extract_model <- extract_models(test_data_sim)

summary(test_extract_model[[1]])
```

```
##     dataset    Instrument   coeff_G_X        coeff_G_X_SE
##  Min.   :1   Min.   : 1   Min.   :0.03006   Min.   :1.591e-16
##  1st Qu.:1   1st Qu.: 7   1st Qu.:0.03791   1st Qu.:1.702e-16
##  Median :1   Median :13   Median :0.05578   Median :1.847e-16
##  Mean   :1   Mean   :13   Mean   :0.06018   Mean   :2.346e-16
##  3rd Qu.:1   3rd Qu.:19   3rd Qu.:0.07998   3rd Qu.:2.441e-16
##  Max.   :1   Max.   :25   Max.   :0.09140   Max.   :7.259e-16
##      gamma            coeff_G_Y           coeff_G_Y_SE          alpha
##  Min.   :0.03006   Min.   :-0.1188256   Min.   :0.0009824   Min.   :-0.120669
##  1st Qu.:0.03791   1st Qu.: 0.0006676   1st Qu.:0.0010520   1st Qu.: 0.000000
##  Median :0.05578   Median : 0.0031161   Median :0.0011837   Median : 0.000000
##  Mean   :0.06018   Mean   :-0.0047291   Mean   :0.0014576   Mean   :-0.008692
##  3rd Qu.:0.07998   3rd Qu.: 0.0068099   3rd Qu.:0.0015114   3rd Qu.: 0.000000
##  Max.   :0.09140   Max.   : 0.1356693   Max.   :0.0040567   Max.   : 0.133513
##       phi         beta      prop_invalid
##  Min.   :0   Min.   :0.1   Min.   :0.3
##  1st Qu.:0   1st Qu.:0.1   1st Qu.:0.3
##  Median :0   Median :0.1   Median :0.3
##  Mean   :0   Mean   :0.1   Mean   :0.3
##  3rd Qu.:0   3rd Qu.:0.1   3rd Qu.:0.3
##  Max.   :0   Max.   :0.1   Max.   :0.3
```

Testing Generation of Data and Models

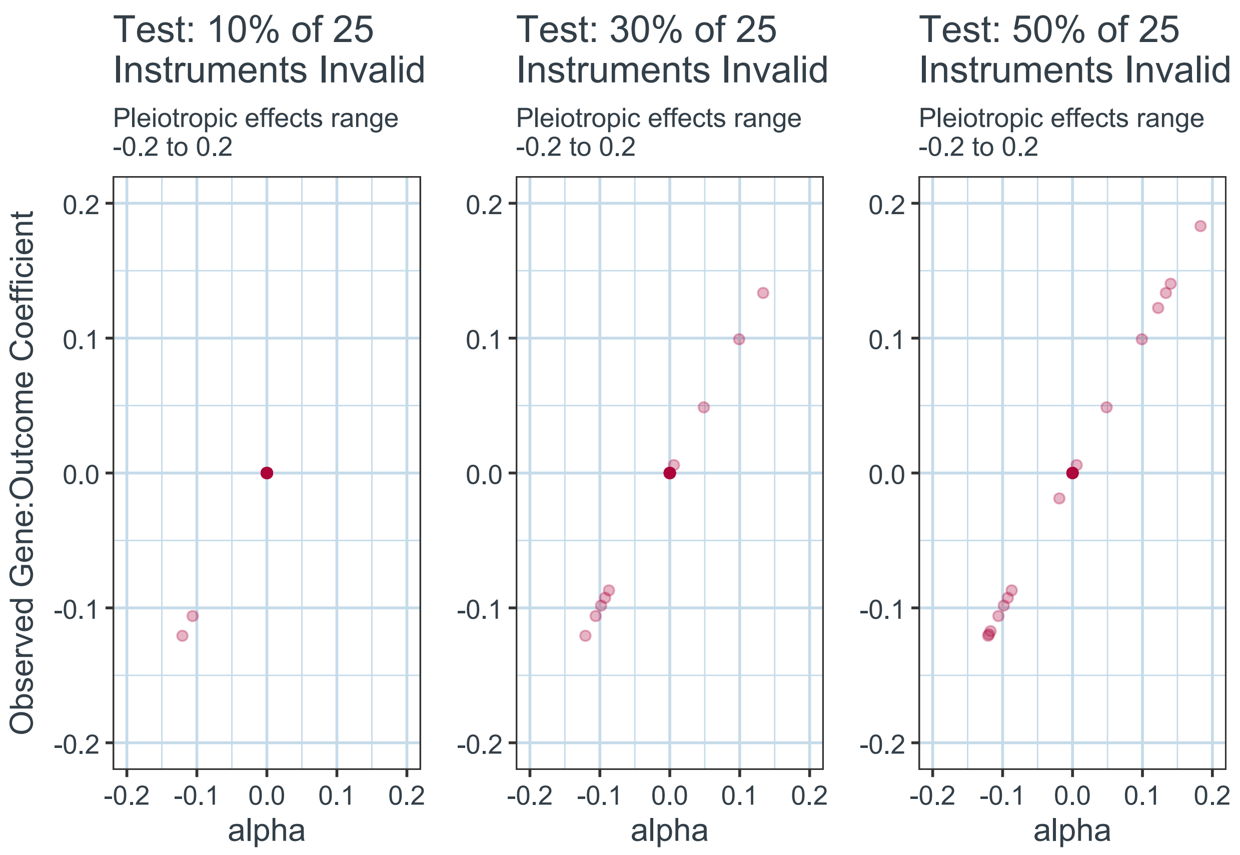
A series of test plots were used to verify that data were simulated as intended under the various conditions specified by input parameters. Test plots were not created for the parameters `n_participants`, n_instruments or n_datasets, as the functioning of these parameters could be readily inferred from the structure of the datasets outputted, as above.

The prop_invalid parameter specifies the proportion of invalid genetic instruments simulated, i.e. the proportion of genetic instruments affecting the outcome via direct/pleiotropic effects, and thus not solely via the exposure of interest. If simulated correctly, increasing the value of prop_invalid should increase the number of instruments with pleiotropic effects, i.e. instruments with alpha =/= 0. With random error terms set to 0 and no causal effect present (i.e. rand_error = FALSE and causal_effect = FALSE), the estimated gene:outcome coefficient estimated using any given instrument will equal the pleiotropic effects of that instrument (i.e. coeff_G_Y = alpha), and therefore will only be non-zero for invalid instruments with non-zero pleiotropic effects on the outcome . Plotting coeff_G_Y against alpha for simulated data with no causal effect or random error should therefore yield a graph where

- For valid instruments: gene:outcome coefficient = alpha = 0
- For invalid instruments: gene:outcome coefficient = alpha =/= 0, with values spread uniformly between alpha_min and alpha_max

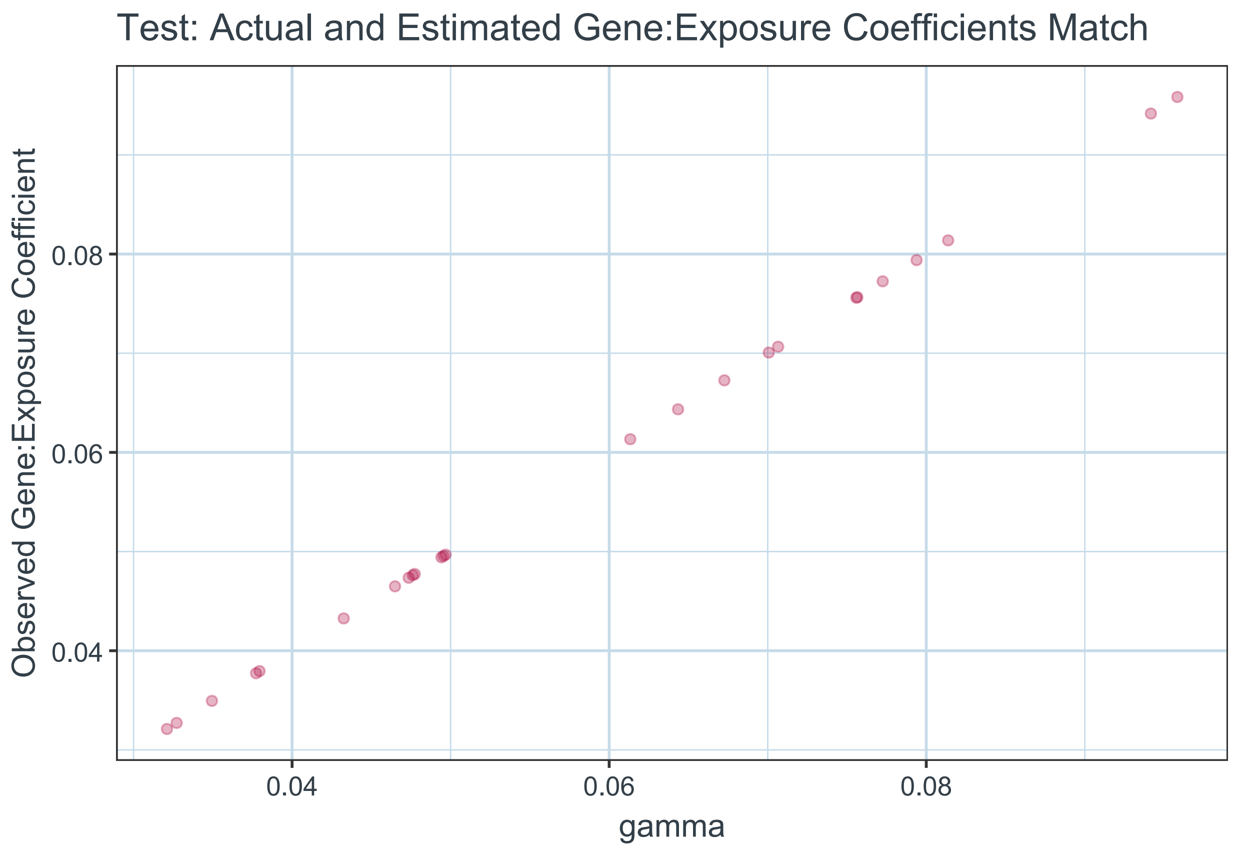
```r
# Check altering proportion of invalid instruments alters
# proportion of instruments displaying pleiotropic effects
# N.B. cluster around alpha = 0 represents valid instruments with
# no pleiotropic effects

# 10% of instruments invalid
set.seed(1701)
sim_test_data_inval_0.1 <- simulate_MR_data(n_participants = 1000,
                                            n_instruments = 25,
                                            n_datasets = 1,
                                            prop_invalid = 0.1,
                                            rand_error = FALSE,
                                            causal_effect = FALSE,
                                            alpha_min = -0.2,
                                            alpha_max = 0.2)

# 30% of instruments invalid
set.seed(1701)
sim_test_data_inval_0.3 <- simulate_MR_data(n_participants = 1000,
                                            n_instruments = 25,
                                            n_datasets = 1,
                                            prop_invalid = 0.3,
                                            rand_error = FALSE,
                                            causal_effect = FALSE,
                                            alpha_max = 0.2)

# 50% of instruments invalid
set.seed(1701)
sim_test_data_inval_0.5 <- simulate_MR_data(n_participants = 1000,
                                            n_instruments = 25,
                                            n_datasets = 1,
                                            prop_invalid = 0.5,
                                            rand_error = FALSE,
                                            causal_effect = FALSE,
                                            alpha_min = -0.2,
                                            alpha_max = 0.2)
```

```r
test_plot_tib_inval_0.1 <- extract_models(sim_test_data_inval_0.1)[[1]]
test_plot_tib_inval_0.3 <- extract_models(sim_test_data_inval_0.3)[[1]]
test_plot_tib_inval_0.5 <- extract_models(sim_test_data_inval_0.5)[[1]]

test_plot_inval_0.1 <- test_plot_tib_inval_0.1 %>%
  select(alpha, coeff_G_Y) %>%
  plot_template() +
  geom_point(colour = edin_bright_red_hex, alpha = 0.3) +
  aes(x = alpha, y = coeff_G_Y ) +
  scale_y_continuous(limits = c(-0.2, 0.2)) +
  scale_x_continuous(limits = c(-0.2, 0.2)) +
  labs(y = "Observed Gene:Outcome Coefficient",
       title = "Test: 10% of 25 \nInstruments Invalid",
       subtitle = "Pleiotropic effects range \n-0.2 to 0.2")

test_plot_inval_0.3 <- test_plot_tib_inval_0.3 %>%
  select(alpha, coeff_G_Y) %>%
  plot_template() +
  geom_point(colour = edin_bright_red_hex, alpha = 0.3) +
  aes(x = alpha, y = coeff_G_Y ) +
  scale_y_continuous(limits = c(-0.2, 0.2)) +
  scale_x_continuous(limits = c(-0.2, 0.2)) +
  labs(y = "Observed Gene:Outcome Coefficient",
       title = "Test: 30% of 25 \nInstruments Invalid",
       subtitle = "Pleiotropic effects range \n-0.2 to 0.2") +
  theme(axis.title.y = element_blank())

test_plot_inval_0.5 <- test_plot_tib_inval_0.5 %>%
  select(alpha, coeff_G_Y) %>%
  plot_template() +
  geom_point(colour = edin_bright_red_hex, alpha = 0.3) +
  aes(x = alpha, y = coeff_G_Y ) +
  scale_y_continuous(limits = c(-0.2, 0.2)) +
  scale_x_continuous(limits = c(-0.2, 0.2)) +
  labs(y = "Observed Gene:Outcome Coefficient",
       title = "Test: 50% of 25 \nInstruments Invalid",
       subtitle = "Pleiotropic effects range \n-0.2 to 0.2") +
  theme(axis.title.y = element_blank())

plot_grid(test_plot_inval_0.1,
          test_plot_inval_0.3,
          test_plot_inval_0.5,
          ncol = 3,
          rel_widths = c(1.1, 1, 1))
```



Similarly, with random error terms set to 0 (`rand_error = FALSE`) and no causal effect present (`causal_effect = FALSE`), gene:exposure coefficients estimated for each instrument should exactly match the actual values simulated, i.e. `coeff_G_X = gamma` for all instruments:

```r
# Check observed gene:exposure coefficients for each instrument
# (coeff_G_X) approximate true values (gamma) when a causal effect
# is present & a large number of participants are included
set.seed(1701)
sim_test_data_gamma_1 <- simulate_MR_data(n_participants = 100,
                                          n_instruments = 25,
                                          n_datasets = 1,
                                          prop_invalid = 0.1,
                                          causal_effect = FALSE,
                                          rand_error = FALSE,
                                          balanced_pleio = TRUE,
                                          InSIDE_satisfied = TRUE)


test_plot_tib_gamma_1 <- extract_models(sim_test_data_gamma_1)[[1]]

test_plot_tib_gamma_1 %>%
  select(gamma, coeff_G_X) %>%
  plot_template() +
  geom_point(colour = edin_bright_red_hex, alpha = 0.3) +
  aes(x = gamma, y = coeff_G_X ) +
  labs(y = "Observed Gene:Exposure Coefficient",
       title = "Test: Actual and Estimated Gene:Exposure Coefficients Match")
```



For the next phase of testing, a function (`plot_GY_GX`) was written to plot the coefficients for gene:exposure versus gene:outcome as estimated using the previously created linear models:

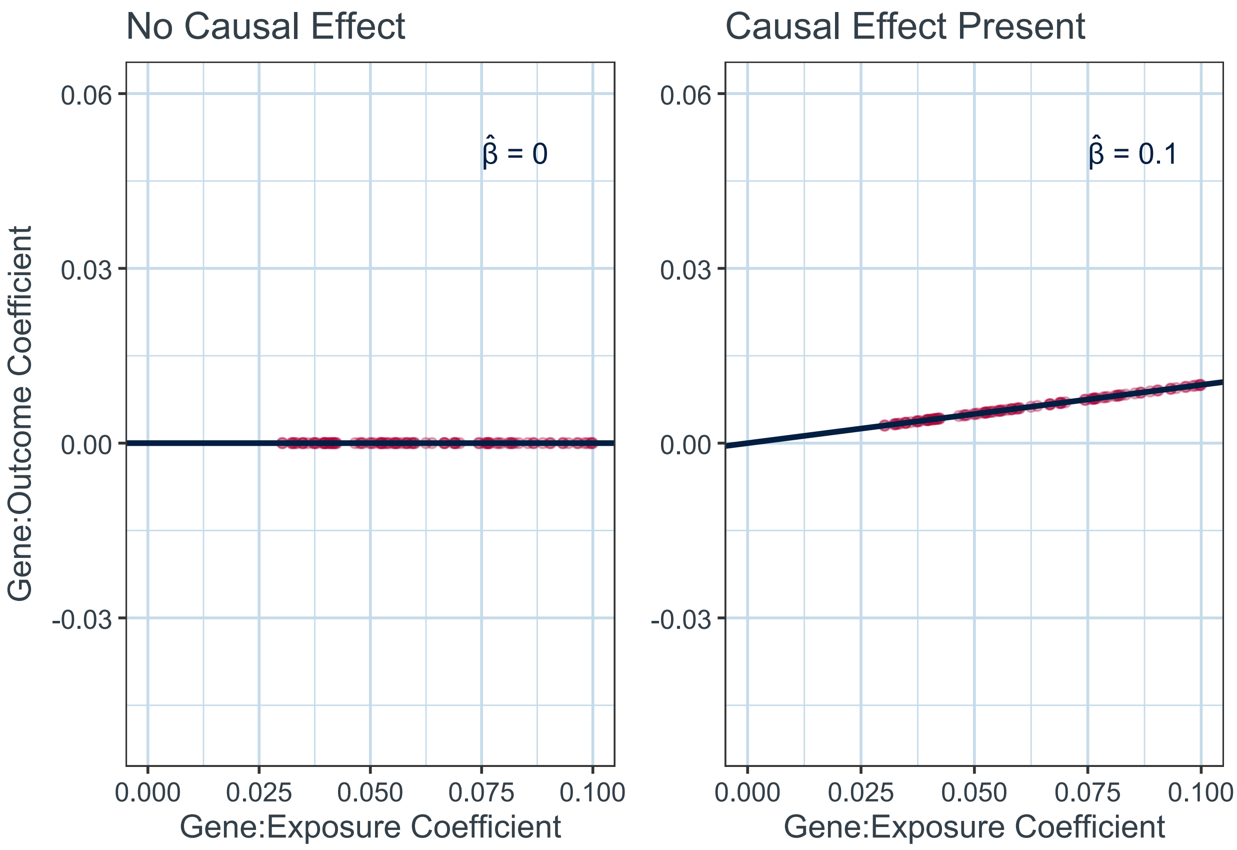
```
plot_GY_GX <- function(model_tib,
                       plot_title = as.character(NA),
                       x_min = 0,                    # set x-axis limits
                       x_max = 0.1,
                       y_min = -0.05,                # set x-axis limits
                       y_max = 0.06,
                       beta_x = 0.075,               # set beta-hat position
                       beta_y = 0.05,
                       hat_offset = 0.003
                       )
  {

  model_tib %>%
    mutate(Gradient = round(coefficients(lm(coeff_G_Y ~ 0 + coeff_G_X)[1], 5), digits = 2)) %>%
    plot_template() +
    aes(x = coeff_G_X, y = coeff_G_Y) +
    geom_point(colour = edin_bright_red_hex, alpha = 0.3) +
    geom_abline(aes(intercept = 0,
                    slope = Gradient),
                size = 1,
                colour = edin_uni_blue_hex) +
```

```r
    geom_text(aes(label = paste0("\U03B2 = ", as.character(Gradient))), #beta
              x = beta_x, # labels with gradient (causal effect estimate)
              y = beta_y,
              colour = edin_uni_blue_hex,
              hjust = 0,
              data = . %>% slice_head()# prevent over-printing
              ) +
    annotate("text",
             x = beta_x,      # add hat to beta
             y = beta_y + hat_offset,
             label = paste("\U02C6"),
             colour = edin_uni_blue_hex,
             hjust = -0.4,
             vjust = 0.9
             ) +
    labs(title = plot_title,
         x = "Gene:Exposure Coefficient",
         y = "Gene:Outcome Coefficient") +
    xlim(x_min, x_max) +
    ylim(y_min, y_max)

}
```

With random error terms set to 0 and no causal effect present, a graph of gene:exposure coefficients versus gene:outcome coefficients should be a straight line through the origin with gradient = 0; causal effect of β = 0.1 present (`beta_val = 0.1`, `causal_effect = TRUE`), the slope of a graph of gene:exposure coefficients versus gene:outcome coefficients from the same sample should be a straight line through the origin with gradient = 0.1:

```r
# No causal effect present
set.seed(1701)
sim_test_data_causal_0 <- simulate_MR_data(n_participants = 10000,
                                           n_instruments = 100,
                                           n_datasets = 1,
                                           prop_invalid = 0,
                                           causal_effect = FALSE,
                                           rand_error = FALSE)

test_plot_tib_causal_0 <- extract_models(sim_test_data_causal_0)[[1]]

test_plot_causal_0 <- plot_GY_GX(test_plot_tib_causal_0, plot_title = "No Causal Effect")

# Causal effect present
set.seed(1701)
sim_test_data_causal_1 <- simulate_MR_data(n_participants = 10000,
                                           n_instruments = 100,
                                           n_datasets = 1,
                                           prop_invalid = 0,
                                           beta_val = 0.1,
                                           causal_effect = TRUE,
                                           rand_error = FALSE,
                                           two_sample = FALSE)
```

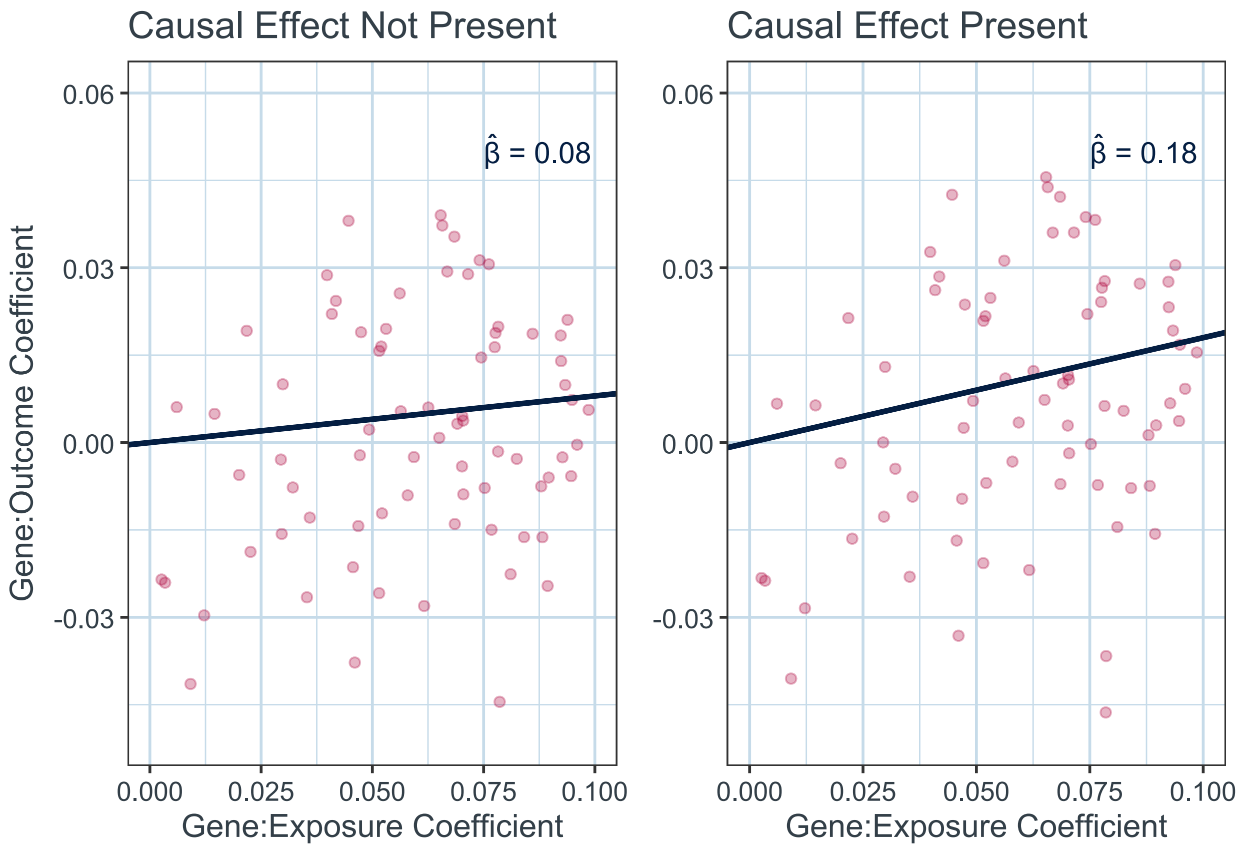
```r
test_plot_tib_causal_1 <- extract_models(sim_test_data_causal_1)[[1]]

test_plot_causal_1 <- plot_GY_GX(test_plot_tib_causal_1, plot_title = "Causal Effect Present")+
  theme(axis.title.y = element_blank())

plot_grid(test_plot_causal_0,
          test_plot_causal_1,
          ncol = 2,
          rel_widths = c(1.05, 1))
```



Re-plotting the same graphs with non-zero random error terms should produce similar graphs with Gaussian spread around lines passing through the origin with gradients of 0 and 0.1 for no causal effect and causal effect, respectively:

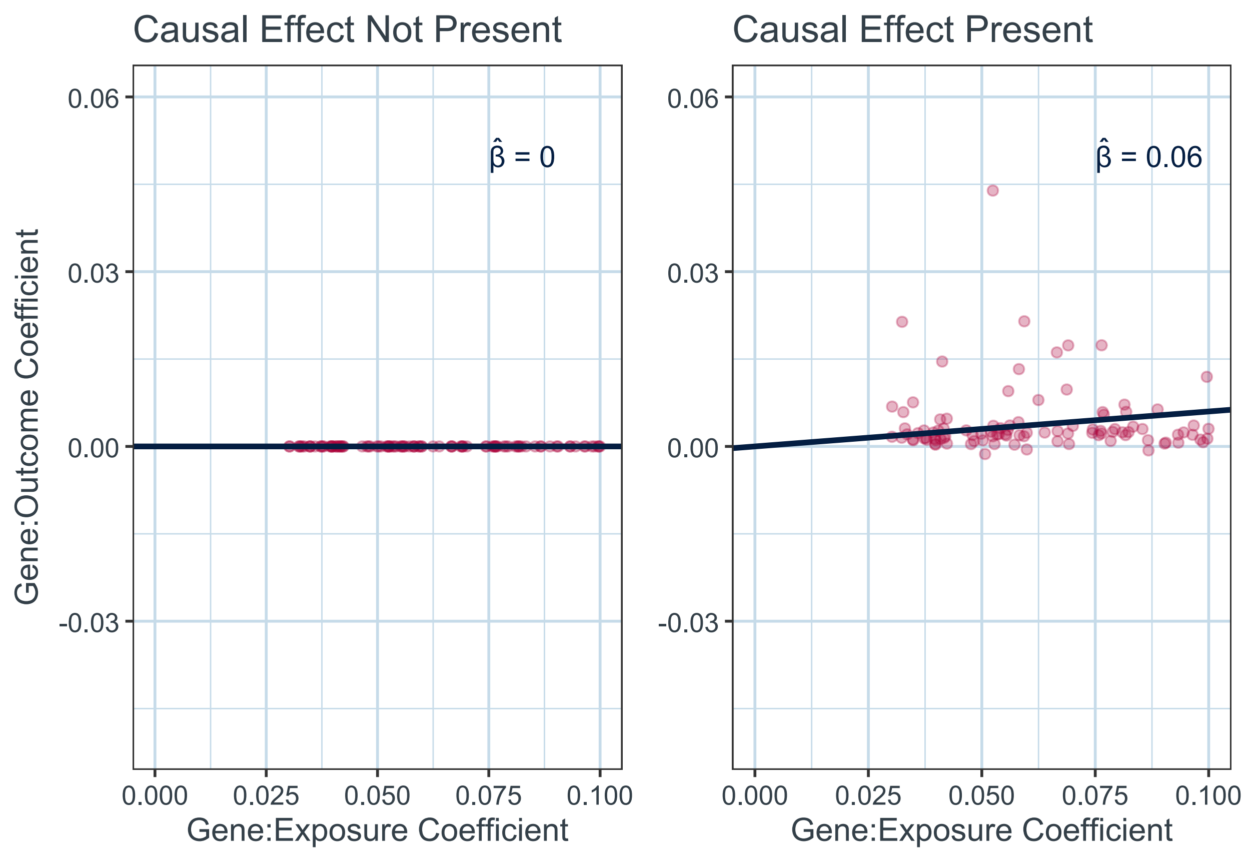
```r
# Causal effect not present
set.seed(1701)
sim_test_data_causal_0_errors <- simulate_MR_data(n_participants = 10000,
                                                  n_instruments = 100,
                                                  n_datasets = 1,
                                                  prop_invalid = 0,
                                                  causal_effect = FALSE,
                                                  rand_error = TRUE,
                                                  two_sample = FALSE)

test_plot_tib_causal_0_errors <- extract_models(sim_test_data_causal_0_errors)[[1]]
```

```
test_plot_causal_0_errors <- plot_GY_GX(test_plot_tib_causal_0_errors, plot_title = "Causal Effect Not I

# Causal effect present
set.seed(1701)
sim_test_data_causal_1_errors <- simulate_MR_data(n_participants = 10000,
                                                  n_instruments = 100,
                                                  n_datasets = 1,
                                                  prop_invalid = 0,
                                                  causal_effect = TRUE,
                                                  rand_error = TRUE,
                                                  two_sample = FALSE)

test_plot_tib_causal_1_errors <- extract_models(sim_test_data_causal_1_errors)[[1]]

test_plot_causal_1_errors <-  plot_GY_GX(test_plot_tib_causal_1_errors, plot_title = "Causal Effect Pres
  theme(axis.title.y = element_blank())

plot_grid(test_plot_causal_0_errors,
          test_plot_causal_1_errors,
          ncol = 2,
          rel_widths = c(1.05, 1))
```



Where gene:exposure coefficients and gene:outcome coefficients are estimated from two separate samples rather than one (i.e. simulating 2 sample MR), even with random error terms set to zero, error will be introduced into causal effect estimation through random sampling of different combinations of effect alleles. However, where a causal effect is not present, the effect estimated will consistently be zero regardless of the combinations of alleles sampled, so random error should not be introducted:

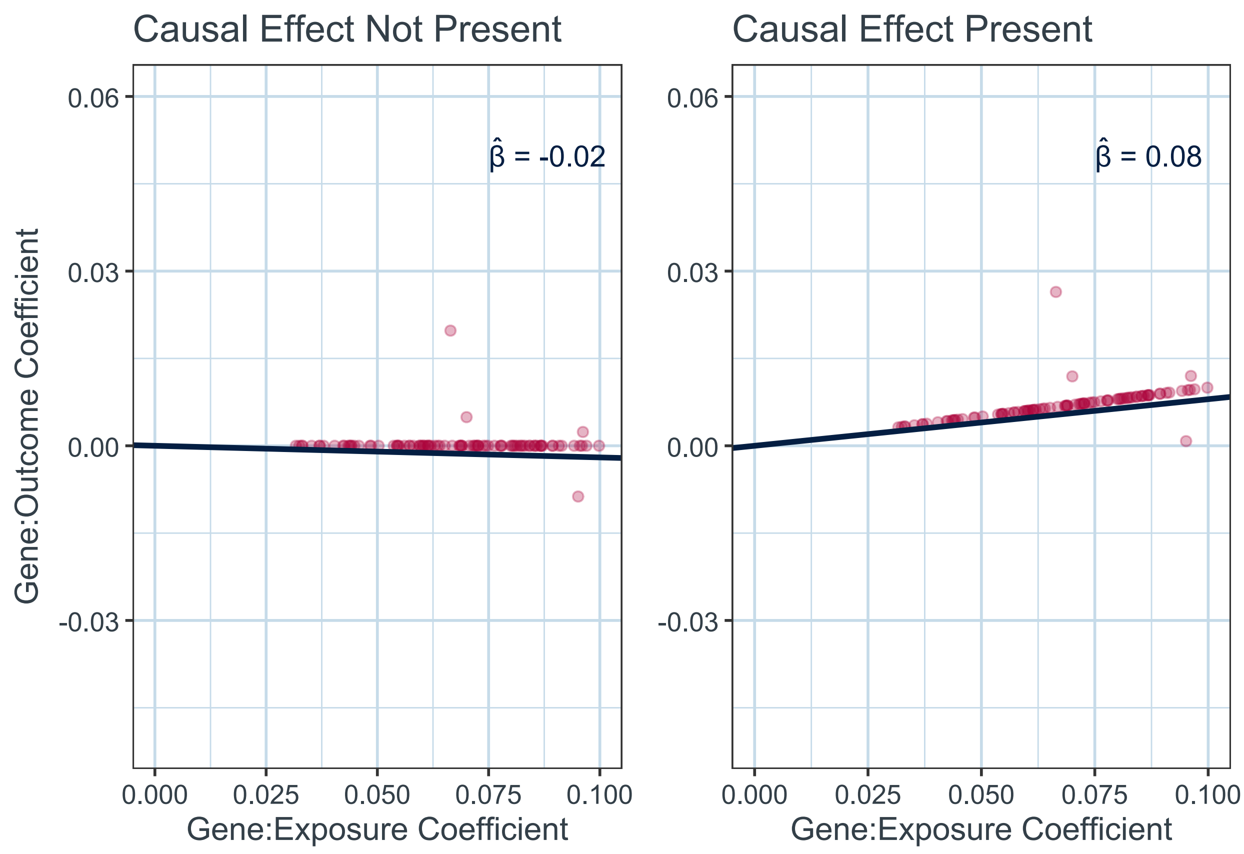
```
# Causal effect not present
set.seed(1701)
sim_test_data_causal_0_2SMR <- simulate_MR_data(n_participants = 10000,
                                                 n_instruments = 100,
                                                 n_datasets = 1,
                                                 prop_invalid = 0,
                                                 causal_effect = FALSE,
                                                 rand_error = FALSE,
                                                 two_sample = TRUE)

test_plot_tib_causal_0_2SMR <- extract_models(sim_test_data_causal_0_2SMR)[[1]]

test_plot_causal_0_2SMR <- plot_GY_GX(test_plot_tib_causal_0_2SMR, plot_title = "Causal Effect Not Prese

# Causal effect present
set.seed(1701)
sim_test_data_causal_1_2SMR <- simulate_MR_data(n_participants = 10000,
                                                 n_instruments = 100,
                                                 n_datasets = 1,
                                                 prop_invalid = 0,
                                                 causal_effect = TRUE,
                                                 rand_error = FALSE,
                                                 two_sample = TRUE)

test_plot_tib_causal_1_2SMR <- extract_models(sim_test_data_causal_1_2SMR)[[1]]

test_plot_causal_1_2SMR <- plot_GY_GX(test_plot_tib_causal_1_2SMR, plot_title = "Causal Effect Present")
  theme(axis.title.y = element_blank())

plot_grid(test_plot_causal_0_2SMR,
          test_plot_causal_1_2SMR,
          ncol = 2,
          rel_widths = c(1.05, 1))
```



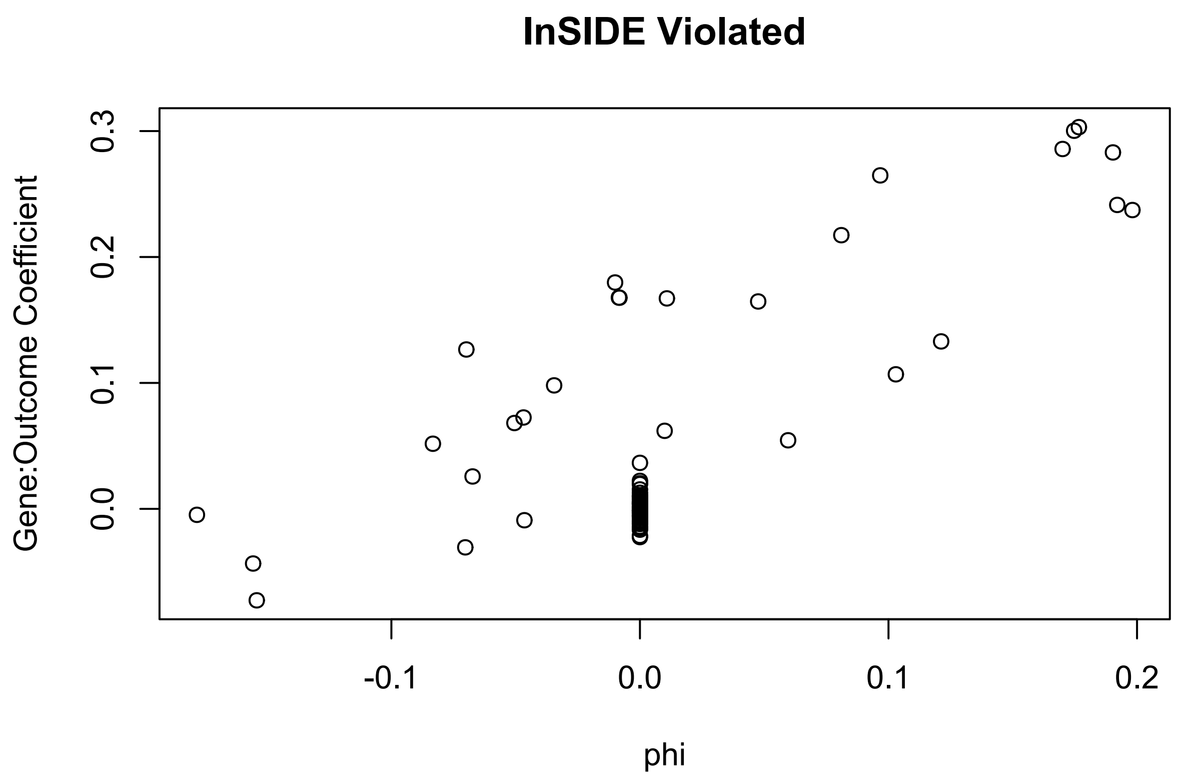
Where invalid instruments are present (i.e. `prop_invalid =\= 0`)

```r
# Causal effect not present
set.seed(1701)
sim_test_data_causal_0_inval <- simulate_MR_data(n_participants = 10000,
                                                 n_instruments = 100,
                                                 n_datasets = 1,
                                                 prop_invalid = 0.1,
                                                 causal_effect = FALSE,
                                                 rand_error = FALSE,
                                                 two_sample = FALSE)

test_plot_tib_causal_0_inval <- extract_models(sim_test_data_causal_0_inval)[[1]]

test_plot_causal_0_inval <- plot_GY_GX(test_plot_tib_causal_0_inval, plot_title = "Causal Effect Not Pre

# Causal effect present
set.seed(1701)
sim_test_data_causal_1_inval <- simulate_MR_data(n_participants = 10000,
                                                 n_instruments = 100,
                                                 n_datasets = 1,
                                                 prop_invalid = 0.1,
                                                 causal_effect = TRUE,
                                                 rand_error = FALSE,
                                                 two_sample = FALSE)
```

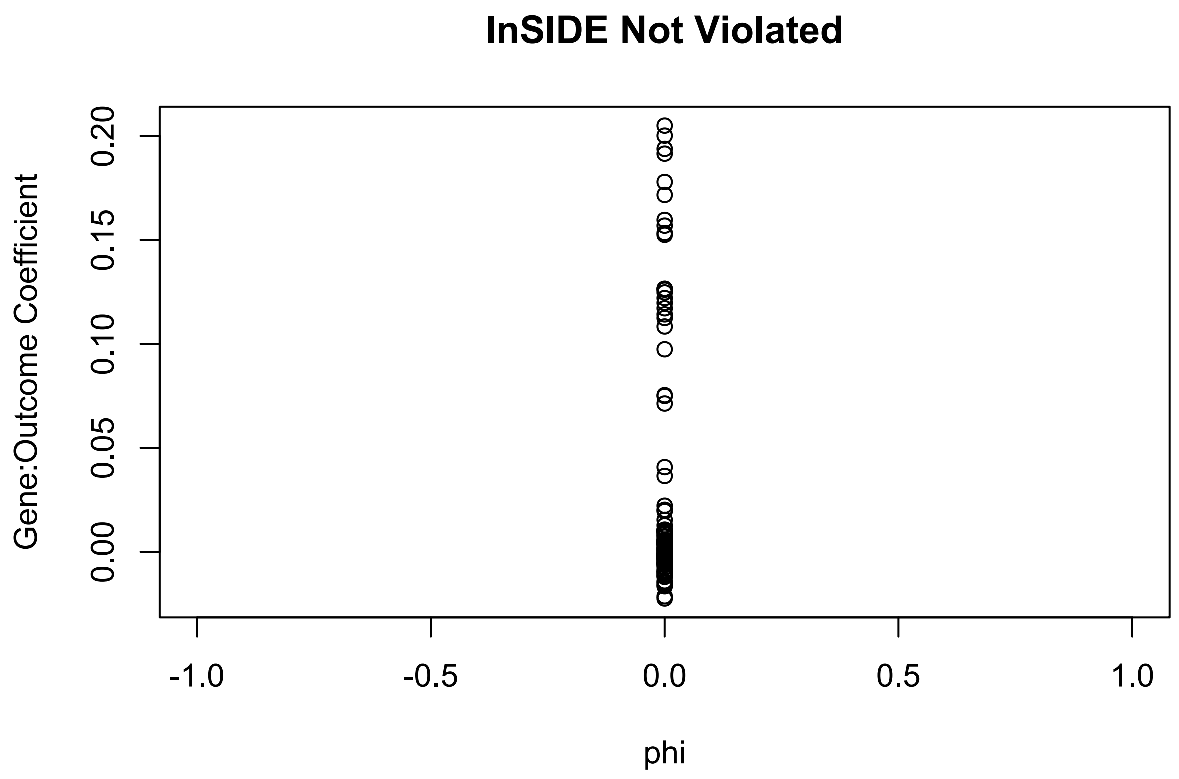
```
test_plot_tib_causal_1_inval <- extract_models(sim_test_data_causal_1_inval)[[1]]

test_plot_causal_1_inval <- plot_GY_GX(test_plot_tib_causal_1_inval, plot_title = "Causal Effect Presen
  theme(axis.title.y = element_blank())

plot_grid(test_plot_causal_0_inval,
          test_plot_causal_1_inval,
          ncol = 2,
          rel_widths = c(1.05, 1))
```



```
# Check violating InSIDE assumption results in distorted
# estimation of pleiotropic effects
# N.B. cluster around alpha = 0 represents valid instruments with
# no pleiotropic effects
set.seed(1701)
sim_test_data_phi_T <- simulate_MR_data(n_participants = 100000,
                                        n_instruments = 100,
                                        n_datasets = 1,
                                        prop_invalid = 0.3,
                                        causal_effect = FALSE,
                                        balanced_pleio = FALSE,
                                        InSIDE_satisfied = FALSE)

set.seed(1701)
sim_test_data_phi_F <- simulate_MR_data(n_participants = 100000,
                                        n_instruments = 100,
                                        n_datasets = 1,
                                        prop_invalid = 0.3,
                                        causal_effect = FALSE,
                                        balanced_pleio = FALSE,
                                        InSIDE_satisfied = TRUE)


test_plot_tib_phi_T <- extract_models(sim_test_data_phi_T)[[1]]
test_plot_tib_phi_F <- extract_models(sim_test_data_phi_F)[[1]]

test_plot_tib_phi_T %>%
  select(phi, coeff_G_Y) %>%
  plot(.,
       main = "InSIDE Violated",
       ylab = "Gene:Outcome Coefficient")
```



```
test_plot_tib_phi_F %>%
  select(phi, coeff_G_Y) %>%
  plot(.,
       main = "InSIDE Not Violated",
       ylab = "Gene:Outcome Coefficient")
```



```
#phi on y, not alpha
```

Appendix C: Citation Search Strategy

1. Bowden J, Smith GD, Haycock PC, Burgess S. Consistent Estimation in Mendelian Randomization with Some Invalid Instruments Using a Weighted Median Estimator. Genetic Epidemiology [Internet]. 2016 Apr [cited 2024 Oct 22];40(4):304. Available from: https://pmc.ncbi.nlm.nih.gov/articles/PMC4849733/