Untitled

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Exploratory Multiverse Analysis (EMA)

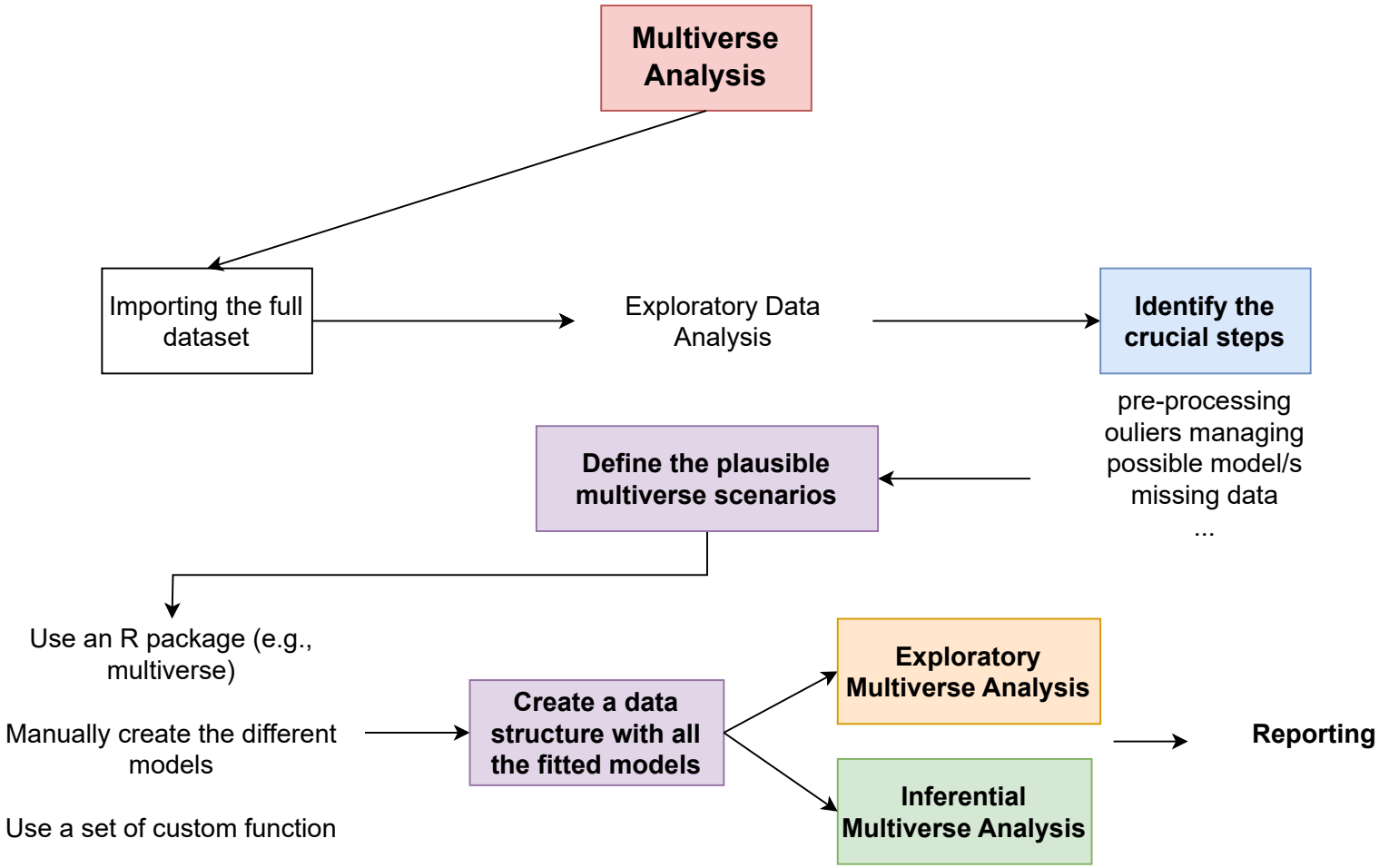
An example, Statistics and Math Anxiety

McCaughey et al. (2022) explored the relationship between self-efficacy anxiety sensitivity and perfectionism would be related to math/statistics anxiety controlling for gender, university program, and education level.

We used the dataset available at https://osf.io/nzhq6.

We are going to do crazy stuff with this dataset that are not related to the original paper and research question! :)

The big picture



Importing

We did a little bit of pre-processing. The `ms_anxiety.rds` file contains the cleaned version of the original dataset.

```
dat <- readRDS(here("data/ms_anxiety.rds"))
vars <- names(dat)
ys <- vars[grepl("^stat.anx|^math", vars)]
ys
##  [1] "stat.anx.tc"   "stat.anx.i"    "stat.anx.ah"   "stat.anx.ws"
##  [5] "stat.anx.fst"  "stat.anx.sc"   "math.anx"      "stat.anx.TOT"
##  [9] "stat.anx.ANX"  "stat.anx.FEEL"

xs <- vars[!vars %in% ys]
xs
## [1] "self.efficacy"   "asi"             "frost.com"
## [4] "frost.da"        "faculty"         "program.type"
## [7] "gender.category"
```

Exploring

Let's see the type of variables of the dataset:

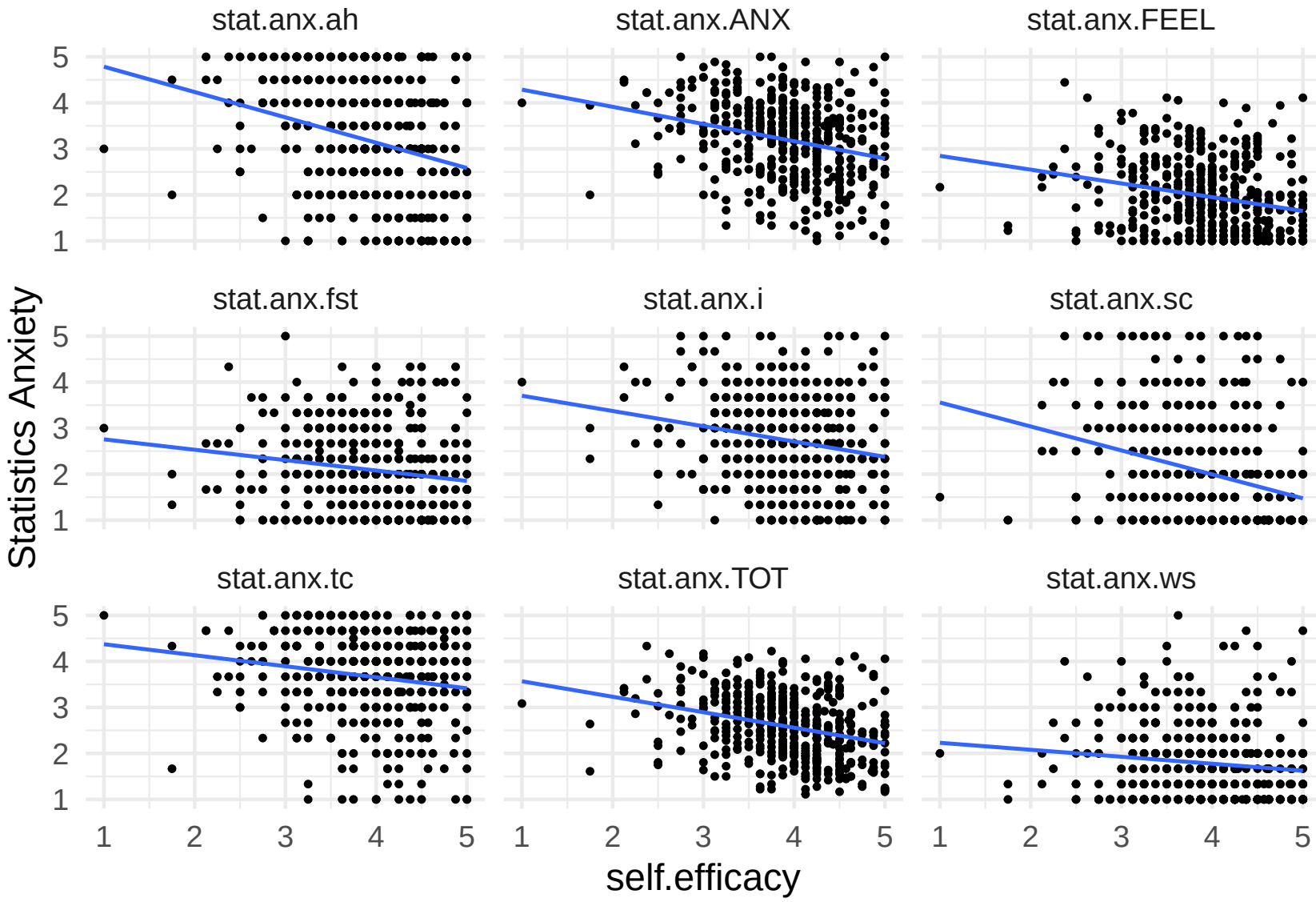
```
sapply(dat[ys], class)
##   stat.anx.tc    stat.anx.i   stat.anx.ah   stat.anx.ws  stat.anx.fst
##     "numeric"     "numeric"     "numeric"     "numeric"     "numeric"
##   stat.anx.sc      math.anx  stat.anx.TOT  stat.anx.ANX stat.anx.FEEL
##     "numeric"     "numeric"     "numeric"     "numeric"     "numeric"
sapply(dat[xs], class)
##   self.efficacy             asi       frost.com        frost.da
##       "numeric"       "numeric"       "numeric"       "numeric"
##         faculty    program.type gender.category
##        "factor"        "factor"        "factor"
```

Main research questions

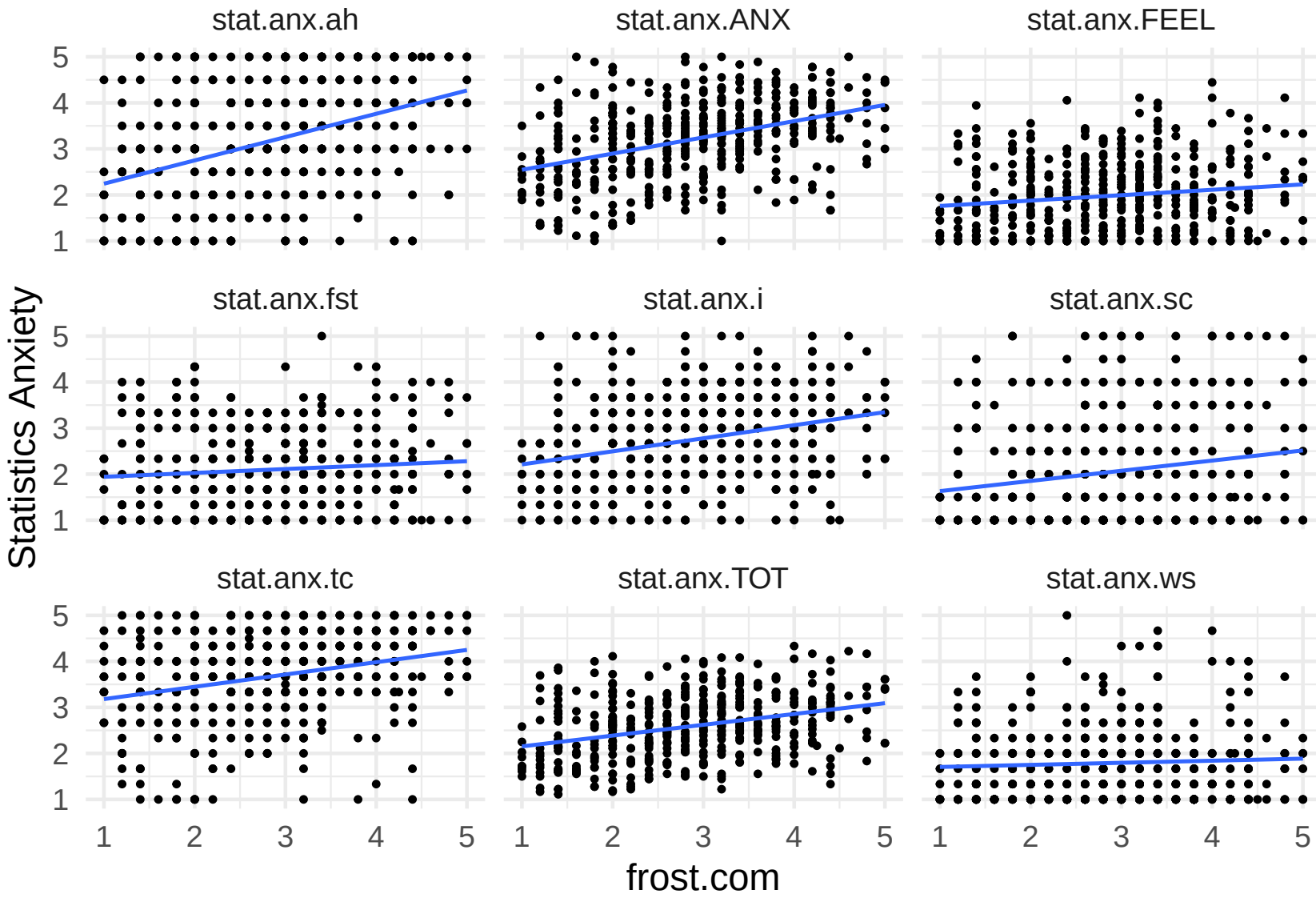
The main idea of the authors is predicting **math** and **statistics** anxiety with self-efficacy and perfectionism. In particular they pre-registered (see https://osf.io/b3g7s):

1. self-efficacy will be negatively related to math/statistics anxiety
2. anxiety sensitivity will be positively related to math/statistics anxiety.
3. self-critical perfectionism will be positively related to math/statistics anxiety.
4. the relationships described above will remain when statistically adjusting for gender, university program (arts vs. science) and student status (undergraduate vs. graduate).

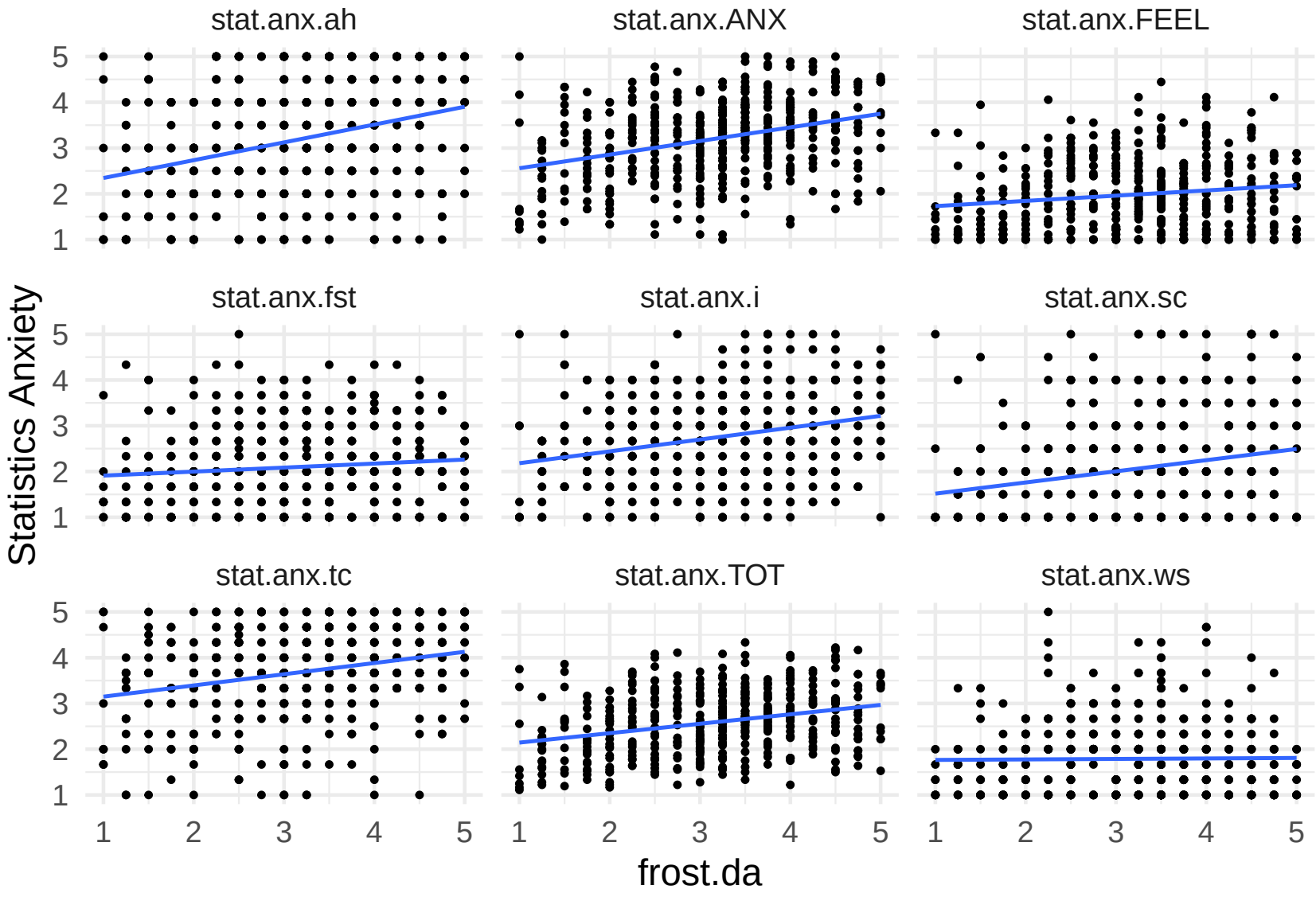
Exploring the relationships



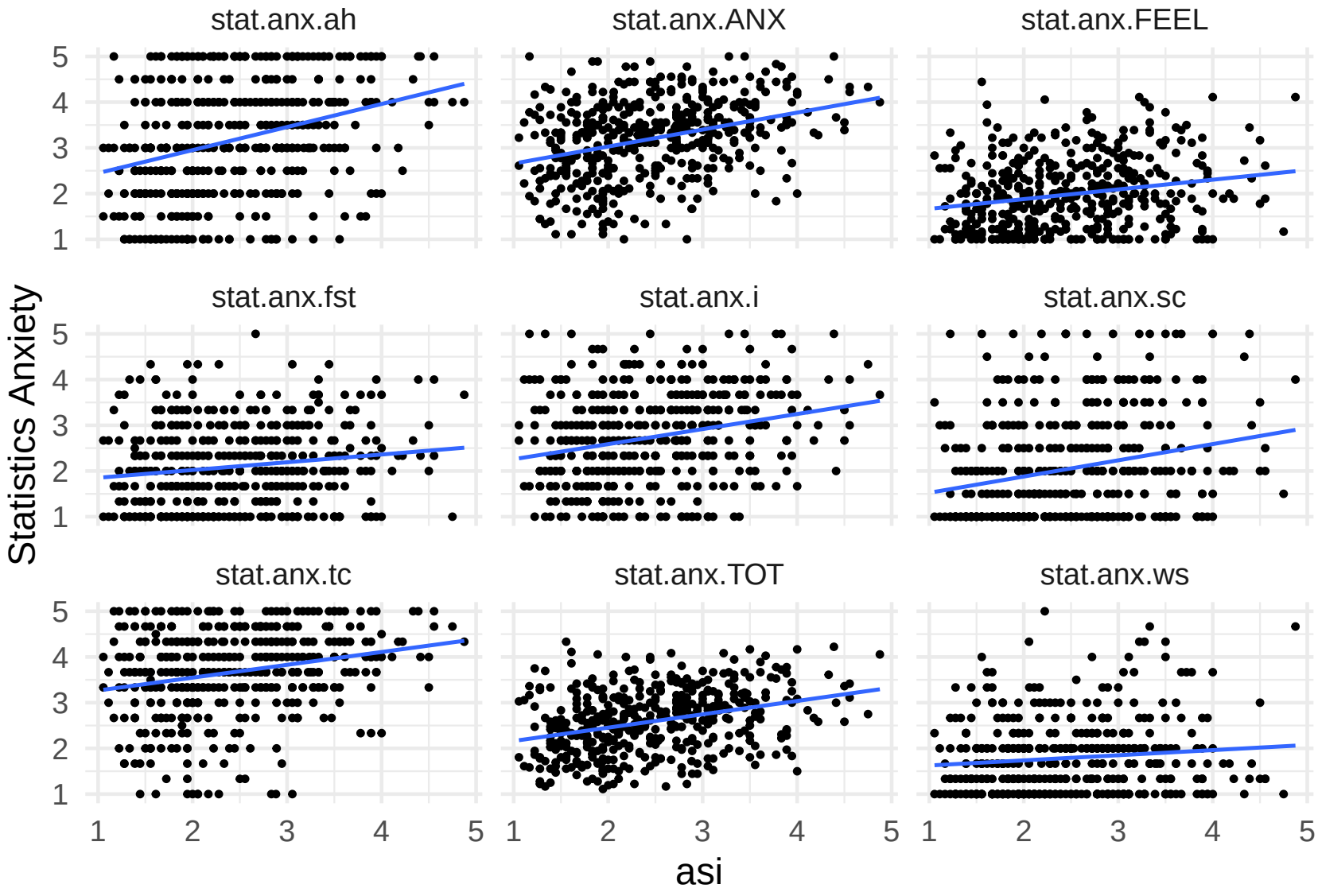
Exploring the relationships



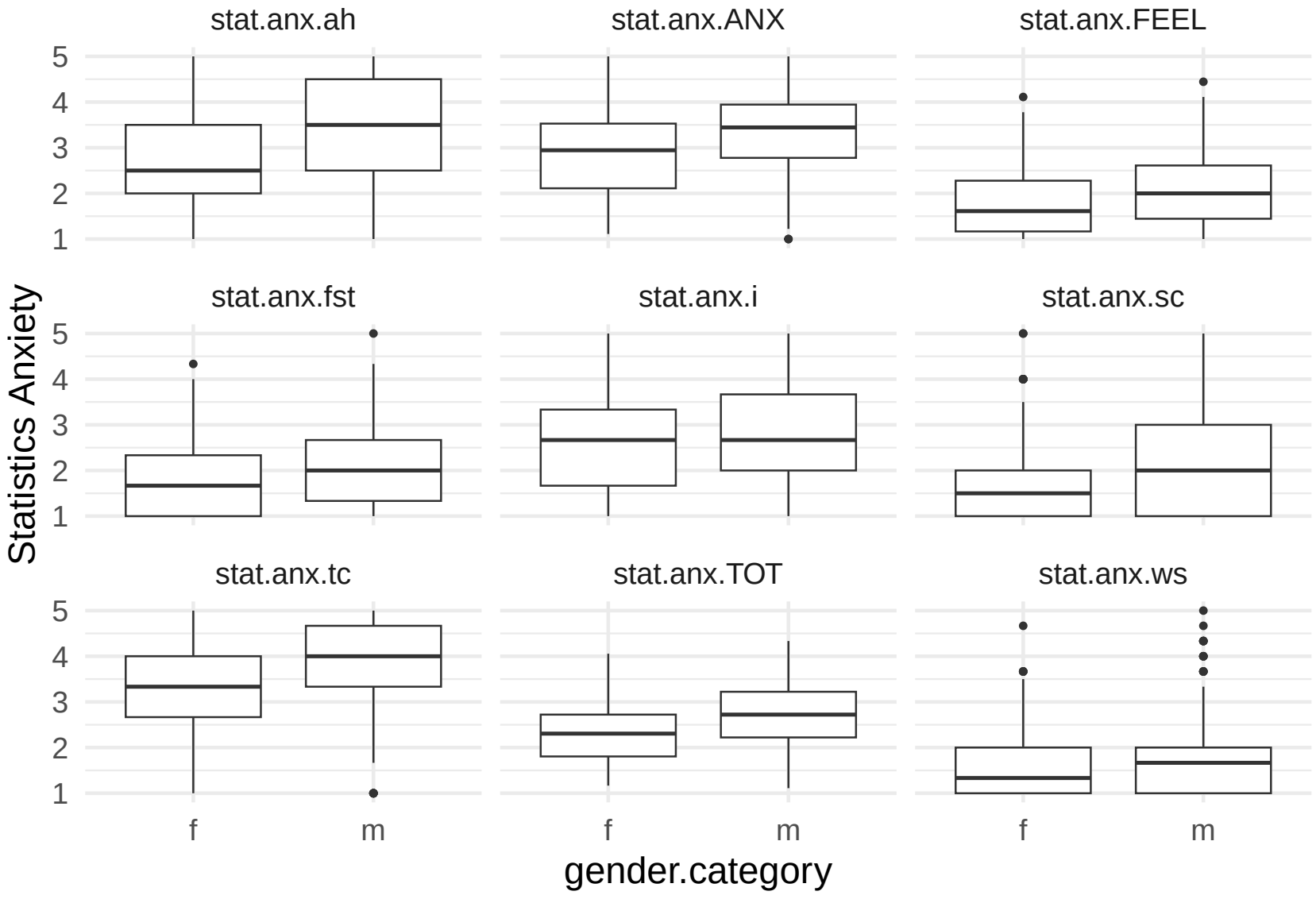
Exploring the relationships



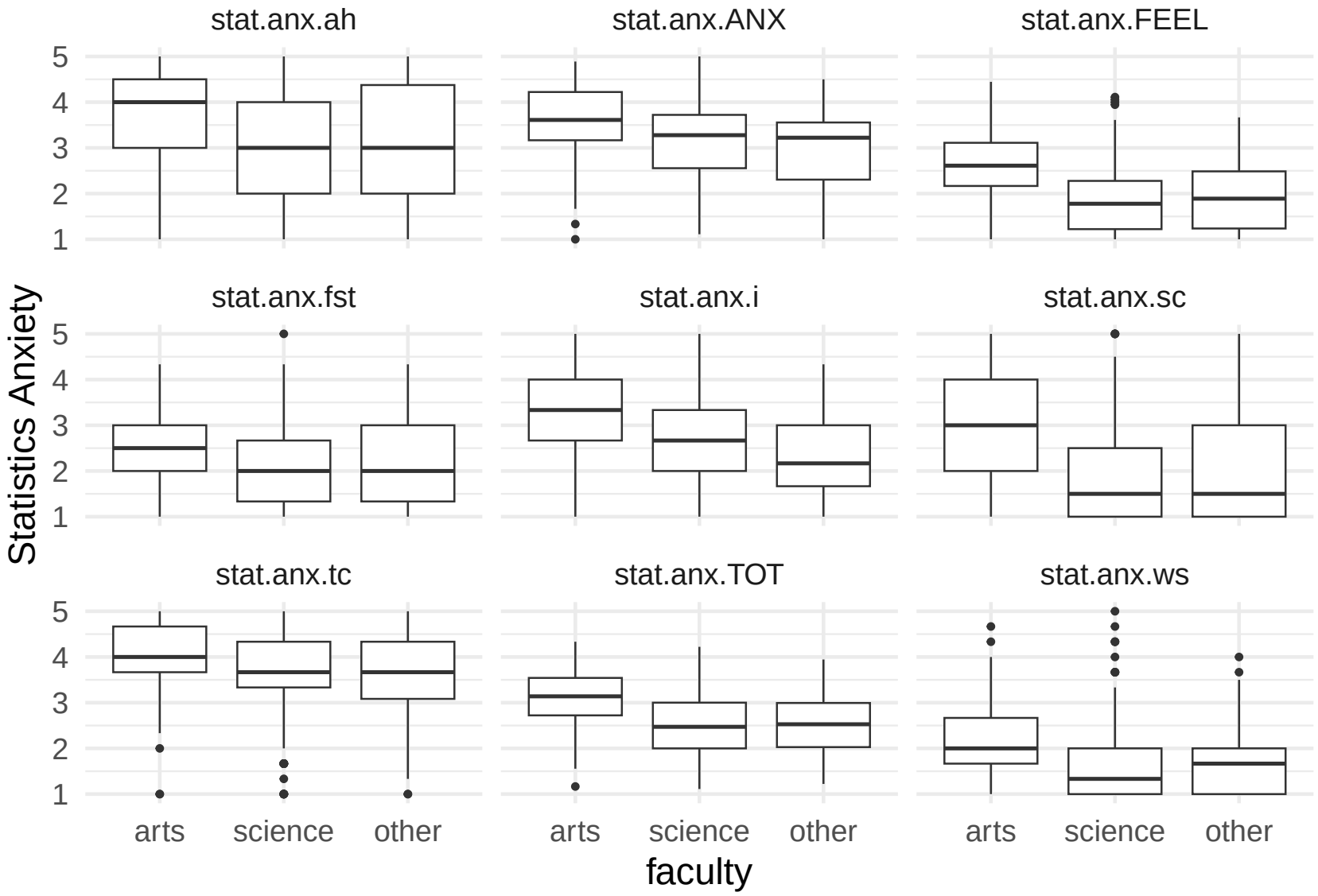
Exploring the relationships



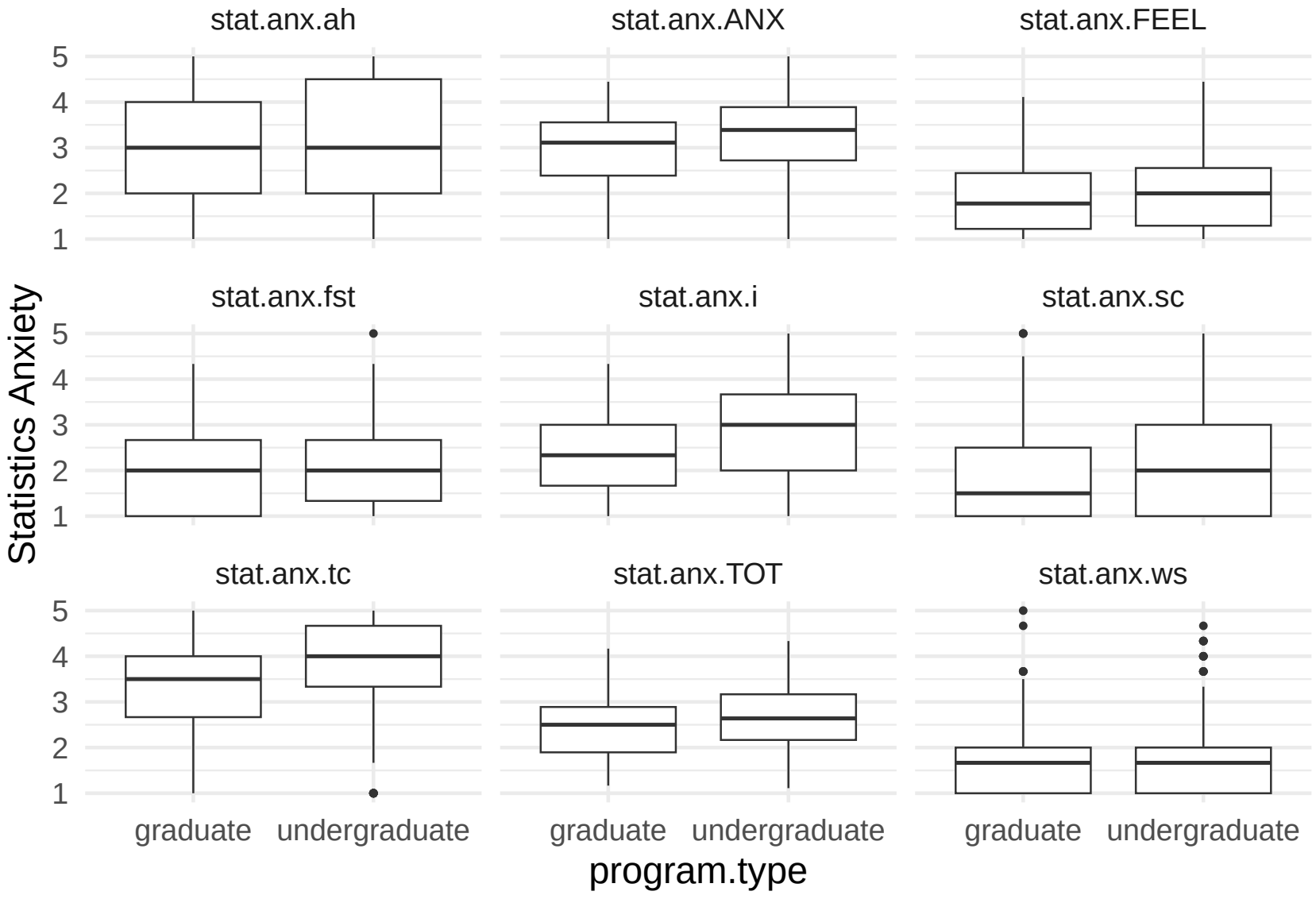
Exploring the relationships



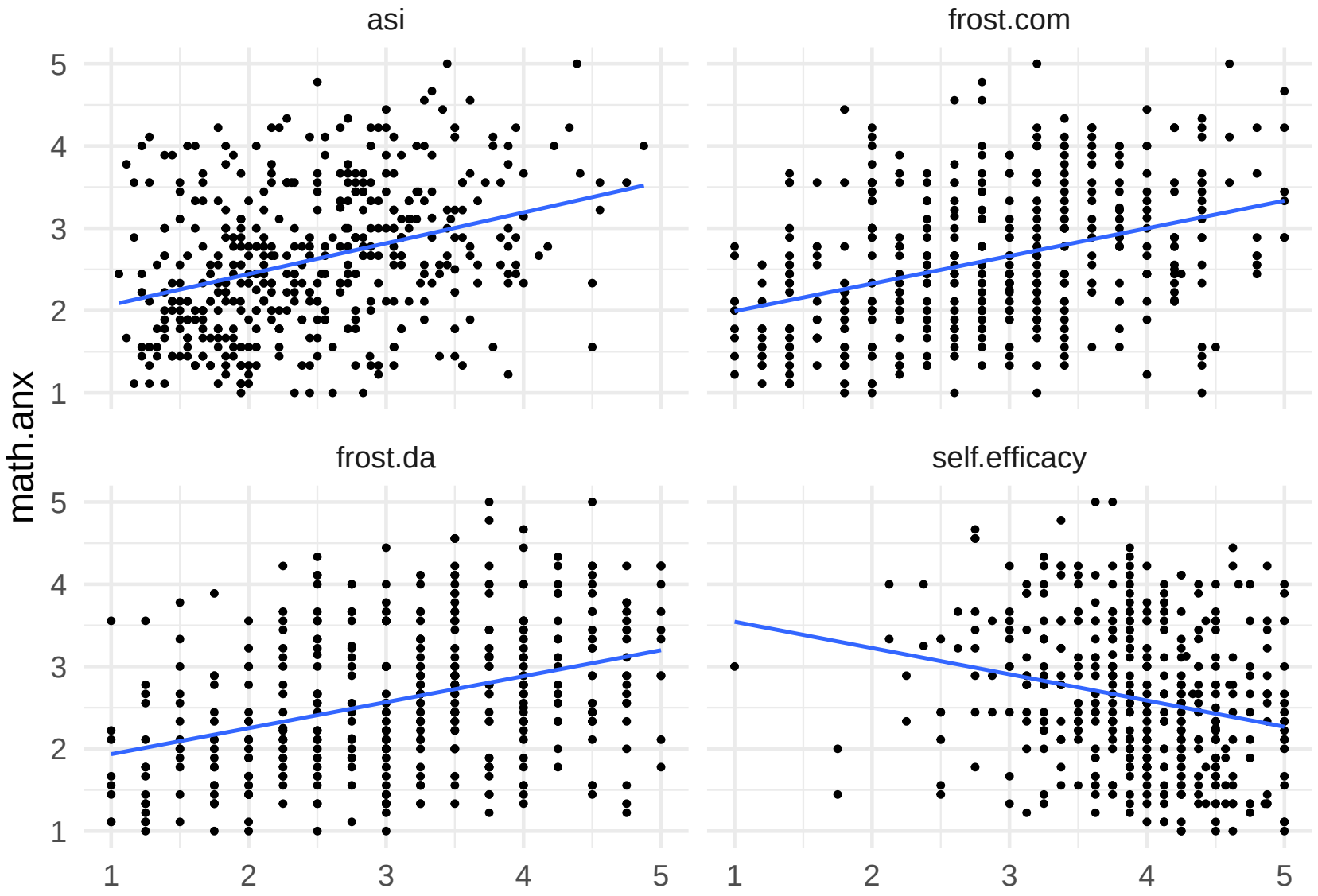
Exploring the relationships



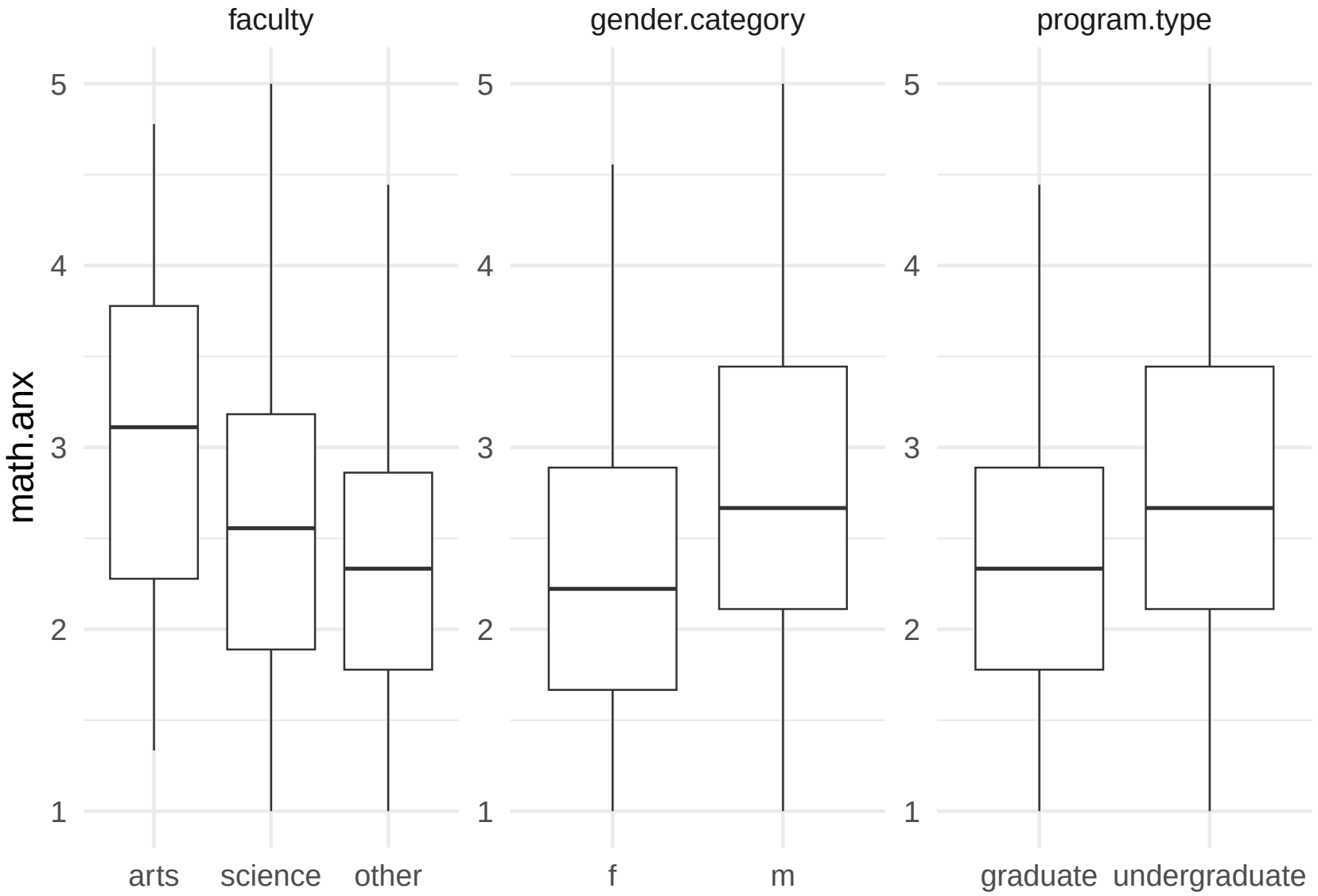
Exploring the relationships



Exploring the relationships



Exploring the relationships



Selecting a sub-sample

For the purpose of the example, we select a subsample of the dataset to increase the variability and simulate a more uncertain scenario with a lower sample size.

```
N <- 100
selected <- sample(1:nrow(dat), size = N, replace = TRUE)
dat <- dat[selected, ]
```

Data structure for specifications

When conducting a multiverse in R (or in whatever language) the data structure is very important.

- how to create and organize the different models?
- how to easily extract all the informations such as coefficients, standard errors, p-values, etc.
- ...

An R `list` is probably the best

A (named) `list` is flexible, easy to index and can be accesed by other functions to extract information and create other list.

A `list` in R can be easily transformed into a `data.frame` for other models, plots, tables, etc.

You can use the `*apply` family (`sapply`, `lapply`, etc.) to compute complex operations on lists.

An R `list` is probably the best

For example, assuming that I have some regression models within a named list:

```
fit1 <- lm(math.anx ~ gender.category + asi, data = dat)
fit2 <- lm(math.anx ~ gender.category + asi + faculty, data = dat)
fit3 <- lm(math.anx ~ gender.category + faculty, data = dat)
fit4 <- lm(math.anx ~ gender.category + asi + program.type, data = dat)

# ... and other thousands of (plausible) models :)

mods <- list(fit1, fit2, fit3, fit4)
names(mods) <- paste0("mod", 1:length(mods))
```

An R `list` is probably the best

Then, I want to extract all the `asi` coefficients and put into a data.frame:

```
get_coef <- function(x, coef = NULL){
  x <- broom::tidy(x, conf.int = TRUE)
  if(!is.null(coef)){
    filter(x, term %in% coef)
  } else{
    x
  }
}

get_coef(mods$mod1, "asi")
```

```
# A tibble: 1 x 7
  term  estimate std.error statistic  p.value conf.low conf.high
  <chr>    <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
1 asi      0.353    0.0483      7.32 1.20e-12    0.258     0.448
```

An R `list` is probably the best

With `lapply` (or `purrr::map()`) and combining the results, you can easily create a nice dataframe with your coefficients:

```
lapply(mods, get_coef, "asi") |>
  dplyr::bind_rows(.id = "mod")
```

```
# A tibble: 3 x 8
  mod   term  estimate std.error statistic  p.value conf.low conf.high
  <chr> <chr>    <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
1 mod1  asi      0.353    0.0483      7.32 1.20e-12    0.258     0.448
2 mod2  asi      0.355    0.0475      7.48 4.13e-13    0.262     0.449
3 mod4  asi      0.377    0.0478      7.88 2.51e-14    0.283     0.471
```

Creating the specifications

There are multiple ways of creating the specifications in practice.
You can do it from scratch:

```
mod1 <- lm(y ~ x1 + x2)
mod2 <- lm(y ~ log(x1) + log(x2))
mod3 <- lm(y ~ x1 + x2) # removing outliers

mods <- list(mod1 = mod1, mod2 = mod2, mod3 = mod3)
# ...
```

Creating the specifications

The `multiverse` R Package and the related paper (**?**) provides a very flexible and complex syntax to define different specifications.

Creating the specifications

For this example we can use some custom functions, in particular the `create_multi()` function. There are no wrong solutions if the results is correct.

```
devtools::load_all()

slog <- function(x) {
  if(any(x == 0)){
    x <- x + 1
  }
  log(x)
}

multi <- create_multi(
  math.anx ~ asi + faculty + stat.anx.TOT, # full model formula
  focal = "asi", # focal predictor, never removed
  nfuns = c("slog"), # functions for the numeric variables
  data = dat
)
```

Creating the specifications

```
$X
       fun             x    type focal .id_fun .id_x
1 identity           asi numeric  TRUE       1     1
2 identity       faculty  factor FALSE       1     2
3 identity stat.anx.TOT numeric FALSE       1     3
5     slog stat.anx.TOT numeric FALSE       2     3
                call
1                asi
2            faculty
3       stat.anx.TOT
5 slog(stat.anx.TOT)

$calls
[1] "~ asi"
[2] "~ asi + faculty"
[3] "~ asi + stat.anx.TOT"
[4] "~ asi + slog(stat.anx.TOT)"
[5] "~ asi + faculty + stat.anx.TOT"
[6] "~ asi + faculty + slog(stat.anx.TOT)"
```

Creating the specifications

Whatever the method we used, we need:

- a list of models
- a way to easily extract the coefficients or other quantities
- a way to extract a summary of the specifications i.e. if a variable is included or not, the type of tranformation, etc.

Pay attention with interactions!

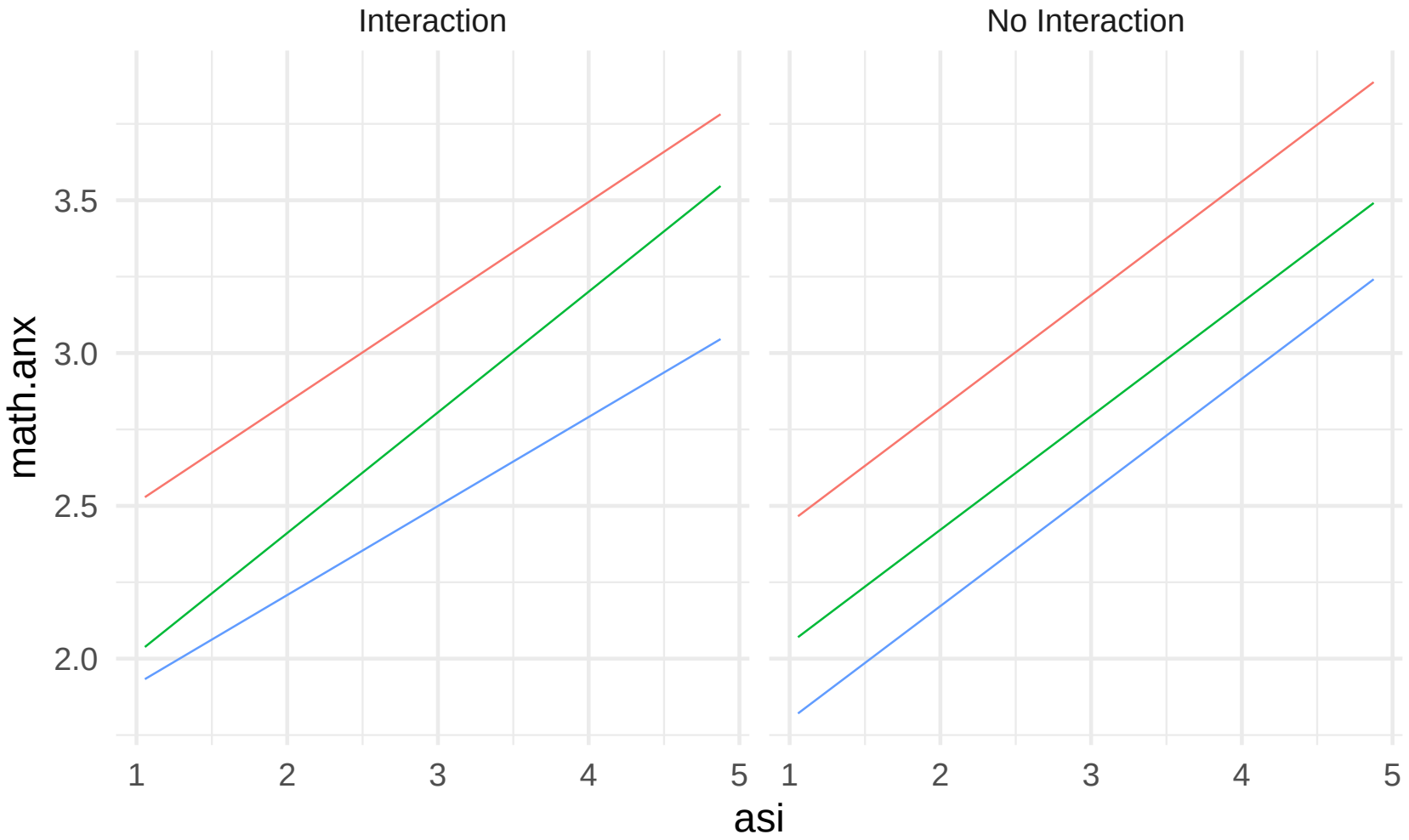
When an interaction is included in the model, the interpretation of the model coefficients completely change, especially if the interaction is consistent. You cannot compare a focal coefficients directly for models with and without interactions.

Let's assume that `asi` is the focal coefficient and we include in the multiverse these two models:

```
fit_int <- lm(math.anx ~ faculty + asi + faculty:asi, data = dat)
fit_no_int <- lm(math.anx ~ faculty + asi, data = dat)
```

Pay attention with interactions!

The `asi` effect in one case is the overall effect (i.e., main effect) controlling for `faculty`. In the other case is the `asi` effect of the reference value.



Pay attention with interactions!

One should adjust the contrasts coding of factors and/or the centering of numeric variables.

```
# sum to zero contrasts i.e. estimating the main effect of asi
update(fit_int, contrasts = list(faculty = contr.sum(3)))
```

```
Call:
lm(formula = math.anx ~ faculty + asi + faculty:asi, data = dat,
    contrasts = list(faculty = contr.sum(3)))

Coefficients:
 (Intercept)      faculty1      faculty2           asi  faculty1:asi
     1.80967       0.37244      -0.18831       0.33809      -0.01002
faculty2:asi
     0.05680
```

```
# with emmeans
emmeans::emtrends(fit_int, ~1, var = "asi")
```

```
 1       asi.trend     SE  df lower.CL upper.CL
 overall     0.338 0.0639 438    0.212    0.464

Results are averaged over the levels of: faculty
Confidence level used: 0.95
```

Why exploring is important?

A multiverse analysis increase the complexity of the data analysis.
There is no longer a single dataset and result to discuss.

Let's create some scenarios :)

Firstly, we use variable transformations directly within the model formula. In this way it is easier to extract the conditions. Thus we define some wrappers:

```
# safe version of log() with 0 variables
slog <- function(x){
  if(any(x == 0)){
    x <- x + 1
  }
  log(x)
}

# function factories, see https://adv-r.hadley.nz/function-factories.html
polyN <- function(degree = 1){
  function(x) poly(x, degree = degree)
}

poly2 <- polyN(2)
poly3 <- polyN(3)
```

Let's create some scenarios :)

More wrappers:

```
cutN <- function(breaks){
  function(x){
    cut(x, breaks = breaks)
  }
}

cut2 <- cutN(2)
cut4 <- cutN(4)
```

Let's create some scenarios :)

Then we can identify some univariate/multivariate outliers or some observations that we may consider removing for some reasons.

Let's create some scenarios :)

```
focal <- "self.efficacy"

multi <- create_multi(
  #math.anx ~ self.efficacy + faculty + asi + gender.category + program.type +
  math.anx ~ self.efficacy + faculty + asi,
  focal = "self.efficacy",
  nfuns = c("slog", "cut2", "poly2", "poly3"),
  data = dat
)
```

Let's fit the models

```r
# faster than before
get_coef <- function(x, coef = NULL){
  xs <- data.frame(summary(x)$coefficients)
  if(!is.null(coef)){
    xs <- xs[coef, ]
  }
  xs$param <- rownames(xs)
  return(xs)
}

fitl <- vector(mode = "list", length = length(multi$calls))

for(i in 1:length(multi$calls)){
  form <- paste0("math.anx", multi$calls[i])
  fitl[[i]] <- glm(form, family = gaussian(link = "identity"), data = dat)
}

resl <- lapply(fitl, get_coef, focal)
res <- bind_rows(resl, .id = "mod")
rownames(res) <- NULL
names(res) <- c("mod", "b", "se", "t", "p", "param")
```

Let's fit the models

Now we have a dataframe with all the model coefficients across the specifications. We can start our multiverse!

```
head(res)
```

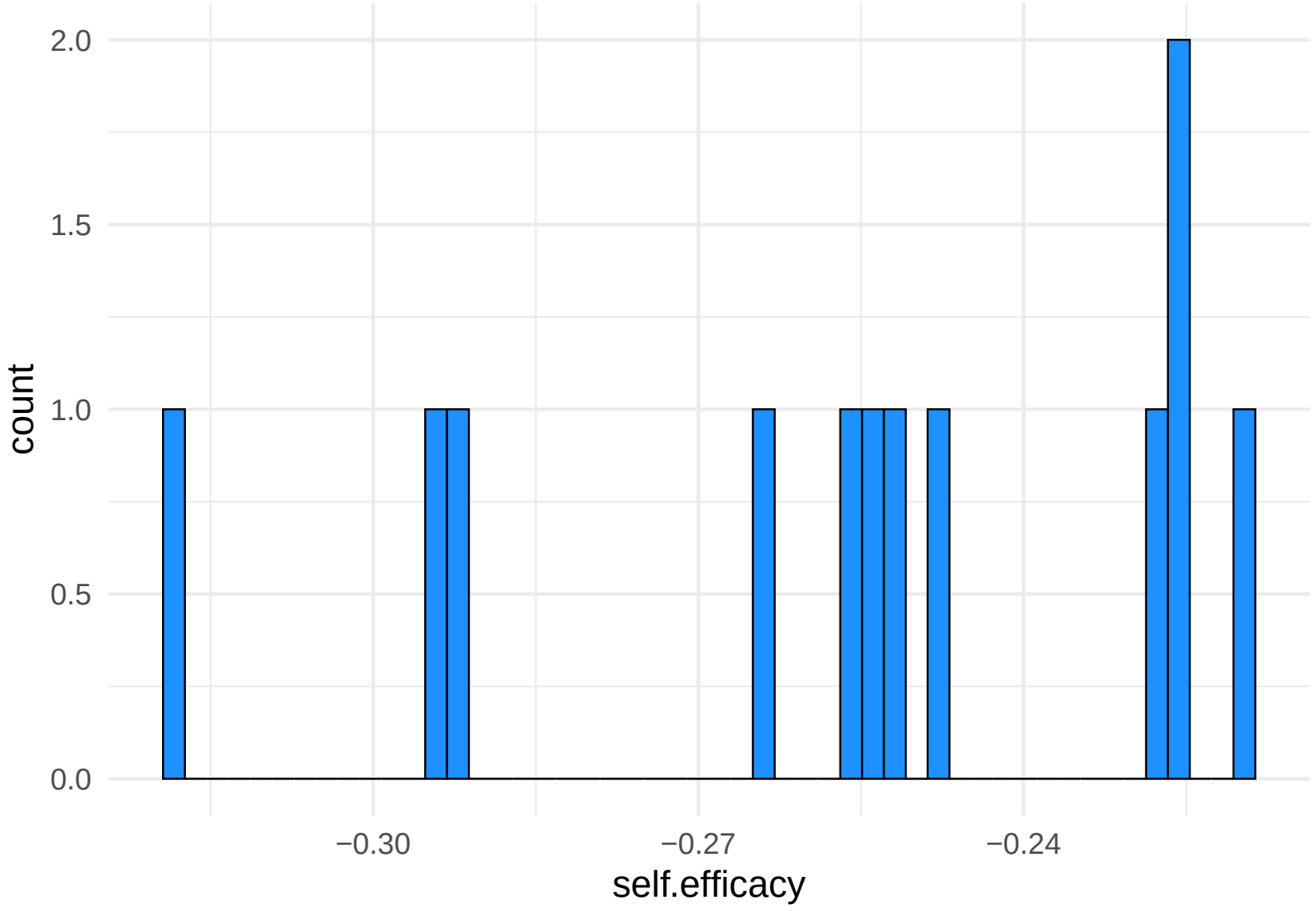
```
  mod          b         se         t             p         param
1   1 -0.3191761 0.06365938 -5.013811 7.738274e-07 self.efficacy
2   2 -0.2933090 0.06298999 -4.656438 4.266628e-06 self.efficacy
3   3 -0.2523166 0.06112503 -4.127876 4.379177e-05 self.efficacy
4   4 -0.2481947 0.06153825 -4.033177 6.484395e-05 self.efficacy
5   5 -0.2914524 0.06144520 -4.743291 2.844147e-06 self.efficacy
6   6 -0.2546701 0.06148965 -4.141675 4.134768e-05 self.efficacy
```

Exploratory tools

- Marginal/Conditional effects
- Vibration of Effects
- Specification Curve

Marginal/Conditional effects

Overall distribution of regression parameters:



Marginal/Conditional effects

We can combine the model results with a table created by all conditions with the custom `get_info_models()` function:

```
info <- get_info_models(multi)
head(info)
```

```
# A tibble: 6 x 4
    mod x_self.efficacy x_faculty x_asi
  <int> <chr>           <chr>     <chr>
1     1 self.efficacy   <NA>      <NA>
2     2 self.efficacy   faculty   <NA>
3     3 self.efficacy   <NA>      asi
4     4 self.efficacy   <NA>      slog(asi)
5     5 self.efficacy   <NA>      cut2(asi)
6     6 self.efficacy   <NA>      poly2(asi)
```

Marginal/Conditional effects

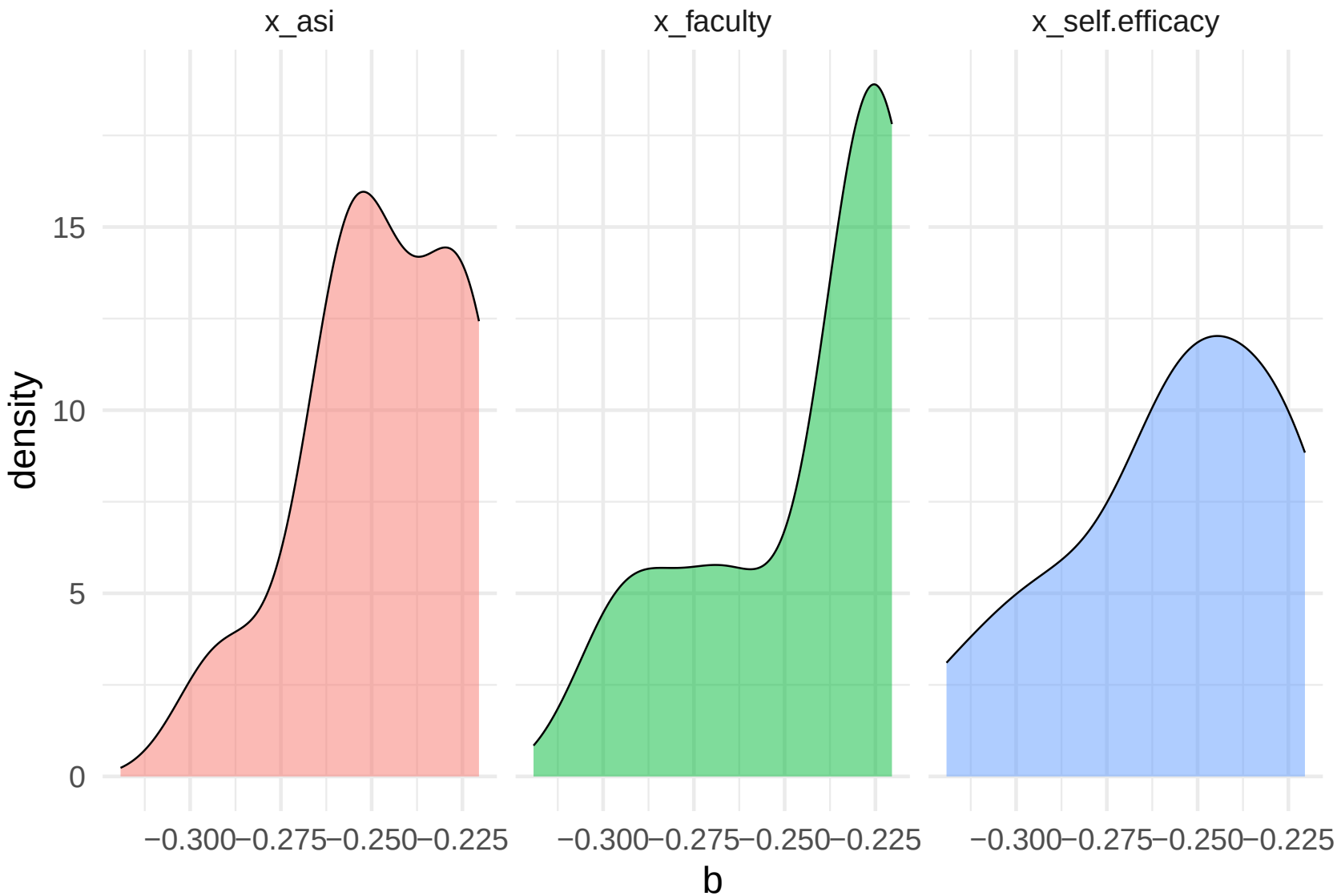
Then we can combine the `info` table with the coefficients table and we have all the important information.

```
# same type
res$mod <- as.numeric(res$mod)
info$mod <- as.numeric(info$mod)
# merging the two tables
multi_res <- left_join(res, info, by = "mod")
head(multi_res)
```

```
  mod          b         se         t             p         param
1   1 -0.3191761 0.06365938 -5.013811 7.738274e-07 self.efficacy
2   2 -0.2933090 0.06298999 -4.656438 4.266628e-06 self.efficacy
3   3 -0.2523166 0.06112503 -4.127876 4.379177e-05 self.efficacy
4   4 -0.2481947 0.06153825 -4.033177 6.484395e-05 self.efficacy
5   5 -0.2914524 0.06144520 -4.743291 2.844147e-06 self.efficacy
6   6 -0.2546701 0.06148965 -4.141675 4.134768e-05 self.efficacy
  x_self.efficacy x_faculty      x_asi
1   self.efficacy      <NA>       <NA>
2   self.efficacy   faculty       <NA>
3   self.efficacy      <NA>        asi
4   self.efficacy      <NA>  slog(asi)
5   self.efficacy      <NA>  cut2(asi)
6   self.efficacy      <NA> poly2(asi)
```

Marginal/Conditional effects

Finally we can plot also the distributions of parameters conditioned on the presence/absence of a particular other predictor:



Vibration of Effects (VoE) (Patel et al., 2015)

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Journal of Clinical Epidemiology

Assessment of vibration of effects due to model specification can demonstrate the instability of observational associations

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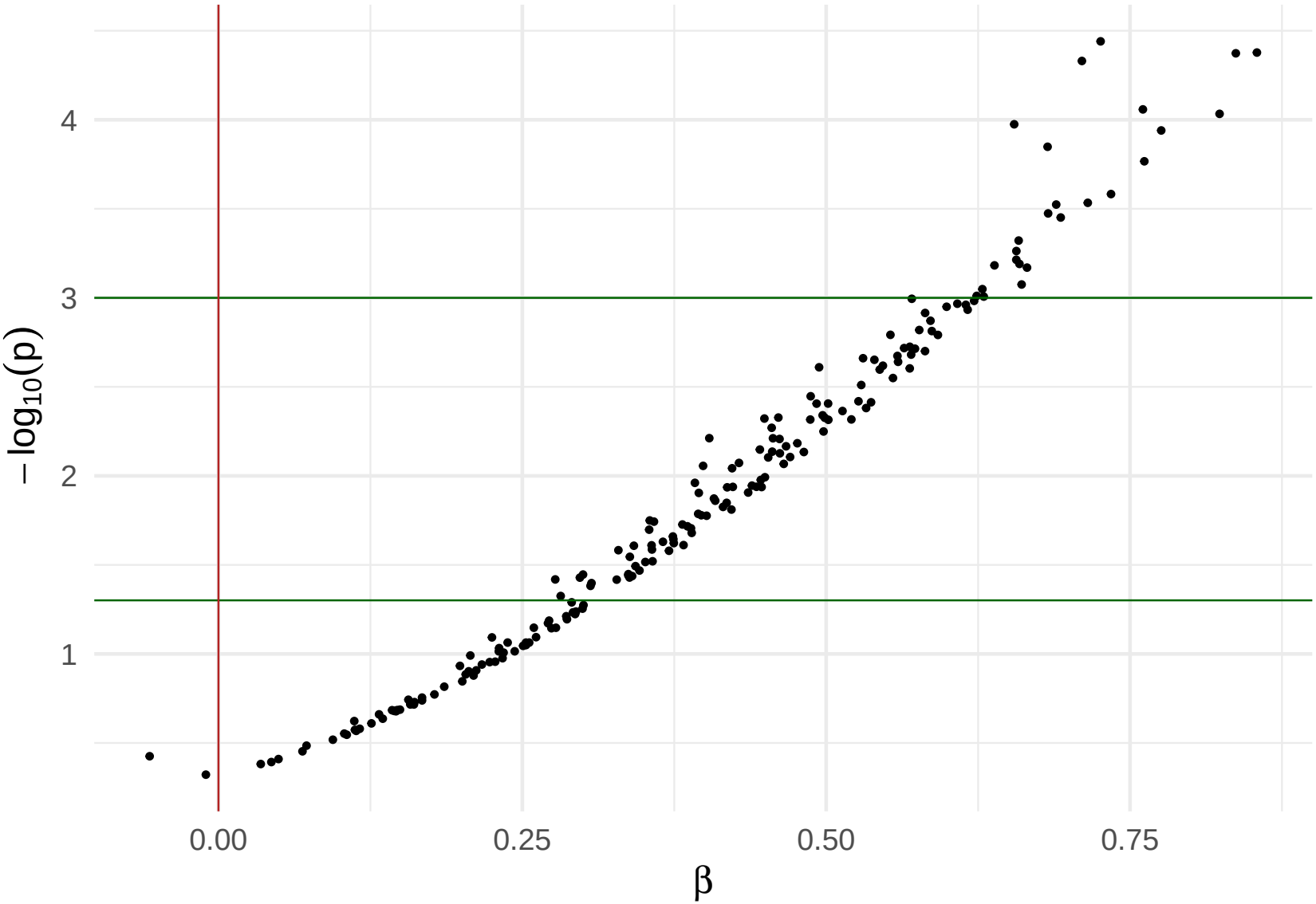
Vibration of Effects (VoE) (Patel et al., 2015)

The VoE is a statistical approach to evaluate the variability in effect estimates and p value due to different sources of variability (i.e., *vibrations*)

- **sampling** vibration: subsets of the full dataset
- **model** vibration: combinations of control variables
- **pre-processing** vibration: inclusio/exclusion criteria, outliers, etc.

Vulcano Plot

The Vulcano Plot is the graphical tool used in the VoE as a diagnostic tool.



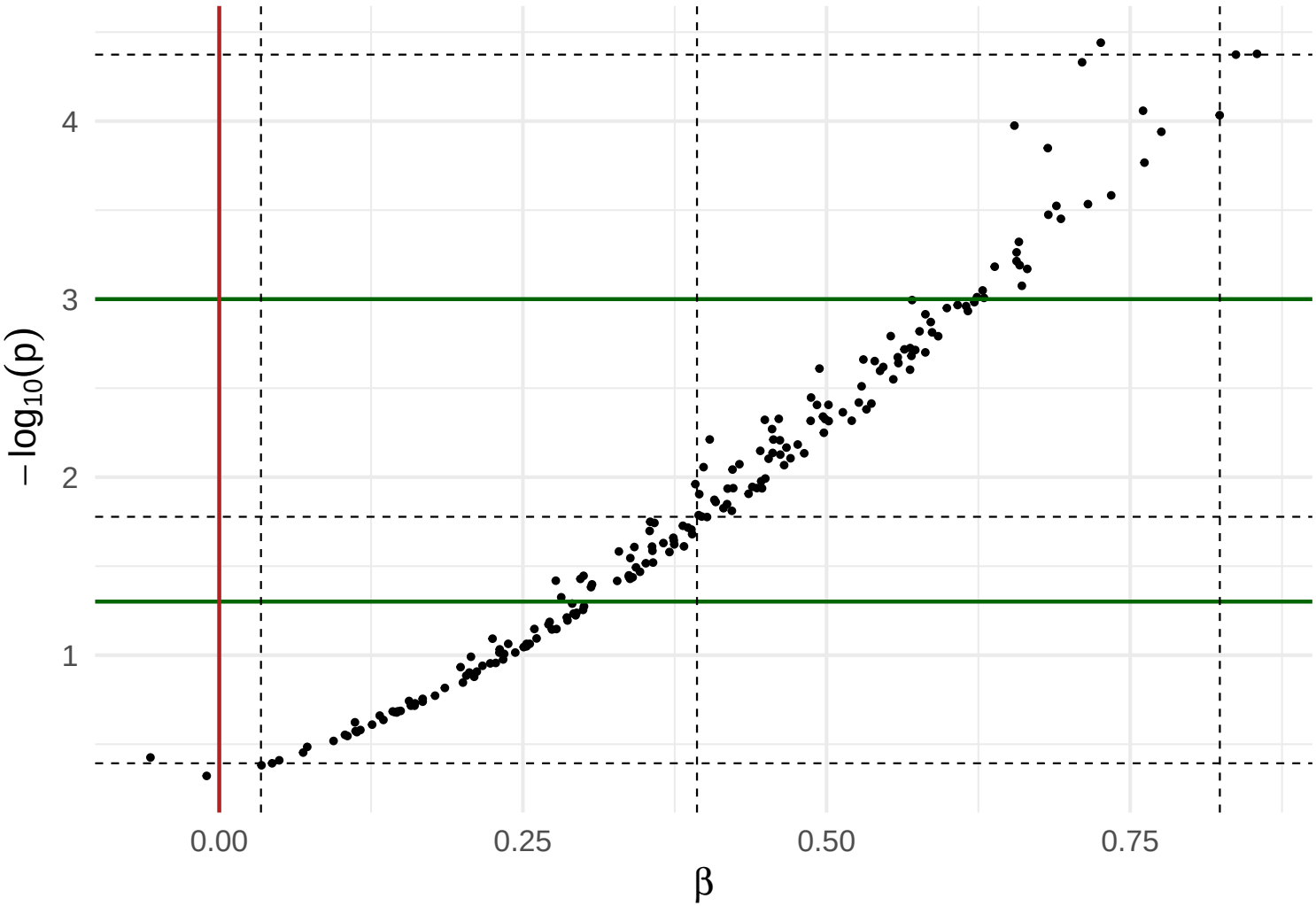
Vulcano Plot

The x axis is the effect size. Usually a regression coefficient of a *focal* parameter. Can be a raw or standardized regression coefficient or whatever effect size measure.

The y axis is the associated p-value transformed in $-\log_{10}(p)$ for better intepretation and visualization. Higher tranformed p values are smaller raw p values.

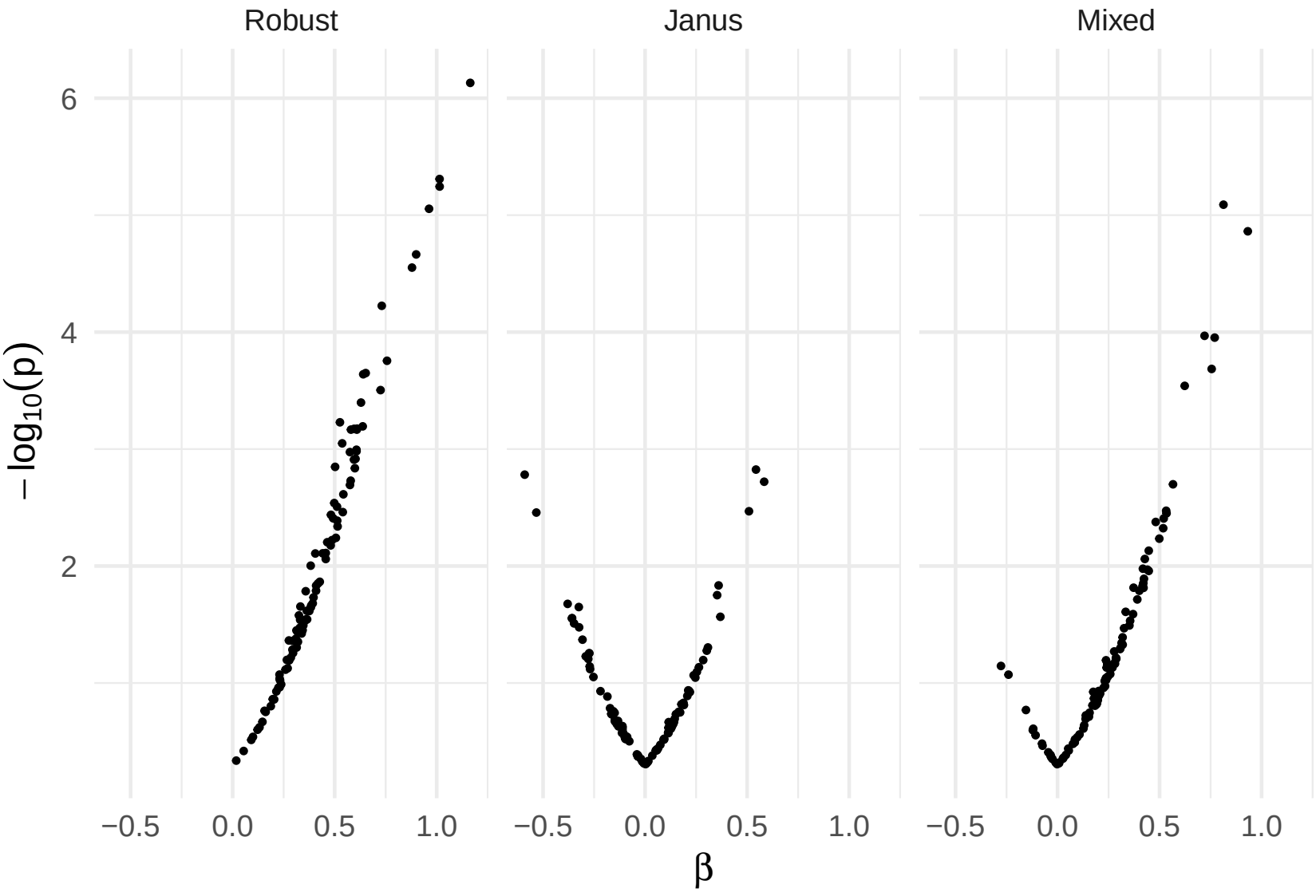
Vibration of Effects (VoE)

The authors proposed to summarise the VoE using the range of effect sizes and p values. In particular the difference between the 99^{th} and 1^{st} percentiles.



Vibration of Effects (VoE)

They identified three usual pattern for a Vulcano Plot:



Vibration of Effects (VoE)

The **Robust** plot suggests a stable pattern across specifications, with the majority if not the total being positive and significant.

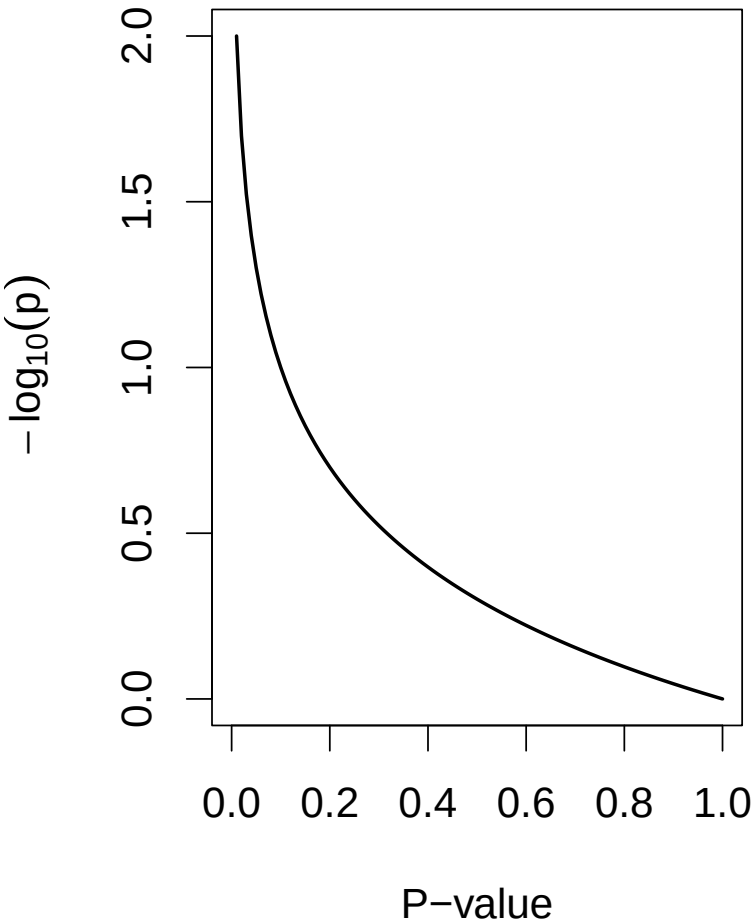
The **Janus**[1] plot suggests the worst scenario where in some conditions the effect is not only not significant but reversed.

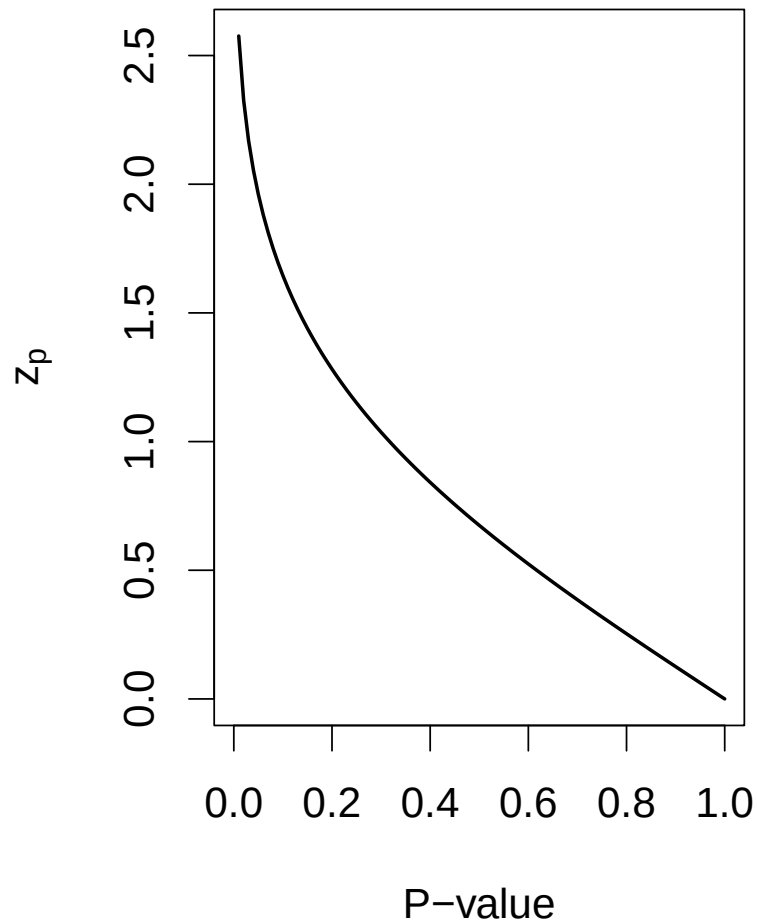
The **Mixed** plot suggests a less robust effect with few effect size reversals in rare specifications.

[1] Fun fact: Janus comes from the Roman/Greek god with two faces :)

P-values transformation

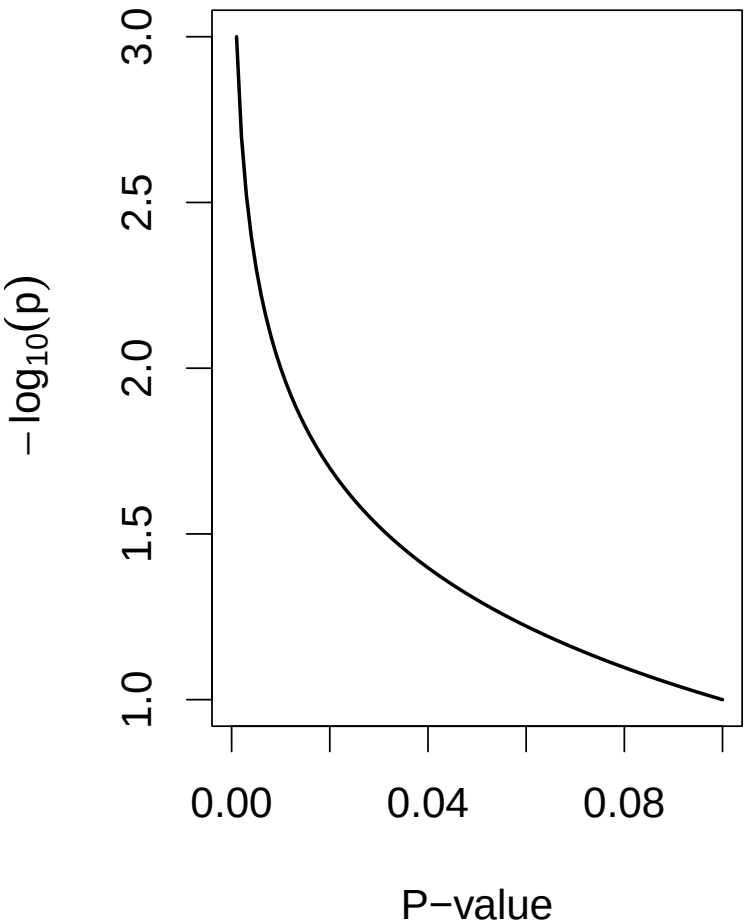
There are different ways to transform p-values to improve the interpretation and visualization.

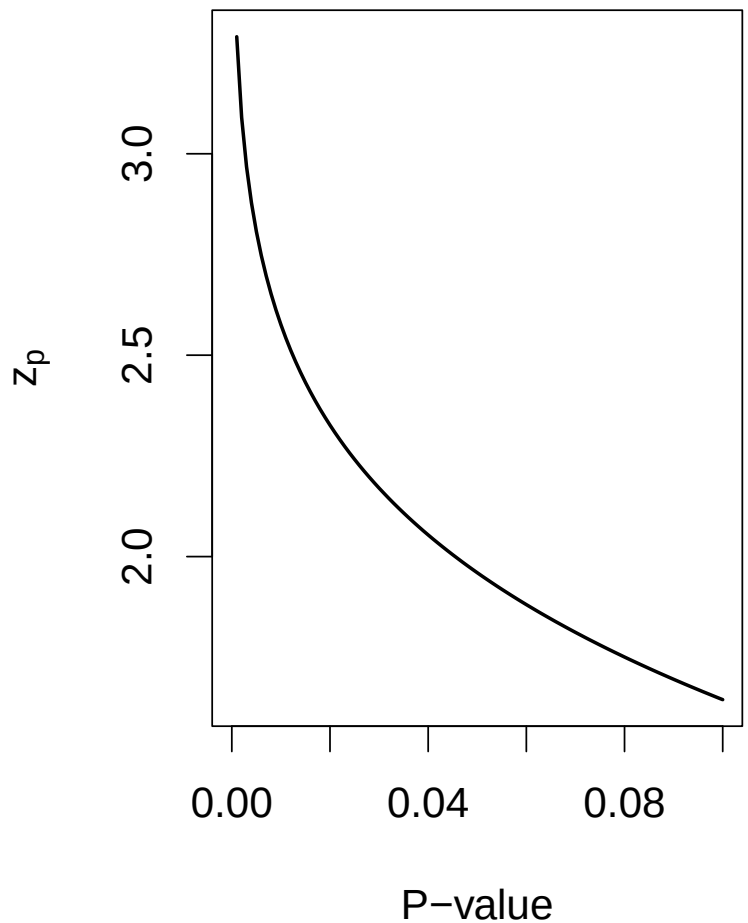




P-values transformation

Values higher than ~1.3 (in $\log_{10}$) or ~2 (z transformation) are significant assuming the traditional $\alpha = 0.05$.



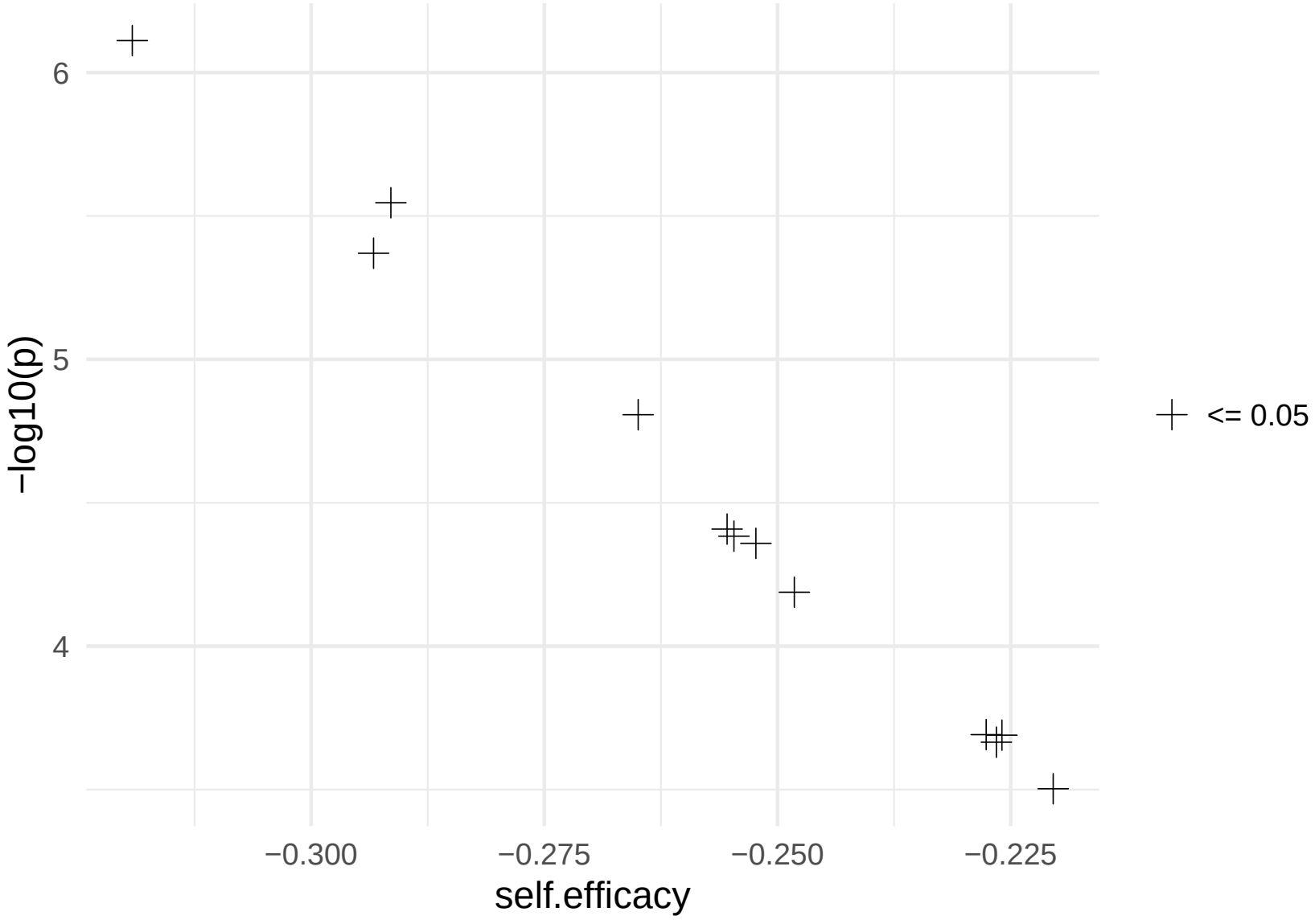


Vulcano plot with our data

We can create a basic version of the vulcano plot with our dataset:

```
multi_res |>
    mutate(sign = ifelse(p <= 0.05, "<= 0.05", "> 0.05"),
           sign = factor(sign, levels = c("<= 0.05", "> 0.05"))) |>
    ggplot(aes(x = b, y = tp(p, "-log10"))) +
    geom_point(aes(shape = sign), size = 5) +
    ylab("-log10(p)") +
    xlab(focal) +
    scale_shape_manual(values = c(3, 16)) +
    theme(legend.title = element_blank())
```

Vulcano plot with our data



Marginal/Conditional effects

A way to evaluate the impact of the multiverse scenario could be to use an ANOVA-style way of thinking. We can fit a regression model on the multiverse where the focal coefficient is the response variable and a series of dummy variables to code the inclusion/exclusion of a certain predictor.

Then we can estimate the % of explained variance of each predictor as an index of the impact in the multiverse results.

A more refined version of this approach can be found in Klau et al. (2023)

Decomposing the multiverse variance

We can create a dataset with dummy variables when a specific predictor is included or not. We are ignoring the transformations of the specific variable.

```
# A tibble: 6 x 3
        b faculty   asi
   <dbl>   <dbl> <dbl>
1 -0.319       0     0
2 -0.293       1     0
3 -0.252       0     1
4 -0.248       0     1
5 -0.291       0     1
6 -0.255       0     1
```

Decomposing the multiverse variance

Then we can fit a linear regression and then evaluate the impact of including/excluding a predictor.

```
fit <- lm(b ~ ., data = multi_fit)
summary(fit)
```

```
Call:
lm(formula = b ~ ., data = multi_fit)

Residuals:
      Min         1Q     Median         3Q        Max
-0.031722  0.000301  0.005604  0.007450  0.012775

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.319779   0.012819 -24.945 1.28e-09 ***
faculty      0.027072   0.009691   2.794  0.02093 *
asi          0.059492   0.013001   4.576  0.00134 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.01678 on 9 degrees of freedom
Multiple R-squared:  0.7615,    Adjusted R-squared:  0.7086
F-statistic: 14.37 on 2 and 9 DF,  p-value: 0.001579
```

Decomposing the multiverse variance

```
car::Anova(fit)
```

```
Anova Table (Type II tests)

Response: b
             Sum Sq Df F value   Pr(>F)
faculty   0.0021987  1  7.8044 0.020929 *
asi       0.0058987  1 20.9382 0.001336 **
Residuals 0.0025355  9
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
effectsize::eta_squared(fit, partial = FALSE)
```

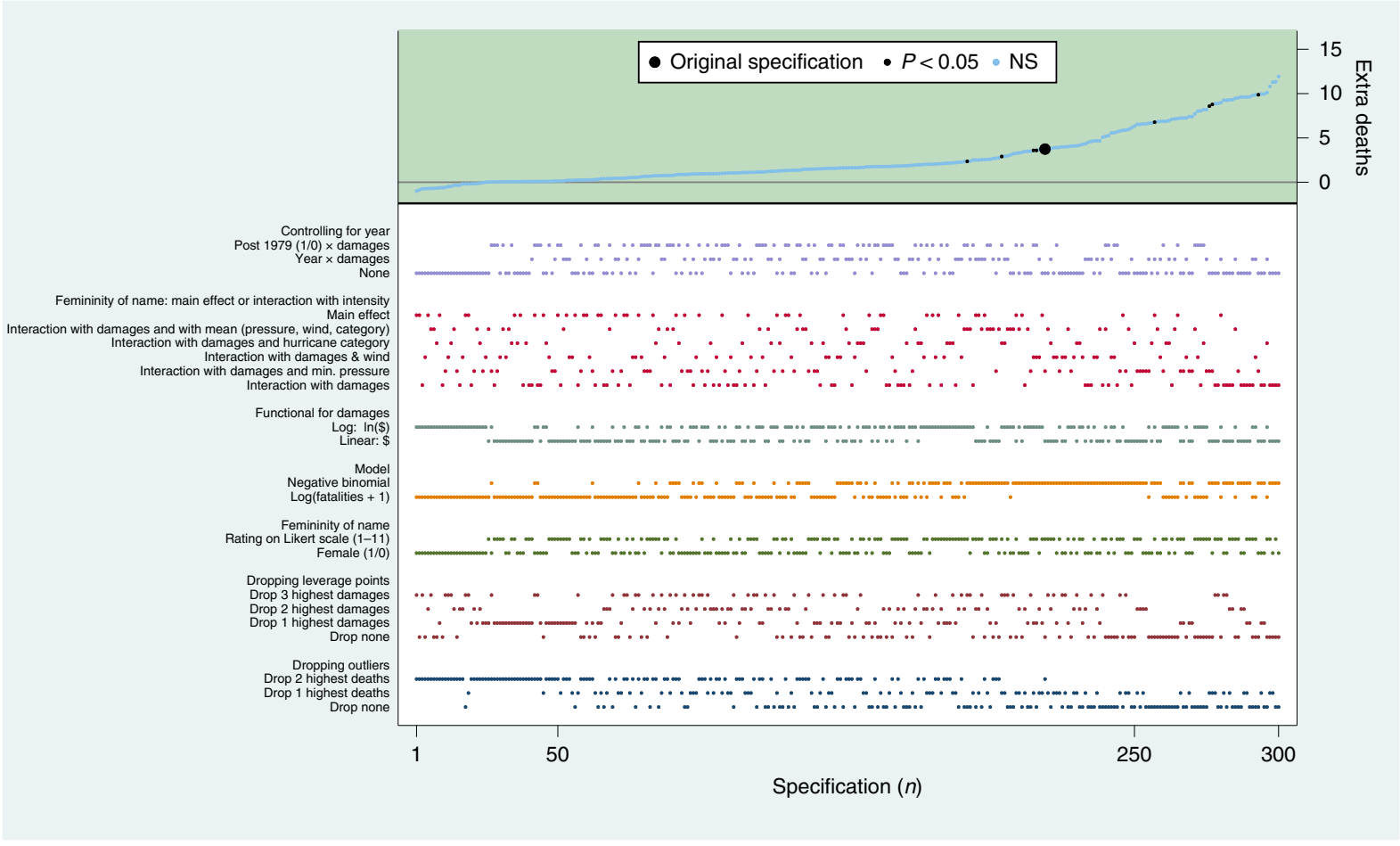
```
# Effect Size for ANOVA (Type I)

Parameter | Eta2 |       95% CI
------------------------------
faculty   | 0.21 | [0.00, 1.00]
asi       | 0.55 | [0.14, 1.00]

- One-sided CIs: upper bound fixed at [1.00].
```

Specification Curve (Simonsohn et al., 2020)

The specification curve is both an inferential and descriptive tool to summarise the results from a multiverse analysis.



Specification Curve as descriptive tool

Basically from M specifications we extract the focal coefficient then:

- we sort the coefficients from the lowest to the highest and assign a progressive index
- we plot the index as a function of the coefficient value
- for each scenario we code the corresponding set of conditions/variables
- we combine the previous plot with a tile-plot (or similar) showing for each scenario the set of variables/choices

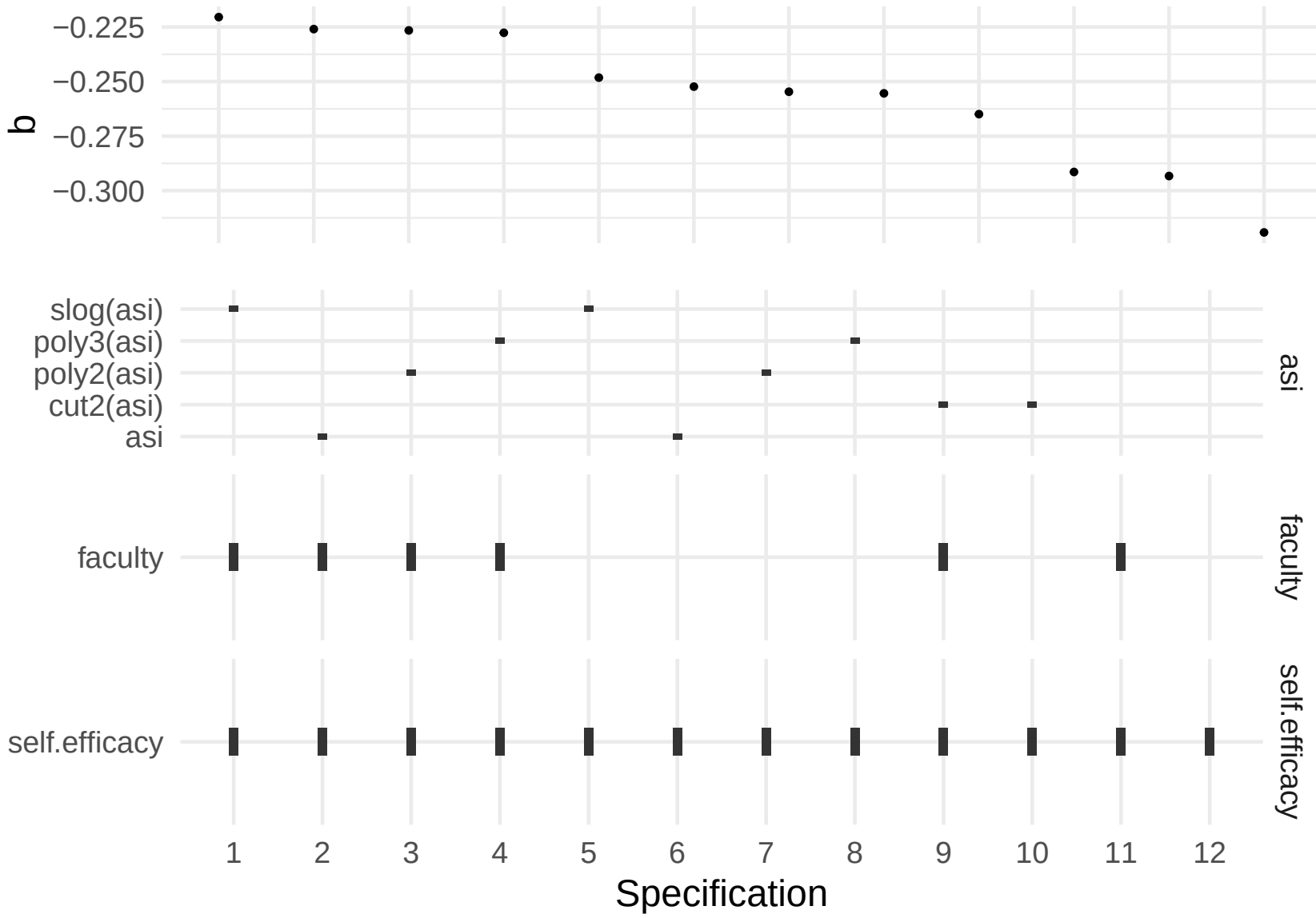
Specification with the dataset

```r
spec_data <- multi_res |>
    # sorting
    arrange(desc(b)) |>
    # index with the order
    mutate(spec = 1:n())

top <- spec_data |>
    # confidence intervals
    mutate(lb = b - se * 2,
           ub = b + se * 2) |>
    ggplot(aes(x = factor(spec), y = b)) +
    geom_point() +
    #geom_segment(aes(y = lb, yend = ub)) +
    theme(axis.text.x = element_blank(),
          axis.title.x = element_blank())

bottom <- spec_data |>
    pivot_longer(starts_with("x_")) |>
    drop_na() |>
    mutate(name = gsub("x_", "", name)) |>
    ggplot(aes(x = factor(spec), y = value)) +
    geom_tile(width = 0.1, height = 0.2) +
    theme(axis.title.y = element_blank()) +
    xlab("Specification") +
    facet_grid(name~., scales = "free")
```

Specification with the dataset



Other descriptive tools

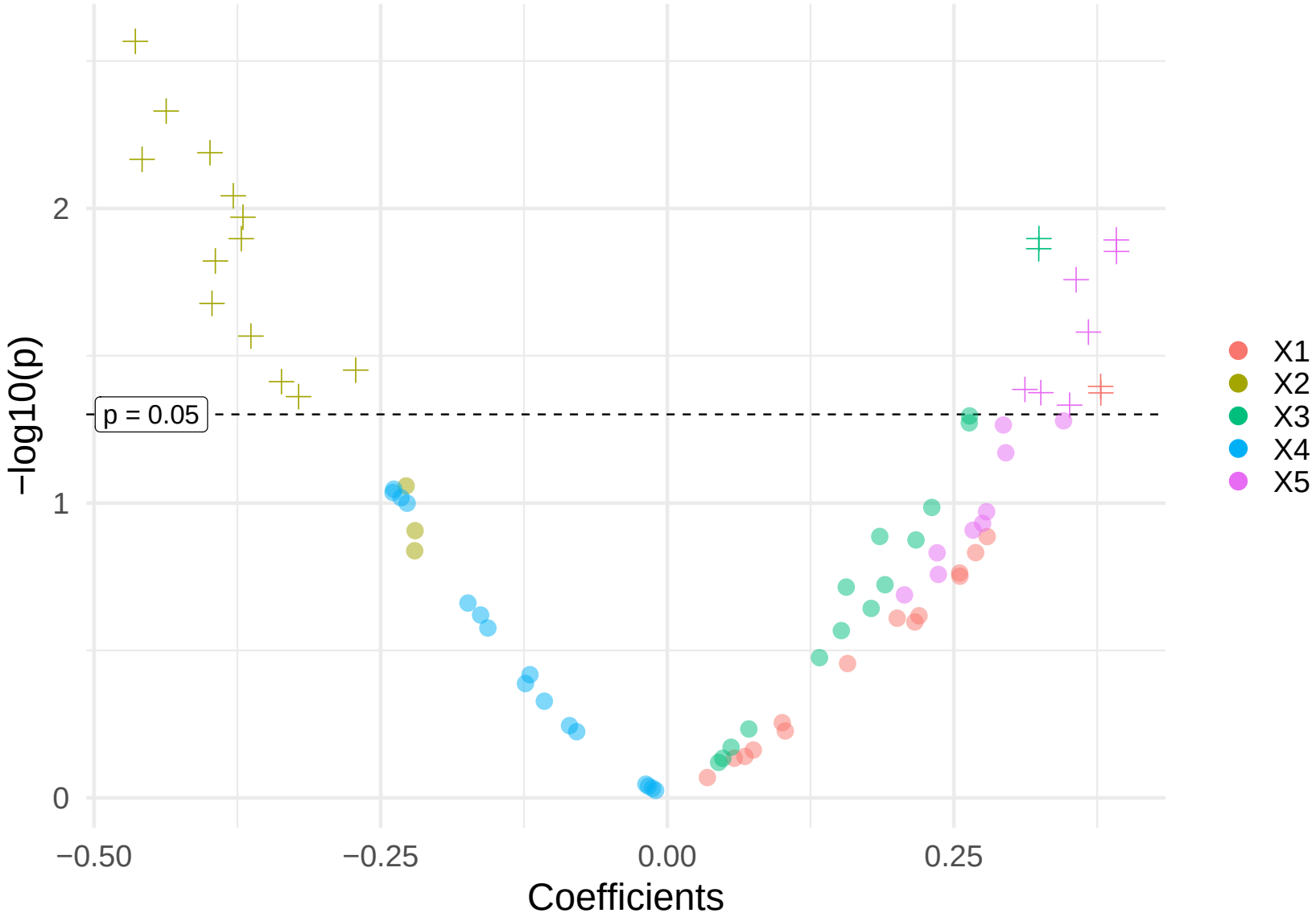
In general, any descriptive statistics can be useful. The main points in a multiverse description are:

- the range of the estimated effects
- the impact of the choices
- the impact on the conclusions (e.g., statistical significance)

Can the EMA be misleading?

Let's have a look to another example

We have a multiverse with 31 scenarios, 50 observations and 5 predictors, this is the vulcano plot. **What do you think?**



Let's have a look to another example[2]

From the previous multiverse it is clear that something is going on. Some of the coefficients are significant and other not. There is also a little bit of Janus effect.

[2] Thanks to Livio Finos for the insightful example

Let's have a look to another example[2]

From the previous multiverse it is clear that something is going on. Some of the coefficients are significant and other not. There is also a little bit of Janus effect.

But, the previous example was a simulated multiverse where all the coefficients $\beta_j = 0$ (the null hypothesis is true). **All the significant scenarios are false positives (type-1 error)!**

[2]Thanks to Livio Finos for the insightful example

Why? multiple testing problem!

A multiverse can be considered as a multiple testing problem because we are testing a set of hypotheses with the same dataset. The type-1 error rate (α) need to be controlled otherwise the actual level is higher than the nominal level.

We can demonstrate this with a simple simulation. We simulate k variables and a one-sample t-test for each variable. The ground truth is that we have $\mu_1, \mu_2, \ldots, \mu_k = 0$ thus H_0 is true.

We repeat the simulation B times and we count how many times $p \leq \alpha$ for at least one of the k tests. This is our estimated type-1 error rate.

Why? multiple testing problem!

```r
k <- 10  # number of variables
n <- 100 # number of observations
R <- 0 + diag(1 - 0, k) # correlation matrix
B <- 1e3

PM <- matrix(NA, B, k)

for(i in 1:B){
    X <- MASS::mvrnorm(n, rep(0, k), R)
    p <- apply(X, 2, function(x) t.test(x)$p.value)
    PM[i, ] <- p
}

# type-1 error for each variable, ignoring multiple testing
apply(PM, 2, function(x) mean(x <= 0.05))
```

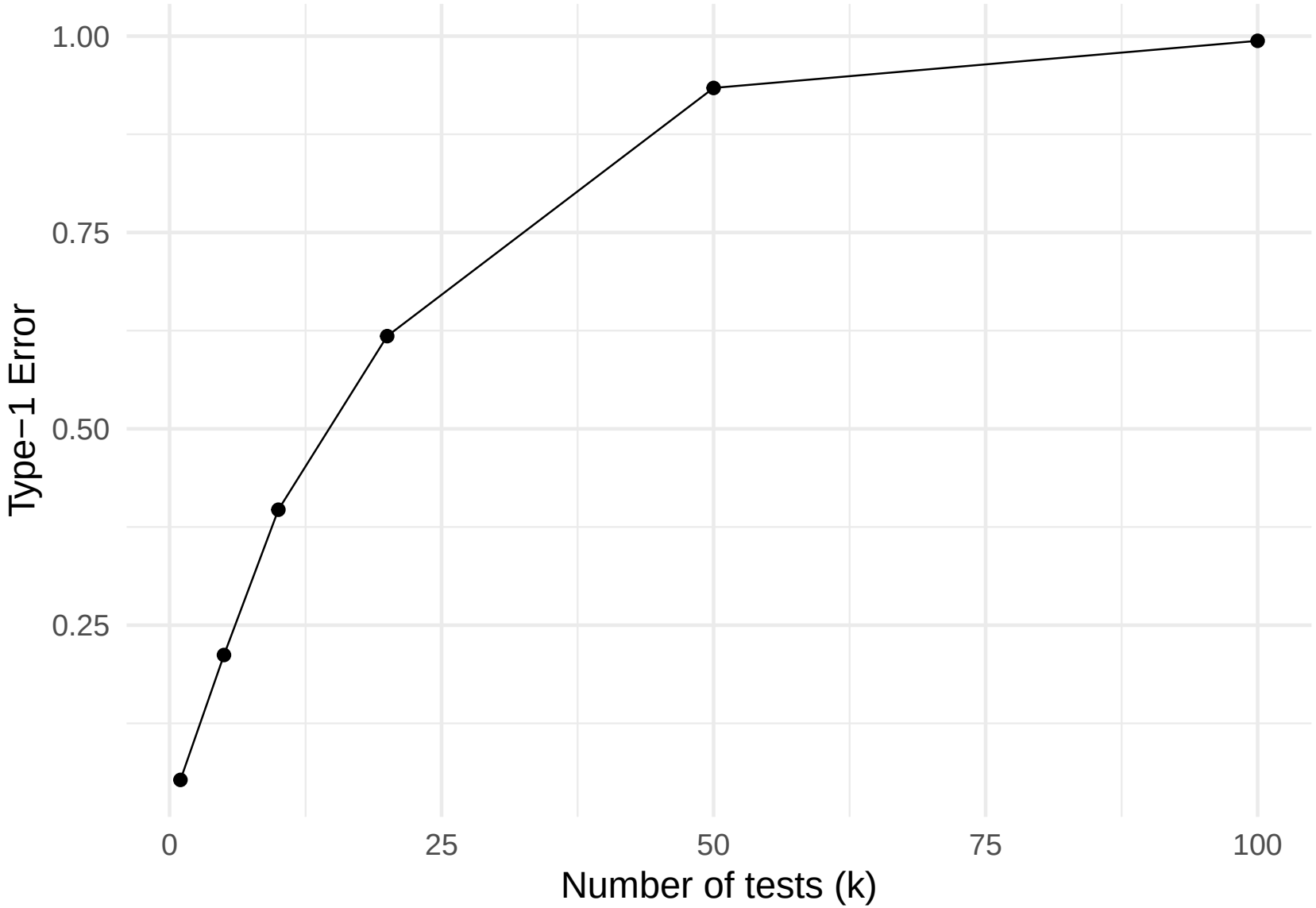
```
 [1] 0.048 0.045 0.055 0.052 0.052 0.061 0.049 0.049 0.056 0.059
```

```r
# type-1 error considering the k tests (should be alpha)
mean(apply(PM, 1, function(x) any(x <= 0.05)))
```

```
[1] 0.427
```

Why? multiple testing problem!

To have a better overview, we can repeat the simulation for different number of k. Quite scary right?



So what? No multiverse?

Exploring is fine and is quite important if not fundamental. But, when we explore the p-values thus the **inferential** results from the single scenarios, we are inflating the type-1 error and our **inferential** conclusions are no longer valid.

So what? No multiverse?

Exploring is fine and is quite important if not fundamental. But, when we explore the p-values thus the **inferential** results from the single scenarios, we are inflating the type-1 error and our **inferential** conclusions are no longer valid.

If we want an inferential answer from our multiverse (not always the case) we need a proper inferential framework. This is the role of the **inferential multiverse analaysis**.

Inferential Multiverse Analysis (IMA)

Correcting the p-values

The main problem is the adjustment for multiple testing. The number of tests in a multiverse can be quite large.

Correcting the p-values

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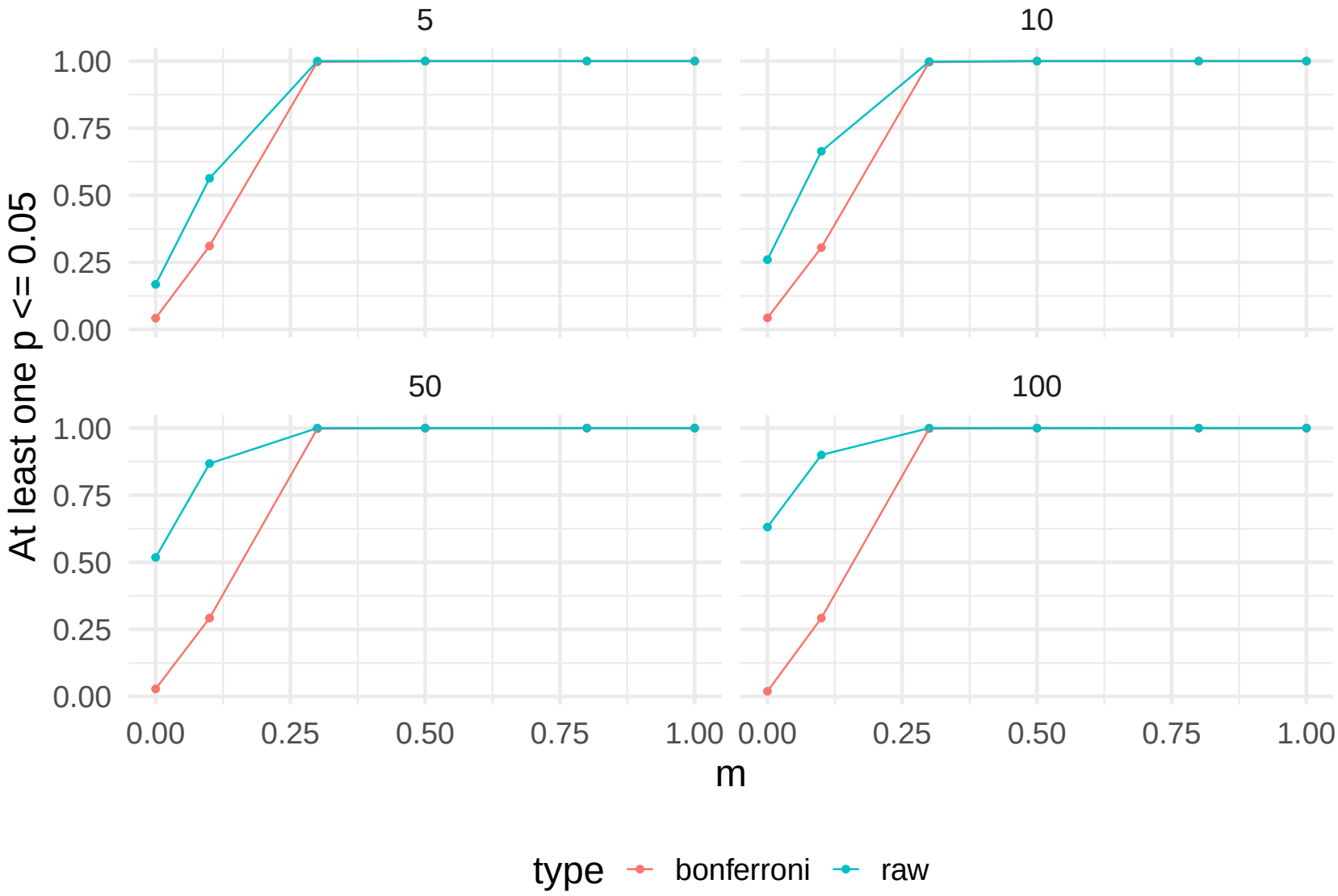
As an example, we simulated a series of tests with different effect size to show the impact on the type-1 error rate and the power.

Correcting the p-values

Using a standard method (e.g., Bonferroni) clearly controls the type-1 error but reduces a lot the statistical power.



Inferential Tools

- Specification Curve
- Post-Selection Inference in Multiverse Analysis (PIMA)

Specification Curve

Intuition of the Specification Curve

The PIMA recipe... (Girardi et al., 2024)

For constructing the inferential approach with PIMA we need:

- a flexible modelling framework: **Generalized Linear Models**
- a permutation-based inferential approach: **Flipscores**
- a permutation-based and powerful method for weak and strong FWER control: **maxT**

Intuition of PIMA

References

Girardi, P., Vesely, A., Lakens, D., Altoè, G., Pastore, M., Calcagnì, A., & Finos, L. (2024). Post-selection inference in multiverse analysis (PIMA): An inferential framework based on the sign flipping score test. *Psychometrika*, *89*, 542–568. https://doi.org/10.1007/s11336-024-09973-6

Klau, S., Felix, Patel, C. J., Ioannidis, J. P. A., Boulesteix, A.-L., & Hoffmann, S. (2023). Comparing the vibration of effects due to model, data pre-processing and sampling uncertainty on a large data set in personality psychology. *Meta-Psychology*, *7*. https://doi.org/10.15626/mp.2020.2556

McCaughey, N. J., Hill, T. G., & Mackinnon, S. P. (2022). The association of self-efficacy, anxiety sensitivity, and perfectionism with statistics and math anxiety. *Personality Science*, *3*. https://doi.org/10.5964/ps.7091

Patel, C. J., Burford, B., & Ioannidis, J. P. A. (2015). Assessment of vibration of effects due to model specification can