

Integrating Proposed Changes into the `subscreenfunnel_fix` Function

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Here's how to integrate the proposed changes into your `subscreenfunnel_fix` function:

1 Step 1: Replace the Current Wrong Approach

Find this section in your function:

```
1 # REMOVE THIS SECTION:
2 if (stratified) {
3   trts <- unique(as.data.frame(data)[,treat])
4   lowest_nr_subject_by_trt <- min(nrow(data[data[treat] == trts[1],]),
5     nrow(data[data[treat] == trts[2],]))
6   sampsize <- ifelse(
7     sampsize > lowest_nr_subject_by_trt,
8     lowest_nr_subject_by_trt,
9     sampsize
10  )
11  all_samples <- replicate(nperm, weightedSampler(data_trimmed, treat,
12    sampsize))
13 } else if (!stratified) {
14   all_samples <- replicate(nperm, dplyr::slice_sample(data_trimmed, n =
15     sampsize))
16 }
```

2 Step 2: Add the Corrected Approach

Replace with this:

```
1 # CORRECT: Permute treatment assignments within subgroups
2 generate_permuted_data <- function(data, treat, nperm) {
3   lapply(1:nperm, function(i) {
4     permuted_data <- data
5     permuted_data[, treat] <- sample(data[, treat]) # Permute
6       treatment labels
7     return(permuted_data)
8   })
9 }
10 # Generate permuted datasets
11 all_samples <- generate_permuted_data(data_trimmed, treat, nperm)
```

3 Step 3: Update the Sampling Logic

Also update the section that processes the samples:

```
1 # OLD CODE:
2 tmp <- furrr::future_map2(rep(1:nperm,length(nsamp)), rep(nsamp, each =
  nperm), function(x, y) {
3   tmp1 <- data.frame(eval_function(data.frame(all_samples[,x])[1:y,]))
4   tmp1$n <- y
5   tmp1
6 }, .options=furrr::furrr_options(seed = TRUE))
7
8 # NEW CODE:
9 tmp <- furrr::future_map2(rep(1:nperm,length(nsamp)), rep(nsamp, each =
  nperm), function(x, y) {
10  # Sample y subjects from the x-th permuted dataset
11  sampled_data <- dplyr::slice_sample(all_samples[[x]], n = y)
12  tmp1 <- data.frame(eval_function(sampled_data))
13  tmp1$n <- y
14  tmp1
15 }, .options=furrr::furrr_options(seed = TRUE))
```

4 Complete Fixed Function

Here's your complete function with all the corrections:

```
1 subscreenfunnel_fix <- function(
2   data,
3   H,
4   eval_function,
5   min_start = 2,
6   n_support_points = 50,
7   nperm = 200,
8   alpha = 0.001,
9   stratified = TRUE,
10  treat = "treat",
11  endpoints = NULL,
12  verbose = TRUE,
13  nkernel = 1,
14  ...
15 ) {
16
17  #### WARNING & ERROR MESSAGES ####
18  if (!is.logical(verbose) || is.na(verbose)) {
19    stop("parameter verbose needs to be logical (TRUE/FALSE) and non-
      missing!")
20  }
21  if (verbose == TRUE) {
22    cat("\n",
23      "subscreenfunnel started at ",
24      format(Sys.time(),
25        format = "%F %R %Z"
26      )
27  )
28  }
```

```

27   )
28   pt1 <- Sys.time()
29 }
30
31 sampsize <- H$results_total$N.of.subjects
32
33 # Generate vector of support points between min and max sample sizes
34 sqrtvec <- seq(
35   sqrt(min_start),
36   by = (sqrt(sampsize) - sqrt(min_start))/n_support_points,
37   length.out = (n_support_points+1)
38 )
39 nsamp <- matrix(round(sqrtvec^2), nrow = 1)
40
41 # First we only remove covariates, since they are not of interest,
42 data_trimmed <- data[,c(treat, endpoints)]
43
44 # CORRECTED: Permute treatment assignments within subgroups
45 generate_permuted_data <- function(data, treat, nperm) {
46   lapply(1:nperm, function(i) {
47     permuted_data <- data
48     permuted_data[, treat] <- sample(data[, treat]) # Permute
49       treatment labels
50     return(permuted_data)
51   })
52 }
53
54 # Generate permuted datasets (replaces the old all_samples logic)
55 all_samples <- generate_permuted_data(data_trimmed, treat, nperm)
56
57 future::plan("multisession", workers = nkernel)
58
59 # CORRECTED: Sample from permuted datasets
60 tmp <- furrr::future_map2(rep(1:nperm, length(nsamp)), rep(nsamp, each
61   = nperm), function(x, y) {
62   # Sample y subjects from the x-th permuted dataset
63   sampled_data <- dplyr::slice_sample(all_samples[[x]], n = y)
64   tmp1 <- data.frame(eval_function(sampled_data))
65   tmp1$n <- y
66   tmp1
67 }, .options=furrr::furrr_options(seed = TRUE))
68
69 # FIXED: Replace rbind.fill with dplyr::bind_rows
70 tmp2 <- dplyr::bind_rows(tmp)
71
72 tmp3 <- tmp2 %>%
73   dplyr::as_tibble() %>%
74   dplyr::group_by(n) %>%
75   dplyr::summarise_all(~quantile(., probs = c(alpha/2, 1-(alpha/2)),
76     na.rm = TRUE)) %>%
77   dplyr::mutate(alpha = c(alpha/2, 1-(alpha/2))) %>%
78   dplyr::ungroup()
79
80 H$funnel_quantiles <- data.frame(tmp3)

```

```

78   pt2 <- Sys.time()
79   if (verbose == TRUE) {
80     cat("\n", "Time for funnel calculation(s): ", pt2 - pt1)
81   }
82   return(H)
83 }

```

5 Key Changes Made:

- **Removed** the problematic `replicate(nperm, slice_sample(...))` approach
- **Added** the `generate_permuted_data()` function that properly permutes treatment assignments
- **Updated** the sampling logic to work with the list of permuted datasets
- **Fixed** the `rbind.fill` issue with `dplyr::bind_rows`
- **Updated** the deprecated `dplyr::funs()` to the modern `syntax`

6 What This Achieves:

- **Proper null hypothesis simulation:** Treatment assignments are permuted while maintaining the original data structure
- **Correct funnel boundaries:** The quantiles now represent the true null distribution
- **Better statistical validity:** Subgroup effects are tested against the appropriate null distribution

The funnel plot will now correctly represent what you'd expect to see under the null hypothesis of no treatment effect.