

Case-Control with Gestational Age Matching

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1 Combine Tables

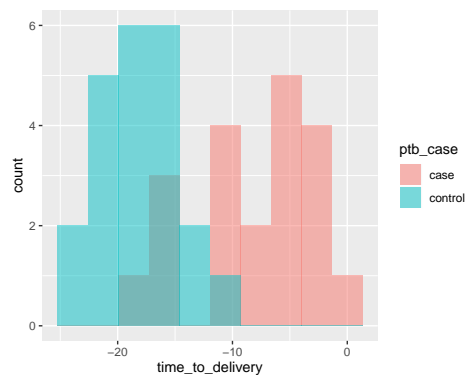
Combine sample tables from stimulated and unstimulated matchings for table in paper.

```
library("readr")
library("dplyr")
library("magrittr")
library("ggplot2")
sample_table_matched_stim = read_csv("sample_table_matched_stim.csv")
sample_table_matched_unstim = read_csv("sample_table_matched_unstim.csv")
sample_table = bind_rows(sample_table_matched_stim,
                          sample_table_matched_unstim)
sample_table %<>% distinct(ptidno, .keep_all = TRUE)
sample_table %<>% dplyr::select(-pair)
write_csv(sample_table, path = "sample_table_case_control_combined.csv")
```

Characteristics of the study population.

```
sample_table %<>% mutate(
  time_to_delivery = gestage_pbmc_collected - gestage_delivery
)
sample_table %>%
  group_by(ptb_case) %>%
  summarize(median_time_to_delivery = median(time_to_delivery))
## # A tibble: 2 x 2
##   ptb_case median_time_to_delivery
##   <chr>          <dbl>
## 1 case          -6.7
## 2 control       -19
wilcox.test(time_to_delivery ~ ptb_case, data = sample_table)
## Warning in wilcox.test.default(x = c(-5.6, -18.3, -14.7, -11.6, -10.2,
## -14.9, : cannot compute exact p-value with ties
##
## Wilcoxon rank sum test with continuity correction
##
## data:  time_to_delivery by ptb_case
## W = 417.5, p-value = 6.98e-07
## alternative hypothesis: true location shift is not equal to 0
ggplot(sample_table, aes(time_to_delivery, fill = ptb_case)) +
  geom_histogram(bins = 10, alpha = 0.5, position = "identity")
```

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Session info.

```
sessionInfo()
## R version 3.5.1 (2018-07-02)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS 10.15.1
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] ggplot2_3.2.1  magrittr_1.5    dplyr_0.8.3    readr_1.3.1
## [5] BiocStyle_2.10.0
##
## loaded via a namespace (and not attached):
## [1] Rcpp_1.0.3      pillar_1.4.2    compiler_3.5.1
## [4] BiocManager_1.30.4 tools_3.5.1      zeallot_0.1.0
## [7] digest_0.6.22   evaluate_0.13    tibble_2.1.3
## [10] gtable_0.3.0    pkgconfig_2.0.3  rlang_0.4.1
## [13] cli_1.1.0       yaml_2.2.0       xfun_0.6
## [16] withr_2.1.2     stringr_1.4.0    knitr_1.22
## [19] vctrs_0.2.0     hms_0.5.2        grid_3.5.1
## [22] tidyselect_0.2.5 glue_1.3.1        R6_2.4.1
## [25] fansi_0.4.0     rmarkdown_1.12   bookdown_0.9
## [28] purrr_0.3.3     backports_1.1.5  scales_1.0.0
## [31] htmltools_0.3.6 assertthat_0.2.1  colorspace_1.4-1
## [34] labeling_0.3     utf8_1.1.4       stringi_1.4.3
## [37] lazyeval_0.2.2   munsell_0.5.0    crayon_1.3.4
```