Test combat-seq

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```r
library(sva)
```

```
## Loading required package: mgcv

## Loading required package: nlme

## This is mgcv 1.8-31. For overview type 'help("mgcv-package")'.

## Loading required package: genefilter

## Loading required package: BiocParallel
```

```r
library(edgeR)
```

```
## Loading required package: limma
```

```r
sessionInfo()
```

```
## R version 3.6.2 (2019-12-12)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Mojave 10.14.5
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.6/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] edgeR_3.28.0        limma_3.42.0        sva_3.33.2
## [4] BiocParallel_1.20.1 genefilter_1.68.0   mgcv_1.8-31
## [7] nlme_3.1-143
##
## loaded via a namespace (and not attached):
## [1] Rcpp_1.0.3          pillar_1.4.3          compiler_3.6.2
```

```
##  [4] bitops_1.0-6        tools_3.6.2        zeallot_0.1.0
##  [7] digest_0.6.23       bit_1.1-15.1       memoise_1.1.0
## [10] annotate_1.64.0     evaluate_0.14      RSQLite_2.2.0
## [13] tibble_2.1.3        lattice_0.20-38    pkgconfig_2.0.3
## [16] rlang_0.4.2         Matrix_1.2-18      DBI_1.1.0
## [19] yaml_2.2.0          parallel_3.6.2     xfun_0.12
## [22] stringr_1.4.0       knitr_1.27         IRanges_2.20.2
## [25] S4Vectors_0.24.3    vctrs_0.2.1        locfit_1.5-9.1
## [28] stats4_3.6.2        bit64_0.9-7        grid_3.6.2
## [31] Biobase_2.46.0      AnnotationDbi_1.48.0 survival_3.1-8
## [34] XML_3.99-0.3        rmarkdown_2.1      blob_1.2.1
## [37] magrittr_1.5        matrixStats_0.55.0 backports_1.1.5
## [40] htmltools_0.4.0     splines_3.6.2     BiocGenerics_0.32.0
## [43] xtable_1.8-4        stringi_1.4.5     RCurl_1.98-1.1
## [46] crayon_1.3.4
```

```r
source("~/Downloads/sva 2/R/ComBat_seq.R")
source("~/Downloads/sva 2/R/helper_seq.R")

dat <- rbind(c(1533, 1503, 1387, 1258, 1657, 1139, 989, 935, 902, 829, 913, 1153),
             c(16, 19, 19, 32, 48, 17, 9, 12, 10, 16, 7, 7),
             c(7, 216, 83, 65, 30, 3, 4, 4, 0, 5, 5, 2),
             c(1, 0, 2, 6, 0, 0, 0, 0, 0, 0, 1, 0),
             c(54963, 47549, 45226, 39082, 53703, 47144, 16344, 18281, 15508, 16260, 16299, 21966),
             c(1177, 1066, 1079, 843, 933, 930, 785, 667, 805, 650, 704, 710),
             c(63, 65, 56, 38, 45, 39, 17, 12, 15, 10, 20, 20),
             c(165, 179, 276, 233, 351, 81, 78, 51, 46, 57, 60, 50),
             c(162, 135, 163, 216, 138, 136, 90, 79, 78, 65, 93, 79),
             c(1809, 1613, 1378, 2227, 1752, 1561, 408, 482, 297, 394, 311, 368))
batch <- c(rep(1, 6), rep(2, 6))
group <- c(0,0,0,1,1,1,0,0,0,2,2,2)

adj_dt <- ComBat_seq(dat, batch=batch, group=group)
```

```
## Found 2 batches
## Using full model in ComBat-seq.
## Adjusting for 2 covariate(s) or covariate level(s)
## Estimating dispersions
## Fitting the GLM model
## Shrinkage off - using GLM estimates for parameters
## Adjusting the data
```

```r
print(class(adj_dt))
```

```
## [1] "matrix"
```

```r
print(dim(adj_dt))
```

```
## [1] 10 12
```