

Decoding Analysis

Run the decoding analysis

```
devtools::install_github("emeyers/NeuroDecodeR")
```

```
## Downloading GitHub repo emeyers/NeuroDecodeR@HEAD
```

```
## vctrs      (0.3.8 -> 0.6.2 ) [CRAN]
## stringi    (1.7.6 -> 1.7.12) [CRAN]
## rlang      (1.0.1 -> 1.1.1 ) [CRAN]
## magrittr   (2.0.2 -> 2.0.3 ) [CRAN]
## lifecycle  (1.0.1 -> 1.0.3 ) [CRAN]
## glue       (1.6.1 -> 1.6.2 ) [CRAN]
## cli        (3.2.0 -> 3.6.1 ) [CRAN]
## withr      (2.4.3 -> 2.5.0 ) [CRAN]
## utf8       (1.2.2 -> 1.2.3 ) [CRAN]
## fansi      (1.0.2 -> 1.0.4 ) [CRAN]
## tidyselect (1.1.2 -> 1.2.0 ) [CRAN]
## tibble     (3.1.6 -> 3.2.1 ) [CRAN]
## pillar     (1.7.0 -> 1.9.0 ) [CRAN]
## generics   (0.1.2 -> 0.1.3 ) [CRAN]
## colorspace (2.0-3 -> 2.1-0 ) [CRAN]
## R.methodsS3 (1.8.1 -> 1.8.2 ) [CRAN]
## R.oo        (1.24.0 -> 1.25.0) [CRAN]
## viridisLite (0.4.0 -> 0.4.1 ) [CRAN]
## RColorBrewer (1.1-2 -> 1.1-3 ) [CRAN]
## farver      (2.1.0 -> 2.1.1 ) [CRAN]
## cpp11       (0.4.2 -> 0.4.3 ) [CRAN]
## stringr     (1.4.0 -> 1.5.0 ) [CRAN]
## purrr       (0.3.4 -> 1.0.1 ) [CRAN]
## dplyr       (1.0.8 -> 1.1.2 ) [CRAN]
## R.utils     (2.11.0 -> 2.12.2) [CRAN]
## gtable      (0.3.0 -> 0.3.3 ) [CRAN]
## scales      (1.1.1 -> 1.2.1 ) [CRAN]
## isoband     (0.2.5 -> 0.2.7 ) [CRAN]
## proxy       (0.4-26 -> 0.4-27) [CRAN]
## tidyr       (1.2.0 -> 1.3.0 ) [CRAN]
## tictoc      (1.0.1 -> 1.2   ) [CRAN]
## R.matlab    (3.6.2 -> 3.7.0 ) [CRAN]
## ggplot2     (3.3.5 -> 3.4.2 ) [CRAN]
## forcats     (0.5.1 -> 1.0.0 ) [CRAN]
## e1071       (1.7-9 -> 1.7-13) [CRAN]
```

```
## Installing 35 packages: vctrs, stringi, rlang, magrittr, lifecycle, glue, cli, withr, utf8, fansi, t.
```

```
## Installing packages into '/vast/palmer/home.grace/em939/R/x86_64-pc-linux-gnu-library/4.1'
## (as 'lib' is unspecified)

## Warning in i.p(...): installation of package 'rlang' had non-zero exit status

## Warning in i.p(...): installation of package 'lifecycle' had non-zero exit
## status

## Warning in i.p(...): installation of package 'vctrs' had non-zero exit status

## Warning in i.p(...): installation of package 'gtable' had non-zero exit status

## Warning in i.p(...): installation of package 'tidyselect' had non-zero exit
## status

## Warning in i.p(...): installation of package 'pillar' had non-zero exit status

## Warning in i.p(...): installation of package 'stringr' had non-zero exit status

## Warning in i.p(...): installation of package 'purrr' had non-zero exit status

## Warning in i.p(...): installation of package 'tibble' had non-zero exit status

## Warning in i.p(...): installation of package 'dplyr' had non-zero exit status

## Warning in i.p(...): installation of package 'ggplot2' had non-zero exit status

## Warning in i.p(...): installation of package 'tidyr' had non-zero exit status

##      checking for file '/tmp/RtmpXkfKZn/remotes59a77764b49b/emeyers-NeuroDecodeR-c9176a8/DESCRIPTION
## - preparing 'NeuroDecodeR':
##      checking DESCRIPTION meta-information ... v checking DESCRIPTION meta-information
## - checking for LF line-endings in source and make files and shell scripts
## - checking for empty or unneeded directories
##      Omitted 'LazyData' from DESCRIPTION
## - building 'NeuroDecodeR_0.1.0.9000.tar.gz'
##
##

## Installing package into '/vast/palmer/home.grace/em939/R/x86_64-pc-linux-gnu-library/4.1'
## (as 'lib' is unspecified)
```

```
library(NeuroDecodeR)
```

```
# I have access to William's files so I can load this data...
```

```
#binned_data <- file.path('/home/wz354/project/NeuralDecoding/NeuralDecoding/data/binned/ZD_150bins_50#
```

```
binned_data <- file.path('/home/em939/research/test_william_cluster_code/gitignore/ZD_150bins_50sampled
```

```

ds <- ds_basic(
  binned_data = binned_data,
  labels = 'combined_ID_position',
  num_label_repeats_per_cv_split = 1,
  num_cv_splits = 2,
  num_resample_sites = 132)

## Automatically selecting sites_IDs_to_use. Since num_cv_splits = 2 and num_label_repeats_per_cv_split

cl <- cl_max_correlation(return_decision_values = TRUE)

fp_zs <- fp_zscore()

fps <- list(fp_zs)

rm_main <- rm_main_results(
  include_norm_rank_results = TRUE)
rm_cm <- rm_confusion_matrix(
  save_TCD_results = TRUE,
  create_decision_vals_confusion_matrix = TRUE)
rms <- list(rm_main, rm_cm)

cv <- cv_standard(
  datasource = ds,
  classifier = cl,
  feature_preprocessors = fps,
  result_metrics = rms)

DECODING_RESULTS <- run_decoding(cv)

## |

paste('The analysis ID is:',
  DECODING_RESULTS$cross_validation_paramaters$analysis_ID)

## [1] "The analysis ID is: 20230501_162621_88927"

log_save_results(DECODING_RESULTS,
  file.path('/home/em939/research/test_william_cluster_code/results', 'decoding_results', 'decoding_r

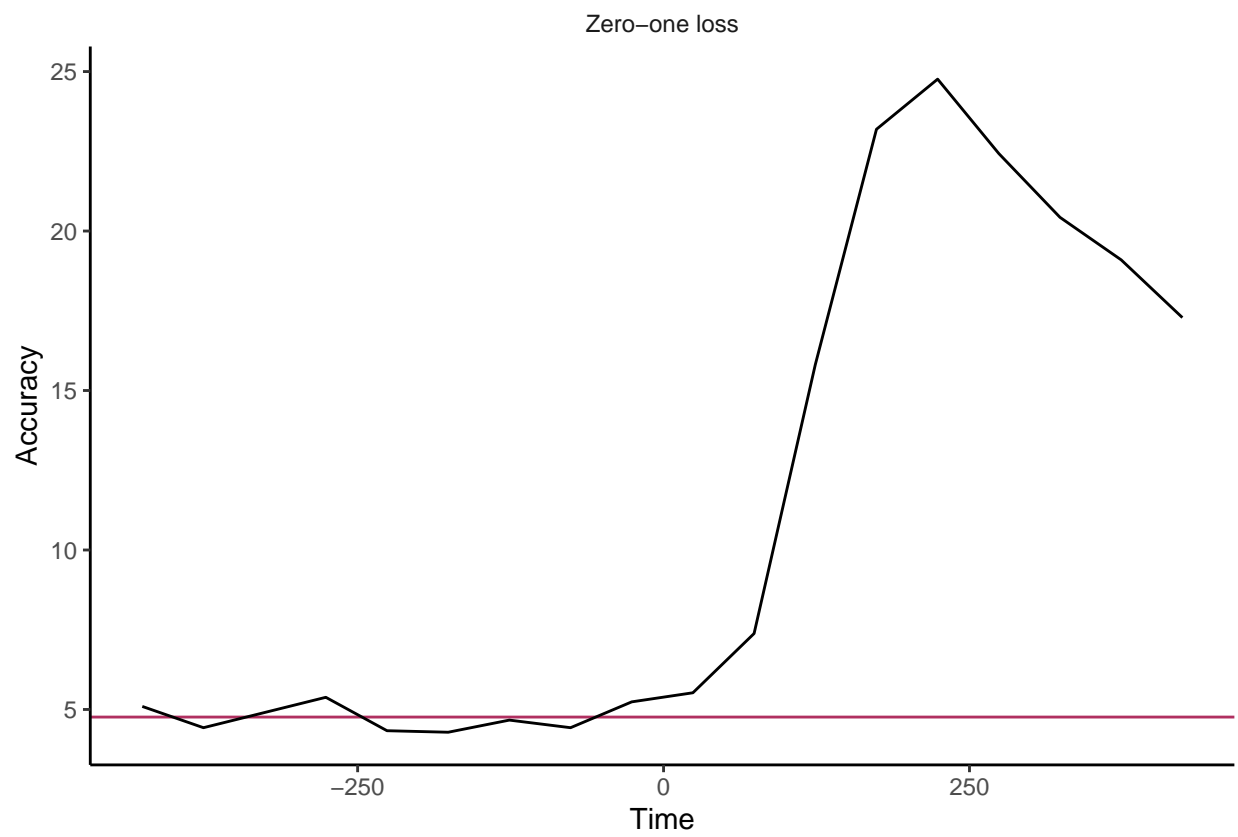
```

Plot some results

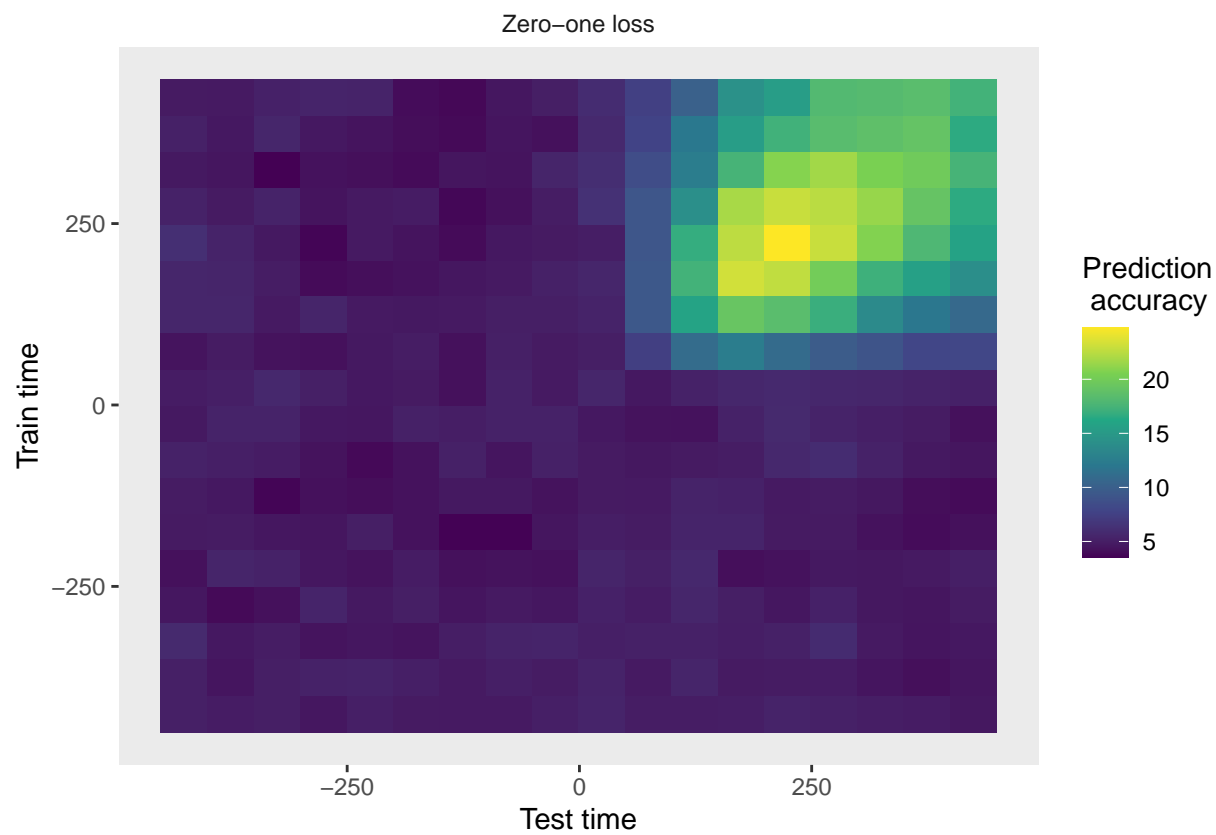
```

plot(DECODING_RESULTS$rm_main_results, type = 'line')

```



```
plot(DECODING_RESULTS$rm_main_results)
```



```
plot(DECODING_RESULTS$rm_confusion_matrix)
```

