Decoding Analysis

Run the decoding analysis

```r
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_50sa


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
```

```r
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)
```
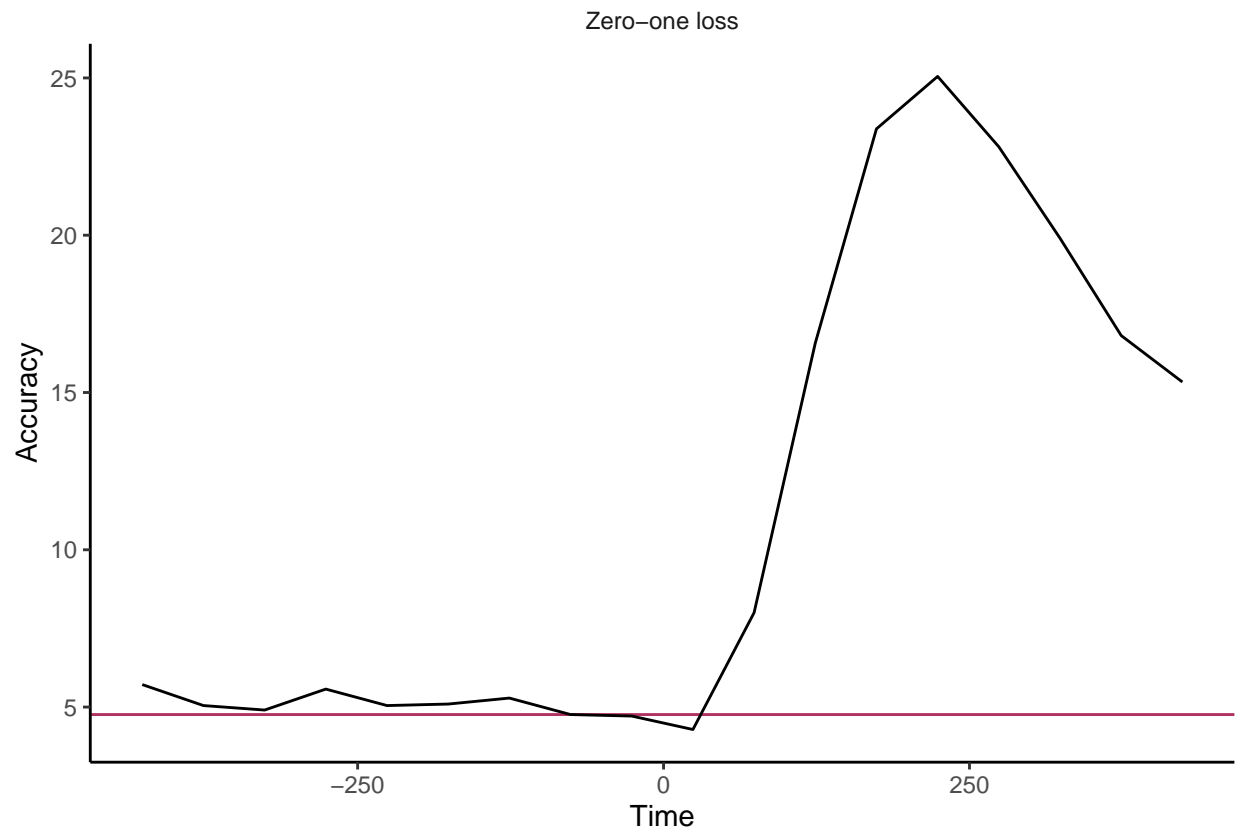
```
## [1] "The analysis ID is: 20230501_144651_62444"
```

```
log_save_results(DECODING_RESULTS,
    file.path('/home/em939/research/test_william_cluster_code/results', 'decoding_results', 'decoding_r
```
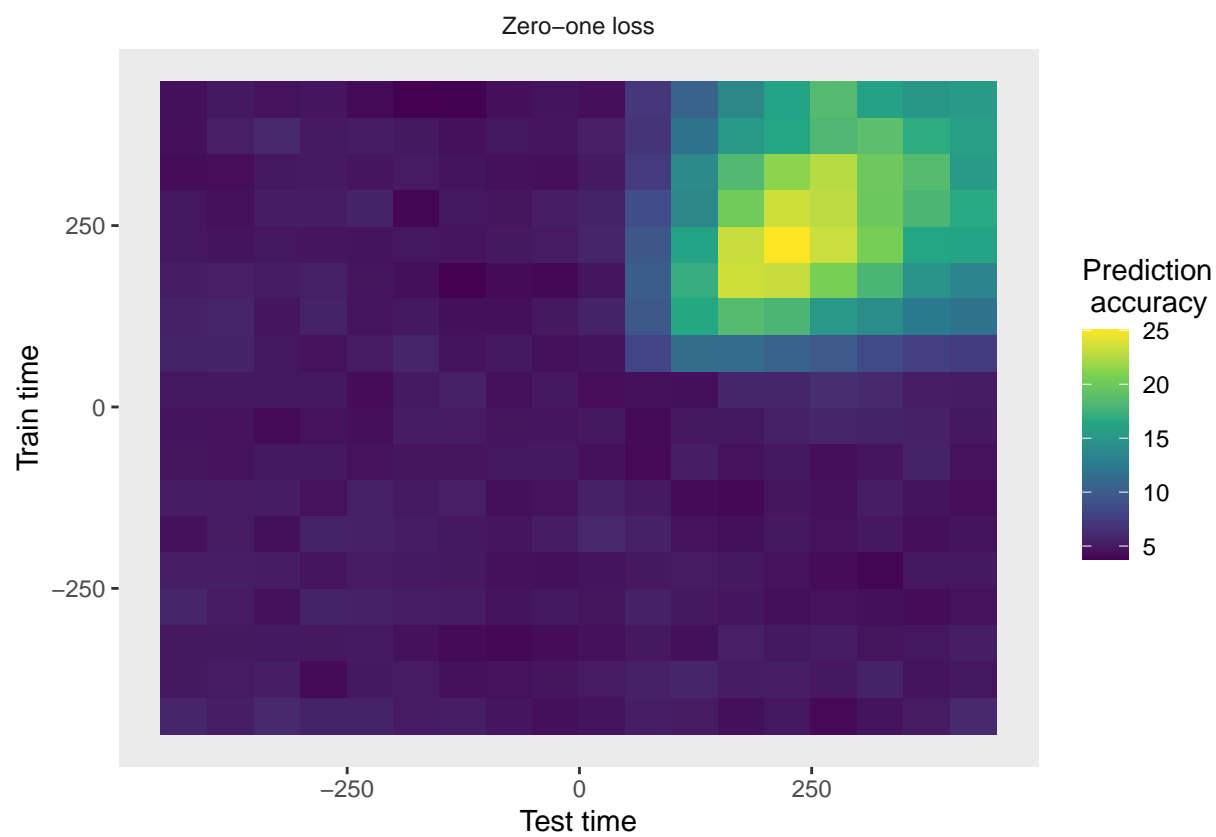
```
## Warning in log_save_results(DECODING_RESULTS,
## file.path("/home/em939/research/test_william_cluster_code/results", : The
## results with the same parameters already exist. Still going ahead and saving the
## results.
```

Plot some results

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



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

Zero–one loss

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

True class

Predicted class

Prediction frequency