

Decoding Analysis

```
load('/home/em939/shared_projects/allen_brain_observatory_data/allen_binned_data/100bins_5sampled/session100bins_5sampled.RData')
nrow(binned_data)
```

```
## [1] 5259800
```

Run the decoding analysis

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

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_50sampled.RData')

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

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)

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)

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)

```