## Decoding Analysis

```
binned_file_name <-'/srv/shiny-server/research/all_NDTr/all_ShinyNDTr/ShinyNDTr/data/binned/ZD_150bins_
variable_to_decode <-'stimulus_ID'</pre>
num_cv_splits <- 5</pre>
ds <- NDTr::ds_basic(binned_file_name, variable_to_decode, num_cv_splits,
                      num_label_repeats_per_cv_split = 2)
cl <- NDTr::cl_max_correlation()</pre>
fps <- list(NDTr::fp_zscore())</pre>
cv <- NDTr::cv standard(ds, cl, fps, NULL, 2)</pre>
DECODING_RESULTS <- NDTr::run_decoding(cv)</pre>
'Decodings results analysis ID:'
## [1] "Decodings results analysis ID:"
DECODING_RESULTS$cross_validation_paramaters$analysis_ID
## [1] "20200807_174618_28269"
NDTr::log_save_results(DECODING_RESULTS, '/srv/shiny-server/research/all_NDTr/all_ShinyNDTr/ShinyNDTr/r
## Warning in NDTr::log_save_results(DECODING_RESULTS, "/srv/shiny-server/
## research/all_NDTr/all_ShinyNDTr/ShinyNDTr/results"): The results with the
## same parameters already exist. Still going ahead and saving the results.
plot(DECODING_RESULTS$rm_main_results)
```

