

Decoding Analysis

```
binmed_file_name <- '/student/15/xf15/GitHub/shinyNDTr/data/binmed/ZD_150_samples_binmed_every_20_samples'
variable_to_decode <- 'combined_ID_position'
num_cv_splits <- 5
ds <- NDTr::basic_DS$new(binmed_file_name, variable_to_decode, num_cv_splits)
ds$num_repeats_per_level_per_cv_split <- 2
cl <- NDTr::max_correlation_CL$new()
fps <- list()
cv <- NDTr::standard_CV$new(ds, cl, fps)
DECODING_RESULTS <- cv$run_decoding()
```

```
## [1] 1
## 7.216 sec elapsed
## [1] 2
## 7.579 sec elapsed
## [1] 3
## 7.392 sec elapsed
## [1] 4
## 7.992 sec elapsed
## [1] 5
## 7.669 sec elapsed
```

```
save('DECODING_RESULTS', file = '/student/15/xf15/GitHub/shinyNDTr/results/rmd.rda')
```