

DRUMLR_Building_example

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```
knitr::opts_chunk$set(echo = TRUE)
#load libraries
library(dplyr)
library(DRUMLR)
```

Import and scale data

```
#import datasets
df_input <- DRUMLRdata::DRUMLphos %>% scale(center = T, scale = T)
df_response <- DRUMLRdata::DRUMLaac

#get list of AML cell lines
aml_cells <-
  DRUMLRdata::DRUMLcellinfo[DRUMLRdata::DRUMLcellinfo$unique.tissue == "AML", "Cell.name"]
input_cells <- DRUMLR::RemoveRepeatNo(colnames(df_input))

#filter input by cell line
df_input_aml <- df_input[, input_cells %in% aml_cells]

#filter drugs by biological range
drugs <-
  DRUMLR::FilterSensitivity(
    sensitivity_database = df_response,
    iqr_tolerance = 0.1,
    n_coverage = 0.8,
    cell_names = aml_cells
  )
```

Generate markers

```
markers <-
  DRUMLR::BuildEMDR(
    df_input = df_input_aml,
    df_response = t(df_response),
    drugs = drugs,
    computational_load = 0.8,
  )
```

##Build Models function .BuildModels contains the paramaters used for the models

```

Model_info <-
  DRUMLR::BuildDRUMLs(
    df_input = df_input_aml,
    .marker_database = markers,
    input_type = "aml_phospho",
    save_path = "~/DRUML_models",
    save_csv = T,
    models = "all",
    df_response = df_response,
    drugs = drugs,
    computational_load = 0.8
  )

```

Predict_validation data

```

df_validation <- external_data

df_validation_dist <-
  DRUMLR::DrugMarkerEnrichment(df = df_validation, marker_database = markers)

df_predictions <-
  DRUMLR::PredictDRUML(df_distance = df_validation_dist,
    models = "all",
    models_dir = "~/DRUML_models")

```