**This folder contains R script to run leave-one-out cross-validation (LOOCV) for metastatic model based on dot blot data.**

**Required software**

The scripts use core R functionality and two publicly R available packages listed below. Version numbers in brackets correspond to the versions of the packages that were used to develop and debug these scripts:

* **R** (4.1.2)
* **RStudio** (1.2.5033) - optional, testing functions and running the code step-by-step
* **pROC** (1.16.2) – display and analyze ROC curves
* **caret** (6.0-90) – perform LOOCV analysis

**Running the scripts**

1. Change path of the data folder on the top of the script.
2. Lauch the script. You can run the eitire script at once or execue commends one by one to see the intermediate outputs.
3. Output results are saved as *.csv* (tables) files.

LOOCV-avNNet model.R

* Data import and process groups (using the data “dot blot samples for metastatic model.csv”, “dot blot samples for metastatic model\_DMvsNM.csv” or “dot blot samples for metastatic model\_LNMvsNM.csv”)
* Set trainControl mode to leave-one-out method
* Train averaged neural network (avNNet) model with four proteins
* Train model with four proteins plus CEA
* Output prediction probabilities