## # breast-cancer-wisconsin-Dataset1

## title: Analysis and ML tests on R

bc\_data <- read.table("breast-cancer-wisconsin.data.txt", header = FALSE, sep = ",") colnames(bc\_data) <- c("sample\_code\_number", "clump\_thickness", "uniformity\_of\_cell\_size", "uniformity\_of\_cell\_shape", "marginal\_adhesion", "single\_epithelial\_cell\_size", "bare\_nuclei", "bland\_chromatin", "normal\_nucleoli", "mitosis", "classes") bc\_dataclasses == "2", "benign", ifelse(bc\_data$classes == "4", "malignant", NA)) bc\_data[bc\_data == "?"] <- NA

# how many NAs are in the data

{r message = FALSE, echo=FALSE, message=FALSE, warning=FALSE} length(which(is.na(bc\_data)))

{r basicconsole, echo=TRUE} x <- 1:10 y <- round(rnorm(10, x, 1), 2) df <- data.frame(x, y) df