Exercise 4

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12 10 2020

We load our data (please use your corresponding path)

```
load("C:/Users/Miriam/Box Sync/Masters/IncompleteDataAnalysis/Assignment1_MF/databp.Rdata")
```

4a: Complete case analysis

We create a dataset only of complete observations

```
data_complete <- databp[complete.cases(databp), ]
```

We calculate the mean and standard error of the complete data For the standard error, we define a function calculating the error.

```
mean(data_complete$recovtime)
```

```
## [1] 19.27273
```

```
# sterror = st deviation divided by squareroot of length of data
sterror <- function(x) sd(x)/sqrt(length(x))
sterror(data_complete$recovtime)
```

```
## [1] 2.603013
```

To calculate the pearson correlation, we need to first calculate the correlation matrix (excluding missing cases). We then divide the corresponding entry by the product of the two variables standard deviation. We note than when calculating their standard deviation, we must use only the entries included in our complete case analysis.

```
covcc <- cov(databp, use = "complete")
```

correlation between recovery and dose

```
covcc["logdose", "recovtime"]/(sd(data_complete$logdose) * sd(data_complete$recovtime))
```

```
## [1] 0.2391256
```

correlation between time and bpressure

```
covcc["bloodp", "recovtime"]/(sd(data_complete$bloodp) * sd(data_complete$recovtime))
```

```
## [1] -0.01952862
```

4b: Mean imputation

We first observe that the time is the only variable with missing observations, we thus only need to perform imputation on this variable

```
mean_recov <- mean(databp$recovtime, na.rm = TRUE)
recov_mi <- ifelse(is.na(databp$recovtime), mean_recov, databp$recovtime)
```

Mean and st error of recovtime with mean imputation

```r
data_mi <- data.frame(logdose = databp$logdose, bloodp = databp$bloodp, recovtime = recov_mi)

mean(data_mi$recovtime)
```

```
## [1] 19.27273
```

```r
sterror(data_mi$recovtime)
```

```
## [1] 2.284135
```

We again calculate the pearson correlation, this time on our new dataset with the missing values filled in with the mean (and we don't need to say we only want complete observations as the data is complete)

```r
covmi <- cov(data_mi)
```

correlation between recovery and dose

```r
covmi["logdose", "recovtime"]/(sd(data_mi$logdose) * sd(data_mi$recovtime))
```

```
## [1] 0.2150612
```

correlation between time and bpressure

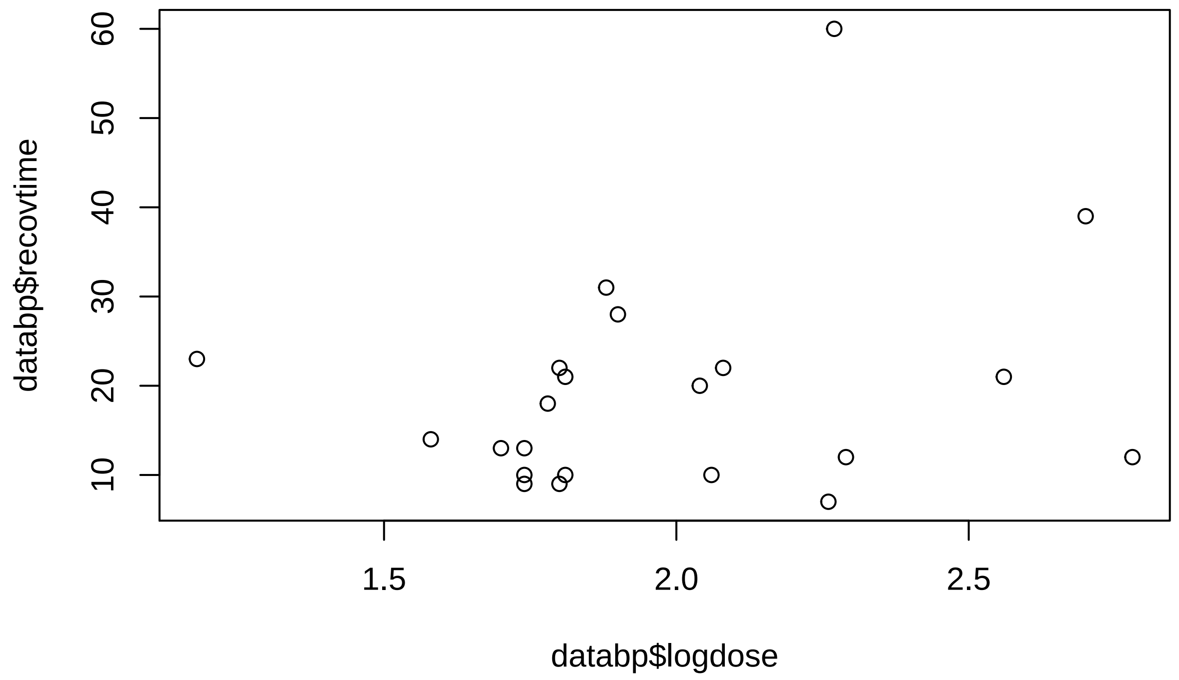
```r
covmi["bloodp", "recovtime"]/(sd(data_mi$bloodp) * sd(data_mi$recovtime))
```

```
## [1] -0.01934126
```

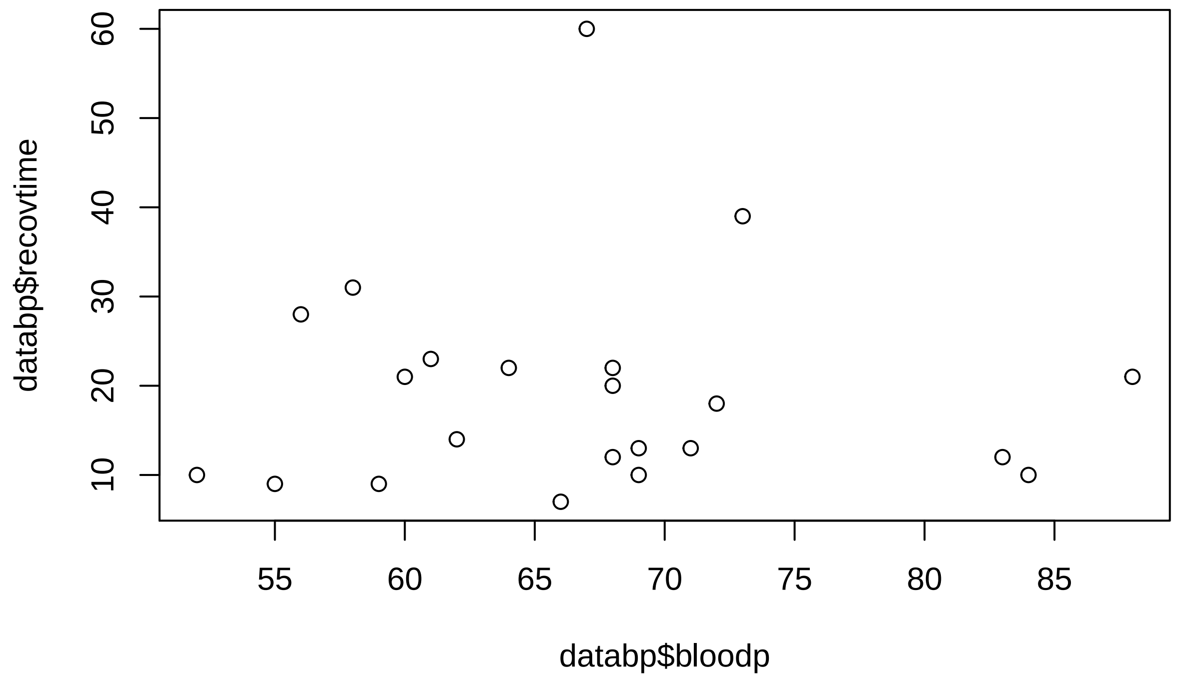
4c: Mean regression imputation

We first plot the variables, to see if the assumption of a linear dependence used for our regression is accurate. Whereas I wouldn't be really confident saying there is a linear dependence, the plots give at least no evidence to say the dependence would be for example logarithmic or quadratic. So in my opinion, this data is more telling us there is no reason not to do linear regression, more than they say there is reason to do linear regression.

```r
plot(databp$logdose, databp$recovtime)
```



```r
plot(databp$bloodp, databp$recovtime)
```



We include both of our observed variables into our regression. Our regressionmodel is

$$\text{Recovtime}_i = \beta_0 + \beta_1 * \text{Logdose}_i + \beta_2 * \text{Bloodpressure}_i + \varepsilon_i$$

assuming $\varepsilon_i \overset{iid}{\sim} N(0, \sigma^2)$. We expect $\beta_1 > 0$ and $\beta_2 < 0$. As we have seen a positive correlation between time and dose and a negative correlation between time and bpressure.

```
fit_mr <- lm(databp$recovtime ~ databp$logdose + databp$bloodp)
fit_mr$coefficients
```

```
##    (Intercept) databp$logdose  databp$bloodp
##     15.2159065     11.4290287     -0.2769265
```

We create a new vector with the predicted times and include it to a new dataset with our new predicted values.

```
predicted_time <- predict(fit_mr, newdata = databp)
recov_predict <- ifelse(is.na(databp$recovtime), predicted_time, databp$recovtime)
data_mr <- data.frame(logdose = databp$logdose, bloodp = databp$bloodp, recovtime = recov_predict)
```

Mean and standard error of the predicted dataset

```
mean(data_mr$recovtime)
```

```
## [1] 19.44428
```

```
sterror(data_mr$recovtime)
```

```
## [1] 2.312845
```

Calculating the correlation matrix

```
covmr <- cov(data_mr)
```

correlation between recovery and dose

```
covmr["logdose", "recovtime"]/(sd(data_mr$logdose) * sd(data_mr$recovtime))
```

```
## [1] 0.2801835
```

correlation between time and bpressure

```
covmr["bloodp", "recovtime"]/(sd(data_mr$bloodp) * sd(data_mr$recovtime))
```

```
## [1] -0.0111364
```

4d:

We use the model of 3c and add a random number

```
set.seed(49)

predicted_sri <- predict(fit_mr, newdata = databp) + rnorm(nrow(databp), 0, sigma(fit_mr))
recov_sri <- ifelse(is.na(databp$recovtime), predicted_sri, databp$recovtime)
```

We calculate the mean and standard error

```
data_sri <- data.frame(logdose = databp$logdose, bloodp = databp$bloodp, recovtime = recov_sri)
mean(data_sri$recovtime)
```

```
## [1] 18.72278
```

```
sterror(data_sri$recovtime)
```

```
## [1] 2.341176
```

Calculating the correlation matrix

```
covsri <- cov(data_sri)
```

correlation between recovery and dose

```
covsri["logdose", "recovtime"]/(sd(data_sri$logdose) * sd(data_sri$recovtime))
```

```
## [1] 0.251039
```

correlation between time and bpressure

```
covsri["bloodp", "recovtime"]/(sd(data_sri$bloodp) * sd(data_sri$recovtime))
```

```
## [1] -0.01514032
```

As we include a random error term, we need to make sure that we don't predict negative times. Further, we might consider to limit the fractional part of the predicted values, thus we might include a floor function to our predicted values, making them nonfractional. In that case, we would use

```
recov_sri_int <- ifelse(is.na(databp$recovtime), floor(predicted_sri), databp$recovtime)
data_sri_int <- data.frame(logdose = databp$logdose, bloodp = databp$bloodp, recovtime = recov_sri_int)
```

giving us the following mean, standard error, correlation matrix:

```
mean(data_sri_int$recovtime)
```

```
## [1] 18.64
```

```r
sterror(data_sri_int$recovtime)
```

```
## [1] 2.347964
```

```r
covsriint <- cov(data_sri_int)
covsriint["logdose", "recovtime"]/(sd(data_sri_int$logdose) * sd(data_sri_int$recovtime))
```

```
## [1] 0.2479823
```

```r
covsriint["bloodp", "recovtime"]/(sd(data_sri_int$bloodp) * sd(data_sri_int$recovtime))
```

```
## [1] -0.01684754
```

4e: predictive mean

We define a function which will calculate the index of the closest observed value to our prediction.

```r
mis_index <- which(is.na(databp$recovtime))

best_replace <- function(val) {

    min <- .Machine$integer.max
    ind <- -1
    available_data <- which(is.na(databp$recovtime) == FALSE)

    for (i in available_data) {
        squaredis <- (val - databp$recovtime[i])^2
        if (squaredis < min) {
            min <- squaredis
            ind <- i
        }
    }
    return(ind)
}

recov_prmtp <- 1:length(databp$recovtime)

for (inde in mis_index) {
    best <- best_replace(predicted_sri[inde])
    recov_prmtp[inde] <- databp$recovtime[best]
    cat("datapoint ", inde, " we take value ", databp$recovtime[best], " of index ",
        best, "\n")
}
```

```
## datapoint  4  we take value  7  of index  1
## datapoint  10  we take value  21  of index  7
## datapoint  22  we take value  18  of index  3
```

```r
recov_prm <- ifelse(is.na(databp$recovtime), recov_prmtp, databp$recovtime)
data_prm <- data.frame(logdose = databp$logdose, bloodp = databp$bloodp, recovtime = recov_prm)
```

We calculate the mean and st error

```r
mean(data_sri_int$recovtime)
```

```
## [1] 18.64
```

```r
sterror(data_sri_int$recovtime)
```

```
## [1] 2.347964
```

and the correlation

```r
covprm <- cov(data_prm)
covprm["logdose", "recovtime"]/(sd(data_prm$logdose) * sd(data_prm$recovtime))
```

```
## [1] 0.2590259
```

```r
covprm["bloodp", "recovtime"]/(sd(data_prm$bloodp) * sd(data_prm$recovtime))
```

```
## [1] -0.01407195
```

4f:

One advantage of predictive mean matching is that we can be certain that our predicted values are values which comply with the pattern of the given variable. With that I mean that if our variable is time, and has only integer values, predictive mean matching will also only predict integer values (as it simply takes already given values). Stochastic regression imputation on the other side calculates the value with regression, and might predict non-integer values. However, predictive mean matching can have similar disadvantages to mean imputation: using already existing values as the values for missing data makes the overall data less variable (as we do not add new values to the dataset, but just have already existing data with higher frequency in the data afte the imputation), leading to changes in the standard deviation of the data.