Exploratory Data Analysis

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1. Data Overview

In this study, the dataset we used is called 'colon', which is found in the 'survival' R package. These are data from one of the first successful trials of adjuvant chemotherapy for colon cancer. Levamisole is a low-toxicity compound previously used to treat worm infestations in animals; 5-FU is a moderately toxic (as these things go) chemotherapy agent. There are two records per person, one for recurrence and one for death. There are 1858 observations and 16 variables.

- id: patient id
- study: 1 for all patients
- rx: treatment - Obs(ervation), Lev(amisole), Lev(amisole)+5-FU
- sex: sex (0 = Female, 1 = Male)
- age: observation age in years
- obstruct: obstruction of colon by tumour (0 = No, 1 = Yes)
- perfor: perforation of colon (0 = No, 1 = Yes)
- adhere: adherence to nearby organs (0 = No, 1 = Yes)
- nodes: number of lymph nodes with detectable cancer
- time: days until event or censoring
- status: censoring status (0 = Censored, 1 = Event)
- differ: differentiation of tumour (1 = Well, 2 = Moderate, 3 = Poor)
- extent: extent of local spread (1 = Submucosa, 2 = Muscle, 3 = Serosa, 4 = Contiguous structures)
- surg: time from surgery to registration (0 = Short, 1 = Long)
- node4: more than 4 positive lymph nodes (0 = No, 1 = Yes)
- etype: event type (1 = recurrence, 2 = death)

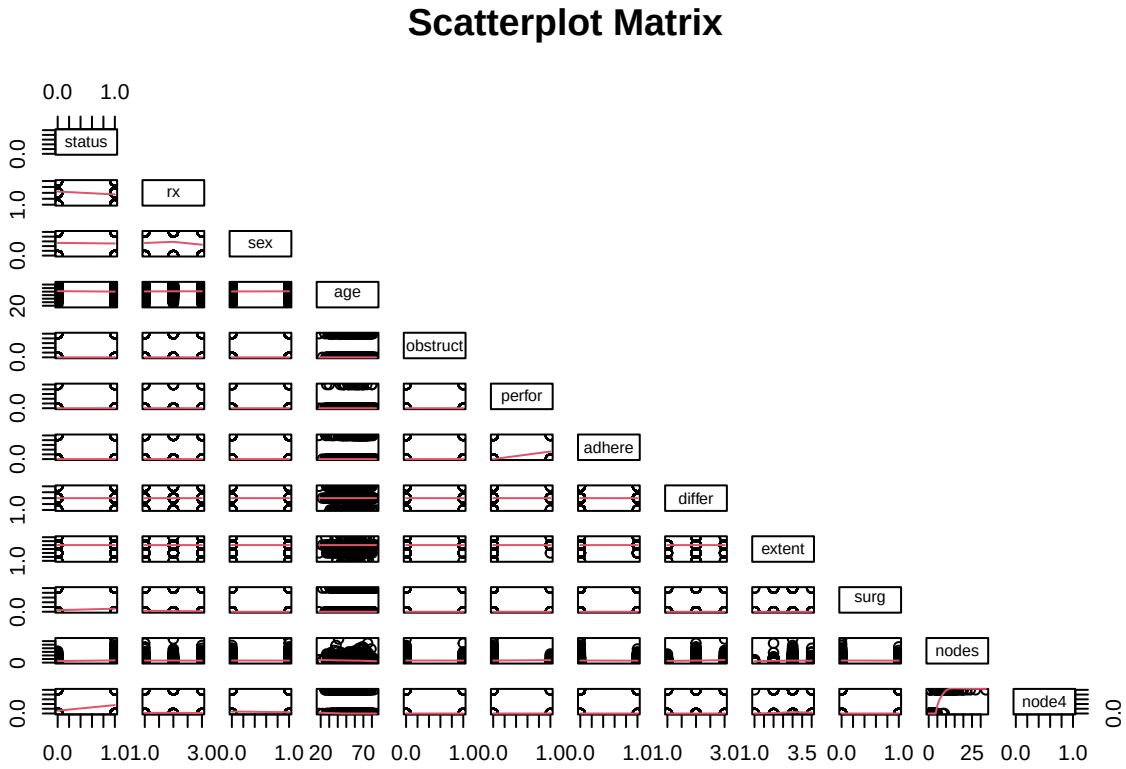
The primary endpoints are the death of patients and the recurrence of patients. The type of censoring is right censoring, which means patients left the study before their death.

```
data(cancer, package = "survival")
colon_tb = as_tibble(colon)
colon_tb = colon_tb

colon_tb$status <- factor(colon_tb$status, levels = c(0,1), labels = c("Censored", "Event"))
colon_tb$sex <- factor(colon_tb$sex, levels = c(0,1), labels = c("Female", "Male"))
colon_tb$obstruct <- factor(colon_tb$obstruct, levels = c(0,1), labels = c("No", "Yes"))
colon_tb$perfor <- factor(colon_tb$perfor, levels = c(0,1), labels = c("No", "Yes"))
colon_tb$adhere <- factor(colon_tb$adhere, levels = c(0,1), labels = c("No", "Yes"))
colon_tb$differ <- factor(colon_tb$differ, levels = c(1,2,3), labels = c("Well", "Moderate","Poor"))
colon_tb$extent <- factor(colon_tb$extent, levels = c(1,2,3,4),
                          labels = c("Submucosa", "Muscle","Serosa","Contiguous structures"))
```

```r
colon_tb$surg <- factor(colon_tb$surg, levels = c(0,1), labels = c("Short", "Long"))
colon_tb$node4 <- factor(colon_tb$node4, levels = c(0,1), labels = c("No", "Yes"))

label(colon_tb$rx) <- "Treatment"
label(colon_tb$sex) <- "Sex"
label(colon_tb$age) <- "Age"
label(colon_tb$obstruct) <- "Obstruction of colon by tumour"
label(colon_tb$perfor) <- "Perforation of colon"
label(colon_tb$adhere) <- "Adherence to nearby organs"
label(colon_tb$status) <- "Censoring status"
label(colon_tb$differ) <- "Differentiation of tumour"
label(colon_tb$extent) <- "Extent of local spread"
label(colon_tb$surg) <- "Time from surgery to registration"
label(colon_tb$node4) <- "More than 4 positive lymph nodes"

units(colon_tb$age) <- "years"
units(colon_tb$time) <- "days"

my.render.cont <- function(x) {
    with(stats.apply.rounding(stats.default(x), digits = 3),
         c("","Mean (SD)" = sprintf("%s (&plusmn;%s)", MEAN, SD)))
}
my.render.cat <- function(x) {
    c("", sapply(stats.default(x), function(y) with(y,
    sprintf("%d (%0.1f%%)", FREQ, PCT))))
}

# Baseline characteristic table for event death
output1 = table1(~ sex + age + obstruct + perfor + adhere + differ + extent + surg + node4| status*rx,
                 data = colon_tb %>% filter(etype == 2),
                 render.continuous = my.render.cont,
                 render.categorical = my.render.cat,
                 render.missing = NULL, overall = FALSE)

# Baseline characteristic table for event recurrence
output2 = table1(~ sex + age + obstruct + perfor + adhere + differ + extent + surg + node4| status*rx,
                 data = colon_tb %>% filter(etype == 1),
                 render.continuous = my.render.cont,
                 render.categorical = my.render.cat,
                 render.missing = NULL, overall = FALSE)


save_table1 = function(output,file_name="temp.html"){
    css_path = system.file("table1_defaults_1.0/table1_defaults.css", package = "table1")
    css = sprintf('<style type="text/css">@import url(%s);</style>',css_path)
    cat(paste(css,output),file = file_name)
}

save_table1(output1,"./table/table1.html")
save_table1(output2,"./table/table2.html")

system("wkhtmltopdf --enable-local-file-access ./table/table1.html ./table/table1.pdf")
system("wkhtmltopdf --enable-local-file-access ./table/table2.html ./table/table2.pdf")
```

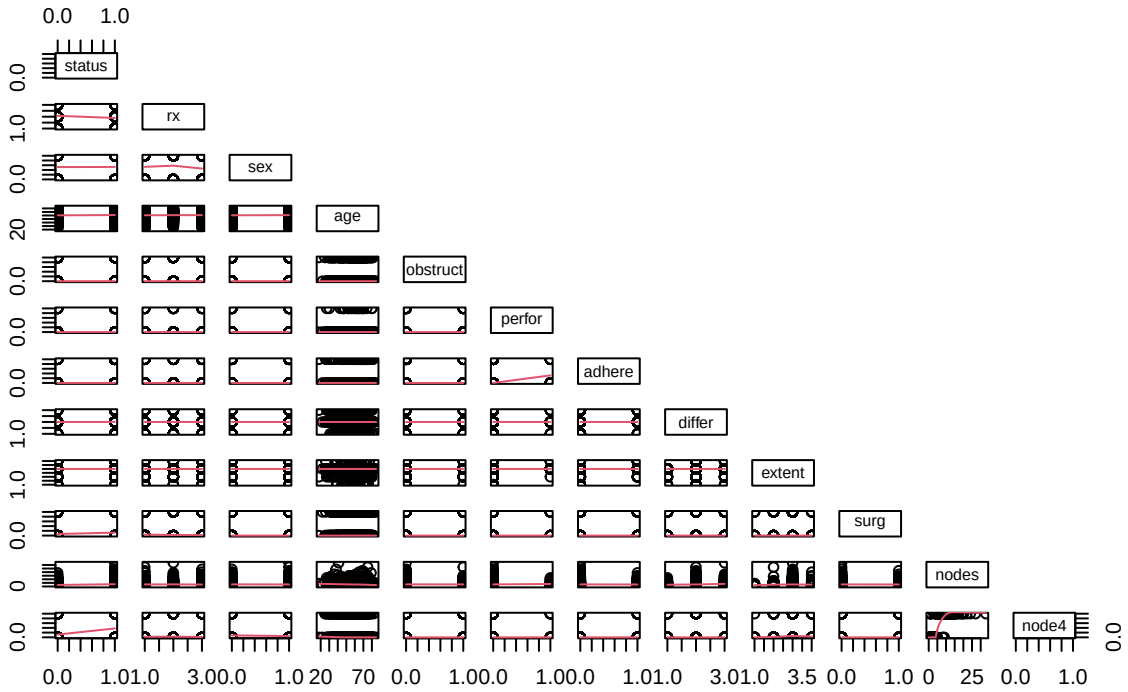
2. Corrlation between Variables

```
pairs(~ status + rx + sex + age + obstruct + perfor + adhere + differ + extent + surg + nodes + node4,
```

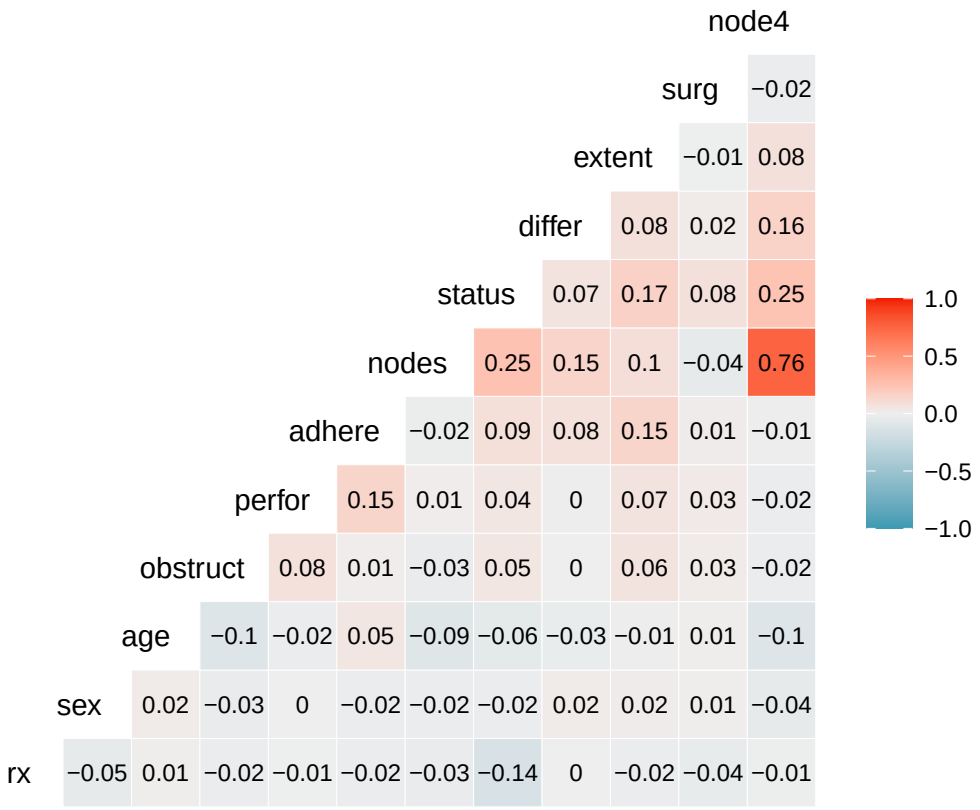



```
pairs(~ status + rx + sex + age + obstruct + perfor + adhere + differ + extent + surg + nodes + node4,
```

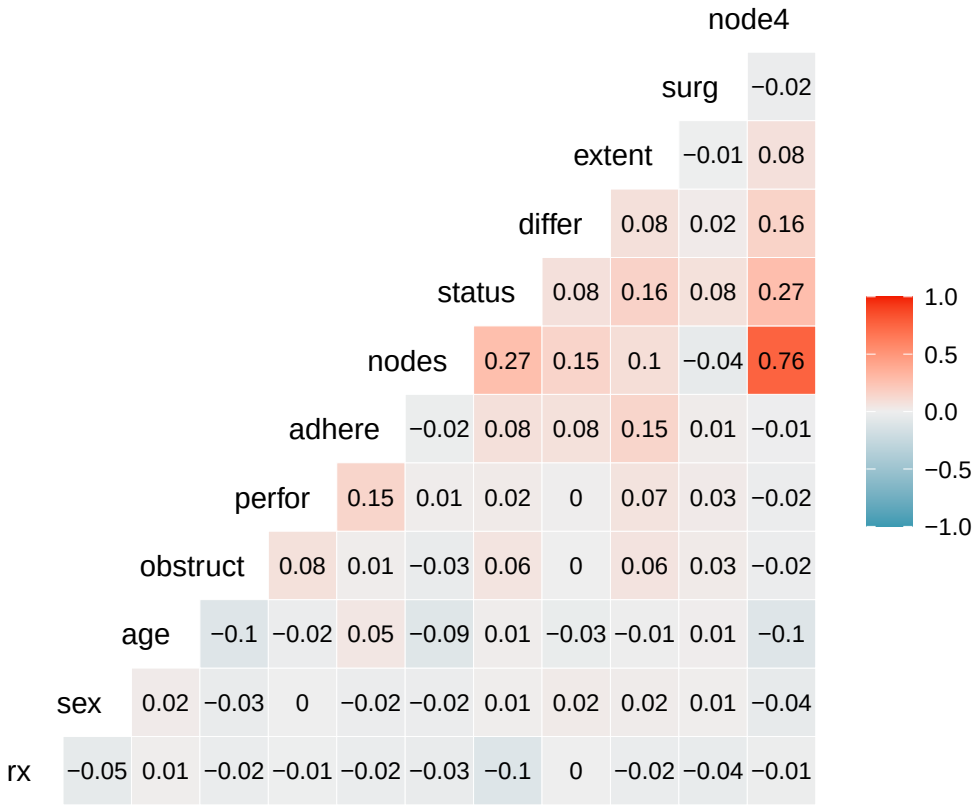
Scatterplot Matrix




```
colon %>%
  subset(etype == 1) %>%
  mutate(rx = as.numeric(rx)) %>%
  dplyr::select(-id, -study,-etype, -time) %>%
  ggcorr(label = TRUE, hjust = 0.9, layout.exp = 2, label_size = 3, label_round = 2)
```




```
colon %>%
  subset(etype == 2) %>%
  mutate(rx = as.numeric(rx)) %>%
  dplyr::select(-id, -study,-etype, -time) %>%
  ggcorr(label = TRUE, hjust = 0.9, layout.exp = 2, label_size = 3, label_round = 2)
```


node4
surg −0.02
extent −0.01 0.08
differ 0.08 0.02 0.16
status 0.08 0.16 0.08 0.27
nodes 0.27 0.15 0.1 −0.04 0.76
adhere −0.02 0.08 0.08 0.15 0.01 −0.01
perfor 0.15 0.01 0.02 0 0.07 0.03 −0.02
obstruct 0.08 0.01 −0.03 0.06 0 0.06 0.03 −0.02
age −0.1 −0.02 0.05 −0.09 0.01 −0.03 −0.01 0.01 −0.1
sex 0.02 −0.03 0 −0.02 −0.02 0.01 0.02 0.02 0.01 −0.04
rx −0.05 0.01 −0.02 −0.01 −0.02 −0.03 −0.1 0 −0.02 −0.04 −0.01
1.0
0.5
0.0
−0.5
−1.0