# 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$sex <- factor(colon_tb$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$status <- factor(colon_tb$status, levels = c(0,1), labels = c("Censored", "Dead"))
colon_tb$differ <- factor(colon_tb$differ, levels = c(1,2,3), labels = c("Well", "Moderate", "Poor"))
colon_tb$extent <- factor(colon_tb$surg, levels = c(1,2,3,4), labels = c("Submucosa", "Muscle", "Seros
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"))</pre>
```

```
label(colon_tb$rx) <- "Treatment"</pre>
label(colon_tb$sex) <- "Sex"</pre>
label(colon_tb$age) <- "Age"</pre>
label(colon_tb$obstruct) <- "Obstruction of colon by tumour"</pre>
label(colon_tb$perfor) <- "Perforation of colon"</pre>
label(colon_tb$adhere) <- "Adherence to nearby organs"</pre>
label(colon_tb$nodes) <- "Number of lymph nodes with detectable cancer"</pre>
label(colon_tb$time) <- "Time until event or censoring"</pre>
label(colon_tb$status) <- "Censoring status"</pre>
label(colon_tb$differ) <- "Differentiation of tumour"</pre>
label(colon_tb$extent) <- "Extent of local spread"</pre>
label(colon_tb$surg) <- "Time from surgery to registration"</pre>
label(colon_tb$node4) <- "More than 4 positive lymph nodes"</pre>
units(colon_tb$age) <- "years"</pre>
units(colon_tb$time) <- "days"</pre>
table1(~ rx + sex + age + obstruct + perfor + adhere + differ + extent + surg + nodes + node4| status,
```

	Censored	Dead	Total	
	(N=461)	(N=468)	(N=929)	
Treatment				
Obs	138 (29.9%)	177 (37.8%)	315 (33.9%)	
Lev	138 (29.9%)	172 (36.8%)	310 (33.4%)	
Lev+5FU	185 (40.1%)	119 (25.4%)	304 (32.7%)	
Sex	,	,	,	
Female	216 (46.9%)	229 (48.9%)	445 (47.9%)	
Male	245 (53.1%)	239 (51.1%)	484 (52.1%)	
Age (years)	( )	(	(	
Mean (SD)	60.5 (11.5)	59.0 (12.4)	59.8 (11.9)	
Median [Min, Max]	61.0 [22.0, 83.0]	61.0 [18.0, 85.0]	61.0 [18.0, 85.0]	
Obstruction of colon b		01.0 [10.0, 00.0]	01.0 [10.0, 00.0]	
No	380 (82.4%)	369 (78.8%)	749 (80.6%)	
Yes	81 (17.6%)	99 (21.2%)	180 (19.4%)	
	01 (17.070)	99 (21.270)	100 (19.470)	
Perforation of colon	451 (05.007)	451 (00 407)	000 (07 107)	
No	451 (97.8%)	451 (96.4%)	902 (97.1%)	
Yes	$10 \ (2.2\%)$	17 (3.6%)	27 (2.9%)	
Adherence to nearby of	9	222 (22 704)	( (04)	
No	408 (88.5%)	386 (82.5%)	794 (85.5%)	
Yes	53 (11.5%)	$82\ (17.5\%)$	$135 \ (14.5\%)$	
Differentiation of tumour				
Well	$49 \ (10.6\%)$	44 (9.4%)	$93\ (10.0\%)$	
Moderate	$337 \ (73.1\%)$	326~(69.7%)	663 (71.4%)	
Poor	62 (13.4%)	88 (18.8%)	$150 \ (16.1\%)$	
Missing	13~(2.8%)	$10 \ (2.1\%)$	23~(2.5%)	
Extent of local spread				
Submucosa	16 (3.5%)	5 (1.1%)	$21\ (2.3\%)$	
Muscle	72 (15.6%)	$34 \ (7.3\%)$	$106 \ (11.4\%)$	
Serosa	359 (77.9%)	400~(85.5%)	759 (81.7%)	
Contiguous structures	14 (3.0%)	29~(6.2%)	$43 \ (4.6\%)$	
Time from surgery to registration				
Short	355 (77.0%)	327 (69.9%)	682 (73.4%)	
Long	106 (23.0%)	141 (30.1%)	$247\ (26.6\%)$	
Number of lymph nodes with detectable cancer				
Mean (SD)	2.76 (2.43)	4.56 (4.25)	3.66(3.57)	
Median [Min, Max]	2.00 [1.00, 16.0]	3.00 [0, 33.0]	$2.00 \ [0, 33.0]$	
Missing	6 (1.3%)	12 (2.6%)	18 (1.9%)	
More than 4 positive lymph nodes				
No	386 (83.7%)	288 (61.5%)	674 (72.6%)	
Yes	75 (16.3%)	180 (38.5%)	255 (27.4%)	
	(==:=///)	()	(+/0)	

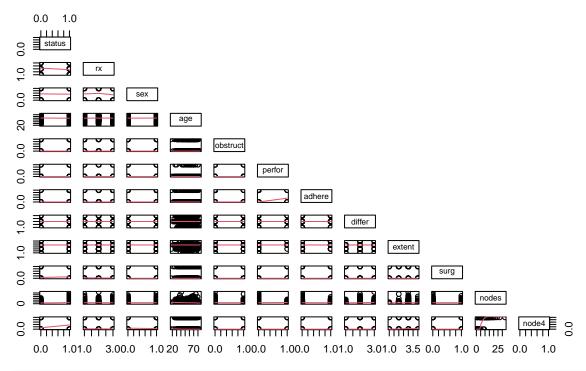
table1(~ rx + sex + age + obstruct + perfor + adhere + differ + extent + surg + nodes + node4| status,

	Censored	Dead	Total	
	(N=477)	(N=452)	(N=929)	
Treatment				
Obs	147 (30.8%)	168 (37.2%)	315 (33.9%)	
Lev	149 (31.2%)	161 (35.6%)	310 (33.4%)	
Lev+5FU	181 (37.9%)	123 (27.2%)	304 (32.7%)	
Sex	,	,	,	
Female	230 (48.2%)	215 (47.6%)	445 (47.9%)	
Male	247 (51.8%)	237 (52.4%)	484 (52.1%)	
Age (years)	(	(	(	
Mean (SD)	59.6 (11.6)	59.9 (12.3)	59.8 (11.9)	
Median [Min, Max]	60.0 [22.0, 83.0]	62.0 [18.0, 85.0]	61.0 [18.0, 85.0]	
Obstruction of colon b		02.0 [10.0, 09.0]	01.0 [10.0, 00.0]	
No	395 (82.8%)	354 (78.3%)	749 (80.6%)	
Yes	82 (17.2%)	98 (21.7%)	180 (19.4%)	
	02 (11.270)	90 (21.170)	100 (19.470)	
Perforation of colon	40F (0F F07)	195 (06 507)	000 (07 107)	
No	465 (97.5%)	437 (96.7%)	902 (97.1%)	
Yes	12 (2.5%)	15 (3.3%)	27 (2.9%)	
Adherence to nearby of	-	a=a (aa =04)	( (04)	
No	421 (88.3%)	373 (82.5%)	794 (85.5%)	
Yes	56 (11.7%)	$79 \ (17.5\%)$	$135 \ (14.5\%)$	
Differentiation of tumour				
Well	$51 \ (10.7\%)$	42 (9.3%)	$93\ (10.0\%)$	
Moderate	352 (73.8%)	311~(68.8%)	663 (71.4%)	
Poor	62 (13.0%)	$88 \ (19.5\%)$	$150 \ (16.1\%)$	
Missing	12~(2.5%)	$11 \ (2.4\%)$	23~(2.5%)	
Extent of local spread				
Submucosa	17 (3.6%)	4~(0.9%)	$21\ (2.3\%)$	
Muscle	$70 \ (14.7\%)$	36~(8.0%)	$106 \ (11.4\%)$	
Serosa	$376 \ (78.8\%)$	383~(84.7%)	759 (81.7%)	
Contiguous structures	14 (2.9%)	29 (6.4%)	$43 \ (4.6\%)$	
Time from surgery to registration				
Short	366 (76.7%)	316 (69.9%)	682 (73.4%)	
Long	111 (23.3%)	136 (30.1%)	$247\ (26.6\%)$	
Number of lymph nodes with detectable cancer				
Mean (SD)	2.72(2.44)	4.66(4.25)	3.66(3.57)	
Median [Min, Max]	2.00 [1.00, 19.0]	3.00 [0, 33.0]	$2.00 \ [0, 33.0]$	
Missing	7 (1.5%)	11 (2.4%)	18 (1.9%)	
More than 4 positive lymph nodes				
No	403 (84.5%)	271 (60.0%)	674 (72.6%)	
Yes	74 (15.5%)	181 (40.0%)	255 (27.4%)	
	( / )	- (//	(	

# 2. Corrlation between Variables

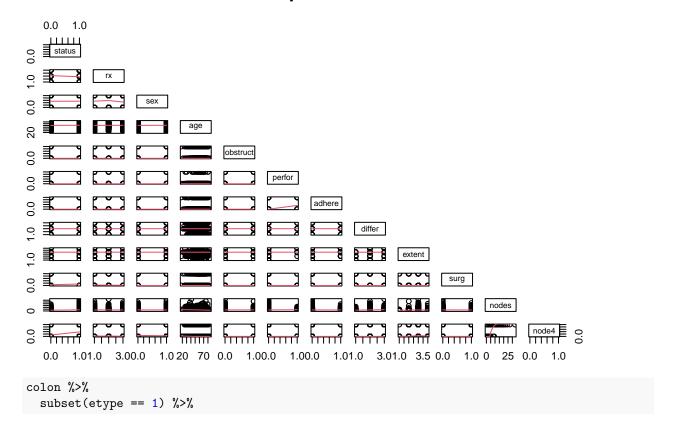
pairs(~ status + rx + sex + age + obstruct + perfor + adhere + differ + extent + surg + nodes + node4,

## **Scatterplot Matrix**

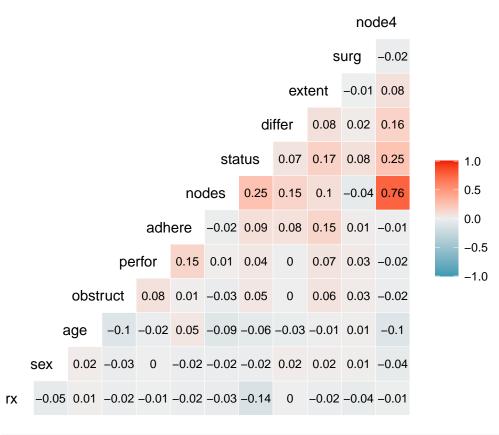


pairs(~ status + rx + sex + age + obstruct + perfor + adhere + differ + extent + surg + nodes + node4,

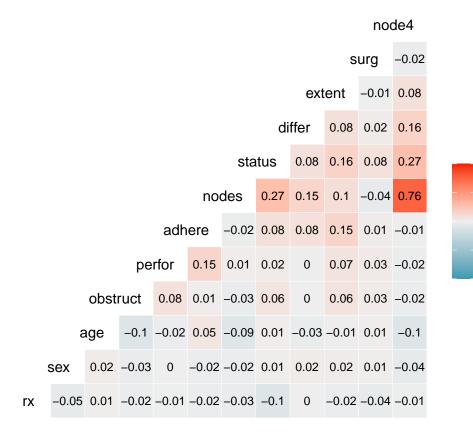
## **Scatterplot Matrix**



```
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)
```



1.0

0.5

0.0

-0.5

-1.0