Supplementary Material.
Statistics for 'Thrombopoietin receptor agonists are effective in treating chemotherapy-induced thrombocytopenia in patients with gliomas undergoing myelotoxic treatment'.

Chris Dardis

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Contents

1 Data collection

A thrombopoetin agonist was prescribed for 40 patients over the 18 months reviewed. Of these, 13 did not start treatment and are not considered further in this analysis. This was due to denial of coverage from their insurer or progressive disease leading to hospice care.

2 Key

```
suppressPackageStartupMessages(library("data.table"))
suppressPackageStartupMessages(library("xtable"))
options("xtable.booktabs"=TRUE)
nrow(k1 <- data.table(read.csv("k1.csv", stringsAsFactors=FALSE)))
```

```
[1] 31
```

```
options("xtable.booktabs"=TRUE)
options("xtable.table.placement"="H")
options("xtable.include.rownames"=FALSE)
options("xtable.NA.string"="NA")
k1 <- data.table(read.csv("k1.csv", stringsAsFactors=FALSE))
print(xtable(k1,
             align=c("l", "c", "l", "c", "l"),
             caption="Key to data",
             label="tab:key"),
      tabular.environment="longtable",
      floating=FALSE)
```

short_name	long_name	values	values_comments
id	unique identifier	1 to 27	one per patient
gr	WHO grade	2 to 4	when chemotherapy started
ageCTx	age when chemotherapy started		
sex	gender	m	male
		f	female
dRT	dosing of radiotherapy	59.4	Gy
dr	dose reduction	0	no
	(of chemotherapy prior to staring treatment)	1	yes
nad	nadir of platelet count		x 10^9/L
ttN	time to nadir		months
nadT	nadir: cumulative dose of temozolomide		mg/m^2
nadB	nadir: cumulative dose of bevacizumab		mg/kg
nadL	nadir: cumulative dose of lomustine		mg/m^2
tx	treatment	e	eltrombopag
		r	romiplostim
dose	dose of treatment	25 to 200	mg, eltrombopag, po daily
		1 or 10	microg/kg, romiplostim, subcut weekly
ttL	time to last observation		months
o	outcome	d	died
		h	hospice care
		o	ongoing
totT	total dose of temozolomide		mg/m^2
totB	total dose of bevacizumab		mg/kg
totL	total dose of lomustine		mg/m^2
addT	additional temozolomide (after tx started)		mg/m^2
addB	additional bevacizumab (after tx started)		mg/kg
addL	additional lomustine (after tx started)		mg/m^2
eff	effective	0	no
		1	yes

se	side effects
notes	

Table 1: Key to data

3 Process data

```
nrow(d1 <- data.table(read.csv("d1.csv", stringsAsFactors=FALSE)))

## [1] 27

d1 <- within(d1, {
  sex <- factor(sex, levels=c("m", "f"))
  tx <- factor(tx, levels=c("e", "r"),
               labels=c("eltrombopag", "romiplostim"))
  grF <- factor(gr, levels=2:4, ordered=TRUE)
  on <- o=="o"
  o <- factor(o, levels=c("d", "h", "o"),
              labels=c("died", "hospice", "ongoing"))
  onF <- factor(on, levels=c(TRUE, FALSE),
                labels=c("ongoing", "ended"))
  p <- rep(1, nrow(d1))
  })
```

4 Useful functions

```
xtable.table <- function(x,
                         caption=paste0(
                           paste(names(dimnames(x)),
                                 collapse=" $\\times$ "),
                           "\\\\ chi-sq=",
                           signif(suppressWarnings(
                             chisq.test(x)$p.value), digits)),
                         label=NULL,
                         align=c("l", rep("c", dim(x)[2])),
                         digits=2,
                         display=NULL){
  identity(caption)
  dn1 <- dimnames(x)
  n1 <- names(dn1)
  names(attr(x, "dimnames")) <- NULL
  rownames(x) <- NULL
  if (length(dim(x))==1) {
    dim(x) <- c(1L, dim(x))
    r1 <- x
    colnames(r1) <- dn1[[1]]
    rownames(r1) <- "."
    class(r1) <- "matrix"
```

```r
  } else {
    r1 <- rbind(dn1[[2]], signif(x, digits))
    rownames(r1) <- c(n1[1], dn1[[1]])
    colnames(r1) <- c(n1[2], rep(".", dim(x)[2] - 1))
  }
  xtable(r1,
         caption=caption,
         label=label,
         align=align,
         digits=digits,
         display=display)
}
suppressPackageStartupMessages(library("survival"))
xtable.survfit <- function(x, caption=NULL, label=NULL,
                           align= NULL, digits=NULL,
                           display=NULL){
  m1 <- survival:::survmean(x, rmean="none")$matrix
  if (is.null(dim(m1))) {
    m1 <- t(as.matrix(m1))
  }
  xtable(m1,
         caption=caption, label=label,
         align=align, digits=digits,
         display=display)
}
```

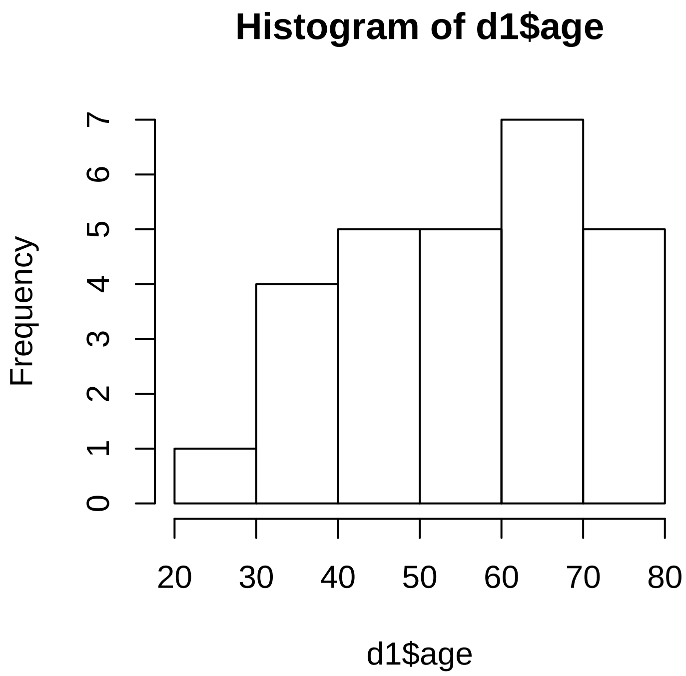
5 Descriptives

```r
options("xtable.include.rownames"=FALSE)
xtable(t(as.matrix(summary(d1$age))),
       caption="Age; Qu. = quantile")
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
26.00	44.00	58.00	55.59	67.00	74.00

Table 2: Age; Qu. = quantile

```r
hist(d1$age)
```

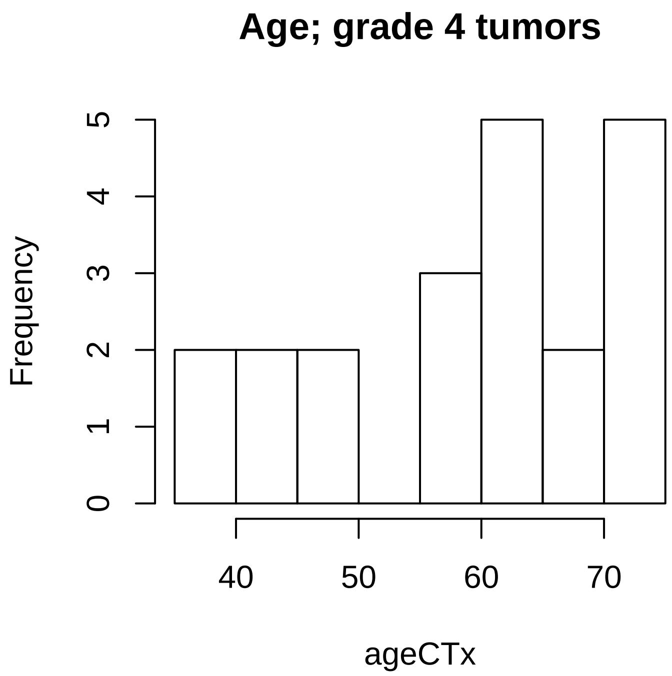


```
xtable(table(d1$gr),
       caption="Grade (counts)")
```

2	3	4
3	3	21

Table 3: Grade (counts)

```
invisible(d1[gr==4, hist(ageCTx, main="Age; grade 4 tumors")])
```

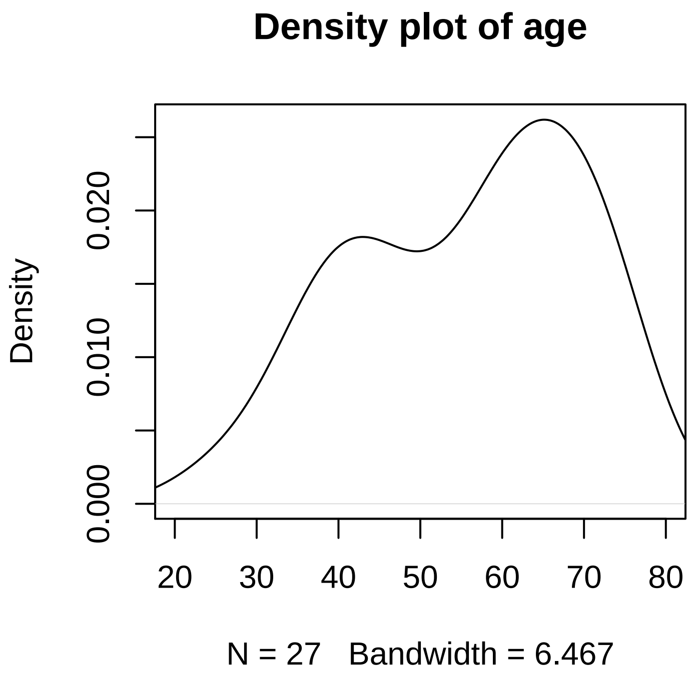


```
t1 <- t.test(d1[gr==4, ageCTx], d1[gr < 4, ageCTx])
t1 <- t(matrix(c(round(t1$estimate, 2), signif(t1$p.value, 2))))
colnames(t1) <- c("mean (grade 4)", "mean (grade < 4)", "p")
xtable(t1,
       caption="Older age for grade 4 tumors \\\\ t-test (2-sided)")
```

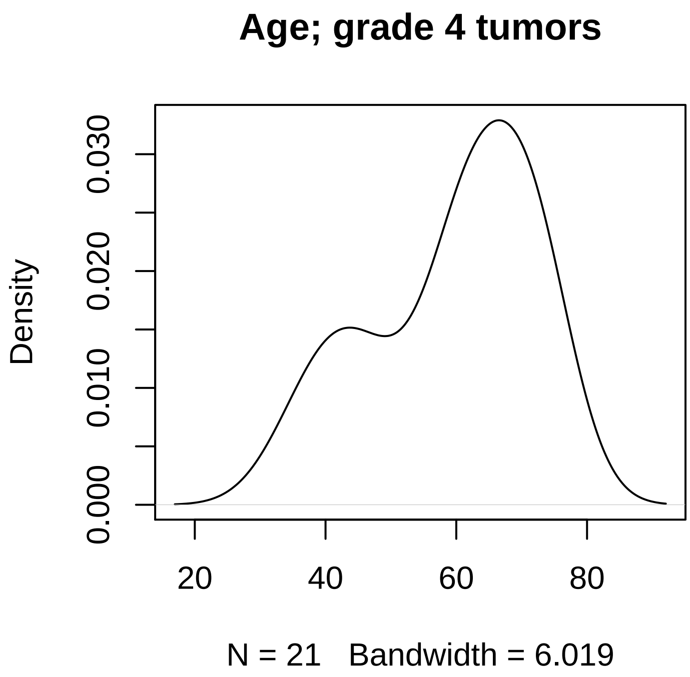
mean (grade 4)	mean (grade $<$ 4)	p
59.38	42.33	0.01

Table 4: Older age for grade 4 tumors
t-test (2-sided)

```
plot(density(sort(d1$age)),
     xlim=c(20,80),
     main="Density plot of age")
```



```
d1[gr==4, plot(density(sort(ageCTx)),
     main="Age; grade 4 tumors")]
```



```
NULL
```

```
round(sd(d1$age), 2)
```

```
[1] 13.89
```

```
xtable(table(d1$sex),
       caption="Gender (counts)")
```

m	f
10	17

Table 5: Gender (counts)

```
xtable(table(d1$tx),
       caption="Treatment (counts)")
```

eltrombopag	romiplostim
22	5

Table 6: Treatment (counts)

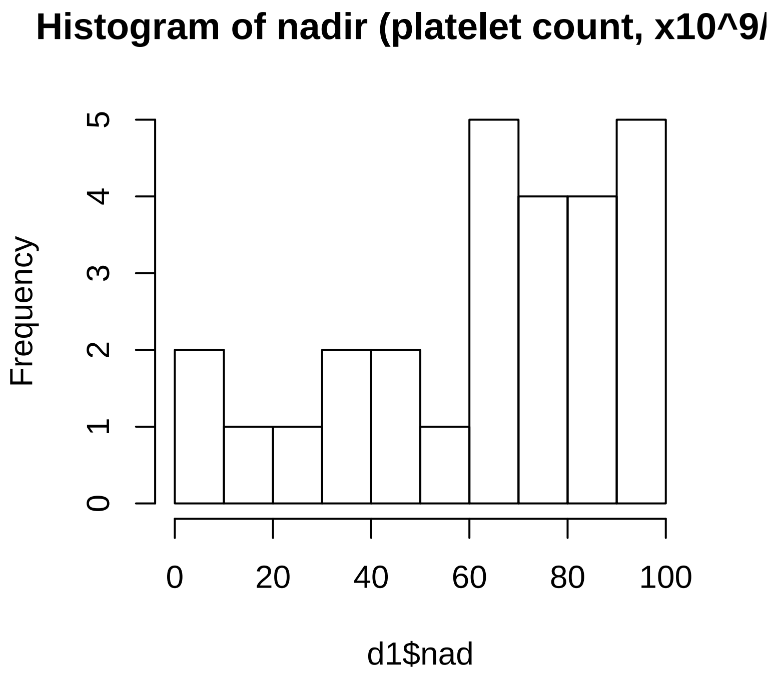
```
options("xtable.include.rownames"=TRUE)
xtable(d1[, table(tx, dose)])
```

	dose	.	.	.	.	.	.
tx	1	10	25	50	100	150	200
eltrombopag	0	0	1	17	1	2	1
romiplostim	4	1	0	0	0	0	0

Table 7: tx × dose
chi-sq=0.00014

6 Nadir

```
hist(d1$nad, 10,
     main="Histogram of nadir (platelet count, x10^9/L)")
```



```
xtable(t(as.matrix(summary(d1$nad))),
       caption="Platelet nadir (x10^9/L); Qu. = quantile")
```

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1	5.00	45.50	69.00	63.67	85.50	98.00

Table 8: Platelet nadir (x10$^9/L); Qu. = quantile$

```
xtable(d1[, anova(lm(nad ~ gr))],
       caption="Nadir does not vary by grade (F test)")
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
gr	1	4.08	4.08	0.01	0.9436
Residuals	25	19977.92	799.12	NA	NA

Table 9: Nadir does not vary by grade (F test)

```
xtable(d1[, summary(lm(nad ~ ageCTx))],
       caption="Nadir does not vary by age (linear regression)")
```

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	57.7342	22.8150	2.53	0.0181
ageCTx	0.1067	0.3986	0.27	0.7911

Table 10: Nadir does not vary by age (linear regression)

7 Dose before nadir

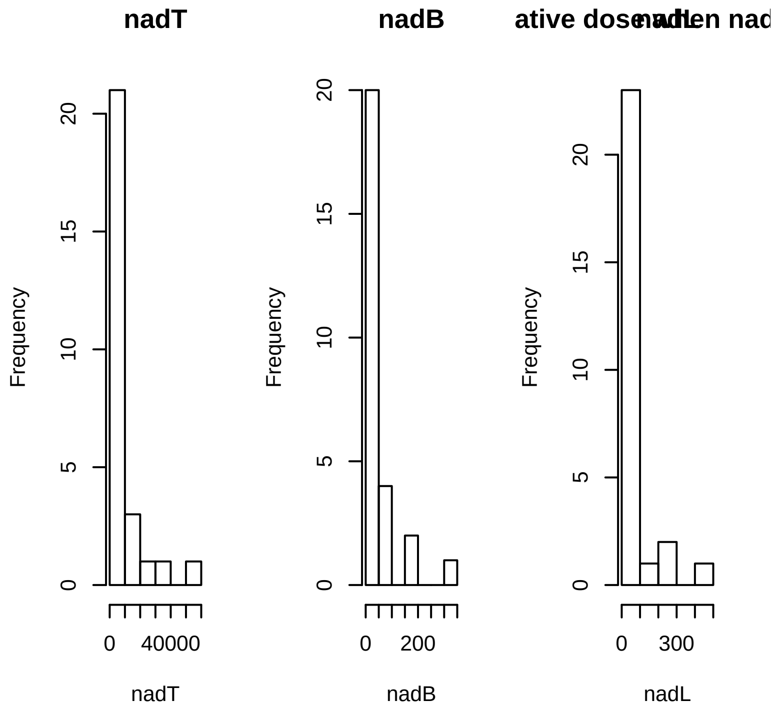
```
t1 <- d1[, sapply(list(nadT, nadB, nadL),
                  function (i) c(summary(i), sd(i)))]
rownames(t1)[7] <- "sDev"
colnames(t1) <- c("nadT", "nadB", "nadL")
options("xtable.include.rownames"=TRUE)
xtable(t1)
```

	nadT	nadB	nadL
Min.	0.00	0.00	0.00
1st Qu.	3150.00	0.00	0.00
Median	4650.00	0.00	0.00
Mean	9485.00	40.93	48.89
3rd Qu.	9900.00	55.00	0.00
Max.	56700.00	320.00	440.00
sDev	12070.30	76.69	115.60

```
cat(c("\n", "No chemotherapy received (counts) - bevacizumb, lomustine: ",
      d1[, sapply(list(nadB, nadL), function(i) sum(i==0))],
      "\n"))
```

```
No chemotherapy received (counts) - bevacizumb, lomustine: 16 22
```

```
p1 <- par()
par(mfrow=c(1, 3))
for (i in c("nadT", "nadB", "nadL")) {
  d1[, hist(get(i), main=i, xlab=i)]
}
title(main="Cumulative dose when nadir reached")
```



```
suppressWarnings(par(p1))
t2 <- d1[, sapply(list(nadT, nadB, nadL),
                  function (i) c(summary(i), sd(i))), by=dr]
t2 <- as.matrix(t2)[, 2]
dim(t2) <- c(7, 6)
rownames(t2) <- rownames(t1)
colnames(t2) <- c(paste0("dr ", c("nadT", "nadB", "nadL")),
                  paste0("No dr ", c("nadT", "nadB", "nadL")))
options("xtable.include.rownames"=TRUE)
xtable(t2,
       caption="Dose reduction did not affect doses given before nadir")
```

	dr nadT	dr nadB	dr nadL	No dr nadT	No dr nadB	No dr nadL
Min.	4650.00	20.00	0.00	0.00	0.00	0.00
1st Qu.	5775.00	50.00	0.00	3150.00	0.00	0.00
Median	6900.00	80.00	0.00	4288.00	0.00	0.00
Mean	15110.00	90.00	33.33	8782.00	34.79	50.83
3rd Qu.	20340.00	125.00	50.00	9900.00	35.00	0.00
Max.	33780.00	170.00	100.00	56700.00	320.00	440.00
sDev	16204.91	75.50	57.74	11714.13	76.15	121.58

Table 11: Dose reduction did not affect doses given before nadir

```
c1 <- "Dose reduction not significant (linear model)"
xtable(d1[, summary(lm(nadT ~ dr))], caption=c1)
```

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	8782.2917	2476.9865	3.55	0.0016
dr	6326.0417	7430.9595	0.85	0.4027

Table 12: Dose reduction not significant (linear model)

```
xtable(d1[, summary(lm(nadB ~ dr))], caption=c1)
```

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	34.7917	15.5335	2.24	0.0342
dr	55.2083	46.6005	1.18	0.2473

Table 13: Dose reduction not significant (linear model)

```
xtable(d1[, summary(lm(nadL ~ dr))], caption=c1)
```

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	50.8333	24.0364	2.11	0.0446
dr	-17.5000	72.1093	-0.24	0.8102

Table 14: Dose reduction not significant (linear model)

8 Try calculate equivalent doses of chemotherapy

We attempt here to determine if there are consistent doses of any of the agents used for chemotherapy when the platelet nadir was reached. We hypothesized, for example, that we might see that a cumulative dose of temozolomide of 1000 mg/m2 was approximately as likely as a cumulative dose of bevacizumab of 100 mg/kg.

As we see below, there was wide individual variablility and no clear consistent relationship could be drawn such as that above.

```
m1 <- as.matrix(d1[, list(nadT, nadB, nadL)])
m1 <- m1[order(m1[, "nadL"], m1[, "nadB"], decreasing=TRUE), ]
m2 <- m1[6:11, 1:2]
e1 <- matrix(rep(100, ncol(m2)), ncol=1)
c1 <- combn(nrow(m2), ncol(m2))
r1 <- t(sapply(1:ncol(c1), function(i) solve(m2[c1[, i], ], e1)))
r1 <- as.matrix(signif(sapply(1:2, function(i) summary(r1[,i])), 2))
colnames(r1) <- c("temozolomide", "bevacizumab")
xtable(r1,
       caption="Equivalent doses; results not clinically meaningful")
```

	temozolomide	bevacizumab
Min.	-1.80	-43.00
1st Qu.	0.00	-2.00
Median	0.01	0.25
Mean	-0.10	25.00
3rd Qu.	0.02	1.10
Max.	0.21	420.00

Table 15: Equivalent doses; results not clinically meaningful

```r
m2 <- m1[apply(m1, 1, function(i) !any(i==0)), ]
e1 <- matrix(rep(100, ncol(m2)), ncol=1)
c1 <- combn(nrow(m2), ncol(m2))
r1 <- t(sapply(1:ncol(c1), function(i) solve(m2[c1[, i], ], e1)))
r1 <- signif(sapply(1:3, function(i) summary(r1[,i])), 2)
colnames(r1) <- c("temozolomide", "bevacizumab", "lomustine")
xtable(r1,
       caption="Equivalent doses; results not clinically meaningful")
```

	temozolomide	bevacizumab	lomustine
Min.	-0.00	-11.00	-0.35
1st Qu.	0.00	-0.91	0.31
Median	0.00	-0.09	0.32
Mean	0.00	-1.40	0.51
3rd Qu.	0.00	-0.07	0.49
Max.	0.02	0.46	2.20

Table 16: Equivalent doses; results not clinically meaningful

9 Time to nadir

```r
options("xtable.include.rownames"=FALSE)
xtable(t(as.matrix(summary(d1$ttN))),
       caption="Time to nadir (months); Qu. = quantile")
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.03	2.17	4.37	17.51	11.98	211.10

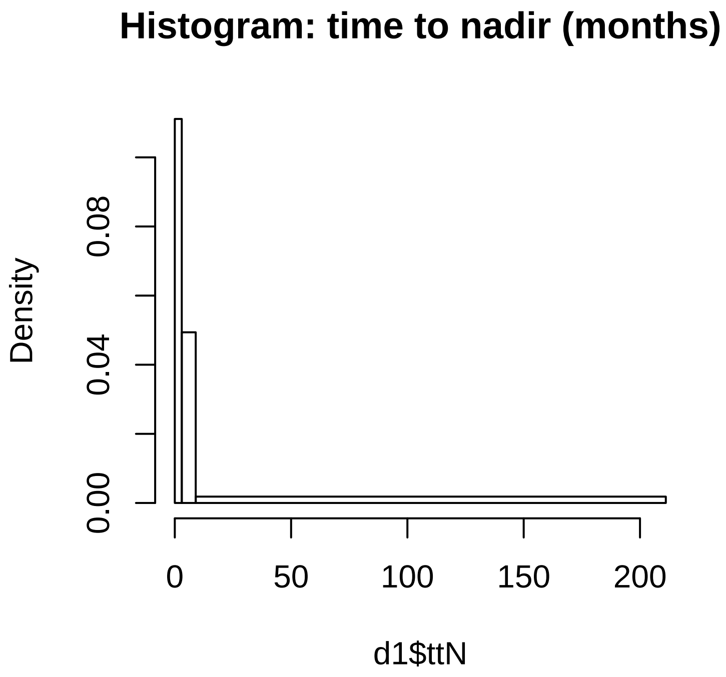
Table 17: Time to nadir (months); Qu. = quantile

```r
xtable(d1[, survfit(Surv(ttN, rep(1, nrow(d1))) ~ 1)],
       caption="Time to nadir (months)")
```

records	n.max	n.start	events	median	0.95LCL	0.95UCL
27.00	27.00	27.00	27.00	4.37	3.06	11.00

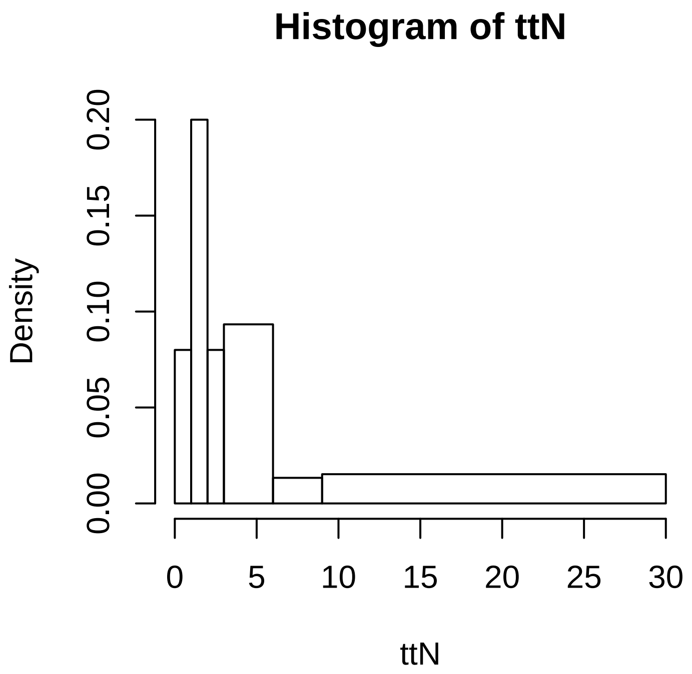
Table 18: Time to nadir (months)

```
hist(d1$ttN, c(0, 3, 9, max(d1$ttN)),
     main="Histogram: time to nadir (months)")
```



```
invisible(d1[ttN < 70, hist(ttN, breaks=c(0,1,2,3,6,9,30))],
          main="Histogram: time to nadir; times > 70 months removed")

## Error in invisible(d1[ttN < 70, hist(ttN, breaks = c(0, 1, 2, 3, 6, 9, :  2 arguments
passed to 'invisible' which requires 1
```



```r
cat(c("\n", "% patients where nadir occurred < 3 months after starting Tx: ",
      100 * round(sum(d1$ttN < 3) / nrow(d1), 2), "\n"))
```

```r
opts_chunk$set(fig.width=7, fig.height=7)
```

10 Last follow-up

```r
xtable(d1[eff==0, ],
       caption="Details of single patient for whom Tx was ineffective")
```

id	gr	ageCTx	sex	dRT	dr	nad	ttN	nadT	nadB	nadL	tx	dose	ttL	o	totT
26	3	37	f	NA	0	7	2.40	3150	0	0	eltrombopag	150	3.85	hospice	3150

Table 19: Details of single patient for whom Tx was ineffective

```r
xtable(t(as.matrix(summary(d1[!eff==0, ttL]))),
       caption="Last follow-up (months) from platelet nadir")
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
2.04	6.09	10.96	12.24	17.15	28.18

Table 20: Last follow-up (months) from platelet nadir

```r
xtable(d1[, table(o)])
```

died	hospice	ongoing
1	13	13

Table 21: o
chi-sq=0.0048

```r
options("xtable.include.rownames"=TRUE)
xtable(d1[, survfit(Surv(ttL, onF=="ended") ~ gr)],
       caption="Last follow-up (months) from platelet nadir by grade")
```

	records	n.max	n.start	events	median	0.95LCL	0.95UCL
gr=2	3.00	3.00	3.00	1.00	16.14	NA	NA
gr=3	3.00	3.00	3.00	2.00	14.66	3.85	NA
gr=4	21.00	21.00	21.00	11.00	15.62	10.06	NA

Table 22: Last follow-up (months) from platelet nadir by grade

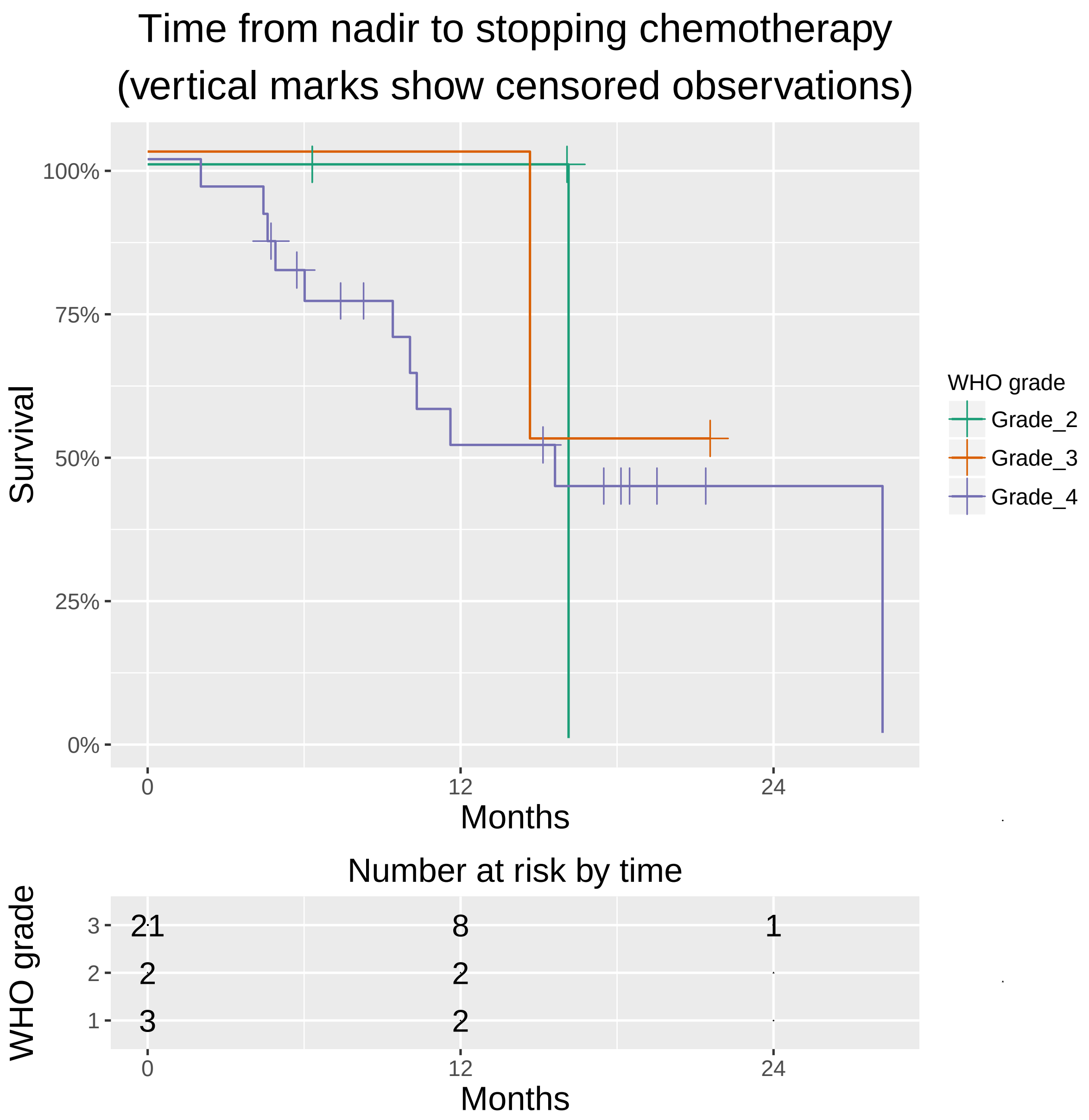
```r
options("xtable.include.rownames"=FALSE)
xtable(d1[, survfit(Surv(ttL, onF=="ended") ~ 1)],
       caption="Survival (months) i.e. time treatment continued after nadir reached")
```

records	n.max	n.start	events	median	0.95LCL	0.95UCL
27.00	27.00	27.00	14.00	15.62	10.32	NA

Table 23: Survival (months) i.e. time treatment continued after nadir reached

```r
suppressPackageStartupMessages(library("survMisc"))
t1 <- ten(Surv(ttL, onF=="ended") ~ gr,
          data=d1[!eff==0, ])
autoplot(t1,
         timeTicks="months",
         xLab="Months",
         title=expression(
           atop("Time from nadir to stopping chemotherapy",
                "(vertical marks show censored observations)")),
         legTitle="WHO grade",
         legLabs=paste0("Grade_", 2:4),
         legOrder=c(3, 2, 1),
         jitter="noEvents")

## Warning:  Removed 2 rows containing missing values (geom_text).
```



11 Overall time on chemotherapy

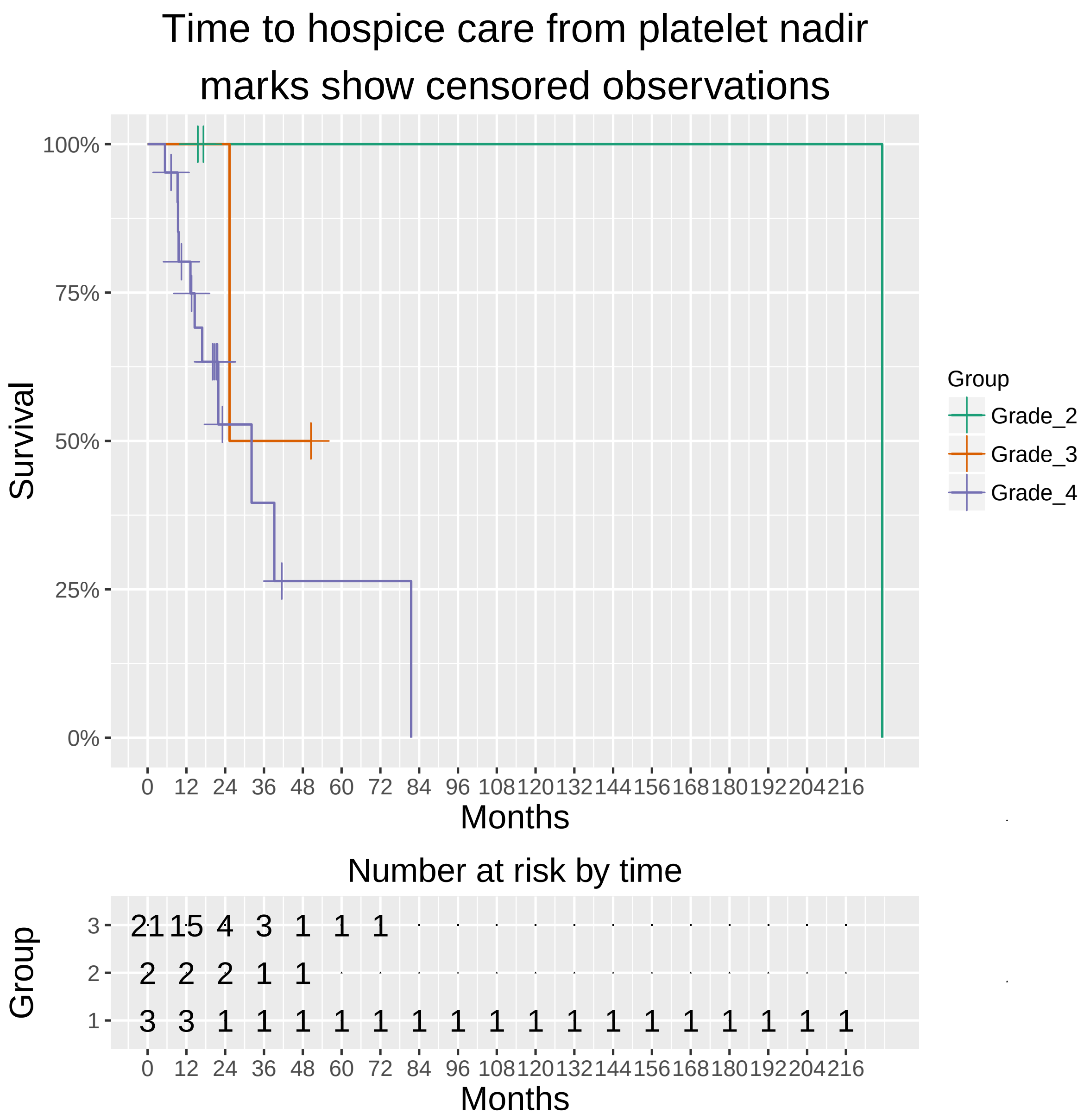
```
options("xtable.include.rownames"=TRUE)
xtable.survfit <- survMisc:::xtable.survfit
xtable(d1[, survfit(Surv(ttN + ttL, onF=="ended") ~ gr)],
                 caption="Total time on chemotherapy (months from nadir), by grade")
```

	records	n.max	n.start	events	median	0.95LCL	0.95UCL
gr=2	3	3	3	1	227	NA	NA
gr=3	3	3	3	2	25	6.2	NA
gr=4	21	21	21	11	32	17	NA

Table 24: Total time on chemotherapy (months from nadir), by grade

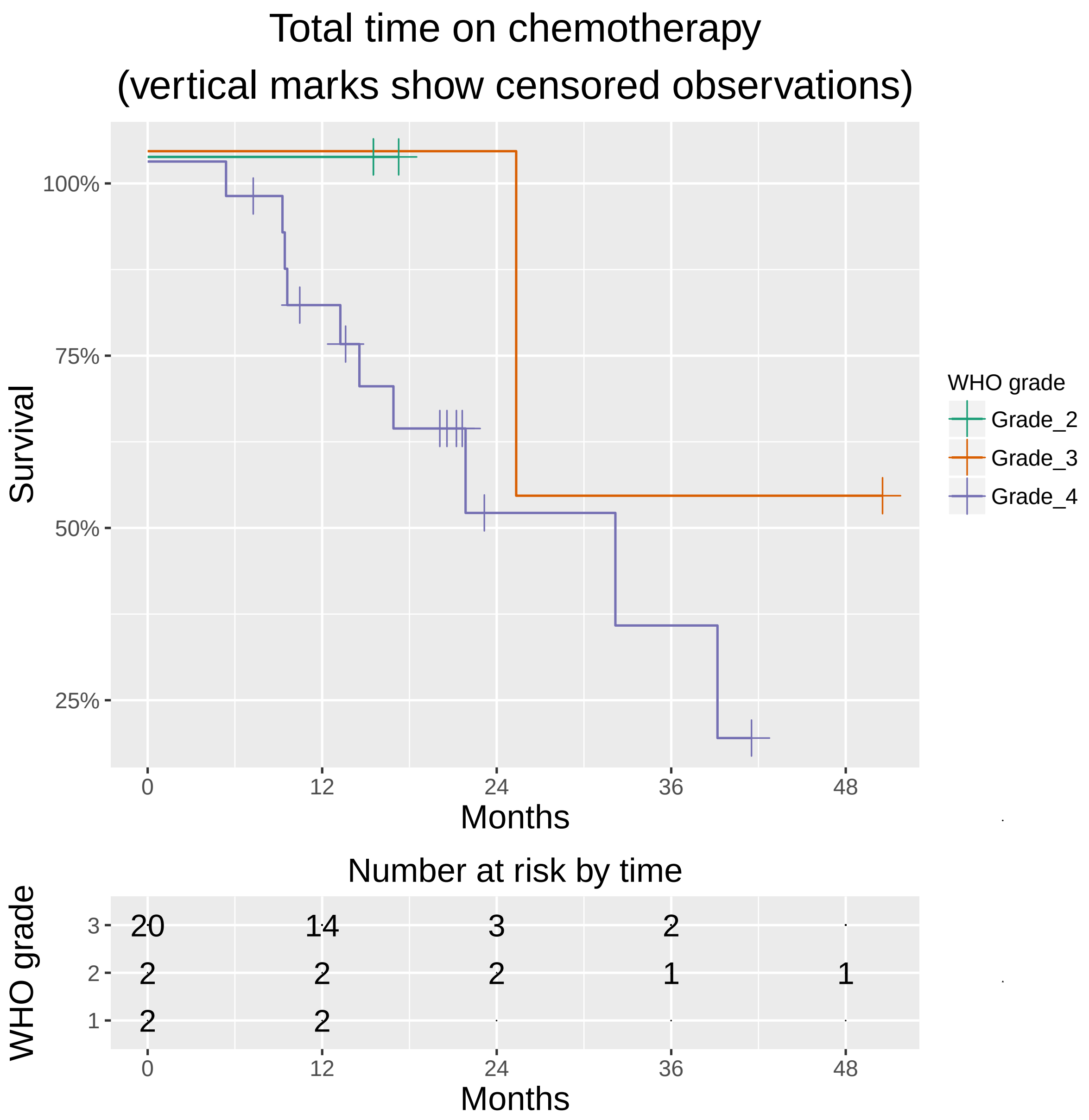
```
t1 <- ten(Surv(ttN + ttL, onF=="ended") ~ gr,
          data=d1[!eff==0, ])
autoplot(t1,
         timeTicks="months",
         xLab="Months",
         title=expression(
           atop("Time to hospice care from platelet nadir",
                "marks show censored observations")),
         legLabs=paste0("Grade_", 2:4),
         legOrder=c(3, 2, 1))

## Warning:  Removed 26 rows containing missing values (geom_text).
```



```
t1 <- ten(Surv(ttN + ttL, onF=="ended") ~ gr,
          data=d1[!eff==0 & (ttN + ttL) < 60, ])
autoplot(t1,
         timeTicks="months",
         xLab="Months",
         title=expression(
           atop("Total time on chemotherapy",
                "(vertical marks show censored observations)")),
         legTitle="WHO grade",
         legLabs=paste0("Grade_", 2:4),
         legOrder=c(3, 2, 1),
         jitter="noEvents")

## Warning:  Removed 4 rows containing missing values (geom_text).
```



```
t1 <- d1[, sapply(list(nadT, nadB, nadL), summary)]
colnames(t1) <- c("temozolomide", "bevacizumab", "lomustine")
xtable.matrix <- xtable:::xtable.matrix
xtable(t1,
       caption="Additional doses of chemotherapy given")
```

	temozolomide	bevacizumab	lomustine
Min.	0.00	0.00	0.00
1st Qu.	3150.00	0.00	0.00
Median	4650.00	0.00	0.00
Mean	9485.00	40.93	48.89
3rd Qu.	9900.00	55.00	0.00
Max.	56700.00	320.00	440.00

Table 25: Additional doses of chemotherapy given

12 Additional chemotherapy

```
t1 <- d1[!eff==0, sapply(list(addT, addB, addL), summary)]
colnames(t1) <- c("addT", "addB", "addL")
xtable(t1,
       caption="Cumulative additional chemoTx given (after nadir)")
```

	addT	addB	addL
Min.	0.00	0.00	0.00
1st Qu.	1625.00	33.75	0.00
Median	5625.00	75.00	0.00
Mean	5784.00	125.80	116.20
3rd Qu.	9000.00	230.00	100.00
Max.	16000.00	390.00	720.00

Table 26: Cumulative additional chemoTx given (after nadir)

```
cat(c("\n", "No additional chemotherapy received (counts) - temozolomide, bevacizumb, lomustine: ",
      d1[!eff==0, sapply(list(addT, addB, addL), function(i) sum(i==0))], "\n"))
```

```
No additional chemotherapy received (counts) - temozolomide, bevacizumb, lomustine: 6 6 18
```

13 Session Info

```
toLatex(sessionInfo())
```

- R version 3.2.1 (2015-06-18), `x86_64-w64-mingw32`
- Locale: `LC_COLLATE=English_United States.1252`, `LC_CTYPE=English_United States.1252`, `LC_MONETARY=English_United States.1252`, `LC_NUMERIC=C`, `LC_TIME=English_United States.1252`
- Base packages: base, datasets, graphics, grDevices, methods, stats, utils
- Other packages: data.table 1.9.4, knitr 1.12.3, survival 2.38-1, survMisc 0.5.3, xtable 1.7-1
- Loaded via a namespace (and not attached): chron 2.3-43, colorspace 1.2-2, digest 0.6.3, evaluate 0.8.3, formatR 0.9, ggplot2 2.1.0, grid 3.2.1, gridExtra 0.9.1, gtable 0.1.2, highr 0.5.1, km.ci 0.5-2, KMsurv 0.1-5, labeling 0.2, lattice 0.20-21, munsell 0.4.2, plyr 1.8, RColorBrewer 1.0-5, Rcpp 0.11.2, reshape2 1.2.2, scales 0.4.0, splines 3.2.1, stringr 0.6.2, tools 3.2.1, zoo 1.7-10

14 Data used

```
dput(d1)
```

```
## structure(list(id = 1:27, gr = c(3L, 4L, 4L, 4L, 4L, 4L, 4L,
## 3L, 4L, 4L, 4L, 4L, 4L, 2L, 4L, 2L, 4L, 4L, 4L, 4L, 4L, 4L, 2L,
## 4L, 4L, 3L, 4L), ageCTx = c(58L, 58L, 72L, 41L, 72L, 73L, 57L,
## 44L, 49L, 35L, 65L, 62L, 39L, 26L, 60L, 38L, 71L, 70L, 63L, 46L,
## 74L, 64L, 51L, 44L, 63L, 37L, 69L), sex = structure(c(1L, 1L,
## 2L, 2L, 1L, 1L, 1L, 2L, 2L, 2L, 2L, 2L, 1L, 2L, 2L, 2L, 2L, 2L,
## 1L, 1L, 2L, 1L, 2L, 2L, 2L, 2L, 1L), .Label = c("m", "f"), class = "factor"),
##     dRT = c(59.4, NA, 60, NA, 60, NA, NA, NA, NA, NA, 25, 60,
##     60, NA, NA, NA, 60, 60, 60, NA, 60, 60, 50.4, 60, NA, NA,
##     NA), dr = c(1L, 0L, 0L, 0L, 0L, 0L, 0L, 0L, 0L, 0L, 0L, 0L,
##     0L, 1L, 0L, 0L, 1L, 0L, 0L, 0L, 0L, 0L, 0L, 0L, 0L, 0L, 0L
##     ), nad = c(98L, 85L, 41L, 58L, 64L, 62L, 69L, 77L, 18L, 61L,
##     5L, 50L, 75L, 86L, 94L, 79L, 81L, 98L, 95L, 40L, 25L, 64L,
##     34L, 73L, 92L, 7L, 88L), ttN = c(10.68, 11, 5, 19.82, 3.62,
##     0.03, 20.12, 28.96, 26.14, 1.61, 1.28, 1.94, 4.14, 211.1,
##     1.64, 1.18, 4.37, 0.95, 5.42, 71.47, 7.89, 4.24, 9.21, 12.95,
##     3.06, 2.4, 2.53), nadT = c(6900L, 9900L, 3900L, 4425L, 3900L,
##     0L, 17900L, 23475L, 17900L, 3150L, 1575L, 3150L, 5400L, 33775L,
##     3150L, 3150L, 4650L, 3150L, 5900L, 56700L, 9900L, 5900L,
##     6900L, 10900L, 4150L, 3150L, 3150L), nadB = c(170L, 70L,
##     0L, 60L, 0L, 0L, 320L, 100L, 30L, 0L, 0L, 0L, 0L, 80L, 0L,
##     0L, 20L, 0L, 0L, 195L, 0L, 10L, 0L, 50L, 0L, 0L, 0L), nadL = c(0L,
##     0L, 0L, 300L, 0L, 0L, 280L, 0L, 200L, 0L, 0L, 0L, 0L, 100L,
##     0L, 0L, 0L, 0L, 0L, 440L, 0L, 0L, 0L, 0L, 0L, 0L, 0L), tx = structure(c(1L,
##     1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 2L, 2L, 1L, 1L, 1L, 1L, 2L,
##     1L, 2L, 1L, 1L, 1L, 1L, 1L, 1L, 2L, 1L, 1L), .Label = c("eltrombopag",
##     "romiplostim"), class = "factor"), dose = c(25L, 50L, 50L,
##     50L, 200L, 50L, 50L, 50L, 50L, 1L, 1L, 50L, 50L, 50L, 50L,
##     10L, 50L, 1L, 50L, 50L, 150L, 50L, 50L, 50L, 1L, 150L, 100L
##     ), ttL = c(14.66, 28.18, 4.6, 2.04, 19.53, 9.4, 21.4, 21.57,
##     6.02, 18.48, 15.62, 18.15, 17.49, 16.14, 11.61, 16.08, 4.9,
##     4.44, 15.16, 10.06, 5.72, 10.32, 6.31, 8.28, 7.4, 3.85, 4.73
##     ), o = structure(c(1L, 2L, 2L, 2L, 3L, 2L, 3L, 3L, 2L, 3L,
##     2L, 3L, 3L, 2L, 2L, 3L, 2L, 2L, 3L, 2L, 3L, 2L, 3L, 3L, 3L,
##     2L, 3L), .Label = c("died", "hospice", "ongoing"), class = "factor"),
##     totT = c(13650L, 18900L, 8900L, 6425L, 9900L, 9850L, 17900L,
##     31475L, 17900L, 12900L, 1575L, 13900L, 21400L, 33775L, 15675L,
##     8400L, 9650L, 5150L, 18900L, 56700L, 14900L, 5900L, 13900L,
##     19900L, 11150L, 3150L, 4650L), totB = c(220L, 390L, 0L, 90L,
##     240L, 60L, 620L, 360L, 75L, 110L, 60L, 230L, 390L, 160L,
##     230L, 60L, 120L, 0L, 0L, 390L, 0L, 260L, 0L, 240L, 0L, 0L,
##     70L), totL = c(0L, 0L, 0L, 300L, 0L, 0L, 1000L, 500L, 400L,
##     100L, 0L, 0L, 0L, 200L, 300L, 0L, 0L, 0L, 0L, 1140L, 0L,
##     400L, 0L, 0L, 0L, 0L, 0L), addT = c(6750L, 9000L, 5000L,
##     2000L, 6000L, 9850L, 0L, 8000L, 0L, 9750L, 0L, 10750L, 16000L,
##     0L, 12525L, 5250L, 5000L, 2000L, 13000L, 0L, 5000L, 0L, 7000L,
##     9000L, 7000L, 0L, 1500L), addB = c(50L, 320L, 0L, 30L, 240L,
```

```
##     60L, 300L, 260L, 45L, 110L, 60L, 230L, 390L, 80L, 230L, 60L,
##     100L, 0L, 0L, 195L, 0L, 250L, 0L, 190L, 0L, 0L, 70L), addL = c(0L,
##     0L, 0L, 0L, 0L, 0L, 720L, 500L, 200L, 100L, 0L, 0L, 0L, 100L,
##     300L, 0L, 0L, 0L, 0L, 700L, 0L, 400L, 0L, 0L, 0L, 0L, 0L),
##     eff = c(1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L,
##     1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 0L, 1L),
##     se = c("died unexpectedly", NA, NA, NA, NA, NA, NA, NA, NA,
##     NA, NA, "bone pain; using every 3 days", NA, NA, NA, NA,
##     NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA), notes = c(NA,
##     "stopped briefly, platelets dropped to 65; dose reduced to 150 when eltrombopag (Promacta) starte
##     "stopped TMZ after 6x cycles due to fatigue", NA, NA, "TP present before starting temozolomide bu
##     "later changed to romiplostim", NA, "Tx interrupted due to infection",
##     NA, "pancytopenia", NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
##     NA, NA, NA, NA, "pancytopenia; PCTx AML", NA), p = c(1, 1,
##     1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
##     1, 1, 1, 1, 1, 1), onF = structure(c(2L, 2L, 2L, 2L, 1L,
##     2L, 1L, 1L, 2L, 1L, 2L, 1L, 1L, 2L, 2L, 1L, 2L, 2L, 1L, 2L,
##     1L, 2L, 1L, 1L, 1L, 2L, 1L), .Label = c("ongoing", "ended"
##     ), class = "factor"), on = c(FALSE, FALSE, FALSE, FALSE,
##     TRUE, FALSE, TRUE, TRUE, FALSE, TRUE, FALSE, TRUE, TRUE,
##     FALSE, FALSE, TRUE, FALSE, FALSE, TRUE, FALSE, TRUE, FALSE,
##     TRUE, TRUE, TRUE, FALSE, TRUE), grF = structure(c(2L, 3L,
##     3L, 3L, 3L, 3L, 3L, 2L, 3L, 3L, 3L, 3L, 3L, 1L, 3L, 1L, 3L,
##     3L, 3L, 3L, 3L, 3L, 1L, 3L, 3L, 2L, 3L), .Label = c("2",
##     "3", "4"), class = c("ordered", "factor"))), .Names = c("id",
## "gr", "ageCTx", "sex", "dRT", "dr", "nad", "ttN", "nadT", "nadB",
## "nadL", "tx", "dose", "ttL", "o", "totT", "totB", "totL", "addT",
## "addB", "addL", "eff", "se", "notes", "p", "onF", "on", "grF"
## ), row.names = c(NA, -27L), class = c("data.table", "data.frame"
## ), .internal.selfref = <pointer: 0x0000000000320788>, index = structure(integer(0), gr = c(14L,
## 16L, 23L, 1L, 8L, 26L, 2L, 3L, 4L, 5L, 6L, 7L, 9L, 10L, 11L,
## 12L, 13L, 15L, 17L, 18L, 19L, 20L, 21L, 22L, 24L, 25L, 27L), eff = c(26L,
## 1L, 2L, 3L, 4L, 5L, 6L, 7L, 8L, 9L, 10L, 11L, 12L, 13L, 14L,
## 15L, 16L, 17L, 18L, 19L, 20L, 21L, 22L, 23L, 24L, 25L, 27L)))
```

References

[Dardis et al.(2015)Dardis, Woolf, and Scheck] Christopher Dardis, Eric C Woolf, and Adrienne C Scheck. Towards reproducible research: From data analysis (in r) to a typeset laboratory notebook (as. pdf) using the text editor emacs with the'mp'package. *F1000Research*, 4, 2015. doi:10.12688/f1000research.6800.2.