Thank you for the many requests to provide some extra info on how best to get finalfit results out of RStudio, and particularly into Microsoft Word.

Here is how.

Make sure you are on the most up-to-date version of finalfit.

Library("finalfit")

What follows is for demonstration purposes and is not meant to illustrate model building.

Does a tumour characteristic (differentiation) predict 5-year survival?

**Demographics table**

First explore variable of interest (exposure) by making it the dependent.

library(finalfit)

library(dplyr)

dependent = "differ.factor"

# Specify explanatory variables of interest

explanatory = c("age", "sex.factor",

"extent.factor", "obstruct.factor",

"nodes")

Note this useful alternative way of specifying explanatory variable lists:

colon\_s %>%

select(age, sex.factor,

extent.factor, obstruct.factor, nodes) %>%

names() -> explanatory

Look at associations between our exposure and other explanatory variables. Include missing data.

colon\_s %>%

summary\_factorlist(dependent, explanatory,

p=TRUE, na\_include=TRUE)

label levels Well Moderate Poor p

Age (years) Mean (SD) 60.2 (12.8) 59.9 (11.7) 59 (12.8) 0.788

Sex Female 51 (11.6) 314 (71.7) 73 (16.7) 0.400

Male 42 (9.0) 349 (74.6) 77 (16.5)

Extent of spread Submucosa 5 (25.0) 12 (60.0) 3 (15.0) 0.081

Muscle 12 (11.8) 78 (76.5) 12 (11.8)

Serosa 76 (10.2) 542 (72.8) 127 (17.0)

Adjacent structures 0 (0.0) 31 (79.5) 8 (20.5)

Obstruction No 69 (9.7) 531 (74.4) 114 (16.0) 0.110

Yes 19 (11.0) 122 (70.9) 31 (18.0)

Missing 5 (25.0) 10 (50.0) 5 (25.0)

nodes Mean (SD) 2.7 (2.2) 3.6 (3.4) 4.7 (4.4) <0.001

Warning messages:

1: In chisq.test(tab, correct = FALSE) :

Chi-squared approximation may be incorrect

2: In chisq.test(tab, correct = FALSE) :

Chi-squared approximation may be incorrect

Note missing data in obstruct.factor. We will drop this variable for now (again, this is for demonstration only). Also that nodes has not been labelled.  
There are small numbers in some variables generating chisq.test warnings (predicted less than 5 in any cell). Generate final table.

Hmisc::label(colon\_s$nodes) = "Lymph nodes involved"

explanatory = c("age", "sex.factor",

"extent.factor", "nodes")

colon\_s %>%

summary\_factorlist(dependent, explanatory,

p=TRUE, na\_include=TRUE,

add\_dependent\_label=TRUE) -> table1

table1

Dependent: Differentiation Well Moderate Poor p

Age (years) Mean (SD) 60.2 (12.8) 59.9 (11.7) 59 (12.8) 0.788

Sex Female 51 (11.6) 314 (71.7) 73 (16.7) 0.400

Male 42 (9.0) 349 (74.6) 77 (16.5)

Extent of spread Submucosa 5 (25.0) 12 (60.0) 3 (15.0) 0.081

Muscle 12 (11.8) 78 (76.5) 12 (11.8)

Serosa 76 (10.2) 542 (72.8) 127 (17.0)

Adjacent structures 0 (0.0) 31 (79.5) 8 (20.5)

Lymph nodes involved Mean (SD) 2.7 (2.2) 3.6 (3.4) 4.7 (4.4) <0.001

**Logistic regression table**

Now examine explanatory variables against outcome. Check plot runs ok.

explanatory = c("age", "sex.factor",

"extent.factor", "nodes",

"differ.factor")

dependent = "mort\_5yr"

colon\_s %>%

finalfit(dependent, explanatory,

dependent\_label\_prefix = "") -> table2

Mortality 5 year Alive Died OR (univariable) OR (multivariable)

Age (years) Mean (SD) 59.8 (11.4) 59.9 (12.5) 1.00 (0.99-1.01, p=0.986) 1.01 (1.00-1.02, p=0.195)

Sex Female 243 (47.6) 194 (48.0) - -

Male 268 (52.4) 210 (52.0) 0.98 (0.76-1.27, p=0.889) 0.98 (0.74-1.30, p=0.885)

Extent of spread Submucosa 16 (3.1) 4 (1.0) - -

Muscle 78 (15.3) 25 (6.2) 1.28 (0.42-4.79, p=0.681) 1.28 (0.37-5.92, p=0.722)

Serosa 401 (78.5) 349 (86.4) 3.48 (1.26-12.24, p=0.027) 3.13 (1.01-13.76, p=0.076)

Adjacent structures 16 (3.1) 26 (6.4) 6.50 (1.98-25.93, p=0.004) 6.04 (1.58-30.41, p=0.015)

Lymph nodes involved Mean (SD) 2.7 (2.4) 4.9 (4.4) 1.24 (1.18-1.30, p<0.001) 1.23 (1.17-1.30, p<0.001)

Differentiation Well 52 (10.5) 40 (10.1) - -

Moderate 382 (76.9) 269 (68.1) 0.92 (0.59-1.43, p=0.694) 0.70 (0.44-1.12, p=0.132)

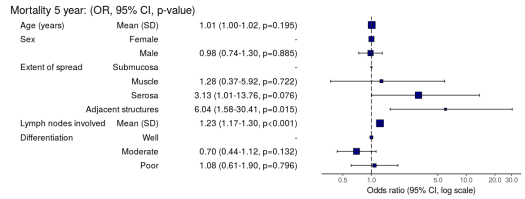
Poor 63 (12.7) 86 (21.8) 1.77 (1.05-3.01, p=0.032) 1.08 (0.61-1.90, p=0.796)

**Odds ratio plot**

colon\_s %>%

or\_plot(dependent, explanatory,

breaks = c(0.5, 1, 5, 10, 20, 30))

[](https://i1.wp.com/www.datasurg.net/wp-content/uploads/2018/05/example_or_plot.png)

**To MS Word via knitr/R Markdown**

Important. In most R Markdown set-ups, environment objects require to be saved and loaded to R Markdown document.

# Save objects for knitr/markdown

save(table1, table2, dependent, explanatory, file = "out.rda")

We use RStudio Server Pro set-up on Ubuntu. But these instructions should work fine for most/all RStudio/Markdown default set-ups.

In RStudio, select File > New File > R Markdown.

A useful template file is produced by default. Try hitting knit to Word on the knitr button at the top of the .Rmd script window.

```{r setup, include=FALSE}

# Load data into global environment.

library(finalfit)

library(dplyr)

library(knitr)

load("out.rda")

```

## Table 1 - Demographics

```{r table1, echo = FALSE, results='asis'}

kable(table1, row.names=FALSE, align=c("l", "l", "r", "r", "r", "r"))

```

## Table 2 - Association between tumour factors and 5 year mortality

```{r table2, echo = FALSE, results='asis'}

kable(table2, row.names=FALSE, align=c("l", "l", "r", "r", "r", "r"))

```

## Figure 1 - Association between tumour factors and 5 year mortality

```{r figure1, echo = FALSE}

colon\_s %>%

or\_plot(dependent, explanatory)

```

**Create Word template file**

Now, edit the Word template. Click on a table. The style should be compact. Right click > Modify... > font size = 9. Alter heading and text styles in the same way as desired. Save this as template.docx. Upload to your project folder. Add this reference to the .Rmd YAML heading, as below. Make sure you get the space correct.

The plot also doesn’t look quite right and it prints with warning messages. Experiment with fig.width to get it looking right.

Now paste this into your .Rmd file and run:

```{r setup, include=FALSE}

# Load data into global environment.

library(finalfit)

library(dplyr)

library(knitr)

load("out.rda")

```

## Table 1 - Demographics

```{r table1, echo = FALSE, results='asis'}

kable(table1, row.names=FALSE, align=c("l", "l", "r", "r", "r", "r"))

```

## Table 2 - Association between tumour factors and 5 year mortality

```{r table2, echo = FALSE, results='asis'}

kable(table2, row.names=FALSE, align=c("l", "l", "r", "r", "r", "r"))

```

## Figure 1 - Association between tumour factors and 5 year mortality

```{r figure1, echo = FALSE, warning=FALSE, message=FALSE, fig.width=10}

colon\_s %>%

or\_plot(dependent, explanatory)

```

**To PDF via knitr/R Markdown**

```{r setup, include=FALSE}

# Load data into global environment.

library(finalfit)

library(dplyr)

library(knitr)

load("out.rda")

```

## Table 1 - Demographics

```{r table1, echo = FALSE, results='asis'}

kable(table1, row.names=FALSE, align=c("l", "l", "r", "r", "r", "r"))

```

## Table 2 - Association between tumour factors and 5 year mortality

```{r table2, echo = FALSE, results='asis'}

kable(table2, row.names=FALSE, align=c("l", "l", "r", "r", "r", "r"))

```

## Figure 1 - Association between tumour factors and 5 year mortality

```{r figure1, echo = FALSE}

colon\_s %>%

or\_plot(dependent, explanatory)

```

We can fix the plot in exactly the same way. But the table is off the side of the page. For this we use the kableExtra package. Install this in the normal manner. You may also want to alter the margins of your page using geometry in the preamble.

```{r setup, include=FALSE}

# Load data into global environment.

library(finalfit)

library(dplyr)

library(knitr)

library(kableExtra)

load("out.rda")

```

## Table 1 - Demographics

```{r table1, echo = FALSE, results='asis'}

kable(table1, row.names=FALSE, align=c("l", "l", "r", "r", "r", "r"),

booktabs=TRUE)

```

## Table 2 - Association between tumour factors and 5 year mortality

```{r table2, echo = FALSE, results='asis'}

kable(table2, row.names=FALSE, align=c("l", "l", "r", "r", "r", "r"),

booktabs=TRUE) %>%

kable\_styling(font\_size=8)

```

## Figure 1 - Association between tumour factors and 5 year mortality

```{r figure1, echo = FALSE, warning=FALSE, message=FALSE, fig.width=10}

colon\_s %>%

or\_plot(dependent, explanatory)```