Visualizing regression using caterpillar plots

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Caterpillar plots can be an effective way to present regression parameters or estimates from multiple sensitivity analyses. This tutorial will demonstrate how to create these plots using **ggplot2** when regression is performed within R, or in another statistical software.

We will need to install the following packages.

```
install.packages("tidyverse")
```

As usual, we will load our packages and set the working directory.

```
library(tidyverse)
library(ggsci)
library(survival)
library(broom)

#The working directory saves the following path when loading files, saving plots, etc
setwd("C:/Users/matth/Documents/R/R code and education/Tutorials/")
```

We will be working with a simulated dataset representing 80 generic cancer patients. The dataset can be loaded directly from GitHub so all the subsequent code will run on your computer.

```
urlRemote  <- "https://raw.githubusercontent.com/"
pathGithub <- "mcas-surg/Tutorials/main/Datasets/"
fileName   <- "generic_cancer.csv"

cancer <- read_csv(paste0(urlRemote, pathGithub, fileName))
```

Suppose we were interested in performing a multivariable Cox proportional hazards model, including 5 covariates: sex, patient age, tumour grade, tumour size, and treating hospital. The **survival** package requires our vital status variable to be binary. We will do this and save our new dataset as *cancer_surv*.

```
cancer_surv <- cancer %>%
  mutate(vital_status = ifelse(vital_status == "Died",
                               1, 0))
```

Now we can create the model. On the left side of the formula we pass variables indicating follow-up time and vital status. On the right side we pass our covariates of interest.

```
cox_model <- coxph(Surv(follow_up, vital_status) ~ male + age + high_grade +
                     tumour_size + hospital,
                   data = cancer_surv)

summary(cox_model)
```

```
## Call:
## coxph(formula = Surv(follow_up, vital_status) ~ male + age +
##     high_grade + tumour_size + hospital, data = cancer_surv)
##
##   n= 80, number of events= 50
##
##                               coef exp(coef) se(coef)      z Pr(>|z|)
## maleMale                   -0.25671   0.77359  0.29118 -0.882   0.3780
## age                         0.04105   1.04190  0.02360  1.740   0.0819 .
## high_gradeYes               0.36677   1.44307  0.38147  0.961   0.3363
## tumour_size                 0.11791   1.12515  0.15341  0.769   0.4421
## hospitalCommunity hospital  0.08044   1.08376  0.32124  0.250   0.8023
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##                            exp(coef) exp(-coef) lower .95 upper .95
## maleMale                      0.7736     1.2927    0.4372     1.369
## age                           1.0419     0.9598    0.9948     1.091
## high_gradeYes                 1.4431     0.6930    0.6832     3.048
## tumour_size                   1.1251     0.8888    0.8330     1.520
## hospitalCommunity hospital    1.0838     0.9227    0.5774     2.034
##
## Concordance= 0.629  (se = 0.044 )
## Likelihood ratio test= 7.99  on 5 df,   p=0.2
## Wald test            = 7.96  on 5 df,   p=0.2
## Score (logrank) test = 8.2  on 5 df,   p=0.1
```

Ideally, we wish to present the hazard ratios and confidence intervals graphically. These values are located within the model object *cox_model*. The **broom** package conveniently converts model objects into datasets than we can manipulate directly.

In this case, we need to exponentiate the estimates, and we would like 95% confidence intervals.

```
tidy_model <- tidy(cox_model,
                   exponentiate = TRUE,
                   conf.int = TRUE)

tidy_model
```

```
## # A tibble: 5 x 7
##   term                   estimate std.error statistic p.value conf.low conf.high
##   <chr>                     <dbl>     <dbl>     <dbl>   <dbl>    <dbl>     <dbl>
## 1 maleMale                  0.774    0.291     -0.882  0.378     0.437      1.37
## 2 age                       1.04     0.0236     1.74   0.0819    0.995      1.09
## 3 high_gradeYes             1.44     0.381      0.961  0.336     0.683      3.05
## 4 tumour_size               1.13     0.153      0.769  0.442     0.833      1.52
## 5 hospitalCommunity hos~    1.08     0.321      0.250  0.802     0.577      2.03
```

Let's clean up our small dataset. We will rename the values in the "term" column, and only keep our hazard ratios and 95% confidence intervals.

```
tidy_model$term <- c("Male sex",
                     "Older age (1 year)",
```

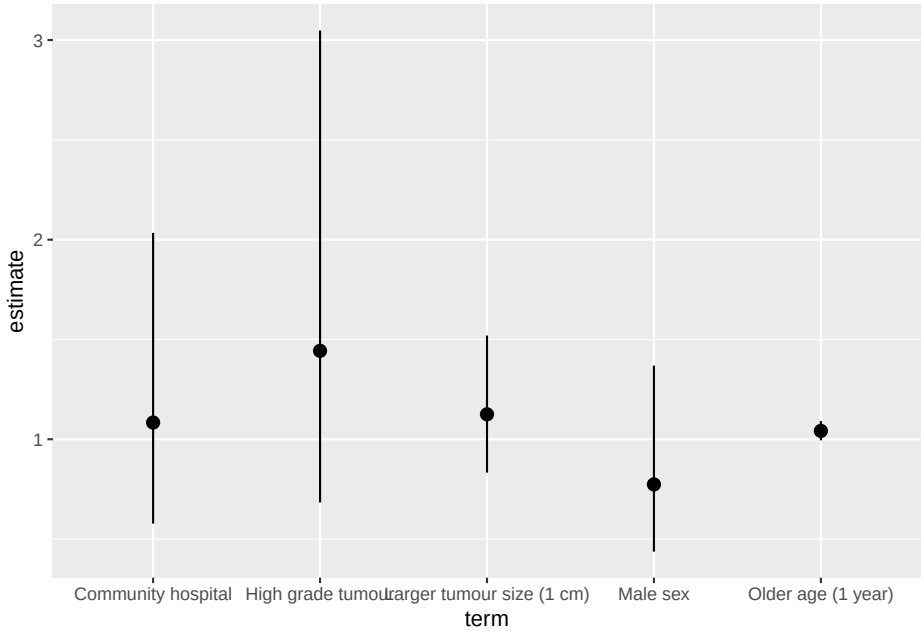
```
                      "High grade tumour",
                      "Larger tumour size (1 cm)",
                      "Community hospital")

tidy_model <- tidy_model %>%
  select(term, estimate, conf.low, conf.high)

tidy_model
```

```
## # A tibble: 5 x 4
##   term                        estimate conf.low conf.high
##   <chr>                          <dbl>    <dbl>     <dbl>
## 1 Male sex                       0.774    0.437      1.37
## 2 Older age (1 year)             1.04     0.995      1.09
## 3 High grade tumour              1.44     0.683      3.05
## 4 Larger tumour size (1 cm)      1.13     0.833      1.52
## 5 Community hospital             1.08     0.577      2.03
```

Now we can begin creating our plot. We will mainly use `geom_pointrange` and `geom_errorbar`, which together will demonstrate each hazard ratio and 95% CI.

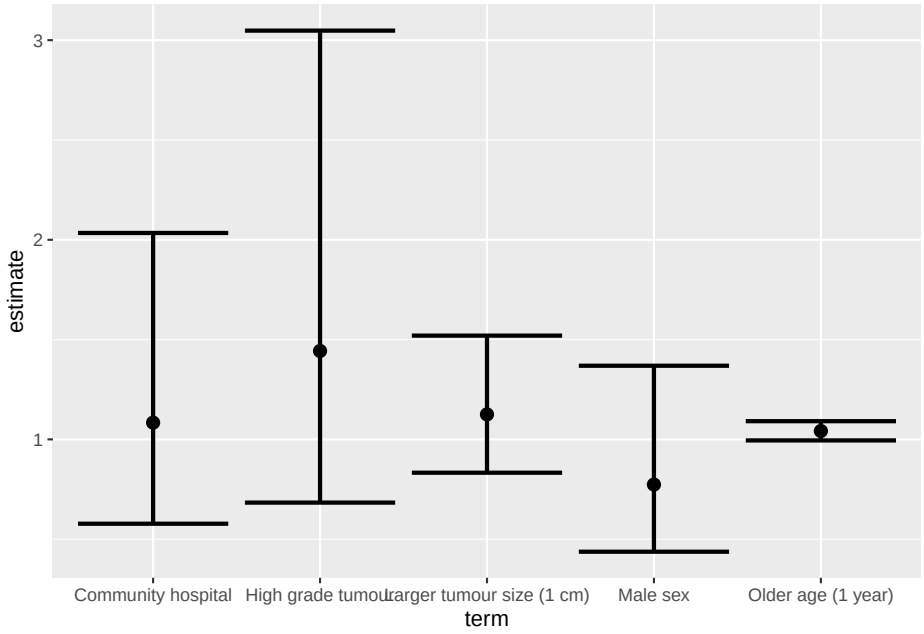
First, starting simply.

```
tidy_model %>%
  ggplot(aes(x = term,
             y = estimate, ymin = conf.low, ymax = conf.high))+
  geom_pointrange(size=0.5)
```



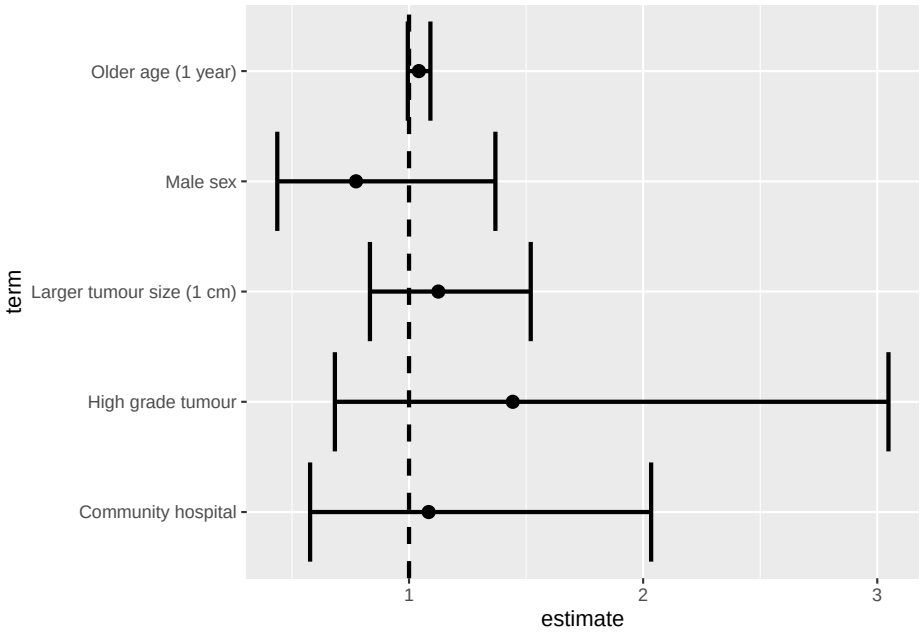
This is `geom_pointrange()` by itself. Here is how adding `geom_errorbar` changes the plot.

```
tidy_model %>%
  ggplot(aes(x = term,
             y = estimate, ymin = conf.low, ymax = conf.high))+
  geom_pointrange(size = 0.5)+
  geom_errorbar(size = 1)
```



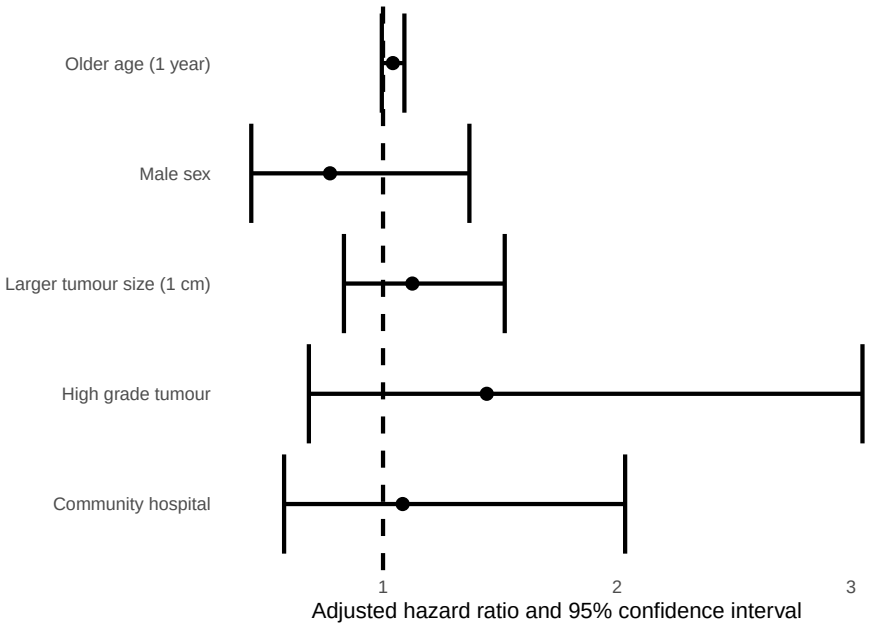
We should flip the plot vertically and add a line showing a HR = 1.

```
tidy_model %>%
  ggplot(aes(x = term,
             y = estimate, ymin = conf.low, ymax = conf.high))+
  geom_pointrange(size = 0.5)+
  geom_errorbar(size = 1)+
  geom_hline(yintercept = 1, linetype = 2, size = 1)+
  coord_flip()
```



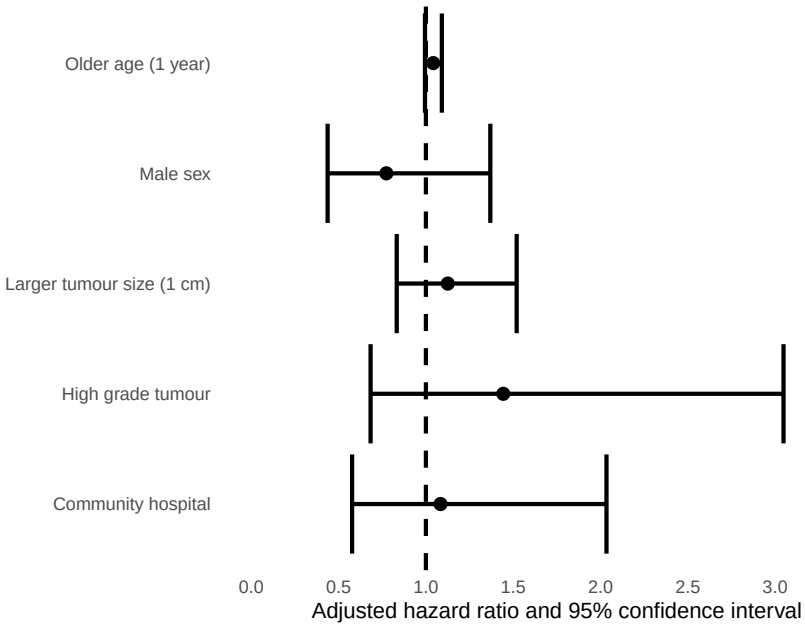
This is already looking better. Next, we can remove the y-axis label, change the x-axis label, and adjust the theme. Remember, when we flip figures the axes don't change in the code.

```
tidy_model %>%
  ggplot(aes(x = term,
             y = estimate, ymin = conf.low, ymax = conf.high))+
  geom_pointrange(size = 0.5)+
  geom_errorbar(size = 1)+
  geom_hline(yintercept = 1, linetype = 2, size = 1)+
  coord_flip()+
  labs(x = "",
       y = "Adjusted hazard ratio and 95% confidence interval")+
  theme_minimal()+
  theme(panel.grid = element_blank())
```



The figure would be improved by shifting the axis and breaks.

```
tidy_model %>%
  ggplot(aes(x = term,
             y = estimate, ymin = conf.low, ymax = conf.high))+
  geom_pointrange(size = 0.5)+
  geom_errorbar(size = 1)+
  geom_hline(yintercept = 1, linetype = 2, size = 1)+
  coord_flip()+
  labs(x = "",
       y = "Adjusted hazard ratio and 95% confidence interval")+
  theme_minimal()+
  theme(panel.grid = element_blank())+
  scale_y_continuous(limits = c(0, 3.5),
                     breaks = seq(0, 3, 0.5))
```



It is also possible to add labels to the figure indicating the hazard ratio. Text can be added dynamically as a layer using `+geom_text()`. This layer requires you to provide labels. We will create our custom labels for each covariate.

First, we need to round the hazard ratios and confidence limits to 2 decimal places, and we will save these as new variables.

```
tidy_model_labels <- tidy_model %>%
  mutate(estimate_round = round(estimate, 2),
         conf.low_round = round(conf.low, 2),
         conf.high_round = round(conf.high, 2))
```

Now we can start building our labels. This will be shown over several steps so you can follow what each piece of code is doing.

```
tidy_model_labels <- tidy_model_labels %>%
  unite("custom_label", estimate_round, conf.low_round,
        remove = TRUE,
        sep = ", 95% CI ")
```

```
## # A tibble: 5 x 1
##   custom_label
##   <chr>
## 1 0.77, 95% CI 0.44
## 2 1.04, 95% CI 0.99
## 3 1.44, 95% CI 0.68
## 4 1.13, 95% CI 0.83
## 5 1.08, 95% CI 0.58
```

The `unite()` function combines chosen columns in a character string, with a custom separator that you can specify. Here, we have combined the estimate and lower confidence limit with the string ", 95% CI"

between. This has been saved to the new variable "custom_label". The `remove = TRUE` argument will delete the original combined columns.

We will continue and add the upper confidence limit.

```
tidy_model_labels <- tidy_model_labels %>%
  unite("custom_label", custom_label, conf.high_round,
        remove = TRUE,
        sep = "-")
```

```
## # A tibble: 5 x 1
##   custom_label
##   <chr>
## 1 0.77, 95% CI 0.44-1.37
## 2 1.04, 95% CI 0.99-1.09
## 3 1.44, 95% CI 0.68-3.05
## 4 1.13, 95% CI 0.83-1.52
## 5 1.08, 95% CI 0.58-2.03
```

Finally, we can paste the string "HR" to the front of each label.

```
tidy_model_labels <- tidy_model_labels %>%
  mutate(custom_label = paste0("HR ", custom_label))
```

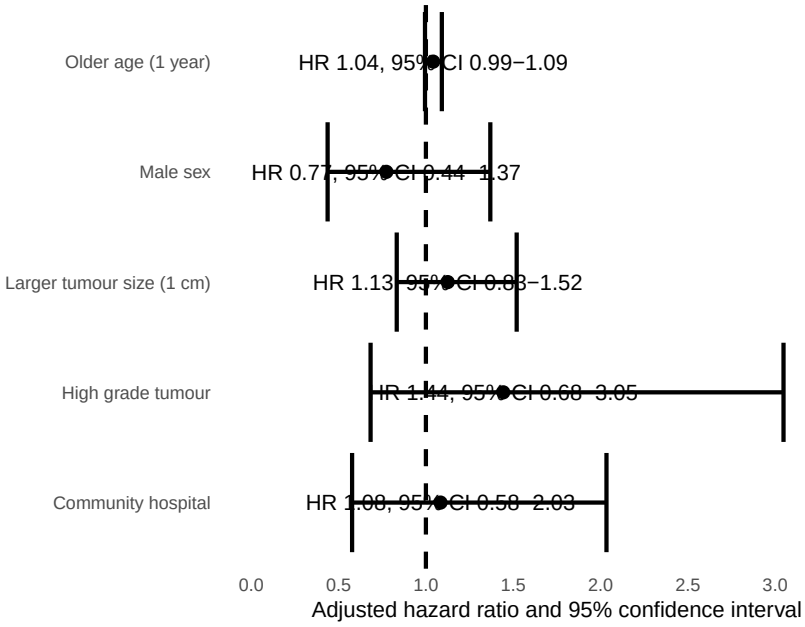
```
## # A tibble: 5 x 1
##   custom_label
##   <chr>
## 1 HR 0.77, 95% CI 0.44-1.37
## 2 HR 1.04, 95% CI 0.99-1.09
## 3 HR 1.44, 95% CI 0.68-3.05
## 4 HR 1.13, 95% CI 0.83-1.52
## 5 HR 1.08, 95% CI 0.58-2.03
```

In reality, all of these data steps could have been piped together to save time. This is what that would look like.

```
tidy_model_labels <- tidy_model %>%
  mutate(estimate_round = round(estimate, 2),
         conf.low_round = round(conf.low, 2),
         conf.high_round = round(conf.high, 2)) %>%
  unite("custom_label", estimate_round, conf.low_round,
        remove = TRUE,
        sep = ", 95% CI ") %>%
  unite("custom_label", custom_label, conf.high_round,
        remove = TRUE,
        sep = "-") %>%
  mutate(custom_label = paste0("HR ", custom_label))
```

Now, let's add these labels to our previous figure using `+geom_text()`. Note I am adding the labels aesthetic directly to `geom_text()`, but it could also have been added to the `ggplot()` statement at the top of the code.

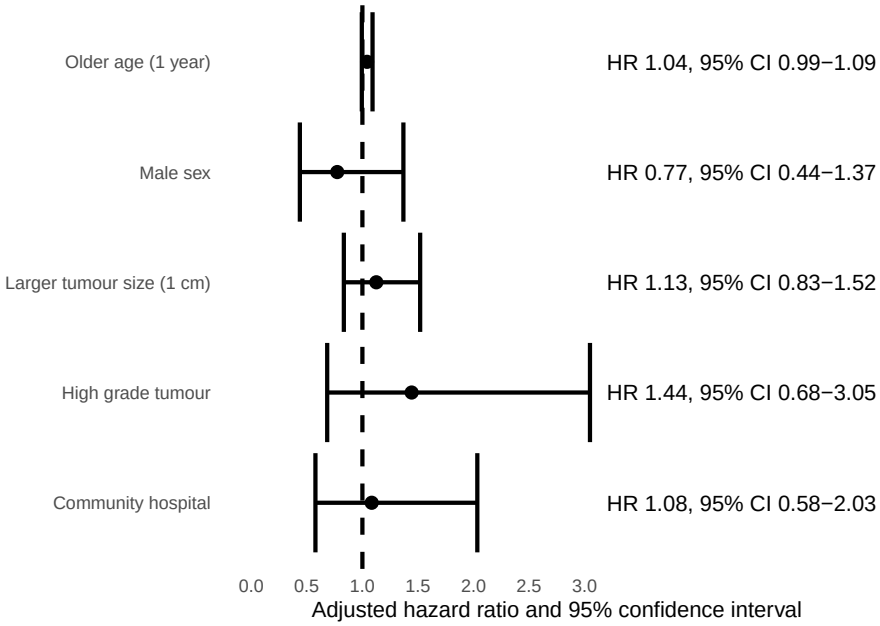
```
tidy_model_labels %>%
  ggplot(aes(x = term,
             y = estimate, ymin = conf.low, ymax = conf.high))+
  geom_pointrange(size = 0.5)+
  geom_errorbar(size = 1)+
  geom_hline(yintercept = 1, linetype = 2, size = 1)+
  coord_flip()+
  labs(x = "",
       y = "Adjusted hazard ratio and 95% confidence interval")+
  theme_minimal()+
  theme(panel.grid = element_blank())+
  scale_y_continuous(limits = c(0, 3.5),
                     breaks = seq(0, 3, 0.5))+
  geom_text(aes(label = custom_label))
```



Unfortunately, `geom_text()` inherited the x and y coordinates in the `ggplot()` statement and the result is not very attractive. We can manually set these values to shift the text. We will also adjust the x-axis limits and breaks to add more space to the right side of the plot without extending the x-axis text. Look at the following code carefully.

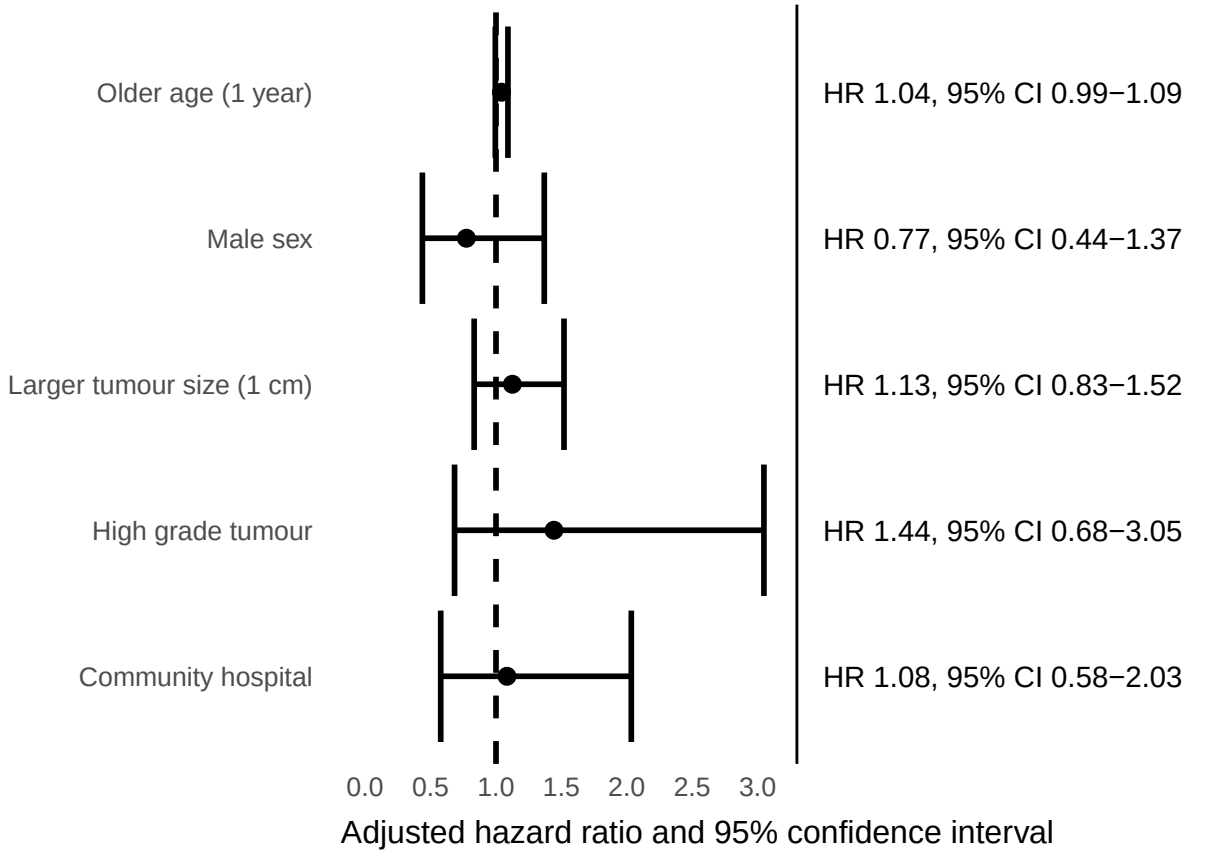
```
tidy_model_labels %>%
  ggplot(aes(x = term,
             y = estimate, ymin = conf.low, ymax = conf.high))+
  geom_pointrange(size = 0.5)+
  geom_errorbar(size = 1)+
  geom_hline(yintercept = 1, linetype = 2, size = 1)+
  coord_flip()+
  labs(x = "",
       y = "Adjusted hazard ratio and 95% confidence interval")+
  theme_minimal()+
  theme(panel.grid = element_blank())+
```

```
  scale_y_continuous(limits = c(0, 5.5),
                     breaks = seq(0, 3, 0.5))+
  geom_text(aes(label = custom_label,
                y = 3.2, hjust = 0))
```



This is looking better. For a final level of customization we can add a vertical line to give the appearance of a divide between the error bars and labels, and manually shift the x-axis title to the left so it remains centered. I will also increase the overall size of the text slightly.

```
tidy_model_labels %>%
  ggplot(aes(x = term,
             y = estimate, ymin = conf.low, ymax = conf.high))+
  geom_pointrange(size = 0.5)+
  geom_errorbar(size = 1)+
  geom_hline(yintercept = 1, linetype = 2, size = 1)+
  coord_flip()+
  labs(x = "",
       y = "Adjusted hazard ratio and 95% confidence interval")+
  theme_minimal()+
  theme(panel.grid = element_blank())+
  scale_y_continuous(limits = c(0, 6),
                     breaks = seq(0, 3, 0.5))+
  geom_text(aes(label = custom_label,
                y = 3.5, hjust = 0))+
  geom_hline(yintercept = 3.3)+
  theme(axis.title.x = element_text(hjust = 0.1, vjust = -0.5),
        text = element_text(size = 12))
```



Remember to save a publication-quality version of your plot.

```
#If you have not set the working directory, include the full file path
ggsave("my_plot.png",
       dpi = 300, dev = "png",
       height = 20, width = 25, units = "cm")
```

Although this example used hazard ratios from a model created in R, this plot can be easily replicated by manually creating an equivalent dataset from estimates given in another statistical software. Creating a .csv file with the following columns and importing this into R will provide an attractive method of presenting regression parameters.

term	estimate	conf.low	conf.high	custom_label

Future tutorials will focus on more complex plots, including using colour and facets to distinguish several different analyses for the same parameter.