

Day 4 : Data Visualization Fundamentals in R



Ambu Vijayan

Bioinformatician

BioLit, Thiruvananthapuram

Visualizations



The ggplot2 library is an extremely popular visualization package that provides an interface for extremely fine control over graphics for plotting.

Install ggplot2 and viridis

```
install.packages("ggplot2")
```

```
library(ggplot2)
```

```
install.packages("viridis")
```

```
library(viridis)
```

Viridis is Colorblind-Friendly Color Maps for R

ggplot2

```
?ggplot
```

```
ggplot(data = birthdata, mapping = aes(x = birthweight))
```

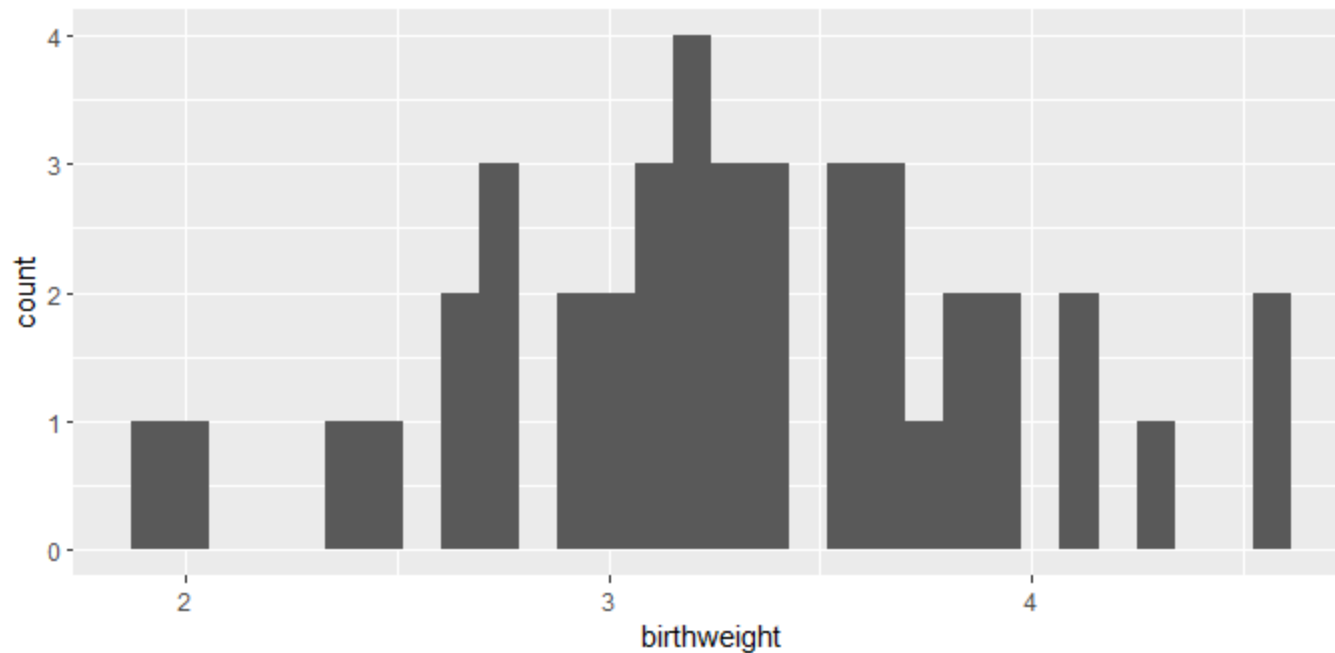
This outputs a blank canvas.



geom

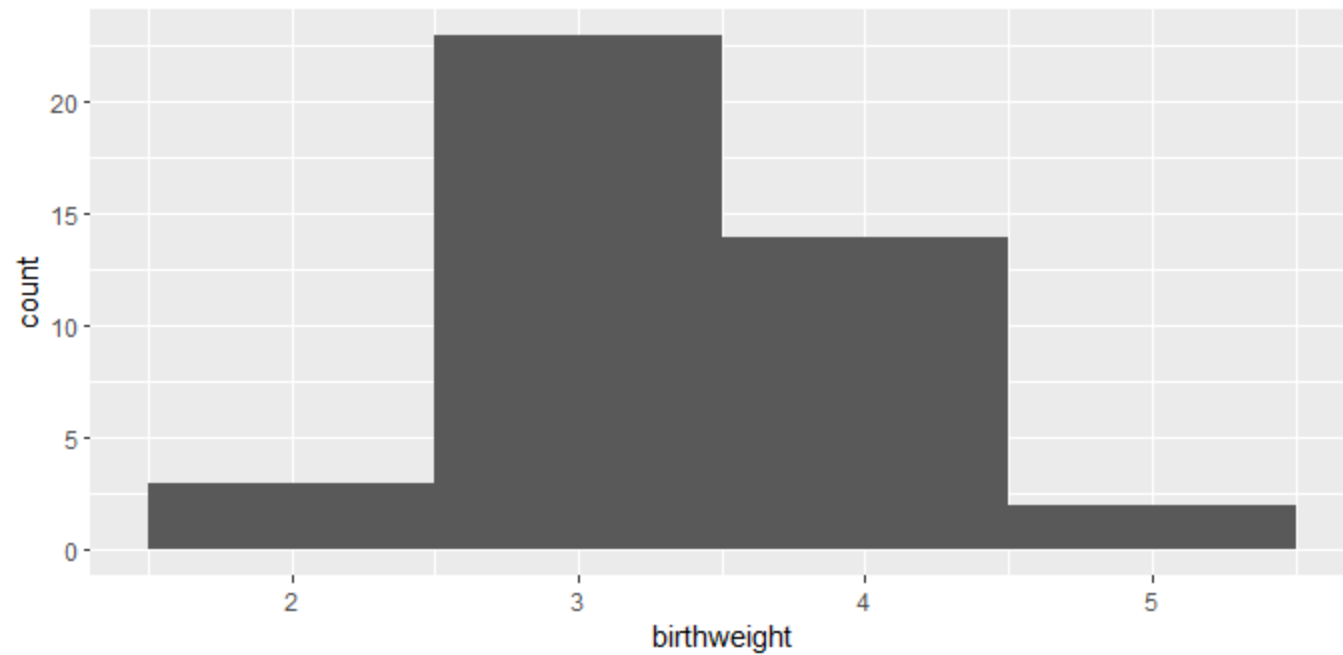
There are 30 geoms in the ggplot2 library, let's start with histogram.

```
ggplot(data = birthdata, mapping = aes(x = birthweight)) + geom_histogram()
```

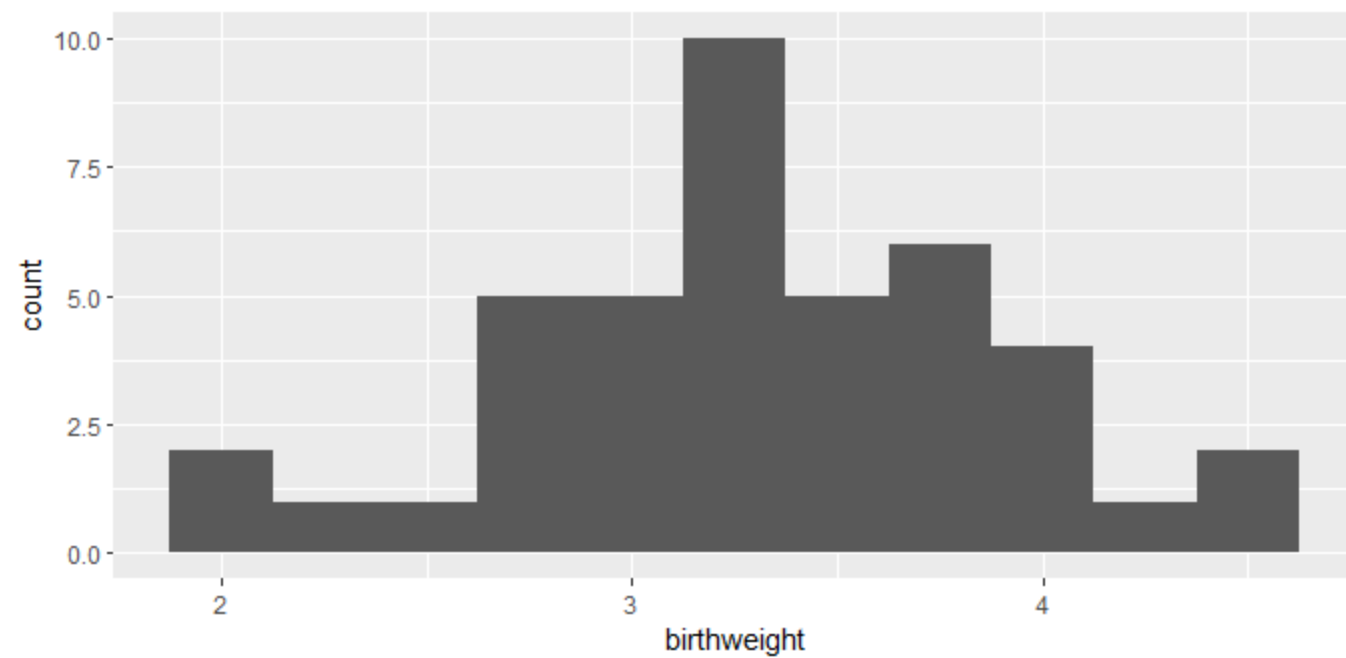


But we get a warning: `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.

```
ggplot(data = birthdata, mapping = aes(x = birthweight)) +  
geom_histogram(binwidth = 1)
```

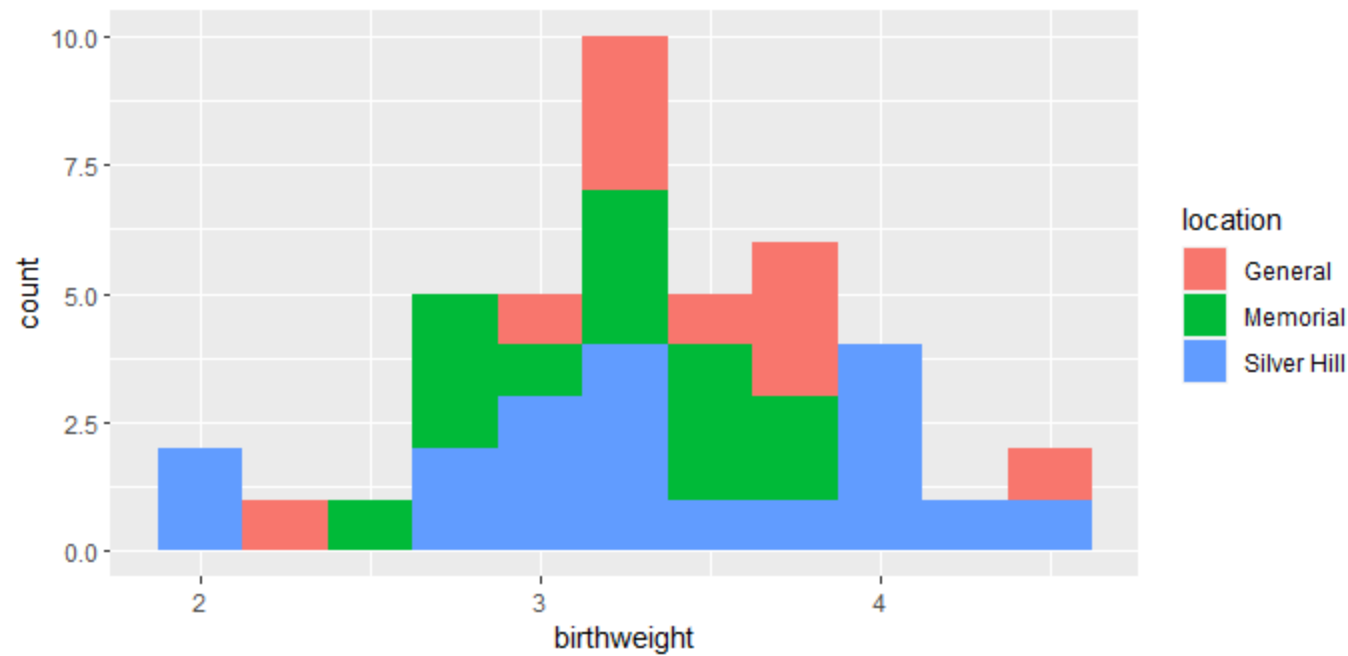


```
ggplot(data = birthdata, mapping = aes(x = birthweight)) +  
geom_histogram(binwidth = 0.25)
```



Adding color (and fill) to geoms

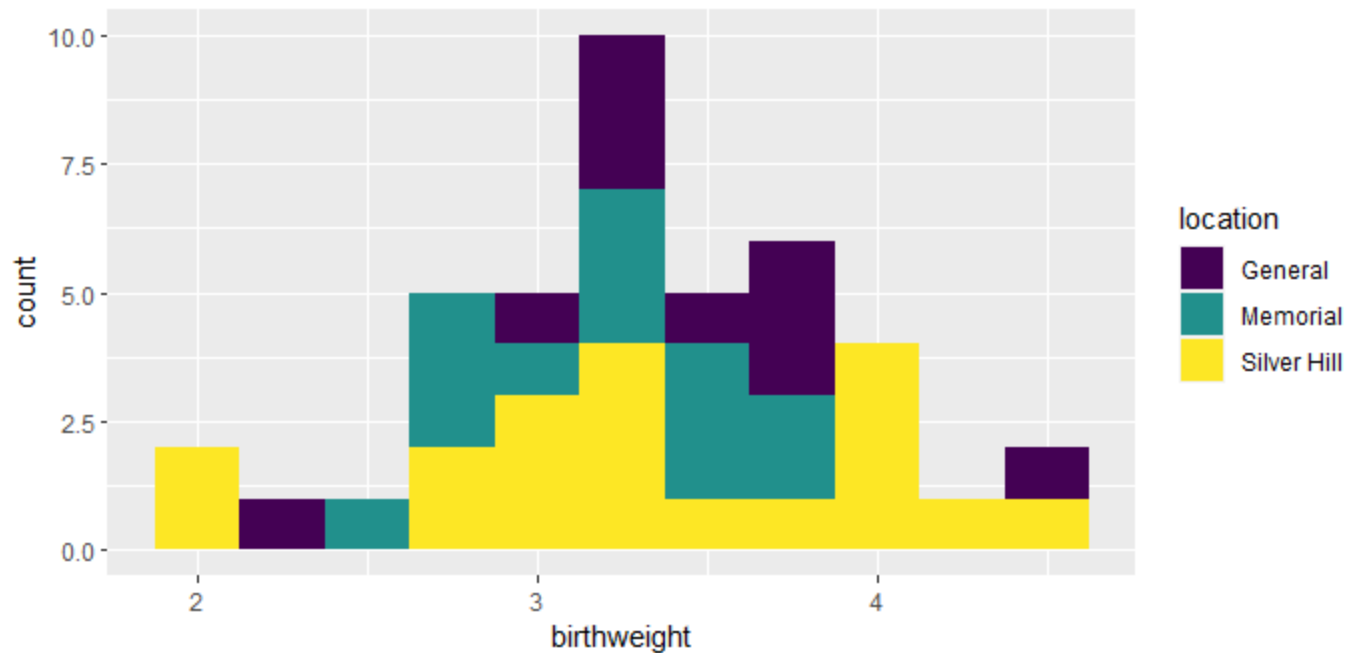
```
ggplot(data = birthdata, mapping = aes(x = birthweight, fill = location)) +  
geom_histogram(binwidth = 0.25)
```



Making it colorblind friendly palette

```
locations.palette <- viridis(3)
```

```
ggplot(data = birthdata, mapping = aes(x = birthweight, fill = location)) +  
geom_histogram(binwidth = 0.25) + scale_fill_manual(values = locations.palette)
```



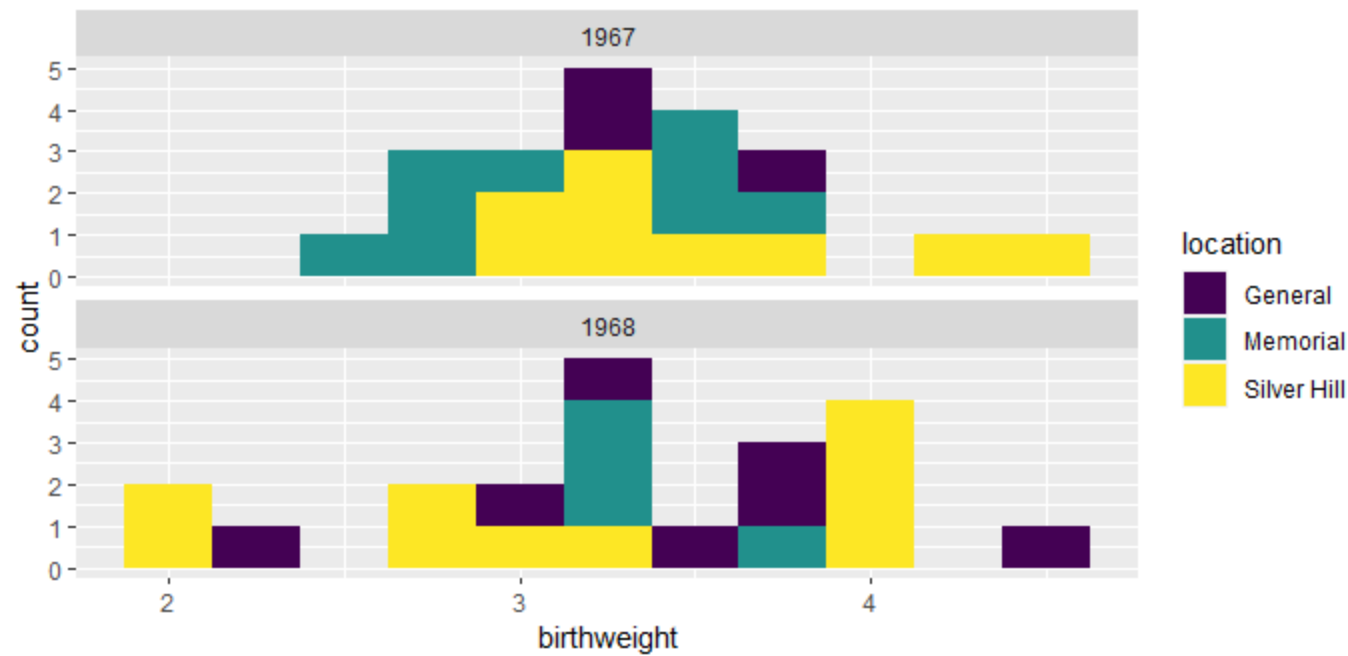
Creating faceted plots

Create multiple sub-plots or “facets” based on categorical values in the data.

The `facet_wrap()` and `facet_grid()` functions allow the user to break the data down into multiple plots by one or two categorical variables, respectively.

```
ggplot(data = birthdata, mapping = aes(x = birthweight, fill = location)) +  
geom_histogram(binwidth = 0.25) + scale_fill_manual(values = locations.palette) +  
facet_wrap(~year, nrow = 2)
```

We used `facet_wrap` to year and grid rows as 2.



Add and modify labels

The `labs()` function offers the option to set the following labels:

- any aesthetic that has been set: in this case, `x` and `fill`
- `title`: main title of the plot
- `subtitle`: displayed below the title
- `caption`: displayed at the bottom right of the plot by default
- `tag`: label that appears at the top left of the plot by default (e.g. 1A)
- `alt`, `alt_insight`: alt text for the plot (used by screen readers)

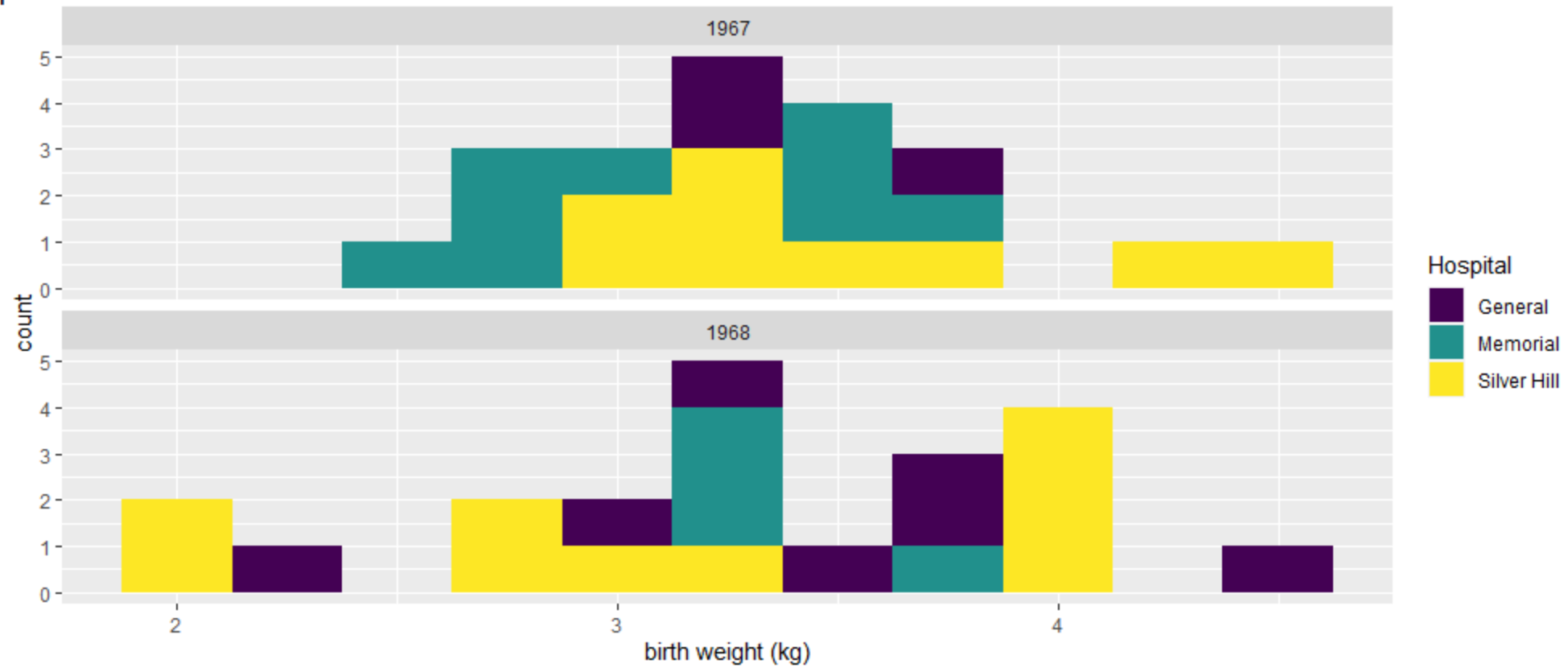
Add and modify labels

```
ggplot(data = birthdata, mapping = aes(x = birthweight, fill = location)) +  
geom_histogram(binwidth = 0.25) + scale_fill_manual(values = locations.palette) +  
facet_wrap(~year, nrow = 2) + labs(x = "birth weight (kg)", fill = "Hospital",  
tag = "fig. 1", caption = "Birth weights by year, color-coded by delivery  
location.", alt = "Pair of histograms displaying the distribution of birth  
weights of infants born at General Hospital, Memorial Hospital, and Silver Hill  
Medical Center in 1967 and 1968.")
```

Breaking down the command

- `ggplot(data = birthdata, mapping = aes(x = birthweight, fill = location)) +`
- `geom_histogram(binwidth = 0.25) +`
- `scale_fill_manual(values = locations.palette) +`
- `facet_wrap(~year, nrow = 2) +`
- `labs(x = "birth weight (kg)",`
 - `fill = "Hospital",`
 - `tag = "fig. 1",`
 - `caption = "Birth weights by year, color-coded by delivery location.",`
 - `alt = "Pair of histograms displaying the distribution of birth weights of infants born at General Hospital, Memorial Hospital, and Silver Hill Medical Center in 1967 and 1968.")`

fig. 1

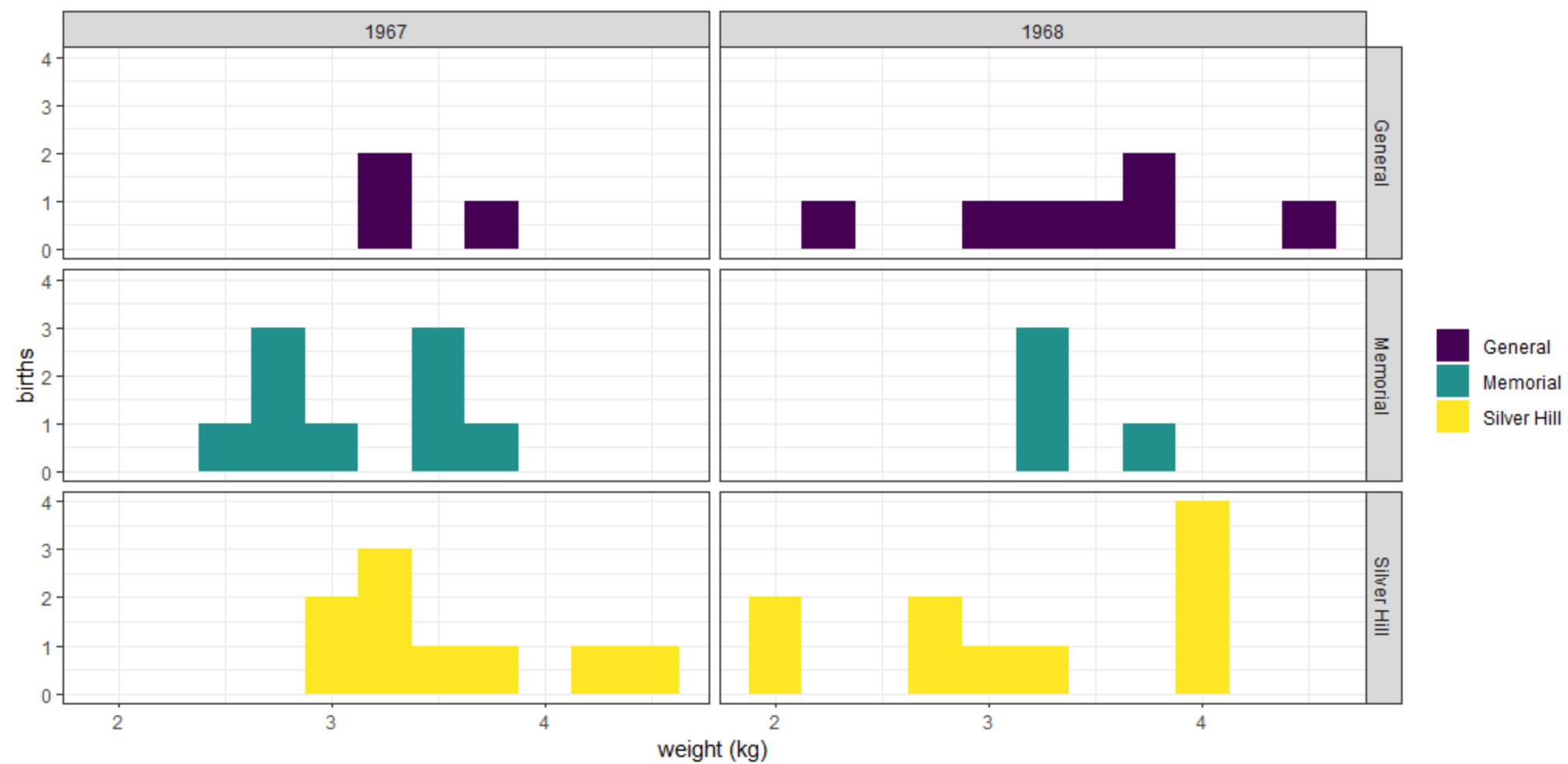


Birth weights by year, color-coded by delivery location.

Plot Themes

```
ggplot(data = birthdata, mapping = aes(x = birthweight, fill = location)) +  
geom_histogram(binwidth = 0.25) + scale_fill_manual(values = locations.palette) +  
facet_grid(location~year) + labs(x = "weight (kg)", y = "births") + theme_bw() +  
theme(legend.title = element_blank())
```

- ggplot(data = birthdata, mapping = aes(x = birthweight, fill = location)) +
- geom_histogram(binwidth = 0.25) +
- scale_fill_manual(values = locations.palette) +
- facet_grid(location~year) +
- labs(x = "weight (kg)", y = "births") +
- theme_bw() +
- theme(legend.title = element_blank())



geom_density()

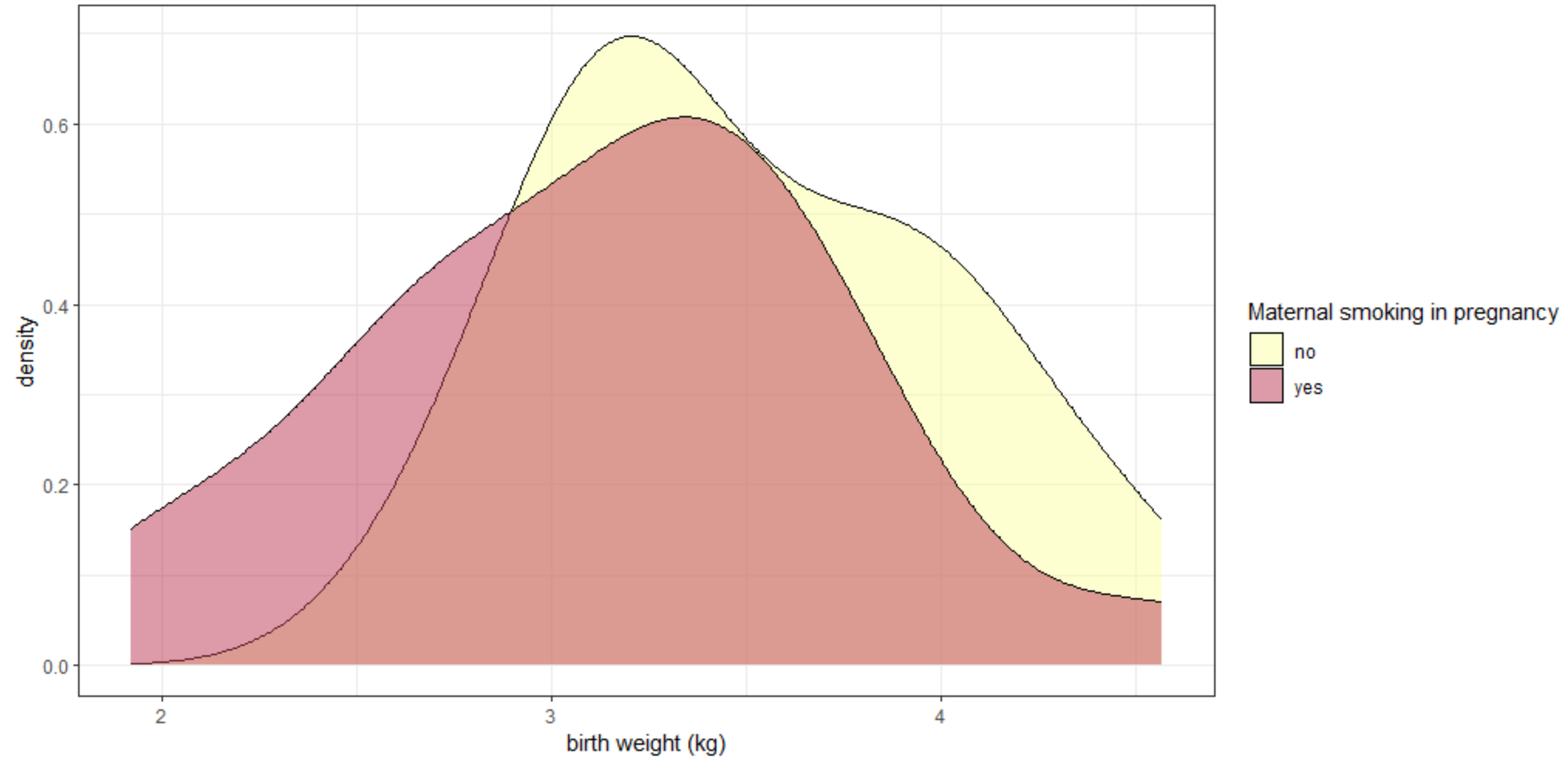
lets create a new color blind palette

```
smoking.palette <- inferno(2, begin = 0.5, direction = -1)
```

?inferno to learn more bout this.

```
ggplot(data = birthdata, mapping = aes(x = birthweight, fill = smoker)) +  
geom_density(alpha = 0.5) + scale_fill_manual(values = smoking.palette) + labs(x  
= "birth weight (kg)", fill = "Maternal smoking in pregnancy") + theme_bw()
```

geom_density() plot



geom_point()

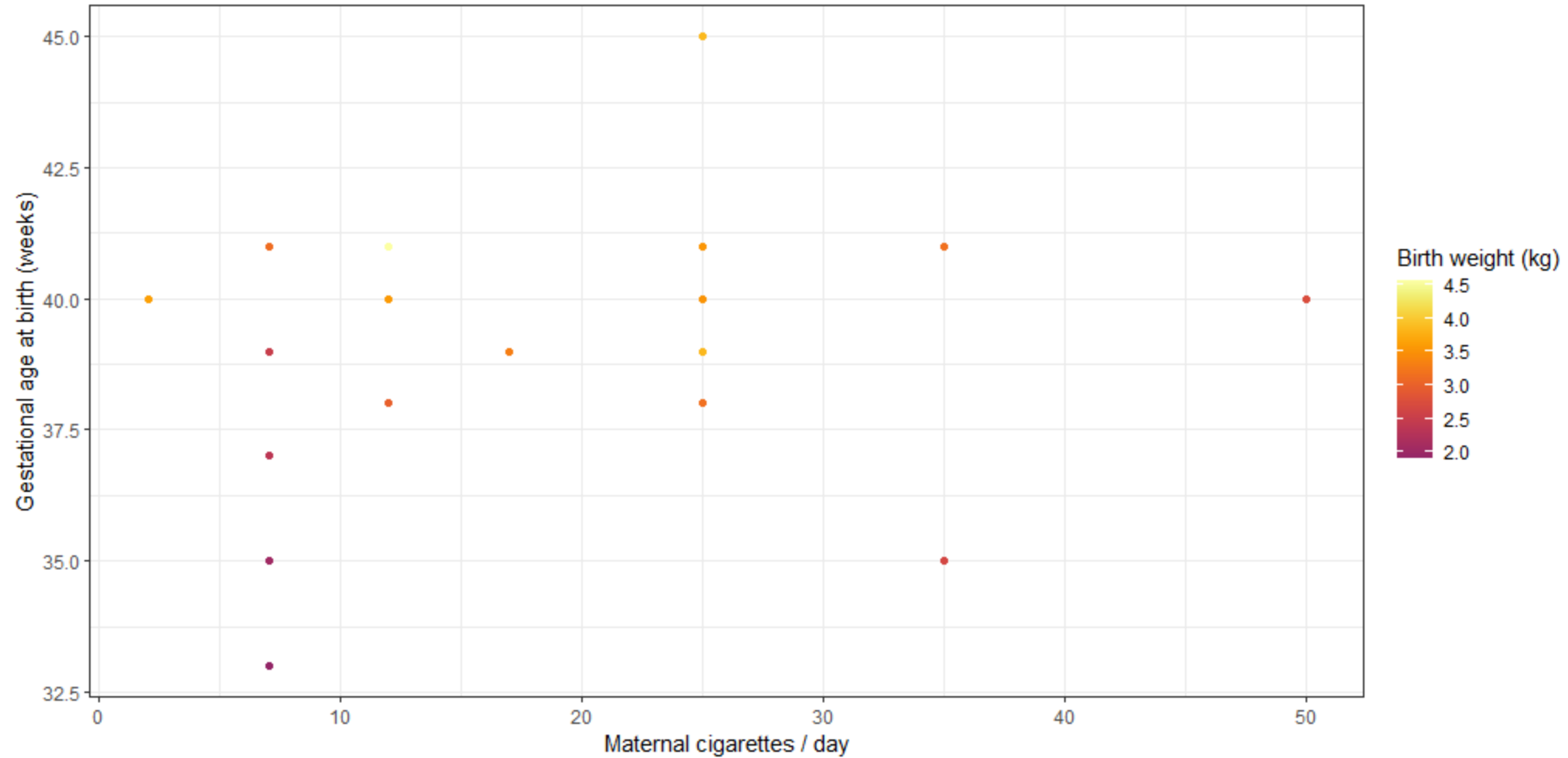
Filter out smokers from birthdata

```
filtered_data <- birthdata[birthdata$smoker == TRUE, ]
```

Plot using geom point

```
ggplot(data = filtered_birthdata, mapping = aes(x = maternal.cigarettes, y =  
weeks.gestation, color = birthweight)) + geom_point() + labs(x = "Maternal  
cigarettes / day", y = "Gestational age at birth (weeks)", color = "Birth weight  
(kg)") + scale_color_viridis(option = "inferno", begin = 0.4) + theme_bw()
```

geom_point() plot



No need to specify a color palette; viridis has a built-in function for ggplot objects.

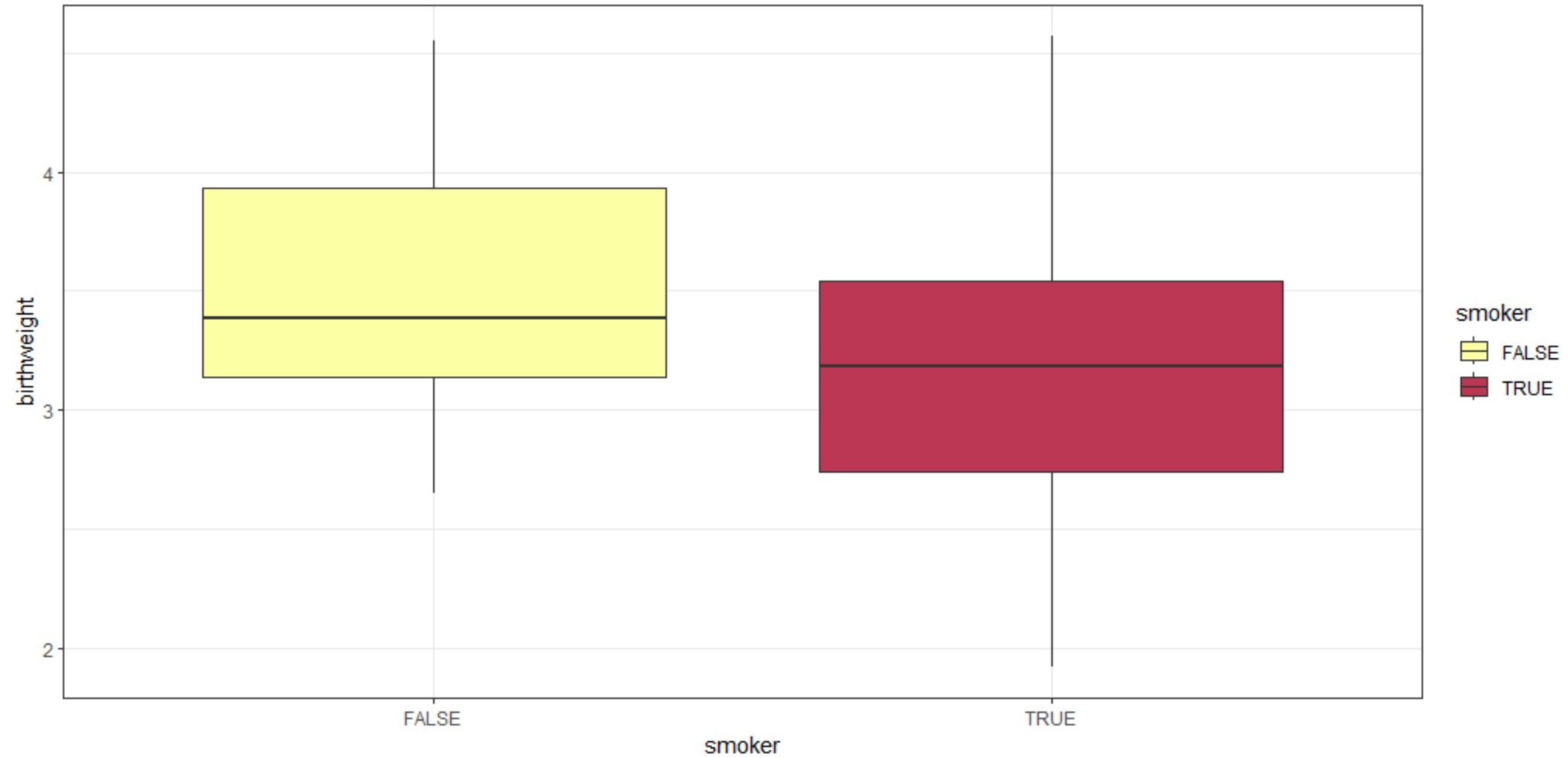
geom_boxplot()

```
ggplot(data = birthdata, mapping = aes(x = smoker, y = birthweight, fill =  
smoker)) + geom_boxplot() + scale_fill_manual(values = smoking.palette) +  
theme_bw()
```

The labels on a categorical axis should be meaningful.

The bar chart above displays the values "TRUE" and "FALSE" on the x-axis.

geom_boxplot() plot



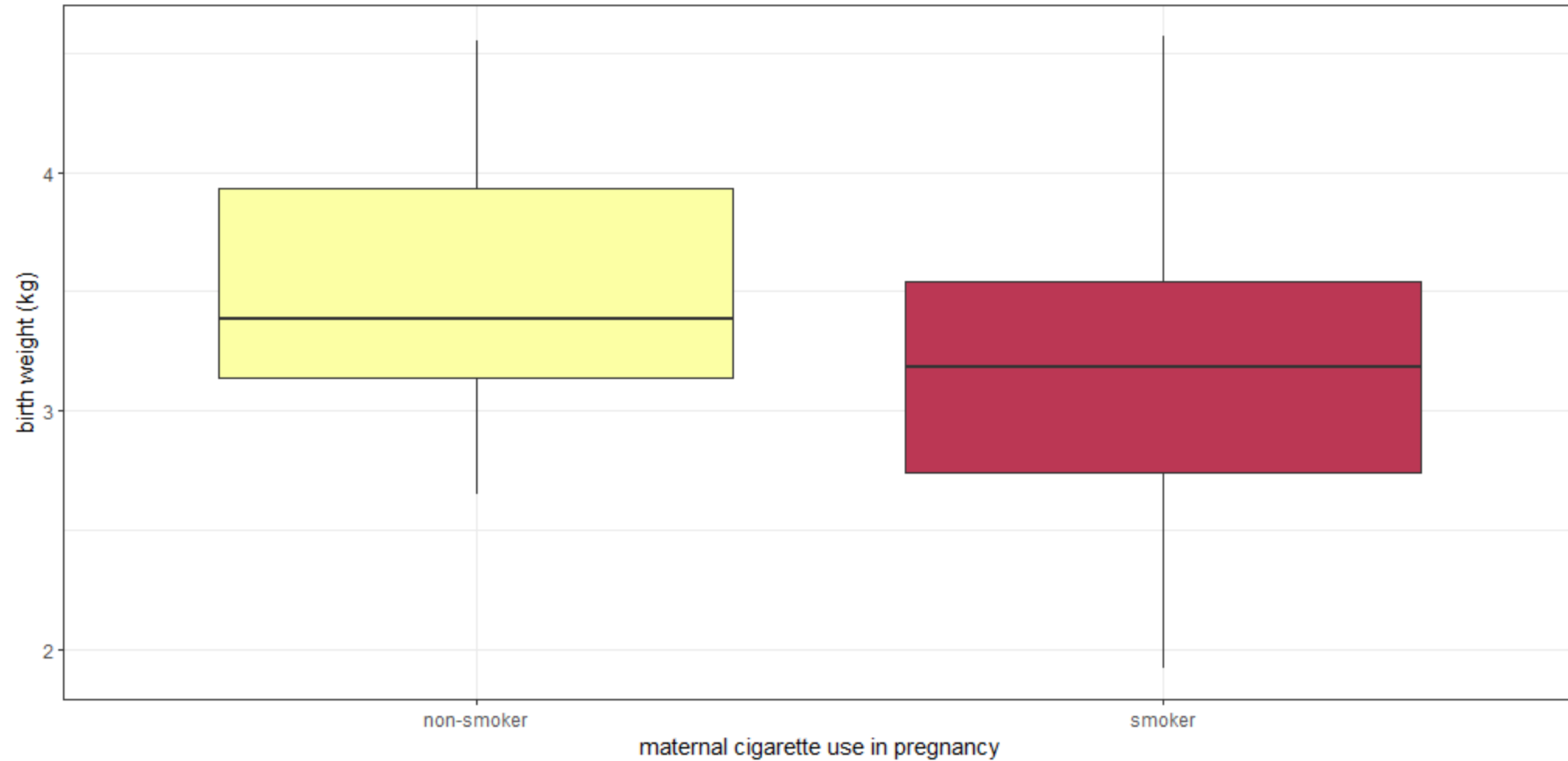
geom_boxplot() for Publications

In a report or publication, it might be more informative to replace "TRUE" and "FALSE" with "smoker" and "non-smoker."

The `scale_x_discrete()` function is used to do that.

```
ggplot(data = birthdata, mapping = aes(x = smoker, y = birthweight, fill =  
smoker)) + geom_boxplot() + scale_fill_manual(values = smoking.palette) +  
scale_x_discrete(labels = c("non-smoker", "smoker")) + guides(fill = "none") +  
labs(y = "birth weight (kg)", x = "maternal cigarette use in pregnancy") +  
theme_bw()
```


geom_boxplot() for Publications Plot



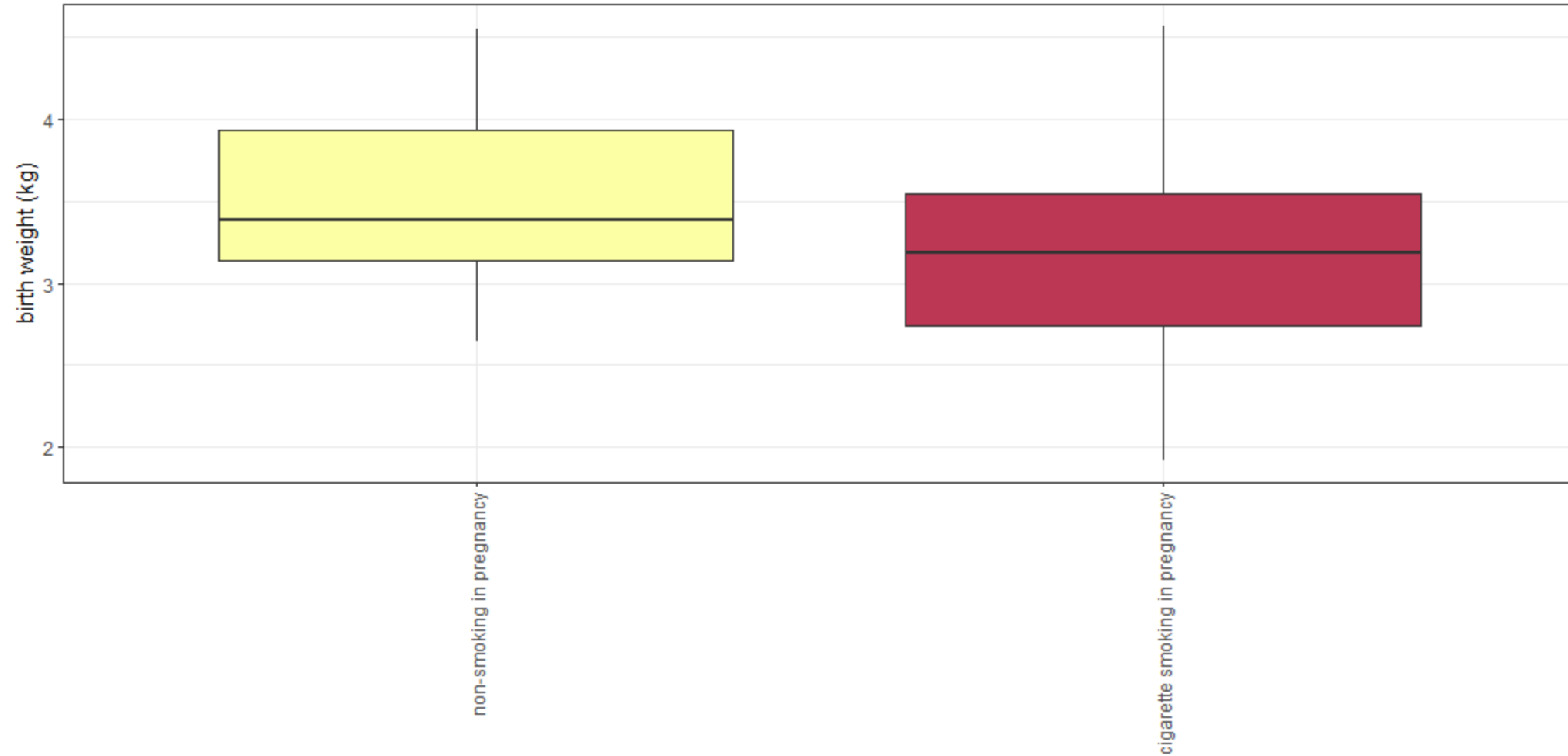
Changing the direction of axes labels

```
ggplot(data = birthdata, mapping = aes(x = smoker, y = birthweight, fill =
smoker)) + geom_boxplot() + scale_fill_manual(values = smoking.palette) +
scale_x_discrete(labels = c("non-smoking in pregnancy", "cigarette smoking in
pregnancy")) + guides(fill = "none") + labs(y = "birth weight (kg)") + theme_bw()
+ theme(axis.title.x = element_blank(), axis.text.x = element_text(angle = 90,
vjust = 0.5, hjust = 1))
```

This last part helps us change angles of labels

```
+ theme(axis.title.x = element_blank(), axis.text.x = element_text(angle = 90,
vjust = 0.5, hjust = 1))
```

Changed label axis plot



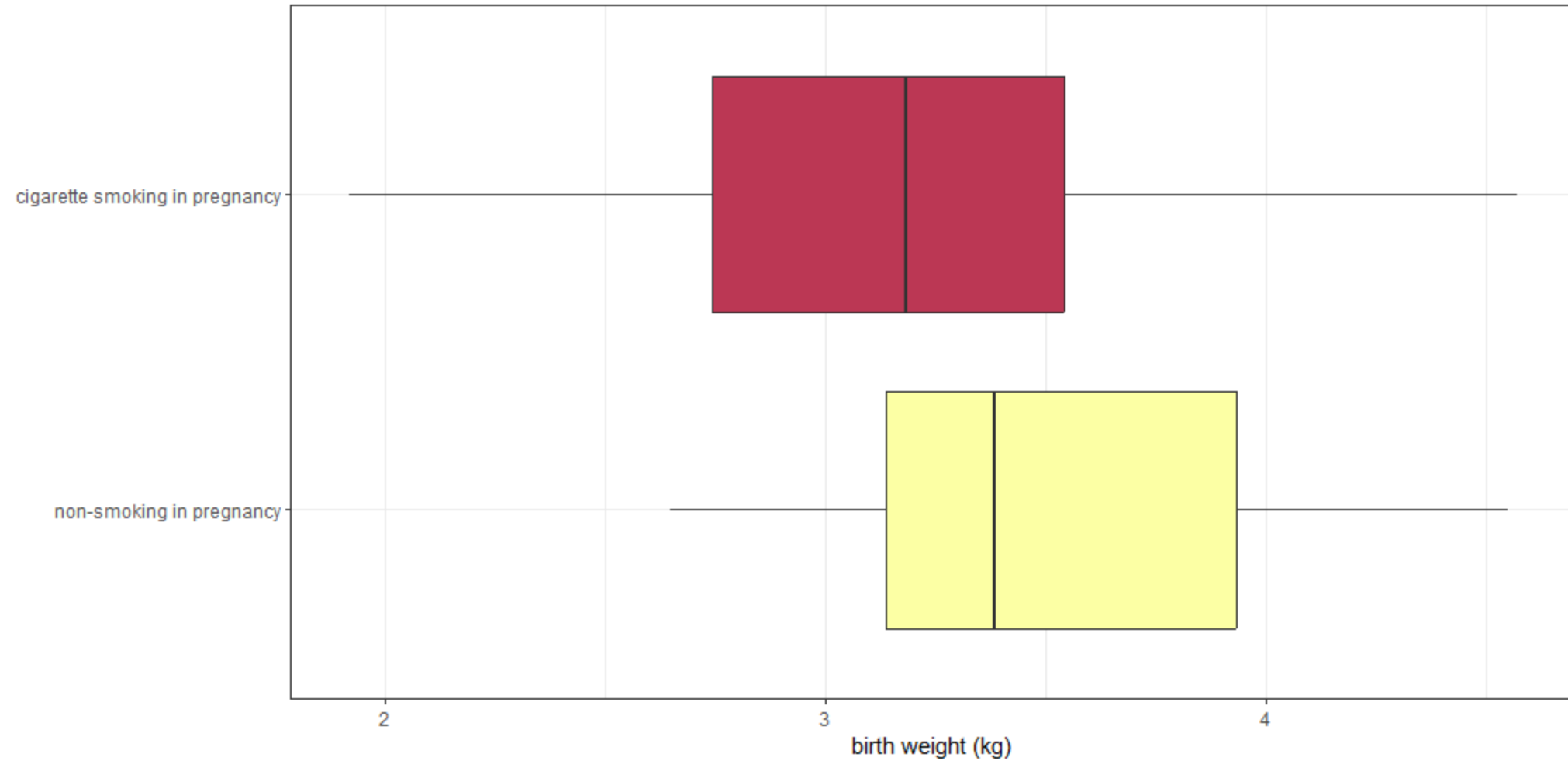
Changing the direction of axes itself

```
ggplot(data = birthdata, mapping = aes(x = smoker, y = birthweight, fill =  
smoker)) + geom_boxplot() + scale_fill_manual(values = smoking.palette) +  
scale_x_discrete(labels = c("non-smoking in pregnancy", "cigarette smoking in  
pregnancy")) + guides(fill = "none") + labs(y = "birth weight (kg)") +  
coord_flip() + theme_bw() + theme(axis.title.y = element_blank())
```

This last part helps us change angles of axis itself

```
+ coord_flip()
```

Changed axis plot

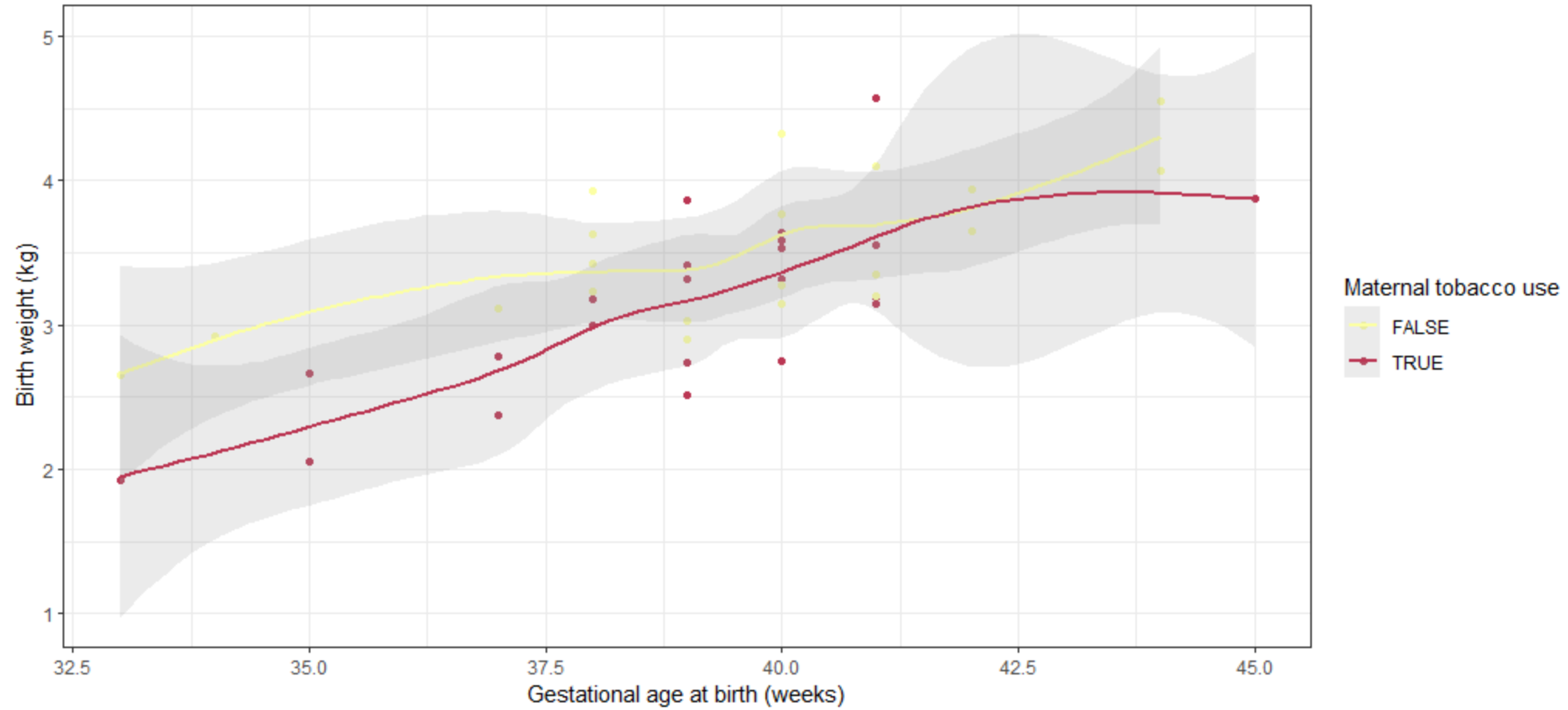


Layer multiple geoms

We used `geom_point` and `geom_smooth` here together.

```
ggplot(birthdata, mapping = aes(x = weeks.gestation, y = birthweight, color =  
smoker)) + geom_point() + geom_smooth(alpha = 0.2) + labs(x = "Gestational age at  
birth (weeks)", y = "Birth weight (kg)", color = "Maternal tobacco use", caption  
= "Birthweight increases with gestational age for infants born to both\nsmokers  
and non-smokers.") + scale_color_manual(values = smoking.palette) + theme_bw() +  
theme(plot.caption = element_text(hjust = 0))
```

multiple geoms plot



Birthweight increases with gestational age for infants born to both smokers and non-smokers.

Remember :

If its point or line of colors, then :

color = data

from above examples : `color = smoker`

Also,

If its an area to be filled by a color, then :

fill = data

from above examples : `fill = smoker`