hw02_gap

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18 September 2019

Exercise 1: Dplyr package

1.1 - Subset gapminder to 3 countries, 1970s.

Countries: Canada, India, Italy

```
filtered <- gapminder %>%
  filter(country %in% c("Canada","India","Italy"),
         year %in% c(1970:1979))
knitr::kable(filtered, format="markdown")
```

country	continent	year	lifeExp	pop	gdpPercap
Canada	Americas	1972	72.880	22284500	18970.5709
Canada	Americas	1977	74.210	23796400	22090.8831
India	Asia	1972	50.651	567000000	724.0325
India	Asia	1977	54.208	634000000	813.3373
Italy	Europe	1972	72.190	54365564	12269.2738
Italy	Europe	1977	73.480	56059245	14255.9847

1.2 - Select country, gdpPercap using %>%

```
country_gdp <- filtered %>%
  select(country,gdpPercap)
knitr::kable(country_gdp, format="markdown")
```

country	gdpPercap
Canada	18970.5709
Canada	22090.8831
India	724.0325
India	813.3373
Italy	12269.2738
Italy	14255.9847

1.3 - Entries with a negative change in life expectancy from previous line

```
exp_list <- gapminder$lifeExp
change <- diff(exp_list,lag=1,differences=1)
# Add NA value to beginning of change vector:
change_2 <- append(change,NA,after=0)
# Create new tibble with delta life expectancy as a column:
gapminder_lifeExp <- gapminder
gapminder_lifeExp$delta <- change_2
# Filter for ALL negative changes
```

```r
gapminder_redExp <- gapminder_lifeExp %>%
  filter(delta < 0)

gapminder_redExp
```

```
## # A tibble: 221 x 7
##    country    continent  year lifeExp      pop gdpPercap   delta
##    <fct>      <fct>     <int>   <dbl>    <int>     <dbl>   <dbl>
##  1 Albania    Europe     1992    71.6  3326498     2497.  -0.419
##  2 Algeria    Africa     1952    43.1  9279525     2449. -33.3
##  3 Angola     Africa     1952    30.0  4232095     3521. -42.3
##  4 Angola     Africa     1987    39.9  7874230     2430.  -0.036
##  5 Australia  Oceania    1952    69.1  8691212    10040.  -6.20
##  6 Austria    Europe     1952    66.8  6927772     6137. -14.4
##  7 Bahrain    Asia       1952    50.9   120447     9867. -28.9
##  8 Bangladesh Asia       1952    37.5 46886859      684. -38.2
##  9 Benin      Africa     1952    38.2  1738315     1063. -41.2
## 10 Benin      Africa     2002    54.4  7026113     1373.  -0.371
## # ... with 211 more rows
```

1.4 - Gapminder: max GDP per capita per country

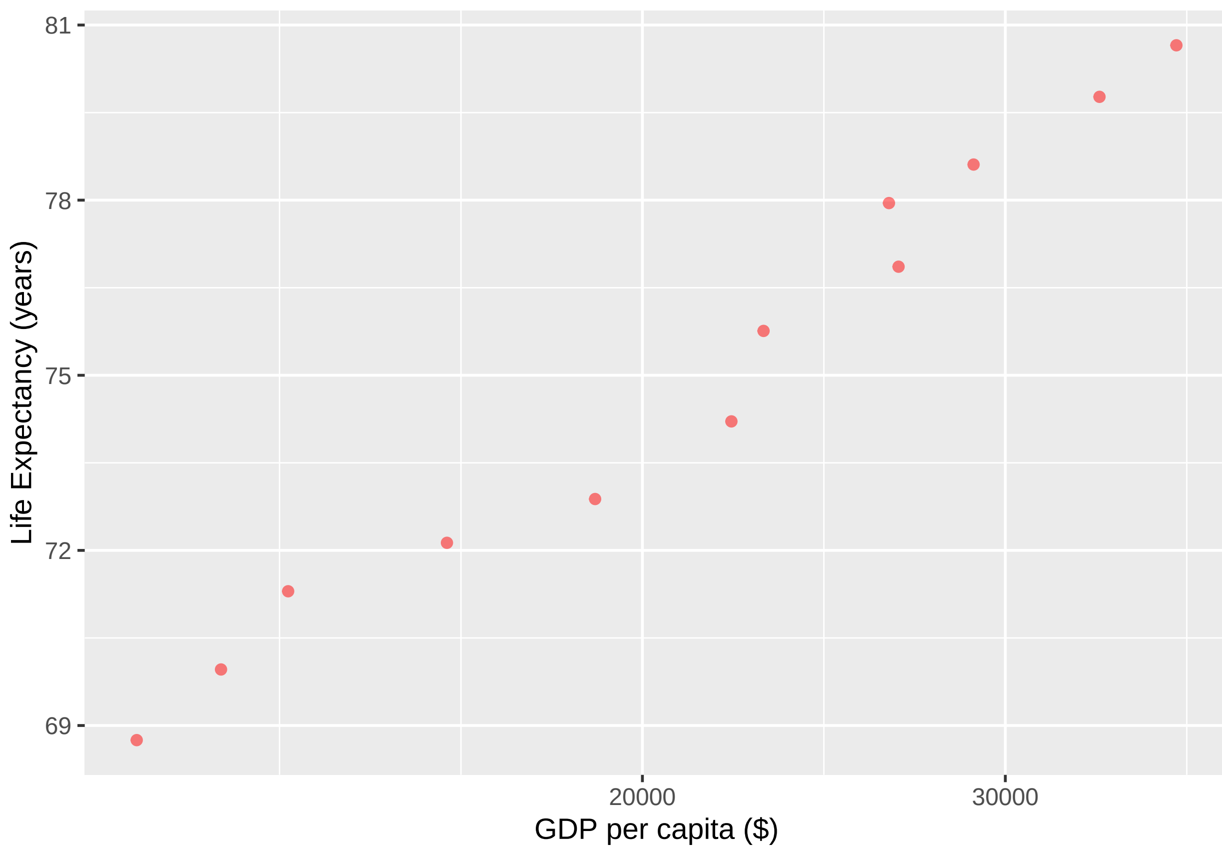
Original question (using group_by())

```r
# Create new column that lists the max GDP per country
gap_max_gdp <- gapminder %>%
  group_by(country) %>%
  mutate(max_gdp = max(gdpPercap)) %>%
  ungroup()

# Filters gapminder to only show max GDP; removes the redundant 'max GDP' column
max_per_country <- gap_max_gdp %>%
  filter(gdpPercap == max_gdp) %>%
  subset(select = -max_gdp)

max_per_country
```

```
## # A tibble: 142 x 6
##    country     continent  year lifeExp       pop gdpPercap
##    <fct>       <fct>     <int>   <dbl>     <int>     <dbl>
##  1 Afghanistan Asia       1982    39.9  12881816      978.
##  2 Albania     Europe     2007    76.4   3600523     5937.
##  3 Algeria     Africa     2007    72.3  33333216     6223.
##  4 Angola      Africa     1967    36.0   5247469     5523.
##  5 Argentina   Americas   2007    75.3  40301927    12779.
##  6 Australia   Oceania    2007    81.2  20434176    34435.
##  7 Austria     Europe     2007    79.8   8199783    36126.
##  8 Bahrain     Asia       2007    75.6    708573    29796.
##  9 Bangladesh  Asia       2007    64.1 150448339     1391.
## 10 Belgium     Europe     2007    79.4  10392226    33693.
## # ... with 132 more rows
```

1.5 - Canadian Life Expectancy vs GDP

```
# Select data
canadians <- gapminder %>%
  filter(country=="Canada") %>%
  select(lifeExp,gdpPercap)

# Plot in ggplot
ggplot(canadians, aes(gdpPercap,lifeExp)) +
  geom_point(alpha=0.5, colour = "red") +
  scale_x_log10("GDP per capita ($)") +
  ylab("Life Expectancy (years)")
```



Exercise 2: Explore individual variables with dplyr

Categorical variable: continent

Possible range of continent

- Assuming we're not creating any new continents, this variable is inherently limited to the seven continents.
  - *Note*: North & South America are grouped into 'Americas'
- Possibilities: c(**Asia, Americas, Europe, Africa, Oceania**, Antarctica)
  - *Note*: Antarctica has no entries in gapminder, as it is a research base.

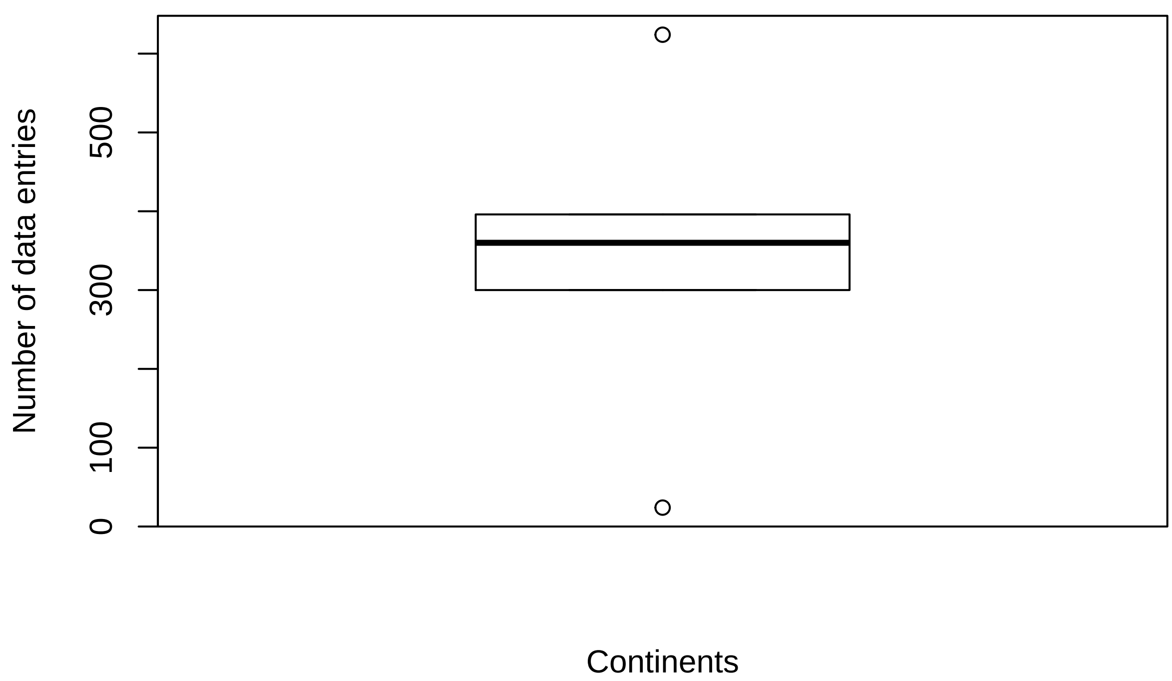
Spread of values

Box and Whisker summary of data:

```
con_only <- gapminder %>%
  select(continent)
con_sum <- count(con_only, continent) %>%  # dplyr: table of counts per continent
  as_tibble()
knitr::kable(summary(con_sum),format="markdown") # Print summary of the data
```

continent	n
Africa :1	Min. : 24.0
Americas:1	1st Qu.:300.0
Asia :1	Median :360.0
Europe :1	Mean :340.8
Oceania :1	3rd Qu.:396.0
NA	Max. :624.0

```
#Visualize the summary in a boxplot
boxplot(con_sum$n,
        ylab="Number of data entries",
        xlab = "Continents")
```



The number of datapoints for each populated continent (e.g. Antarctica not included) **ranged from 24 to 624**. The **mean and median were 341 and 360** respectively, with 50% of the data falling between 300 and 396 entries.

Visual representation of distribution:

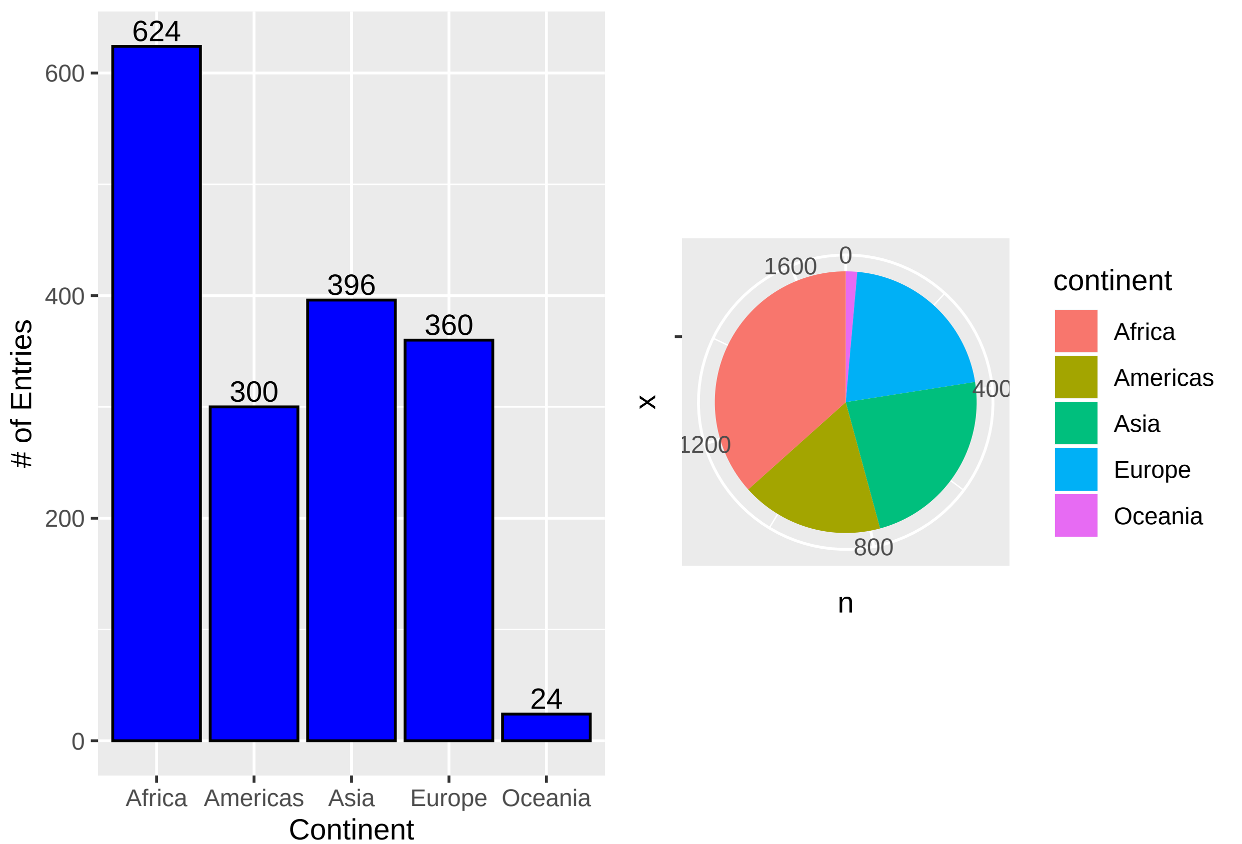
```
bar_plot <- ggplot(con_sum, aes(continent,n)) +
  geom_col(colour="black",fill="blue") +
  geom_text(aes(label=n), vjust=-0.25) +
  ylab("# of Entries") +
  xlab("Continent")

pie_plot <- ggplot(con_sum, aes(x='',y=n,fill=continent)) +
  geom_bar(width=1, stat = "identity") +
  coord_polar(theta="y")

require(gridExtra) # Arrange them side by side
```

```
## Loading required package: gridExtra
```

```
##
## Attaching package: 'gridExtra'
```

```
## The following object is masked from 'package:dplyr':
##
##     combine
```

```
gridExtra::grid.arrange(bar_plot,pie_plot,ncol=2)
```



Generally, Oceania is very underrepresented, comprising just 24 out of 1704 entries. Conversely, African data was included at twice the rate of the average at 624 entries. The other three continents are relatively evenly represented.

Quantitative variable: pop (population)

Range of pop

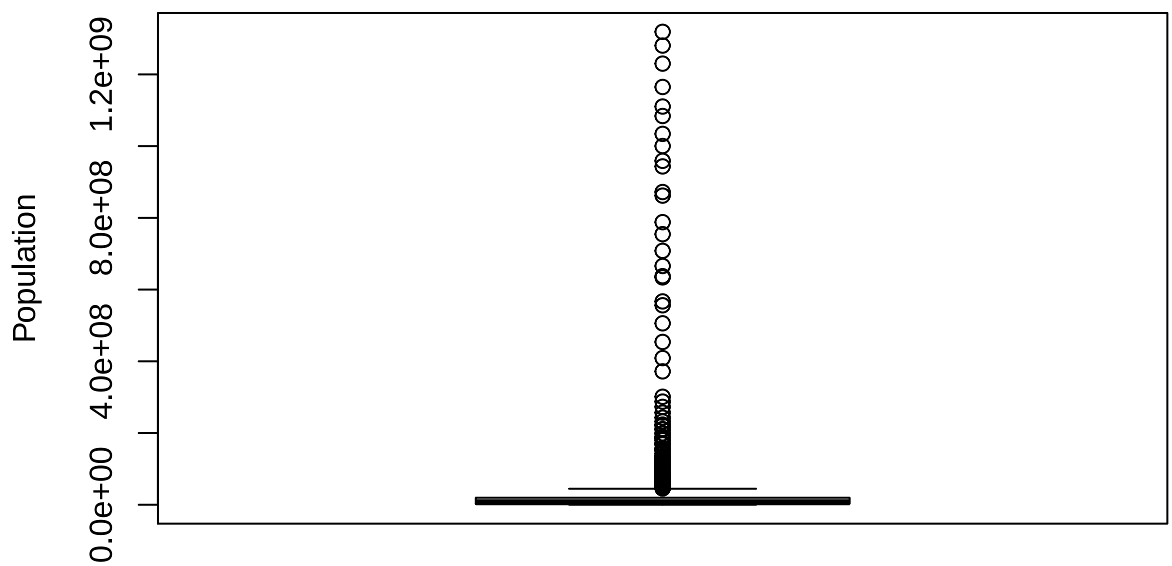
The value of pop must be a Natural (>0) number. No strict upper limit is specified, but should logically be approximately 1.4 billion (the population of China).

Visualizing the spread of all population data:

```
pop_only <- gapminder %>%
  select(pop)
knitr::kable(summary(pop_only),format="markdown")
```

pop
Min. :6.001e+04
1st Qu.:2.794e+06
Median :7.024e+06
Mean :2.960e+07
3rd Qu.:1.959e+07
Max. :1.319e+09

```
boxplot(pop_only$pop,
        ylab="Population",
        xlab = "")
```

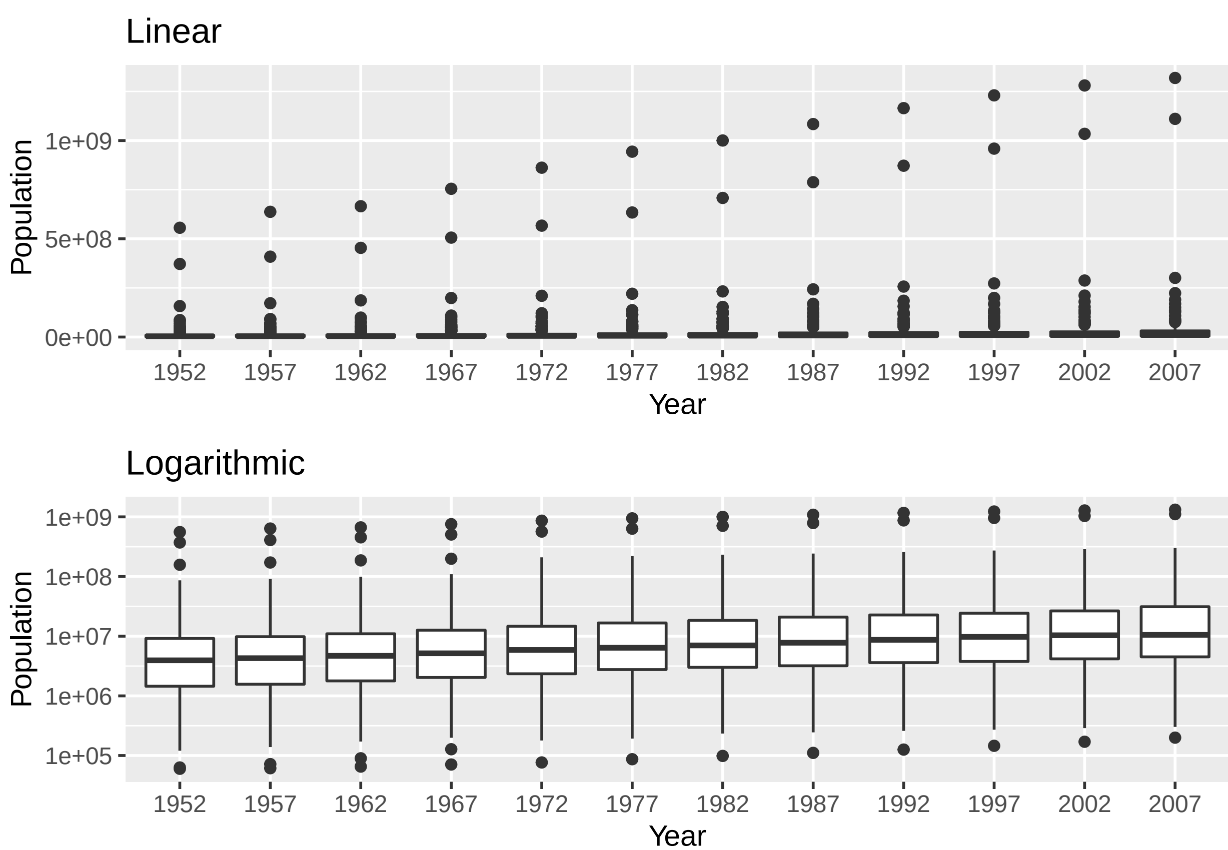


As demonstrated by the boxplot, the vast majority of the data (all data within the whiskers/confidence interval) comprise a tiny fraction of the possible range of population values. **50% of the data decribes a**

population between 2.8-19.6 million, with the median population being **7 million**. The average is much higher at **29.6 million** as the high-population outliers are skewing the data. The minimum and maximum populations are **60 000 and 1.32 billion** respectively.

There are 12 entries for each country, as they were sampled at every time point. We can divide the data by year to see how the **average populations change over time**:

```
# Linear Plot
pop_time <- gapminder %>% # gapminder is gapminder in tibble format
  select(year, pop)
pop_time$year <- as.factor(pop_time$year) # Only factors can be used to plot side-by-side boxplots
pop_time_plot <- ggplot(pop_time, aes(year, pop)) +
  geom_boxplot() +
  xlab("Year") +
  ylab("Population") +
  ggtitle("Linear")

# Log Transformed
log_plot <- pop_time_plot +
  scale_y_log10() +
  ggtitle("Logarithmic")

# Side by Side Output
require(gridExtra)
gridExtra::grid.arrange(pop_time_plot,log_plot,nrow=2)
```



The above graph makes it easier to see that there are only a couple of countries that have populations significantly outside of the statistical range. In the linear plot, the significant population size and fast growth of China and India in particular make the population growth of the rest of the world less apparent. By transforming the y axis to a log 10 scale, all of the outliers can be captured and the general trends become apparent: the **IQR (middle 50%) of the data moves up the y axis, showing exponential population growth**.

Exercise 3: Plot Exploration

Scatterplot of [CO2]ambient vs [CO2]uptake

Dataset: **CO2 - *Carbon Dioxide Uptake in Grass Plants***

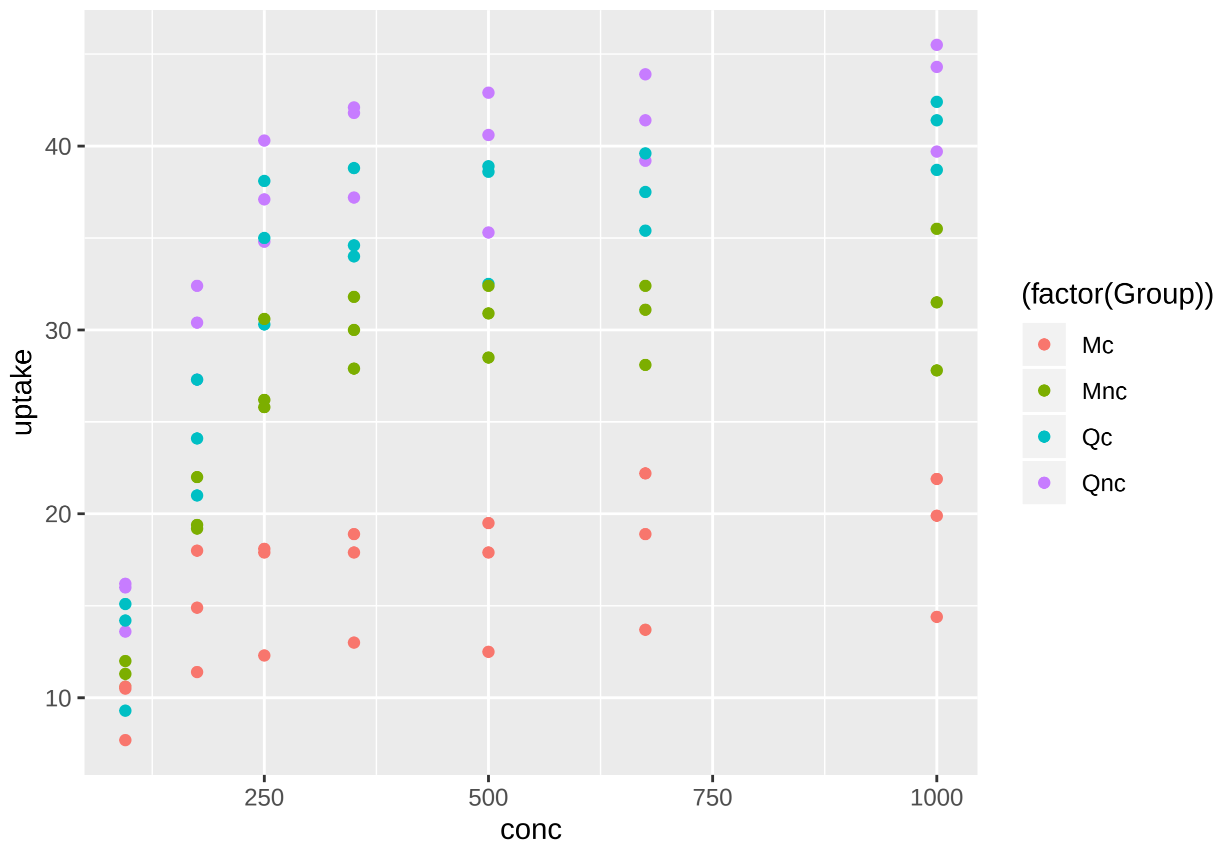
Here are the main parameters of the CO2 dataset:

```
knitr::kable(summary(CO2),format="markdown")
```

Plant	Type	Treatment	conc	uptake
Qn1 : 7	Quebec :42	nonchilled:42	Min. : 95	Min. : 7.70
Qn2 : 7	Mississippi:42	chilled :42	1st Qu.: 175	1st Qu.:17.90
Qn3 : 7	NA	NA	Median : 350	Median :28.30
Qc1 : 7	NA	NA	Mean : 435	Mean :27.21
Qc3 : 7	NA	NA	3rd Qu.: 675	3rd Qu.:37.12
Qc2 : 7	NA	NA	Max. :1000	Max. :45.50
(Other):42	NA	NA	NA	NA

Plant is the type of plant, Type is the location of the plant, conc is the ambient CO2 concentration, and uptake is the CO2 absorbed by the plant.

```
CO2 %>%
  mutate(Group = (if_else
                (Type=="Quebec",
                  if_else
                  (Treatment=="nonchilled","Qnc","Qc"),
                   if_else(Treatment=="nonchilled","Mnc","Mc")))) %>%
  ggplot(aes(conc,uptake)) +
    geom_point(aes(colour=(factor(Group))))
```



The above graph shows the change in CO_2 uptake as a function of CO_2 ambient concentration. In the legend, M/Q denote location (Mississippi vs Quebec) and c/nc denote treatment (chilled/not chilled).

From the plot, it can be seen that Quebec plants are more efficient at carbon fixation than Mississippi plants, and chilling the plants reduces their efficiency.

Graph #2

Dataset: **esoph - *Smoking, Alcohol and (O)esophageal Cancer***

Here are the main parameters of the CO2 dataset:

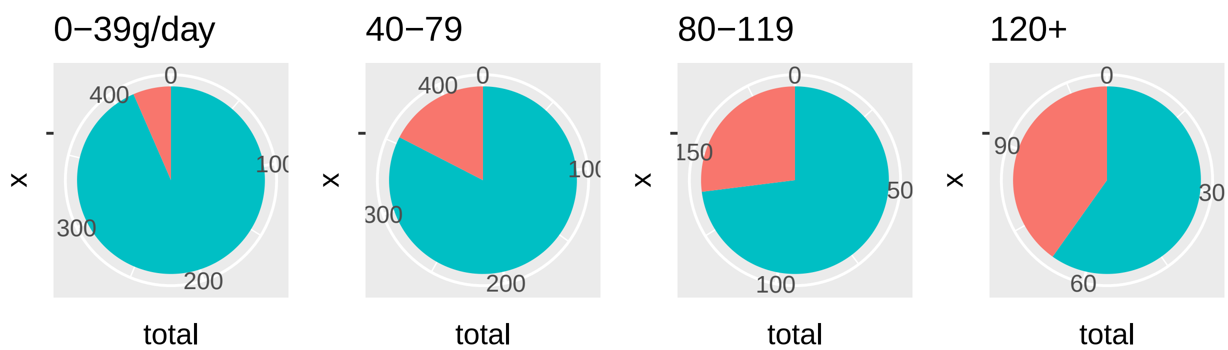
```
esoph_cancer <- esoph %>%
  rename("Alcohol Intake"=alcgp) %>%
  rename("Tobacco Intake"=tobgp)

knitr::kable(summary(esoph_cancer),format="markdown")
```

agegp	Alcohol Intake	Tobacco Intake	ncases	ncontrols
25-34:15	0-39g/day:23	0-9g/day:24	Min. : 0.000	Min. : 1.00
35-44:15	40-79 :23	10-19 :24	1st Qu.: 0.000	1st Qu.: 3.00
45-54:16	80-119 :21	20-29 :20	Median : 1.000	Median : 6.00
55-64:16	120+ :21	30+ :20	Mean : 2.273	Mean :11.08
65-74:15	NA	NA	3rd Qu.: 4.000	3rd Qu.:14.00
75+ :11	NA	NA	Max. :17.000	Max. :60.00

Note: Ncases and ncontrols summaries are meaningless, as they supply weightings to the alcohol and tobacco groups.

We will be looking at the **rate of esophageal cancer relative to alcohol consumption** and irrespective of age.

```r
# Collapse data: sum cases/controls by alcohol group
p2 <- aggregate(cbind(esoph_cancer$ncases,esoph_cancer$ncontrols),
                by=list(esoph_cancer$`Alcohol Intake`),
                FUN=sum)

cases <- mutate(p2,status="case") %>%
  rename("total"=V1) %>%
  select(-V2)
ctrls <- mutate(p2,status="ctrl") %>%
  rename("total"=V2) %>%
  select(-V1)
all_data <- merge(cases,ctrls,all=TRUE)

all_39 <- filter(all_data,Group.1=="0-39g/day")
all_79 <- filter(all_data,Group.1=="40-79")
all_119 <- filter(all_data,Group.1=="80-119")
all_120 <- filter(all_data,Group.1=="120+")

esoph_pie <- function(df){
  ggplot(df, aes(x='',y=total,fill=status,)) +
      geom_bar(width=1,stat="identity") +
      coord_polar(theta="y") +
      guides(fill = FALSE, color = FALSE, linetype = FALSE, shape = FALSE) +
      ggtitle(df$Group.1[1])
}

g1 <- esoph_pie(all_39)
g2 <- esoph_pie(all_79)
g3 <- esoph_pie(all_119)
g4 <- esoph_pie(all_120)

require(gridExtra)
gridExtra::grid.arrange(g1,g2,g3,g4,ncol=4)
```



The esophageal cancer cases are represented by pink, while the controls are in blue. Titles indicate the number of grams of alcohol ingested per day. As the alcohol intake increases, so do the overall cancer rate.

Recycling

Code in question:

```
filter(gapminder, country == c("Rwanda", "Afghanistan"))
```

```
## # A tibble: 12 x 6
##    country     continent  year lifeExp      pop gdpPercap
##    <fct>       <fct>     <int>   <dbl>    <int>     <dbl>
##  1 Afghanistan Asia       1957    30.3  9240934      821.
##  2 Afghanistan Asia       1967    34.0 11537966      836.
##  3 Afghanistan Asia       1977    38.4 14880372      786.
##  4 Afghanistan Asia       1987    40.8 13867957      852.
##  5 Afghanistan Asia       1997    41.8 22227415      635.
##  6 Afghanistan Asia       2007    43.8 31889923      975.
##  7 Rwanda      Africa     1952    40    2534927      493.
##  8 Rwanda      Africa     1962    43    3051242      597.
##  9 Rwanda      Africa     1972    44.6  3992121      591.
## 10 Rwanda      Africa     1982    46.2  5507565      882.
## 11 Rwanda      Africa     1992    23.6  7290203      737.
## 12 Rwanda      Africa     2002    43.4  7852401      786.
```

Though at first glance this code appears to select the data for Afghanistan and Rwanda, but **half of the data is missing**. Every other entry is omitted, in a way where both countries are never represented in the same year. (ex. Rwanda 1952, Afghanistan 1957…)

Because of the inclusion of a list, the function will go along the year-sorted data, taking turns selecting each country for each value of year. The code can be fixed by using an 'or' statement:

```
filter(gapminder, country == "Rwanda" | country == "Afghanistan")
```

```
## # A tibble: 24 x 6
##    country     continent  year lifeExp      pop gdpPercap
##    <fct>       <fct>     <int>   <dbl>    <int>     <dbl>
##  1 Afghanistan Asia       1952    28.8  8425333      779.
##  2 Afghanistan Asia       1957    30.3  9240934      821.
##  3 Afghanistan Asia       1962    32.0 10267083      853.
##  4 Afghanistan Asia       1967    34.0 11537966      836.
##  5 Afghanistan Asia       1972    36.1 13079460      740.
##  6 Afghanistan Asia       1977    38.4 14880372      786.
##  7 Afghanistan Asia       1982    39.9 12881816      978.
##  8 Afghanistan Asia       1987    40.8 13867957      852.
##  9 Afghanistan Asia       1992    41.7 16317921      649.
## 10 Afghanistan Asia       1997    41.8 22227415      635.
## # ... with 14 more rows
```

In this way, all of the data are collected.

Tibbles

All small tables as knitr::kable(). **DT::datatable() only works in html; therefore, the .Rmd and html file on github contains datatable() format for large tables, but as_tibble() is used in the .md file.**