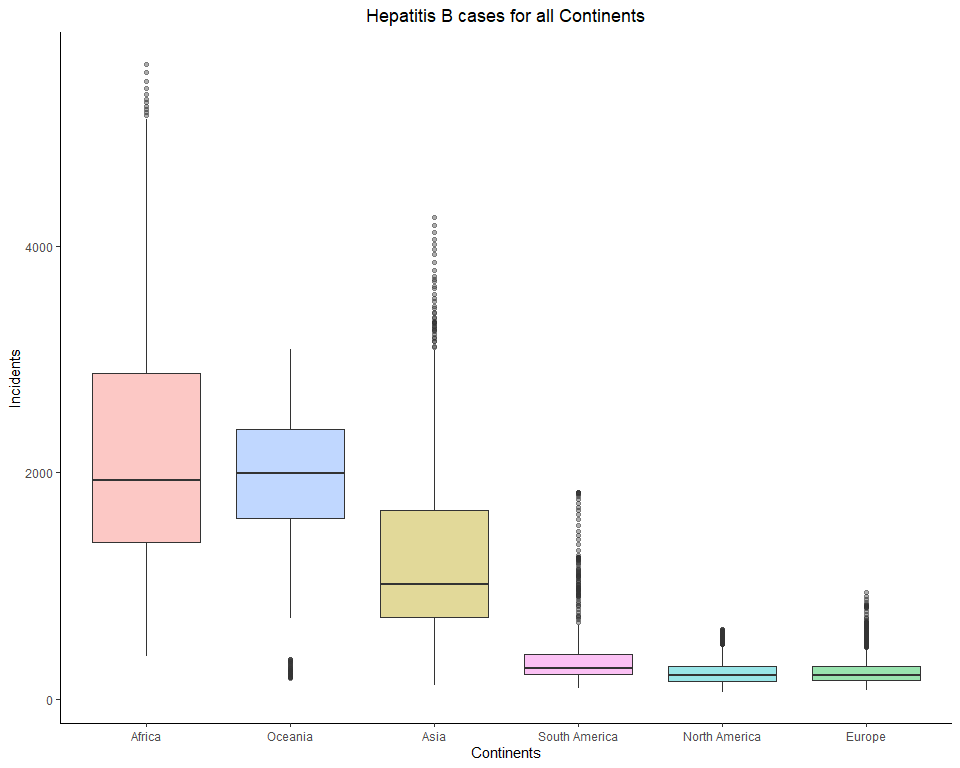
File Org and RDBMS Final Term Project

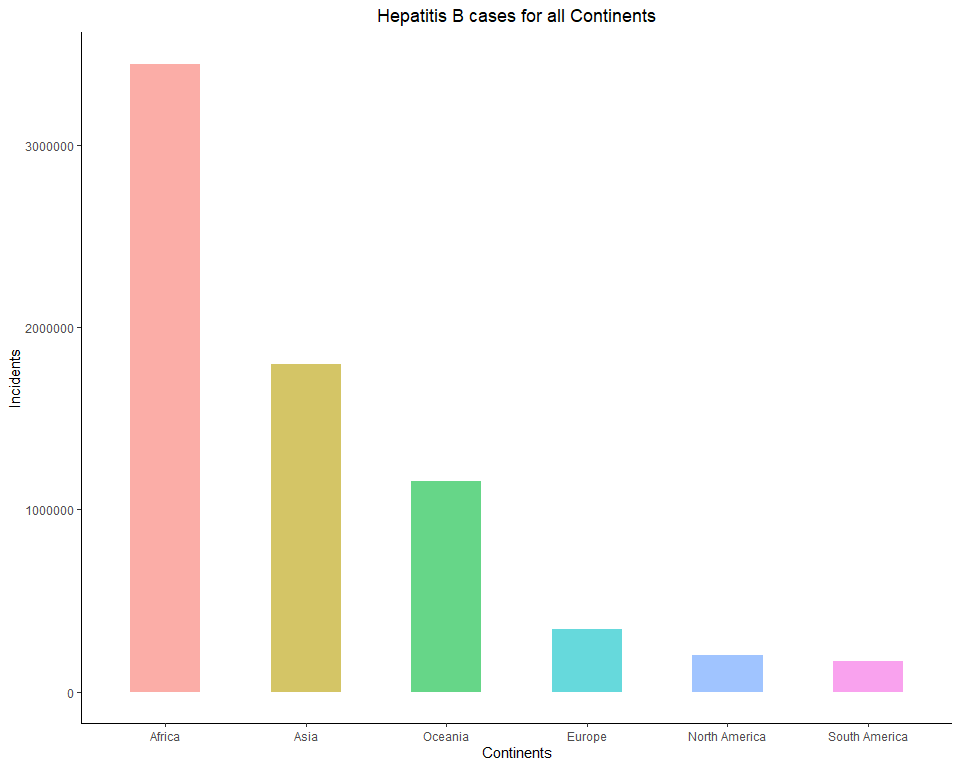
# Hepatitis B

# Hepatitis B cases among continents and regions

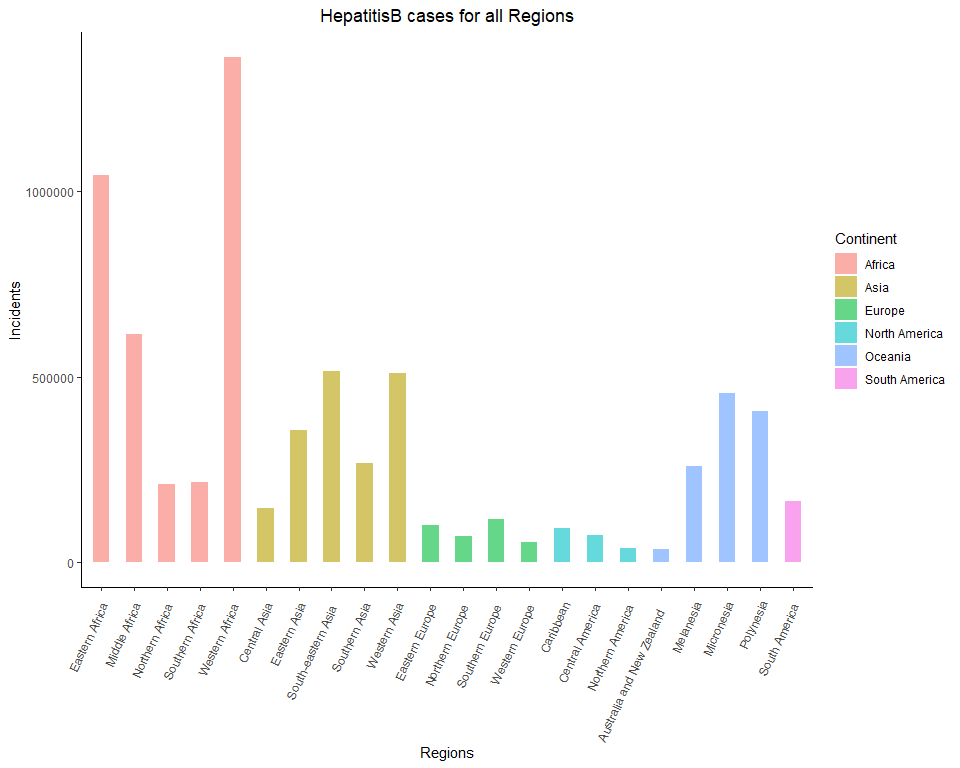
# Boxplot for Hepatitis B cases by all continents  
HepatitisB %>% filter(Continent != "#N/A") %>% ggplot(aes(x = reorder(Continent, -Incidence), y = Incidence, fill = Continent)) + geom\_boxplot(alpha = 0.4) + labs(title = 'Hepatitis B cases for all Continents', x = 'Continents', y = 'Incidents') + theme(legend.position = "none")



# Barplot for Hepatitis B cases by all continents  
# Arrange (order) data by descending Total Cases  
HepatitisB\_Cont = HepatitisB %>% group\_by(Continent) %>% summarize(TotalCases = sum(Incidence)) %>% arrange(desc(TotalCases))  
# Reorder level of Continent factor based on descending Total Cases  
HepatitisB\_Cont$Continent = factor(HepatitisB\_Cont$Continent, level = HepatitisB\_Cont$Continent[order(-HepatitisB\_Cont$TotalCases)])  
  
HepatitisB\_Cont %>% filter(Continent != "#N/A") %>% ggplot(aes(x = Continent, y = TotalCases, fill = Continent)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'Hepatitis B cases for all Continents', x = 'Continents', y = 'Incidents') + theme(legend.position = "none")

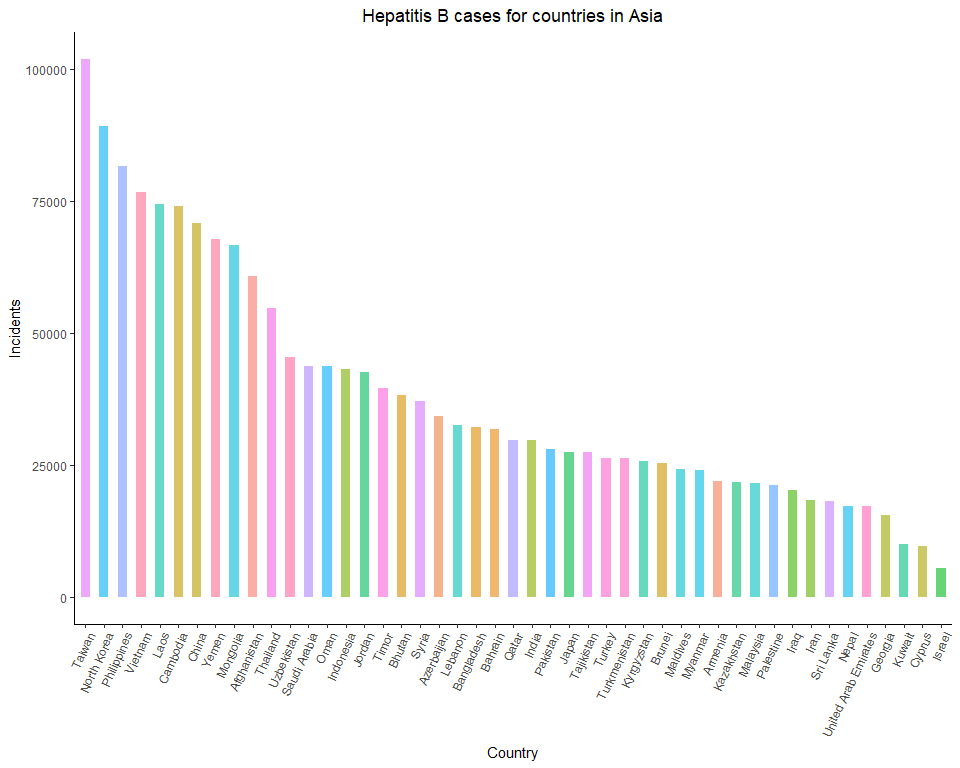


# Barplot for HepatitisB cases by all regions  
HepatitisB$Region <- factor(HepatitisB$Region, levels=unique(HepatitisB$Region[order(HepatitisB$Continent,HepatitisB$Region)]), ordered=TRUE)  
  
HepatitisB %>% filter(Region != "#N/A") %>% ggplot(aes(x = Region, y = Incidence, fill = Continent)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'HepatitisB cases for all Regions', x = 'Regions', y = 'Incidents') + theme(axis.text.x = element\_text(angle = 65, hjust = 1.1))

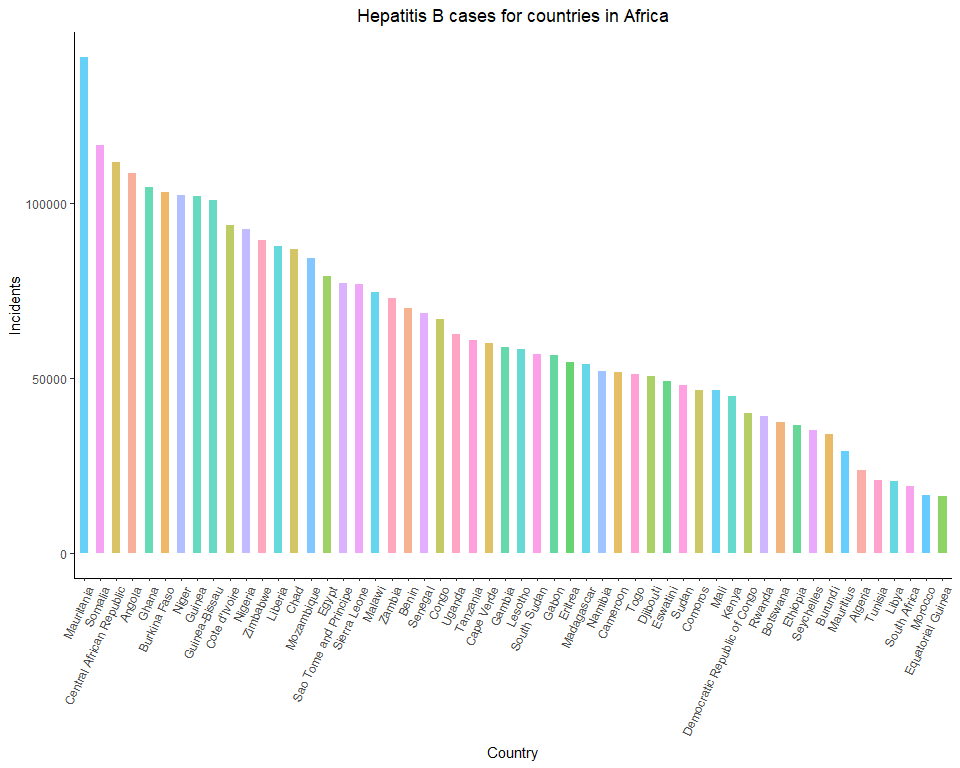


# Hepatitis B total cases in each country in a continent

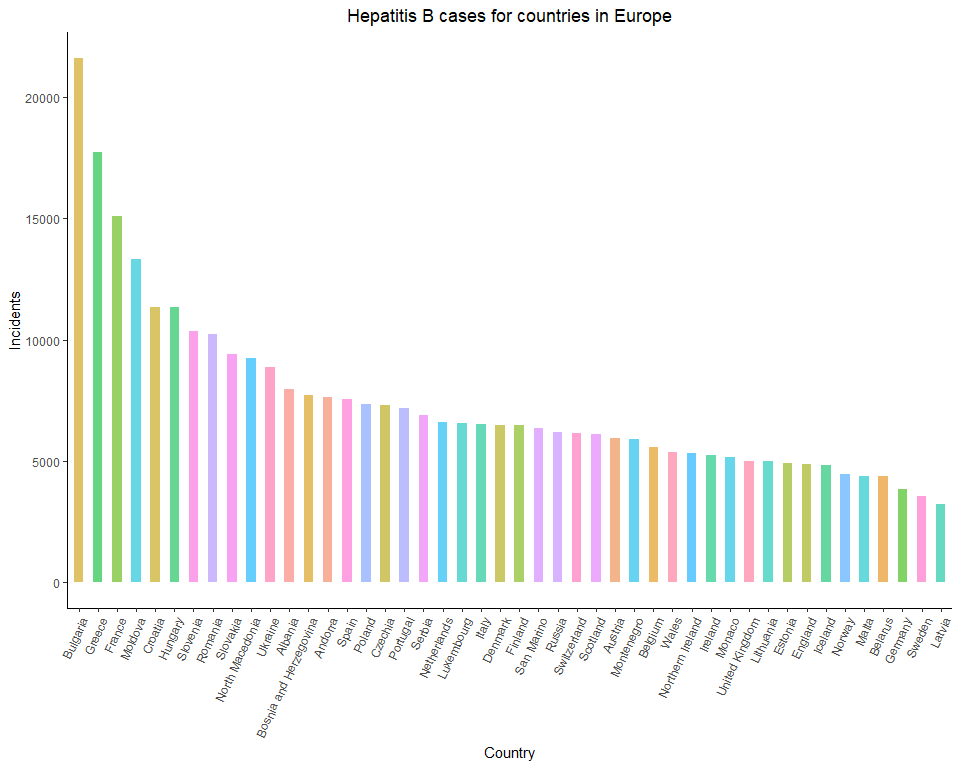
# Barplot for Hepatitis B cases in Asia by Country  
HepatitisB %>% filter(Continent == "Asia") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill=Country)) + geom\_bar(stat="identity", width = 0.5, alpha=0.6) + labs(title = 'Hepatitis B cases for countries in Asia', x= 'Country', y = 'Incidents') + theme(legend.position="none", axis.text.x = element\_text(angle=65, hjust=1, vjust=1))



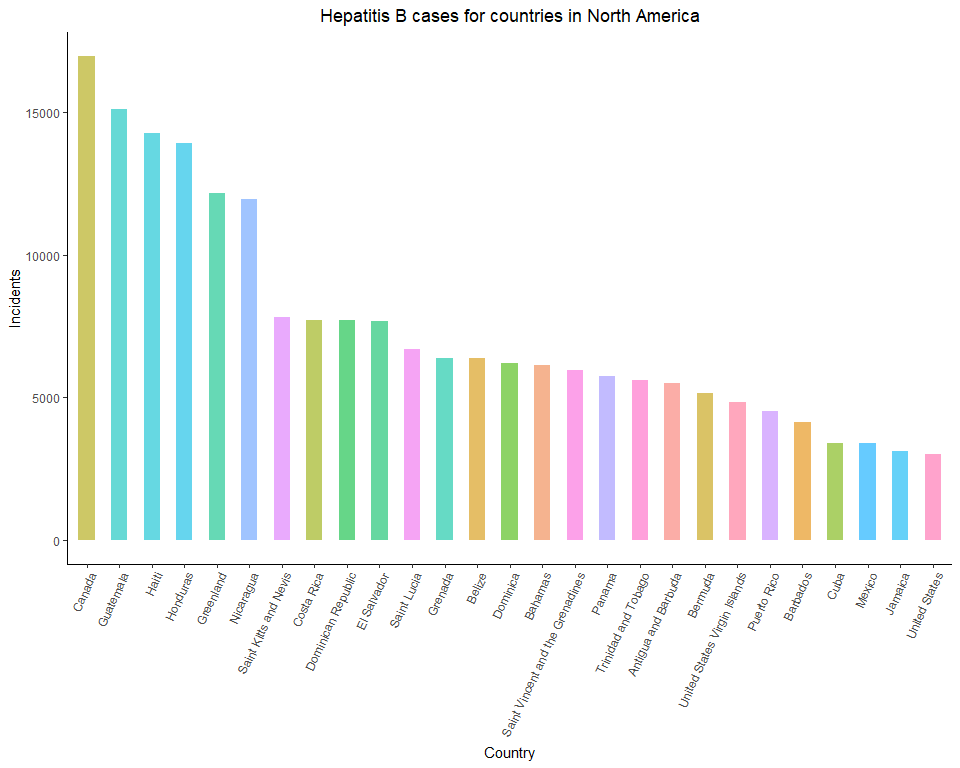
# Barplot for Hepatitis B cases in Africa by Country  
HepatitisB %>% filter(Continent == "Africa") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill=Country)) + geom\_bar(stat="identity", width = 0.5, alpha=0.6) + labs(title = 'Hepatitis B cases for countries in Africa', x= 'Country', y = 'Incidents') + theme(legend.position="none", axis.text.x = element\_text(angle=65, hjust=1))



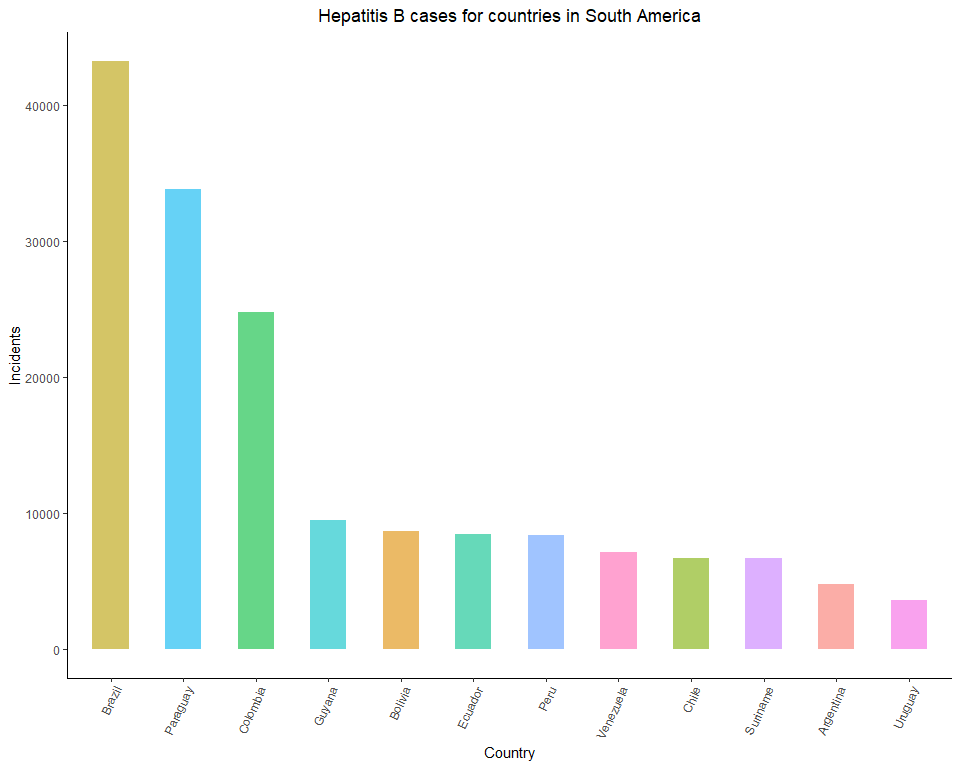
# Barplot for Hepatitis B cases in Europe by Country  
HepatitisB %>% filter(Continent == "Europe") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill=Country)) + geom\_bar(stat="identity", width = 0.5, alpha=0.6) + labs(title = 'Hepatitis B cases for countries in Europe', x= 'Country', y = 'Incidents') + theme(legend.position="none", axis.text.x = element\_text(angle=65, hjust=1))



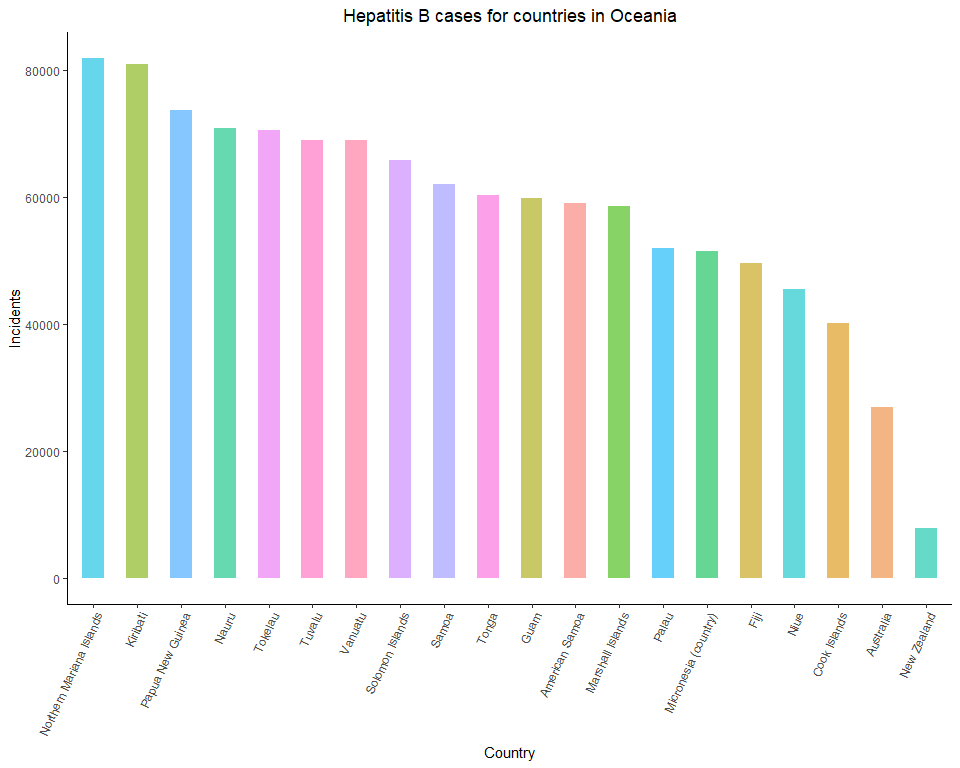
# Barplot for Hepatitis B cases in North America by Country  
HepatitisB %>% filter(Continent == "North America") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill=Country)) + geom\_bar(stat="identity", width = 0.5, alpha=0.6) + labs(title = 'Hepatitis B cases for countries in North America', x= 'Country', y = 'Incidents') + theme(legend.position="none", axis.text.x = element\_text(angle=65, hjust=1))



# Barplot for Hepatitis B cases in South America by Country  
HepatitisB %>% filter(Continent == "South America") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill=Country)) + geom\_bar(stat="identity", width = 0.5, alpha=0.6) + labs(title = 'Hepatitis B cases for countries in South America', x= 'Country', y = 'Incidents') + theme(legend.position="none", axis.text.x = element\_text(angle=65, hjust=1))

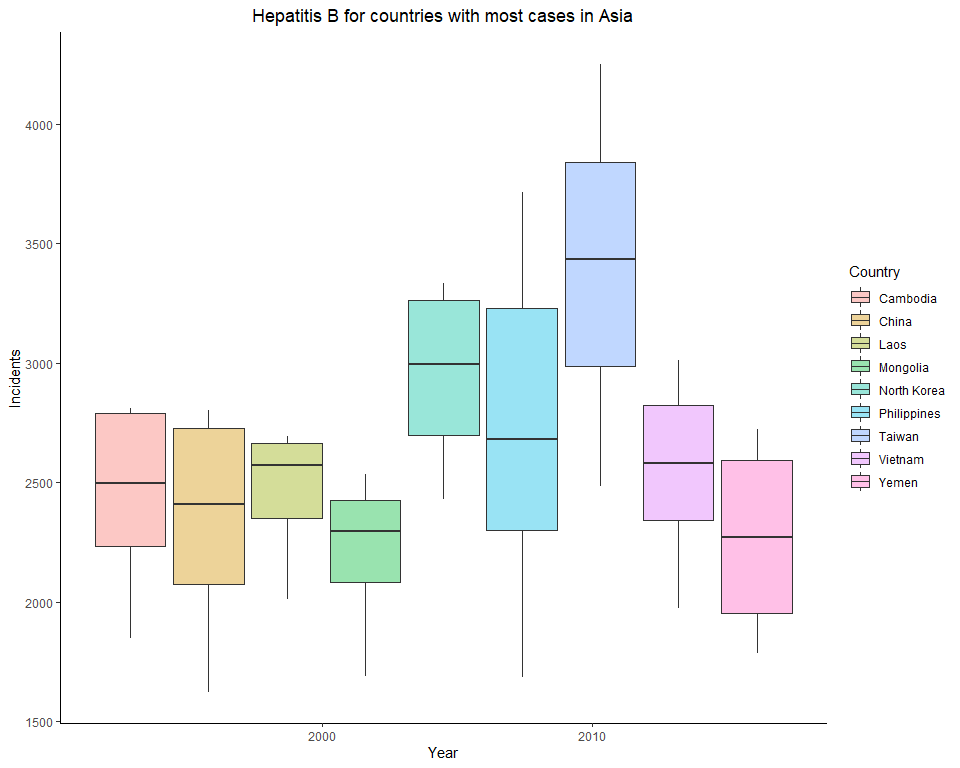


# Barplot for Hepatitis B cases in Oceania by Country  
HepatitisB %>% filter(Continent == "Oceania") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill=Country)) + geom\_bar(stat="identity", width = 0.5, alpha=0.6) + labs(title = 'Hepatitis B cases for countries in Oceania', x= 'Country', y = 'Incidents') + theme(legend.position="none", axis.text.x = element\_text(angle=65, hjust=1))

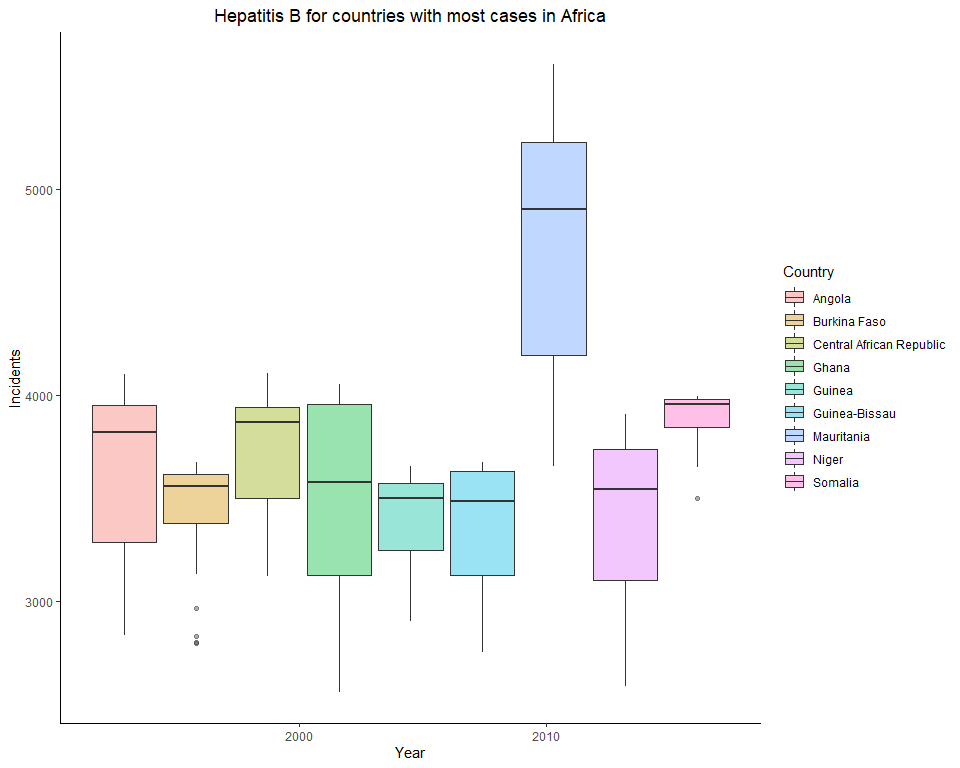


# Hepatitis B cases in SELECT top countries within each continent

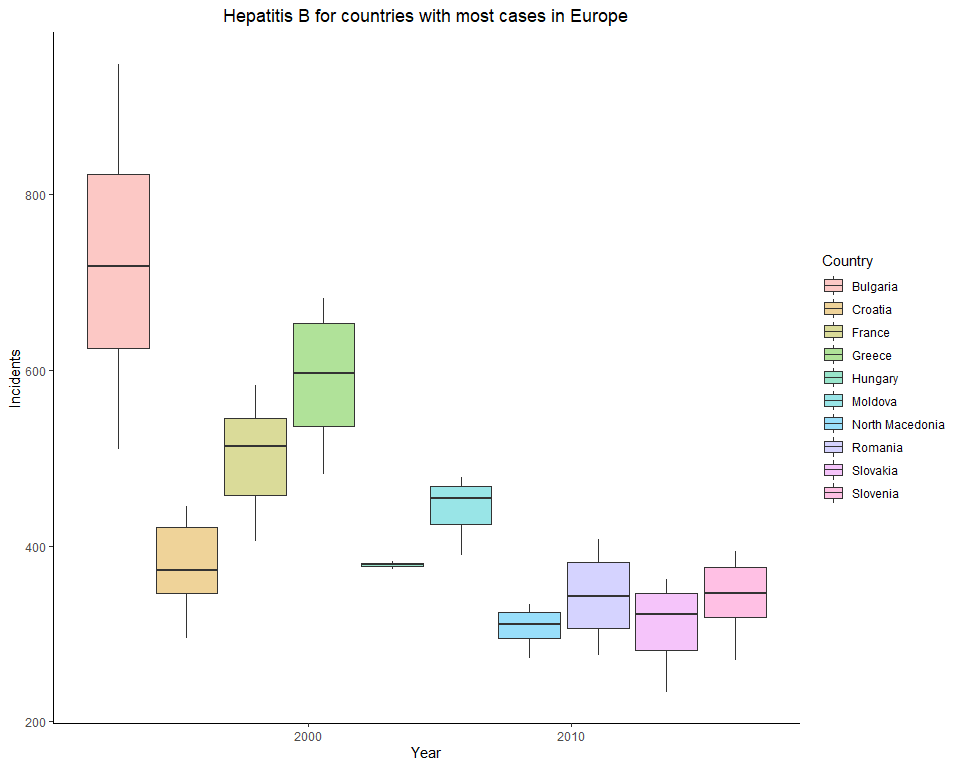
# Boxplot for Hepatitis B cases in SELECT countries in Asia  
HepatitisB %>% filter(Continent == "Asia" & Country %in% c("Taiwan","North Korea","Philippines","Vietnam","Laos","Cambodia","China","Yemen","Mongolia","Afganistan")) %>% ggplot(aes(x = Year, y = Incidence, fill=Country)) + geom\_boxplot(alpha=0.4) + labs(title = 'Hepatitis B for countries with most cases in Asia', x= 'Year', y = 'Incidents')



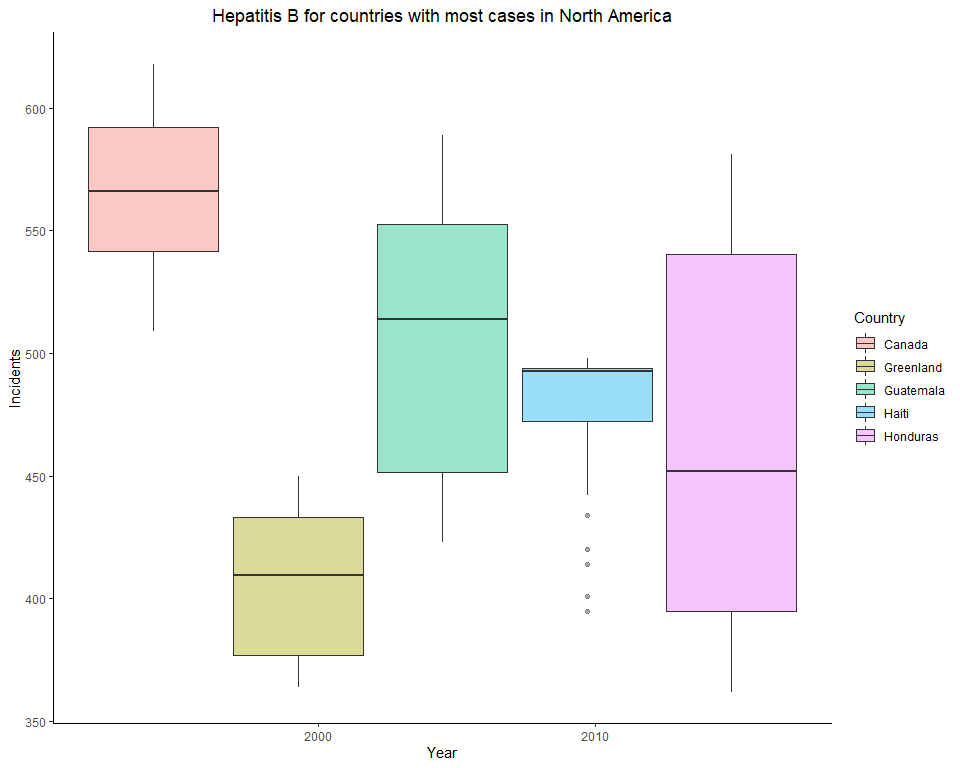
# Boxplot for Hepatitis B cases in SELECT countries in Africa  
HepatitisB %>% filter(Continent == "Africa" & Country %in% c("Mauritania","Somalia","Central African Republic","Angola","Ghana","Burkina Faso","Niger","Guinea","Guinea-Bissau")) %>% ggplot(aes(x = Year, y = Incidence, fill=Country)) + geom\_boxplot(alpha=0.4) + labs(title = 'Hepatitis B for countries with most cases in Africa', x= 'Year', y = 'Incidents')



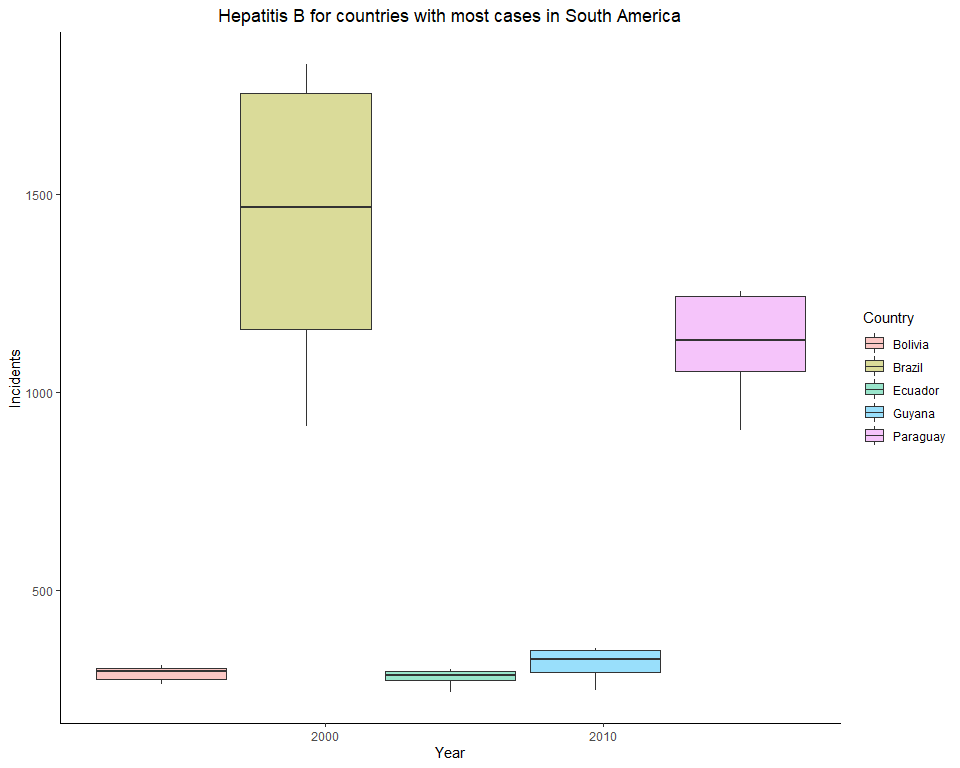
# Boxplot for Hepatitis B cases in SELECT countries in Europe  
HepatitisB %>% filter(Continent == "Europe" & Country %in% c("Bulgaria","Greece","France","Moldova","Croatia","Hungary","Slovenia","Romania","Slovakia", "North Macedonia")) %>% ggplot(aes(x = Year, y = Incidence, fill=Country)) + geom\_boxplot(alpha=0.4) + labs(title = 'Hepatitis B for countries with most cases in Europe', x= 'Year', y = 'Incidents')



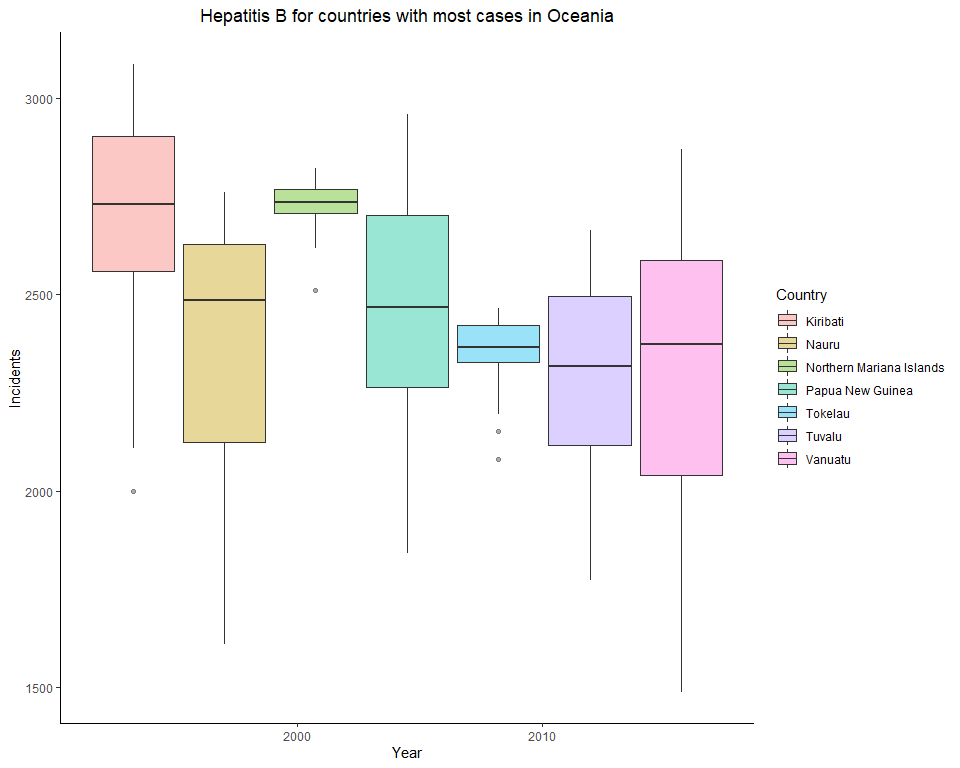
# Boxplot for Hepatitis B cases in SELECT countries in North America  
HepatitisB %>% filter(Continent == "North America" & Country %in% c("Canada","Guatemala","Haiti","Honduras","Greenland","Nicragua")) %>% ggplot(aes(x = Year, y = Incidence, fill=Country)) + geom\_boxplot(alpha=0.4) + labs(title = 'Hepatitis B for countries with most cases in North America', x= 'Year', y = 'Incidents')



# Boxplot for Hepatitis B cases in SELECT countries in South America  
HepatitisB %>% filter(Continent == "South America" & Country %in% c("Brazil","Paraguay","Columbia","Guyana","Bolivia","Ecuador")) %>% ggplot(aes(x = Year, y = Incidence, fill=Country)) + geom\_boxplot(alpha=0.4) + labs(title = 'Hepatitis B for countries with most cases in South America', x= 'Year', y = 'Incidents')



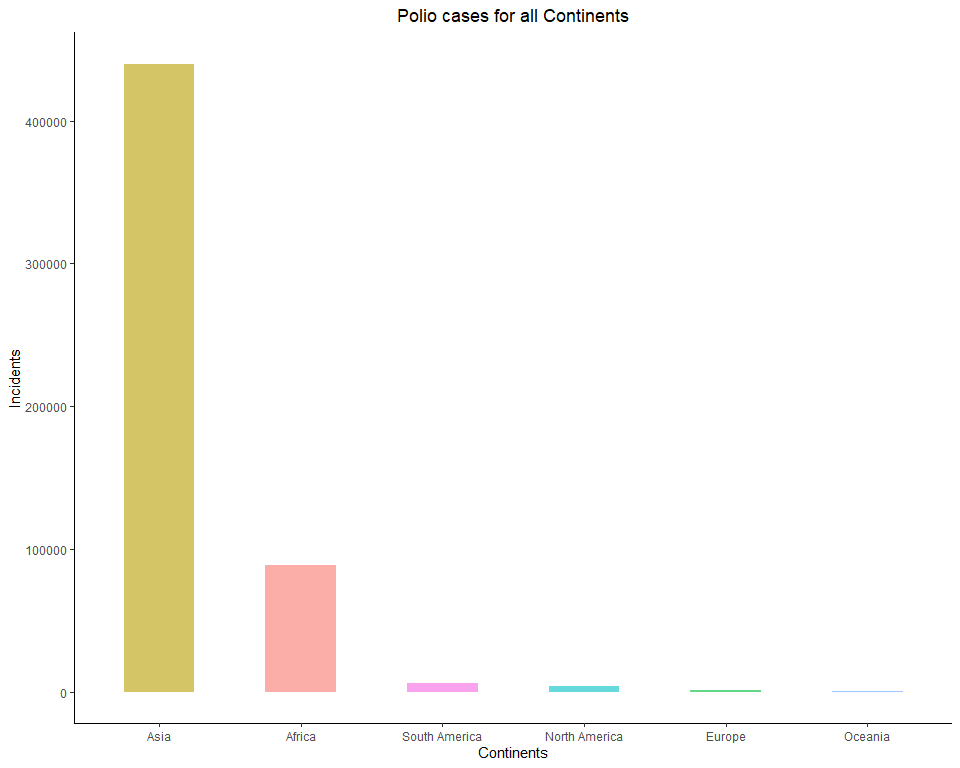
# Boxplot for Hepatitis B cases in SELECT countries in Oceania  
HepatitisB %>% filter(Continent == "Oceania" & Country %in% c("Northern Mariana Islands","Kiribati","Papua New Guinea","Nauru","Tokelau","Tuvalu","Vanuatu")) %>% ggplot(aes(x = Year, y = Incidence, fill=Country)) + geom\_boxplot(alpha=0.4) + labs(title = 'Hepatitis B for countries with most cases in Oceania', x= 'Year', y = 'Incidents')



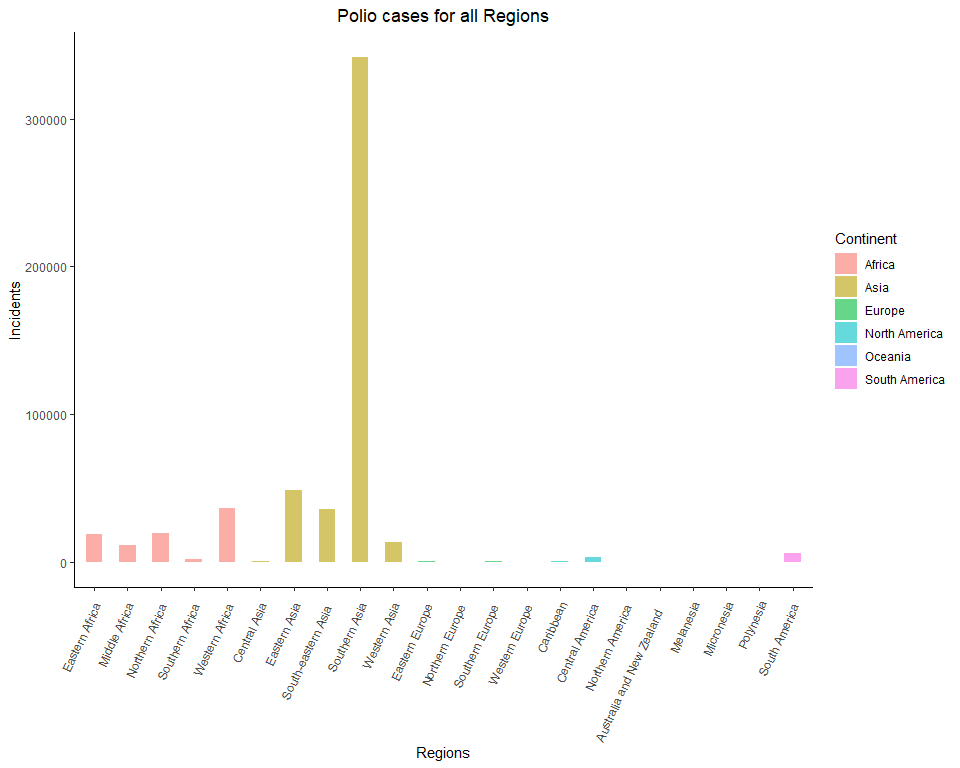
# Polio

# Polio cases among continents and regions

# Barplot for Polio cases by all continents  
Polio %>% filter(Continent != "#N/A") %>% ggplot(aes(x = reorder(Continent, -Incidence), y = Incidence, fill=Continent)) + geom\_bar(stat="identity", width = 0.5, alpha=0.6) + labs(title = 'Polio cases for all Continents', x= 'Continents', y = 'Incidents') + theme(legend.position="none")

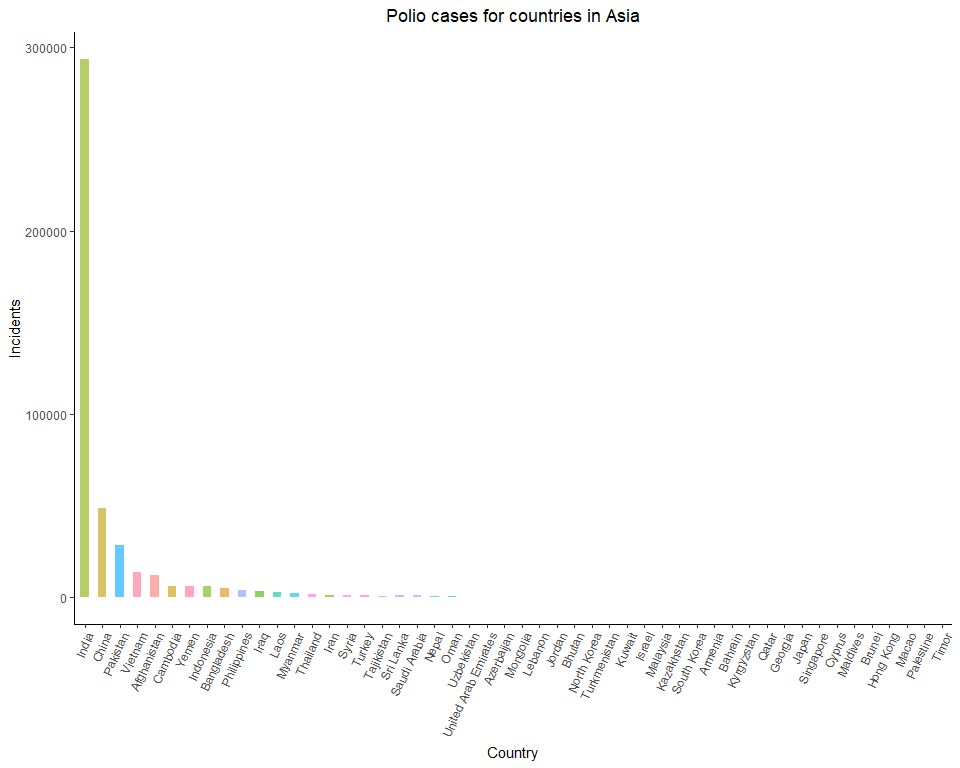


# Barplot for Polio cases by all regions  
Polio$Region <- factor(Polio$Region, levels=unique(Polio$Region[order(Polio$Continent,Polio$Region)]), ordered=TRUE)  
  
Polio %>% filter(Region != "#N/A") %>% ggplot(aes(x = Region, y = Incidence, fill = Continent)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'Polio cases for all Regions', x = 'Regions', y = 'Incidents') + theme(axis.text.x = element\_text(angle = 65, hjust = 1.1))

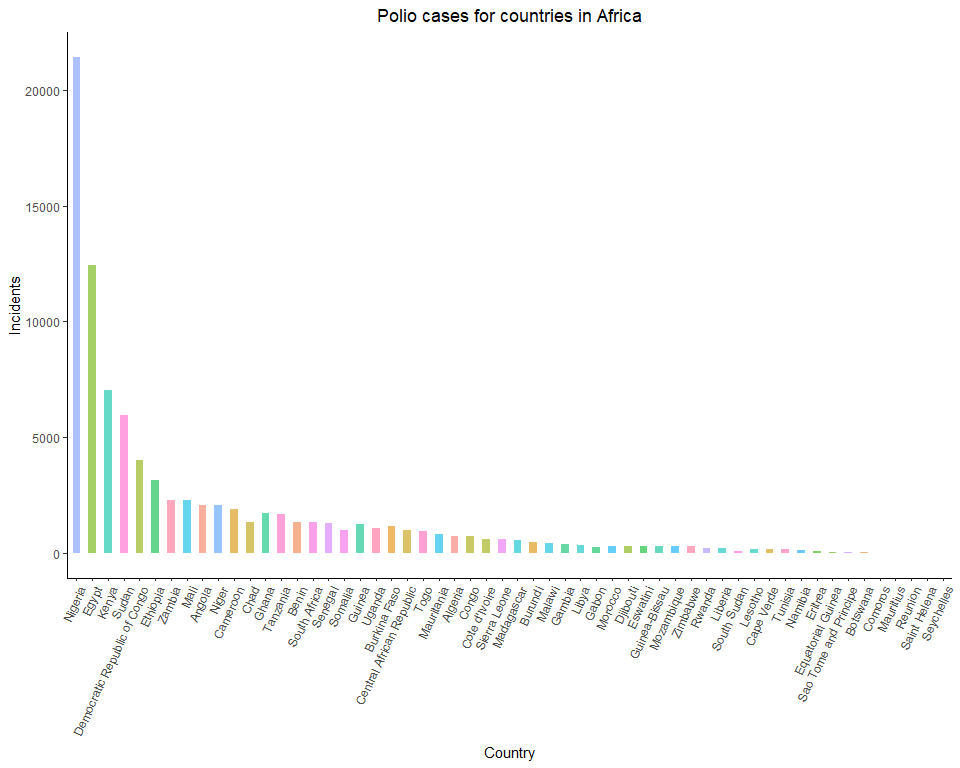


# Polio total cases in each country in a continent

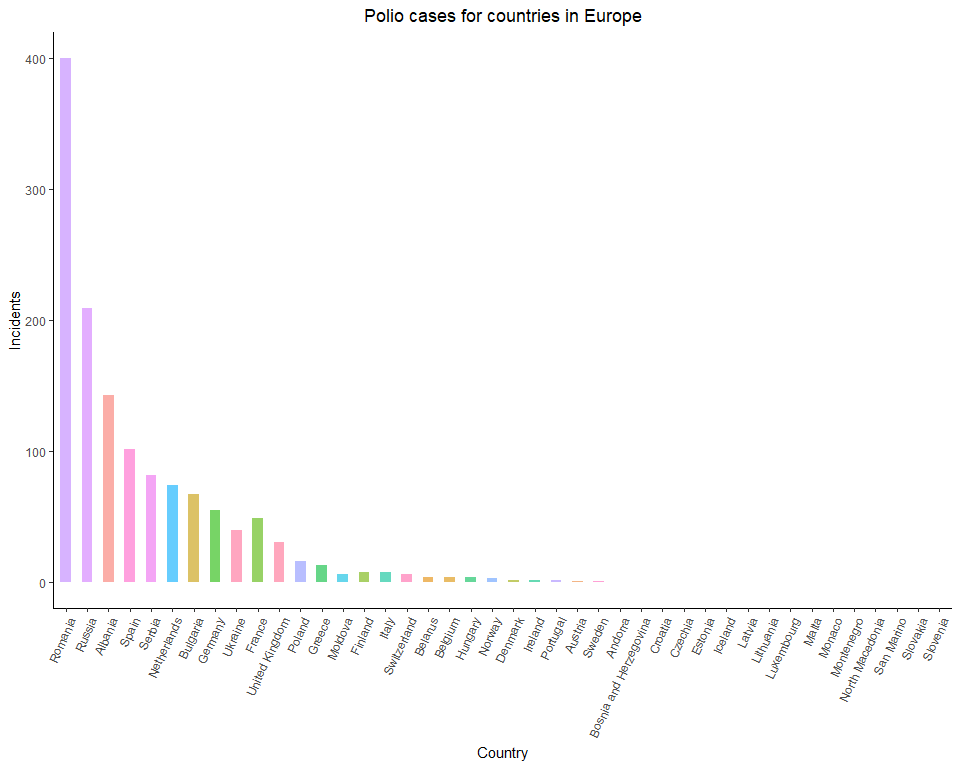
# Barplot for Polio cases in Asia by Country  
Polio %>% filter(Continent == "Asia") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill=Country)) + geom\_bar(stat="identity", width = 0.5, alpha=0.6) + labs(title = 'Polio cases for countries in Asia', x= 'Country', y = 'Incidents') + theme(legend.position="none", axis.text.x = element\_text(angle=65, hjust=1))



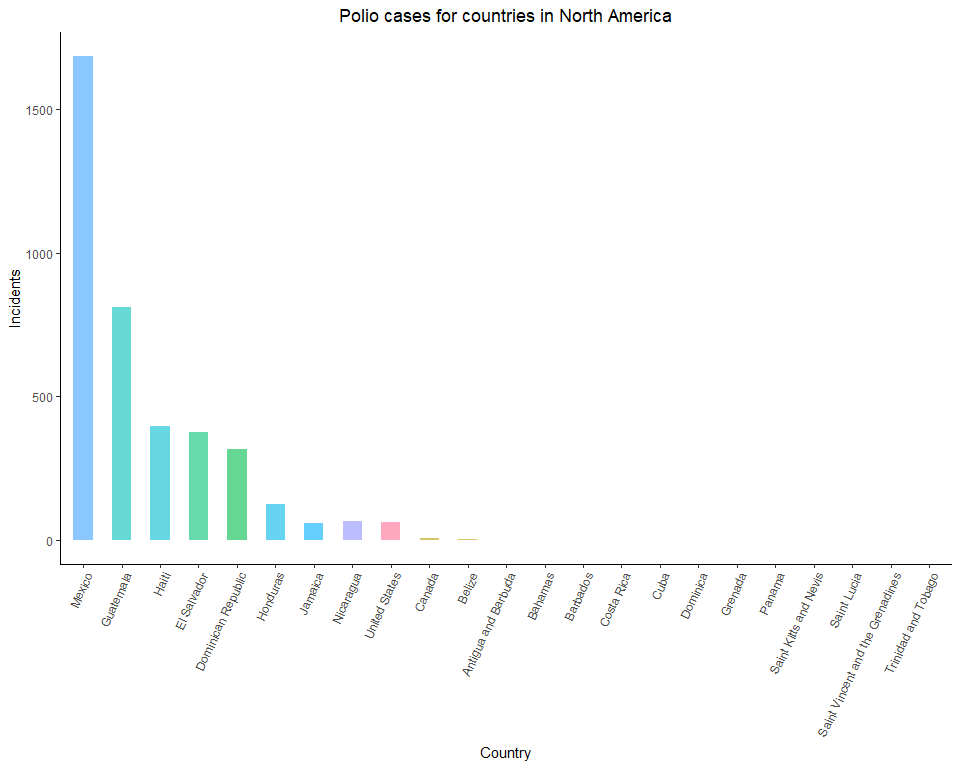
# Barplot for Polio cases in Africa by Country  
Polio %>% filter(Continent == "Africa") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill=Country)) + geom\_bar(stat="identity", width = 0.5, alpha=0.6) + labs(title = 'Polio cases for countries in Africa', x= 'Country', y = 'Incidents') + theme(legend.position="none", axis.text.x = element\_text(angle=65, hjust=1))



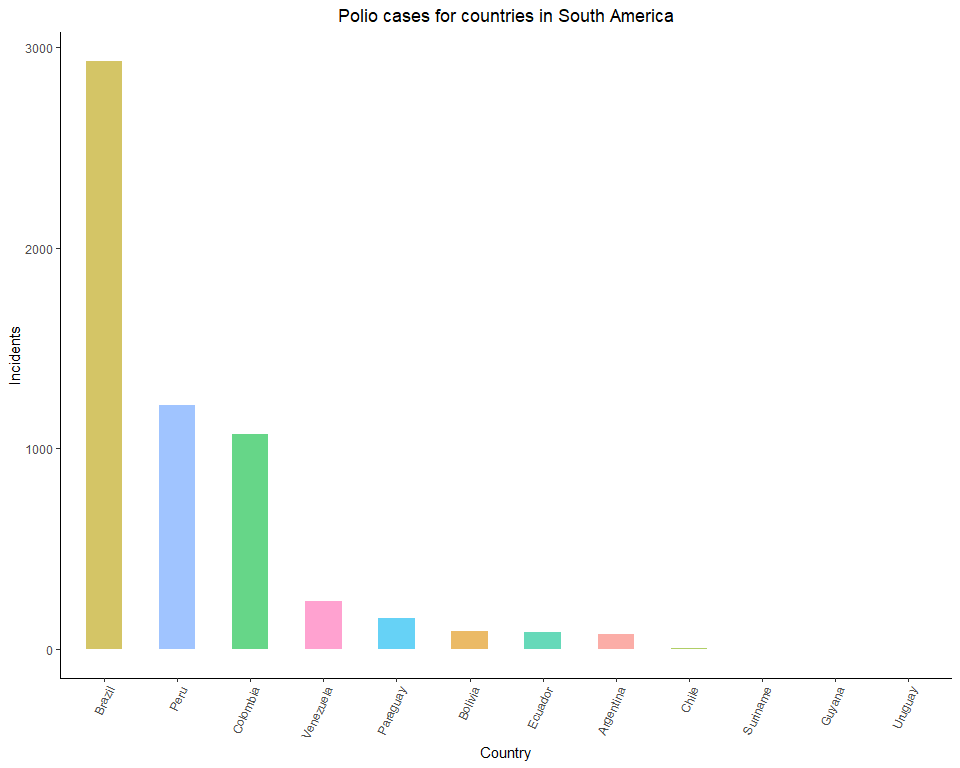
# Barplot for Polio cases in Europe by Country  
Polio %>% filter(Continent == "Europe") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill=Country)) + geom\_bar(stat="identity", width = 0.5, alpha=0.6) + labs(title = 'Polio cases for countries in Europe', x= 'Country', y = 'Incidents') + theme(legend.position="none", axis.text.x = element\_text(angle=65, hjust=1))



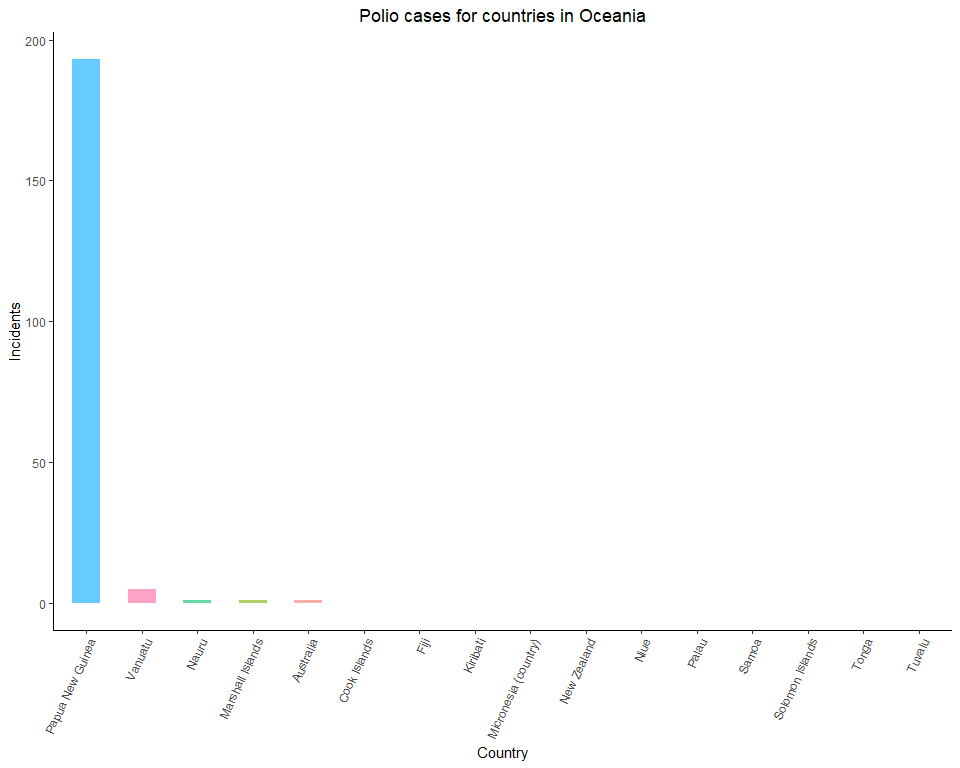
# Barplot for Polio cases in North America by Country  
Polio %>% filter(Continent == "North America") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill=Country)) + geom\_bar(stat="identity", width = 0.5, alpha=0.6) + labs(title = 'Polio cases for countries in North America', x= 'Country', y = 'Incidents') + theme(legend.position="none", axis.text.x = element\_text(angle=65, hjust=1))



# Barplot for Polio cases in South America by Country  
Polio %>% filter(Continent == "South America") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill=Country)) + geom\_bar(stat="identity", width = 0.5, alpha=0.6) + labs(title = 'Polio cases for countries in South America', x= 'Country', y = 'Incidents') + theme(legend.position="none", axis.text.x = element\_text(angle=65, hjust=1))

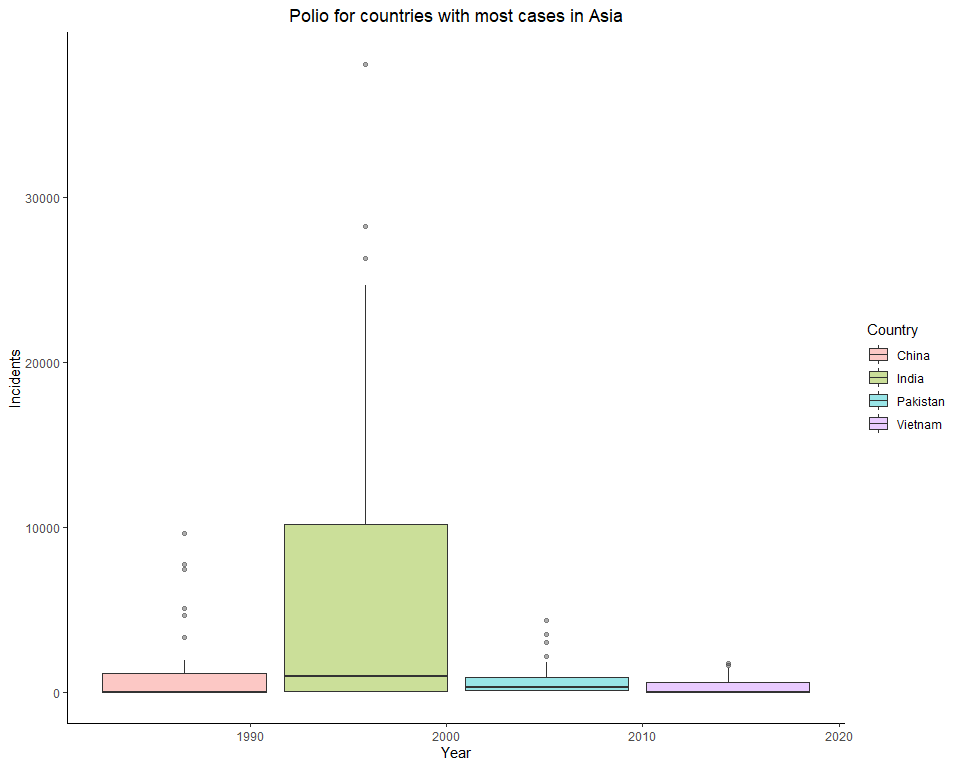


# Barplot for Polio cases in Oceania by Country  
Polio %>% filter(Continent == "Oceania") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill=Country)) + geom\_bar(stat="identity", width = 0.5, alpha=0.6) + labs(title = 'Polio cases for countries in Oceania', x= 'Country', y = 'Incidents') + theme(legend.position="none", axis.text.x = element\_text(angle=65, hjust=1))

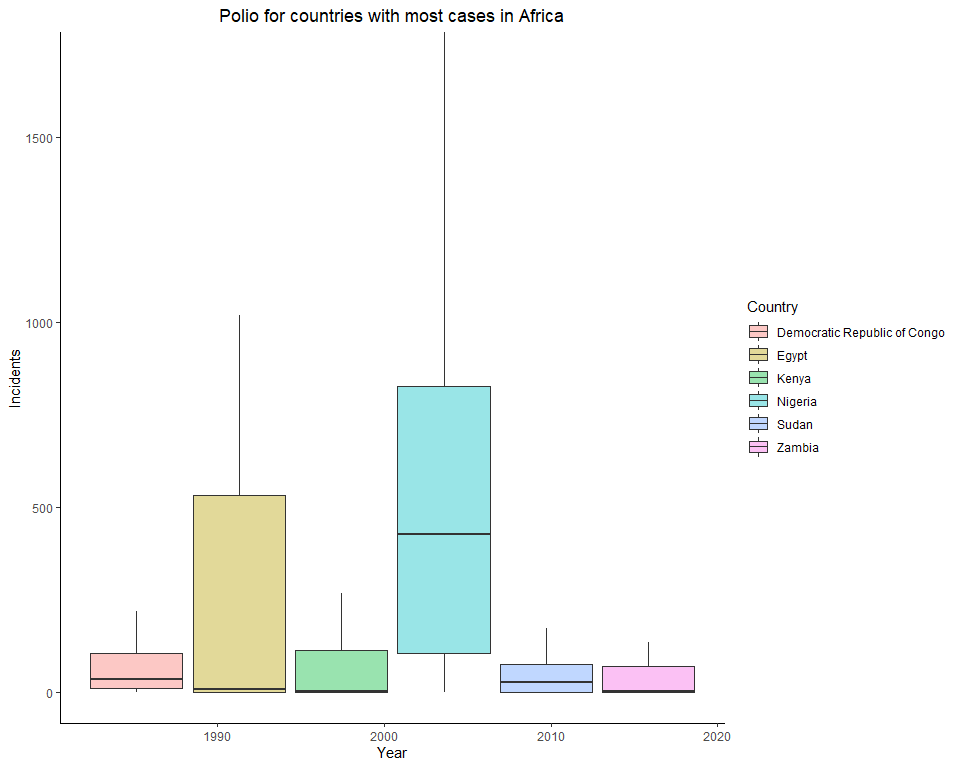


# Polio cases in SELECT top countries within each continent

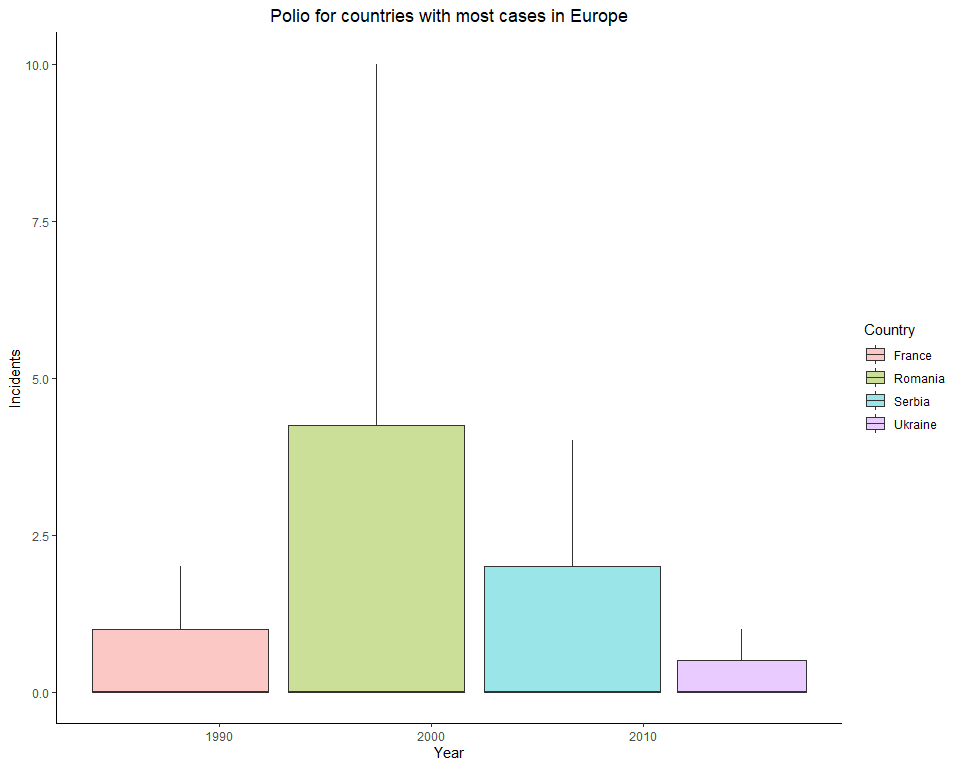
# Boxplot for Polio cases in SELECT countries in Asia  
Polio %>% filter(Continent == "Asia" & Country %in% c("India","China","Pakistan","Vietnam","Afganistan")) %>% ggplot(aes(x = Year, y = Incidence, fill=Country)) + geom\_boxplot(alpha=0.4) + labs(title = 'Polio for countries with most cases in Asia', x= 'Year', y = 'Incidents')



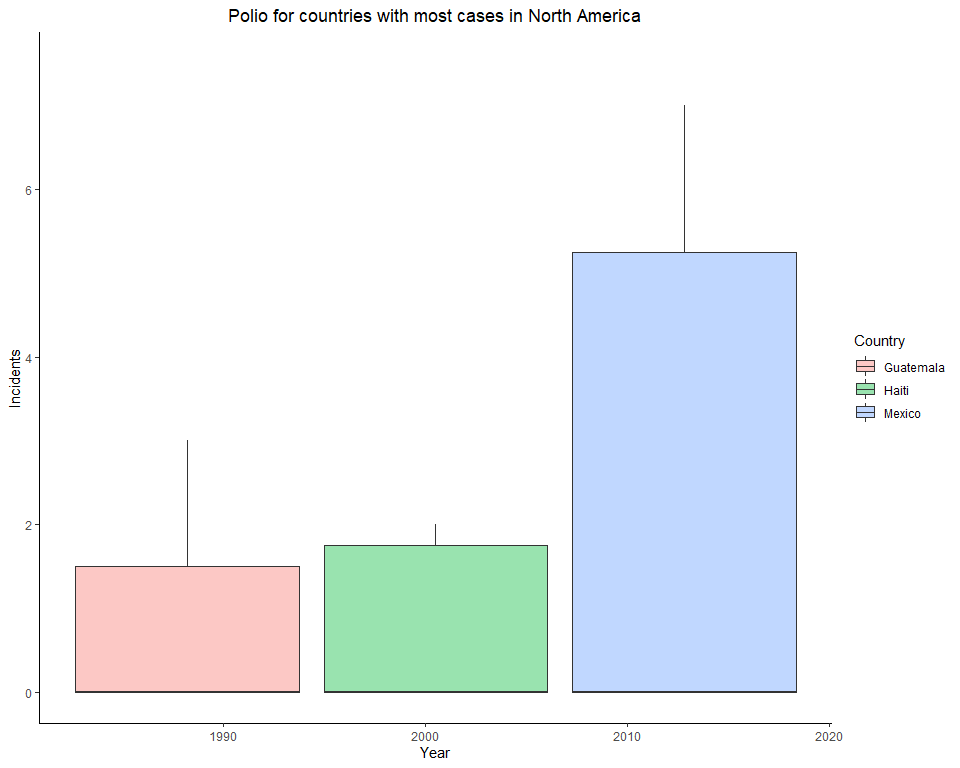
# Boxplot for Polio cases in SELECT countries in Africa  
Polio %>% filter(Continent == "Africa" & Country %in% c("Nigeria","Egypt","Kenya","Sudan","Democratic Republic of Congo","Ehiopia","Zambia")) %>% ggplot(aes(x = Year, y = Incidence, fill=Country)) + geom\_boxplot(outlier.shape=NA, alpha=0.4) + coord\_cartesian(ylim=c(0, 1700)) + labs(title = 'Polio for countries with most cases in Africa', x= 'Year', y = 'Incidents')



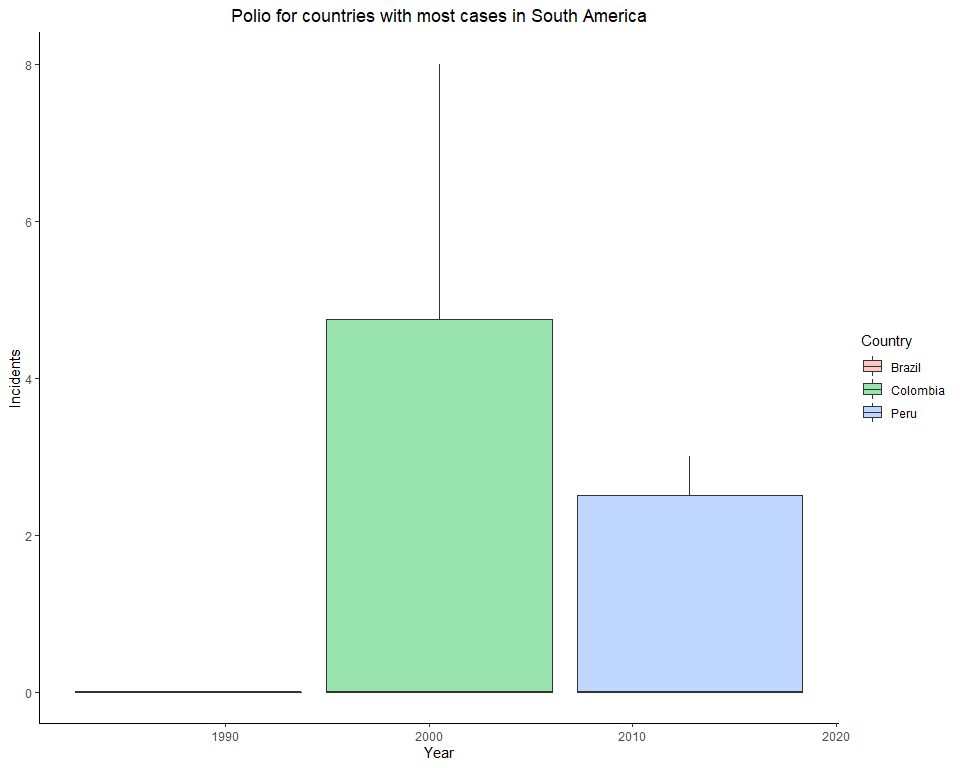
# Boxplot for Polio cases in SELECT countries in Europe  
Polio %>% filter(Continent == "Europe" & Country %in% c("Romania","Serbia","France","Ukraine")) %>% ggplot(aes(x = Year, y = Incidence, fill=Country)) + geom\_boxplot(outlier.shape=NA, alpha=0.4) + coord\_cartesian(ylim=c(0, 10)) + labs(title = 'Polio for countries with most cases in Europe', x= 'Year', y = 'Incidents')



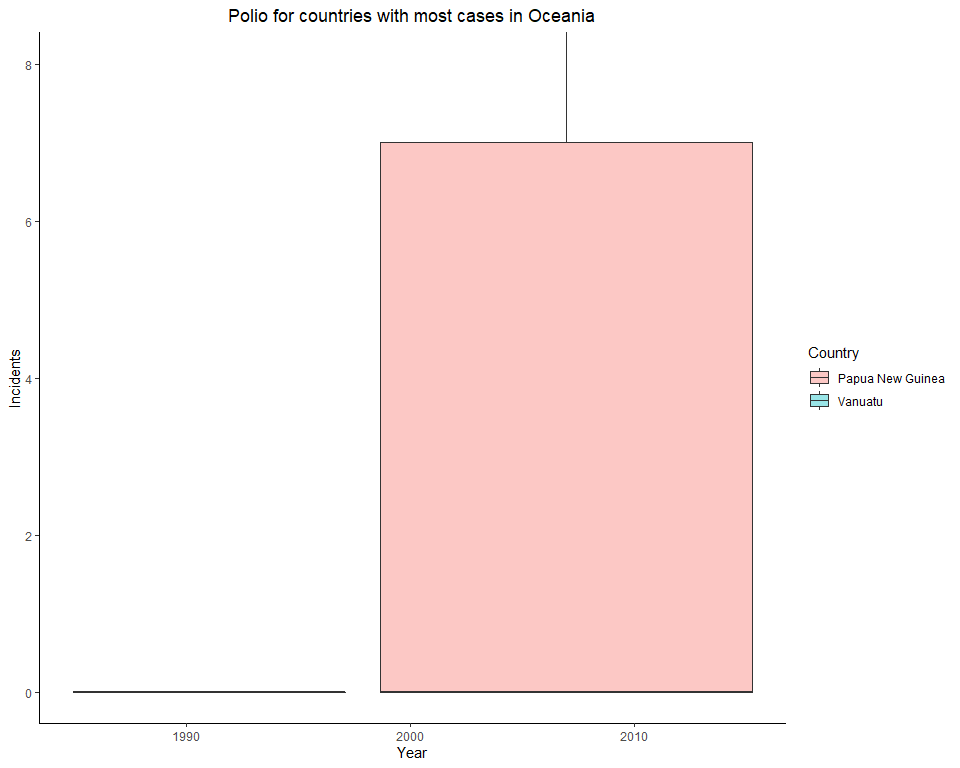
# Boxplot for Polio cases in SELECT countries in North America  
Polio %>% filter(Continent == "North America" & Country %in% c("Mexico","Guatemala","Haiti")) %>% ggplot(aes(x = Year, y = Incidence, fill=Country)) + geom\_boxplot(outlier.shape=NA, alpha=0.4) + coord\_cartesian(ylim=c(0, 7.5)) + labs(title = 'Polio for countries with most cases in North America', x= 'Year', y = 'Incidents')



# !!!! BRAZIL doesn't show up !!!!  
# Boxplot for Polio cases in SELECT countries in South America  
Polio %>% filter(Continent == "South America" & Country %in% c("Brazil","Peru","Colombia")) %>% ggplot(aes(x = Year, y = Incidence, fill=Country)) + geom\_boxplot(outlier.shape=NA, alpha=0.4) + coord\_cartesian(ylim=c(0,8)) + labs(title = 'Polio for countries with most cases in South America', x= 'Year', y = 'Incidents')



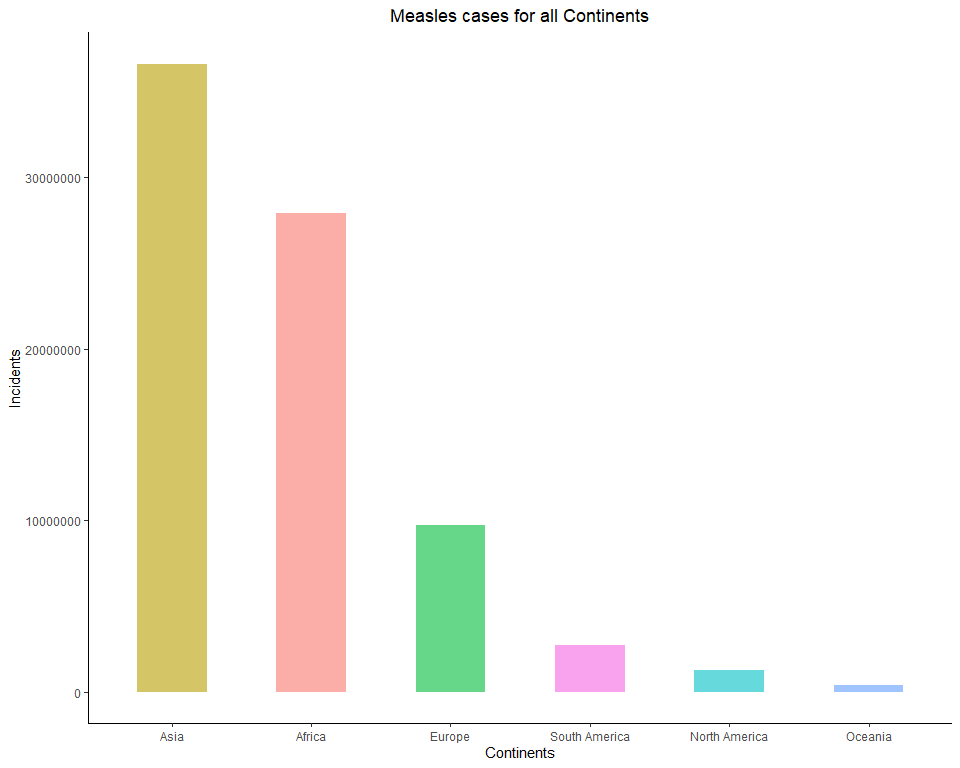
# Boxplot for Polio cases in SELECT countries in Oceania  
Polio %>% filter(Continent == "Oceania" & Country %in% c("Papua New Guinea","Vanuatu")) %>% ggplot(aes(x = Year, y = Incidence, fill=Country)) + geom\_boxplot(outlier.shape=NA, alpha=0.4) + coord\_cartesian(ylim=c(0,8)) + labs(title = 'Polio for countries with most cases in Oceania', x= 'Year', y = 'Incidents')



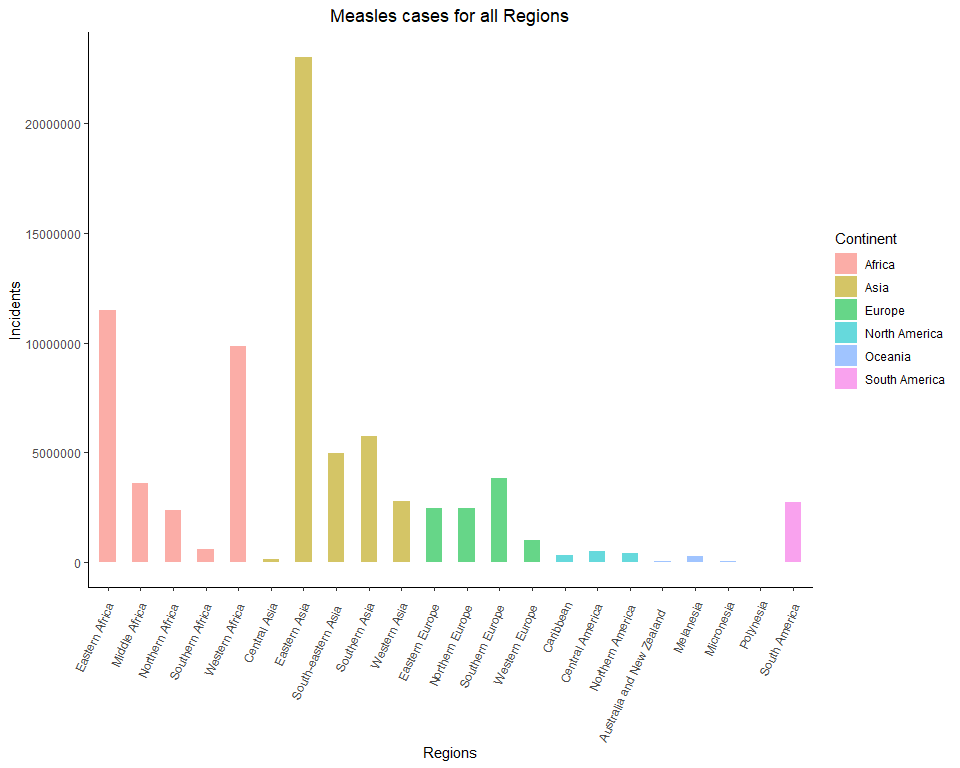
# Measles

# Measles cases among continents and regions

# Barplot for Measles cases by all continents  
Measles %>% filter(Continent != "#N/A") %>% ggplot(aes(x = reorder(Continent, -Incidence), y = Incidence, fill=Continent)) + geom\_bar(stat="identity", width = 0.5, alpha = 0.6) + labs(title = 'Measles cases for all Continents', x= 'Continents', y = 'Incidents') + theme(legend.position="none")

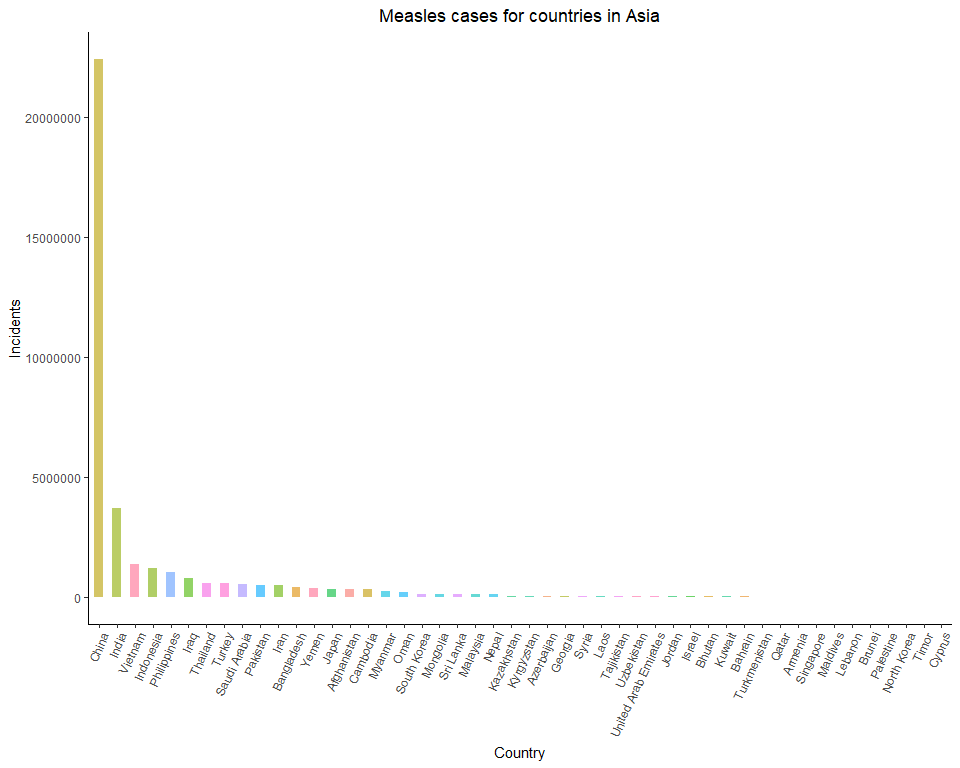


# Barplot for Measles cases by all regions  
Measles$Region <- factor(Measles$Region, levels=unique(Measles$Region[order(Measles$Continent,Measles$Region)]), ordered=TRUE)  
  
Measles %>% filter(Region != "#N/A") %>% ggplot(aes(x = Region, y = Incidence, fill = Continent)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'Measles cases for all Regions', x = 'Regions', y = 'Incidents') + theme(axis.text.x = element\_text(angle = 65, hjust = 1.1))

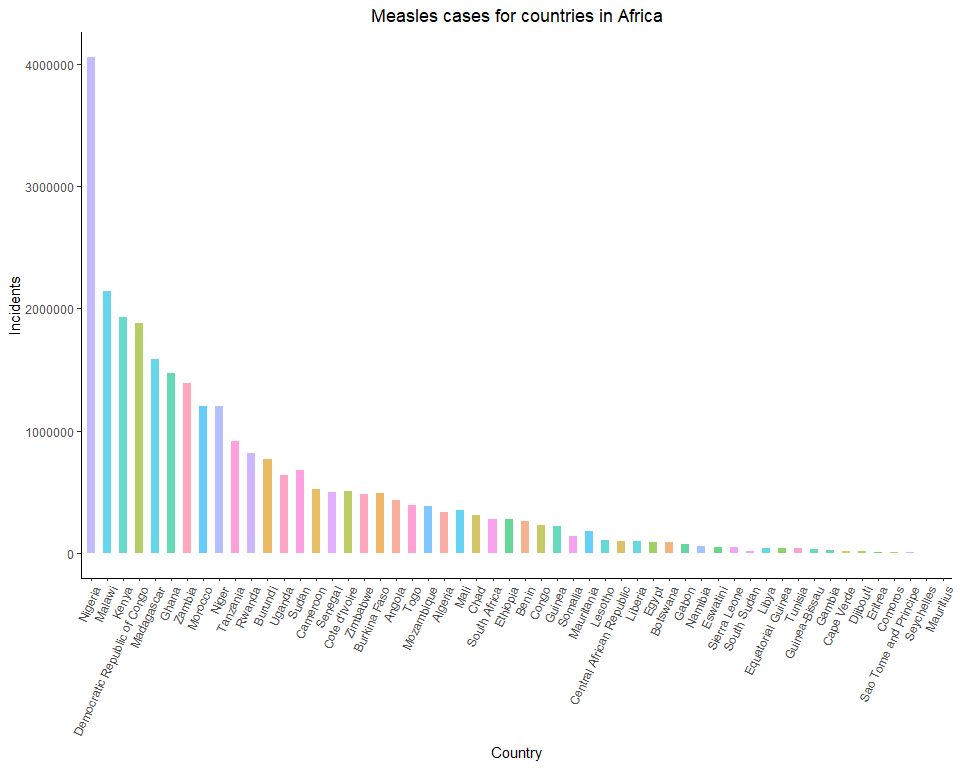


# Measles total cases in each country in a continent

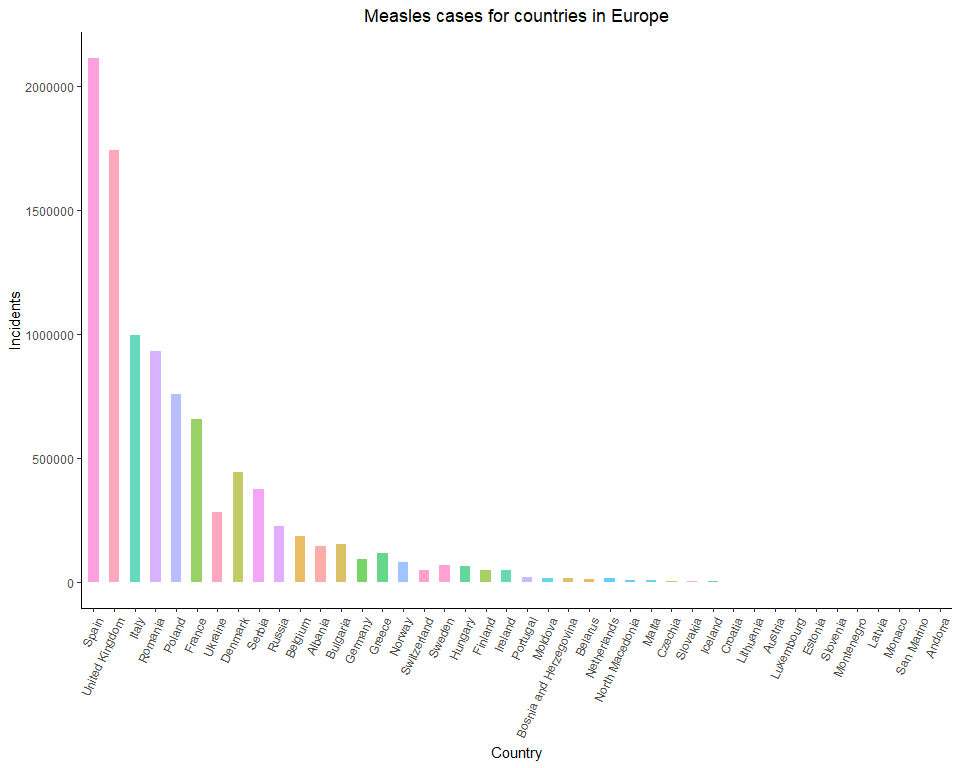
# Barplot for Measles cases in Asia by Country  
Measles %>% filter(Continent == "Asia") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill = Country)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'Measles cases for countries in Asia', x = 'Country', y = 'Incidents') + theme(legend.position = "none", axis.text.x = element\_text(angle = 65, hjust = 1))



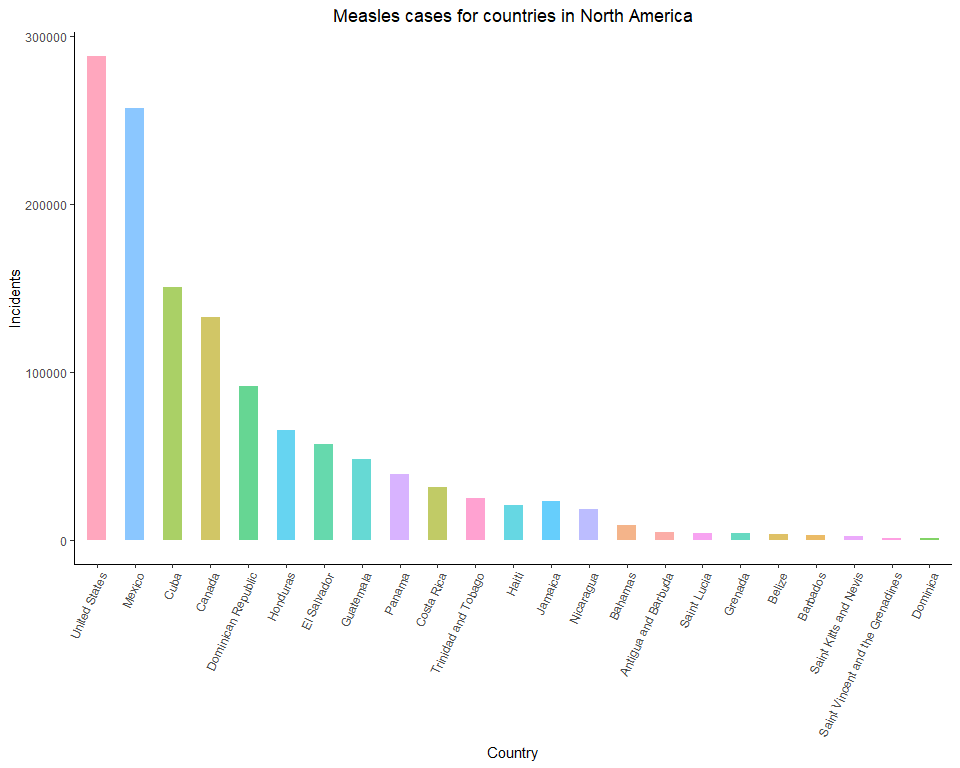
# Barplot for Measles cases in Africa by Country  
Measles %>% filter(Continent == "Africa") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill = Country)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'Measles cases for countries in Africa', x = 'Country', y = 'Incidents') + theme(legend.position = "none", axis.text.x = element\_text(angle = 65, hjust = 1))



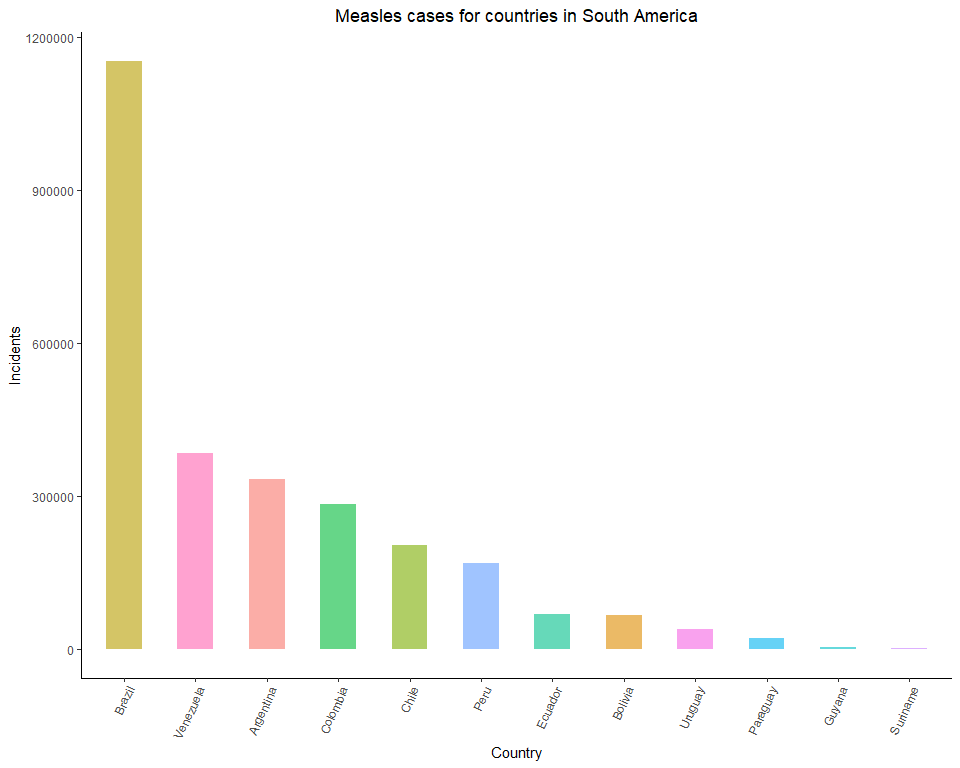
# Barplot for Measles cases in Europe by Country  
Measles %>% filter(Continent == "Europe") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill = Country)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'Measles cases for countries in Europe', x = 'Country', y = 'Incidents') + theme(legend.position = "none", axis.text.x = element\_text(angle = 65, hjust = 1))



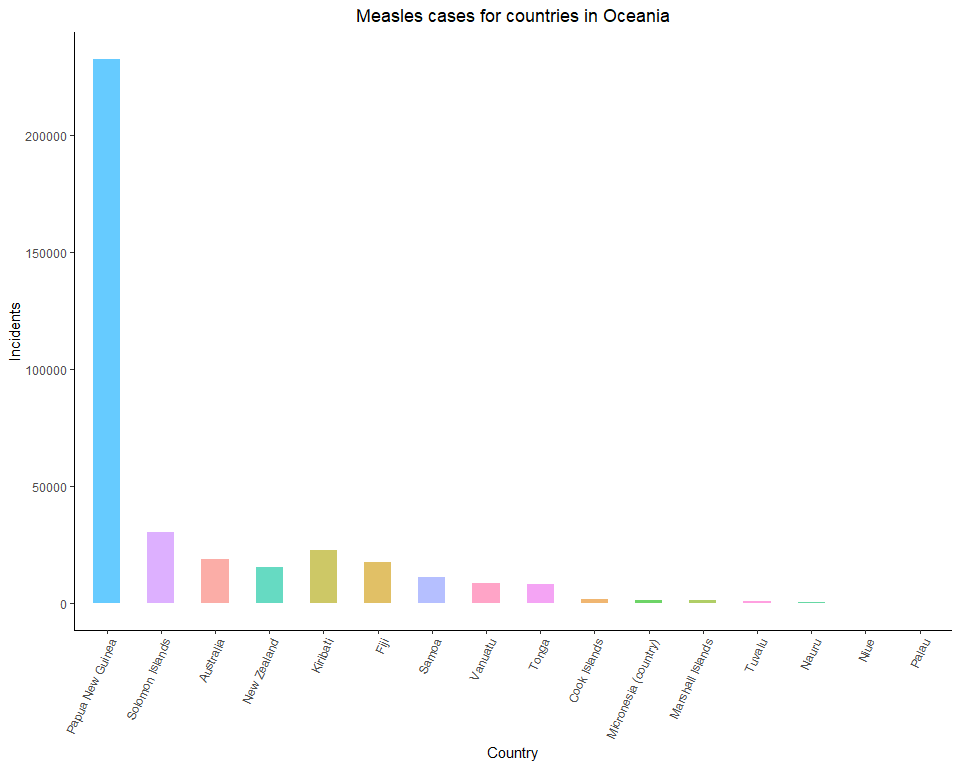
# Barplot for Measles cases in North America by Country  
Measles %>% filter(Continent == "North America") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill = Country)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'Measles cases for countries in North America', x = 'Country', y = 'Incidents') + theme(legend.position = "none", axis.text.x = element\_text(angle = 65, hjust = 1))



# Barplot for Measles cases in South America by Country  
Measles %>% filter(Continent == "South America") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill = Country)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'Measles cases for countries in South America', x = 'Country', y = 'Incidents') + theme(legend.position = "none", axis.text.x = element\_text(angle = 65, hjust = 1))

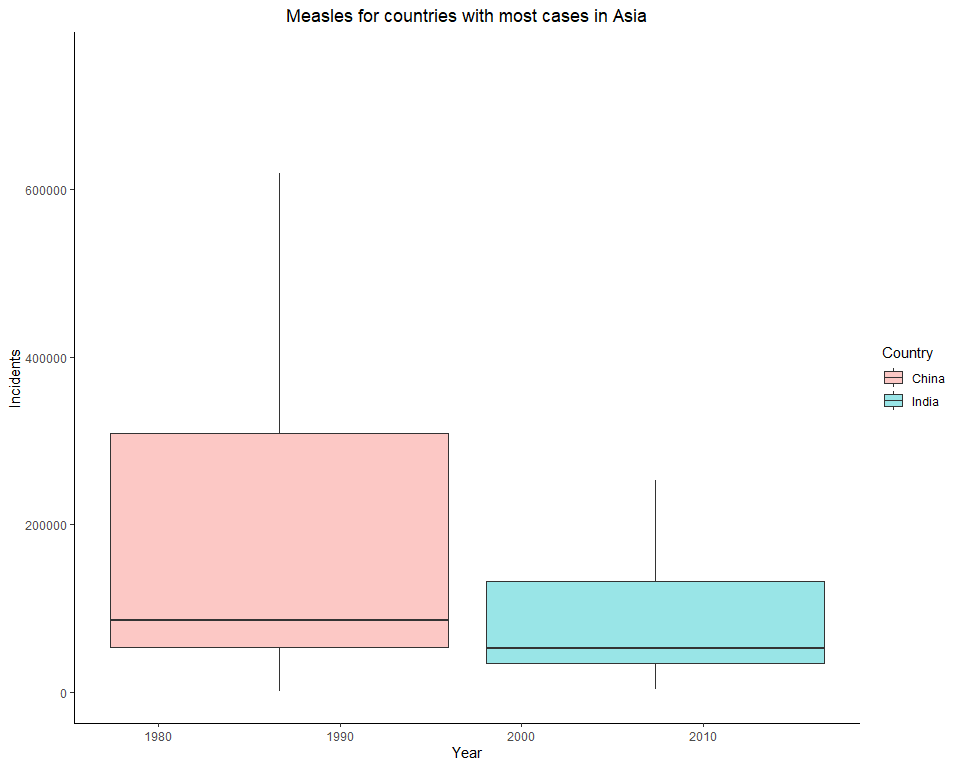


# Barplot for Measles cases in Oceania by Country  
Measles %>% filter(Continent == "Oceania") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill = Country)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'Measles cases for countries in Oceania', x = 'Country', y = 'Incidents') + theme(legend.position = "none", axis.text.x = element\_text(angle = 65, hjust = 1))

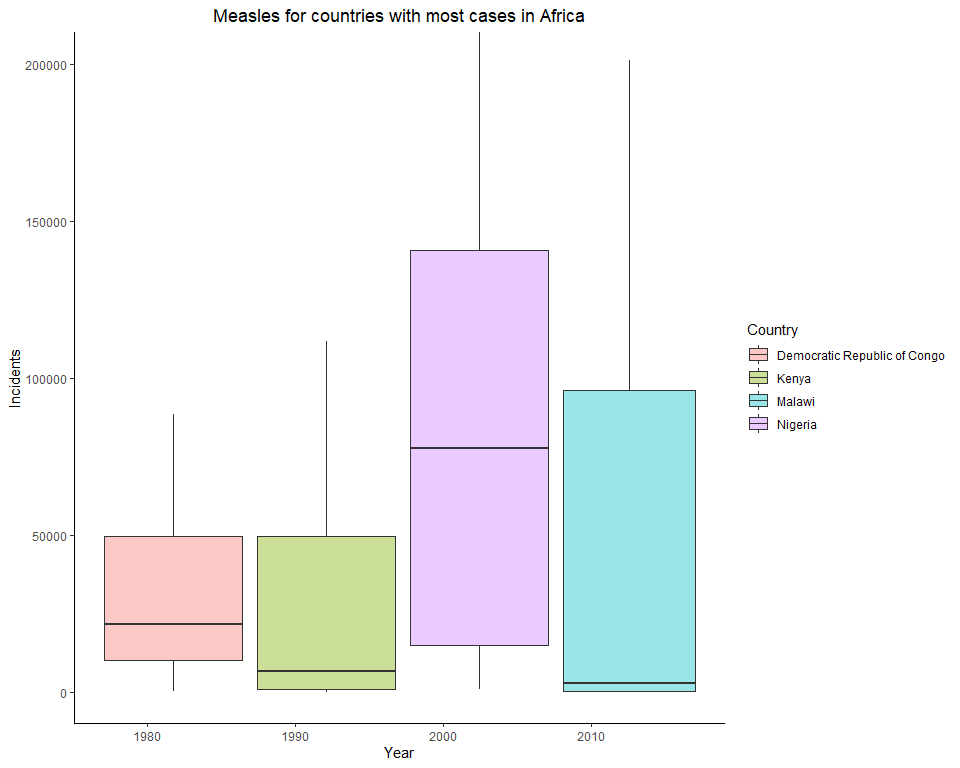


# Measles cases in SELECT top countries within each continent

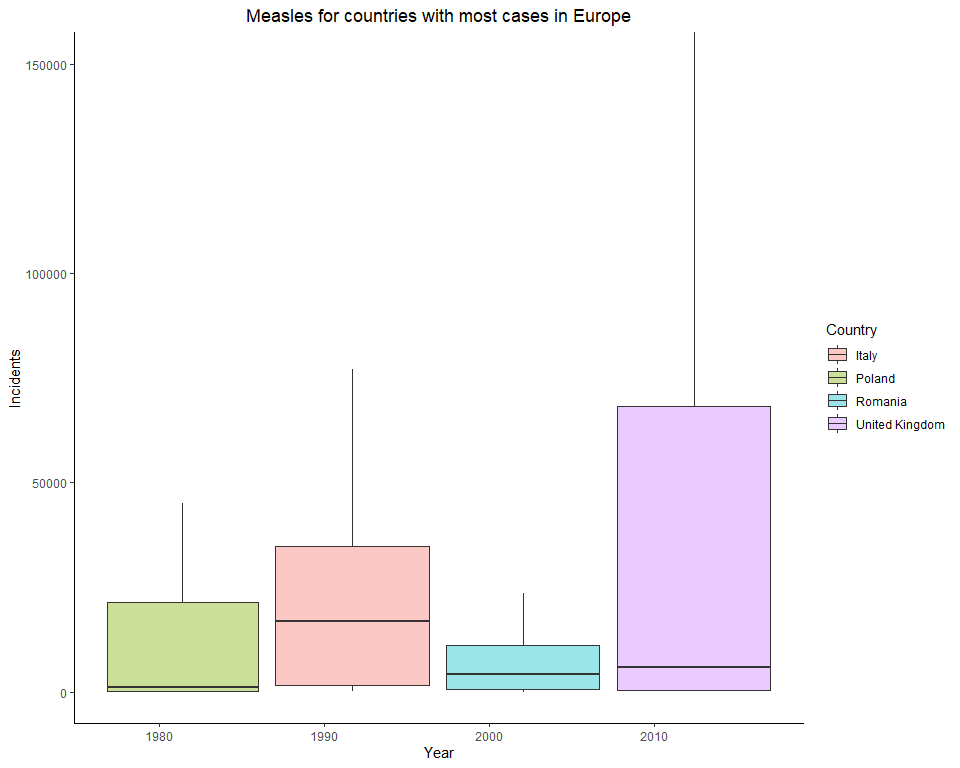
# Boxplot for Measles cases in SELECT countries in Asia  
Measles %>% filter(Continent == "Asia" & Country %in% c("China","India")) %>% ggplot(aes(x = Year, y = Incidence, fill = Country)) + geom\_boxplot(outlier.shape = NA, alpha = 0.4) + coord\_cartesian(ylim = c(0,750000)) + labs(title = 'Measles for countries with most cases in Asia', x = 'Year', y = 'Incidents')



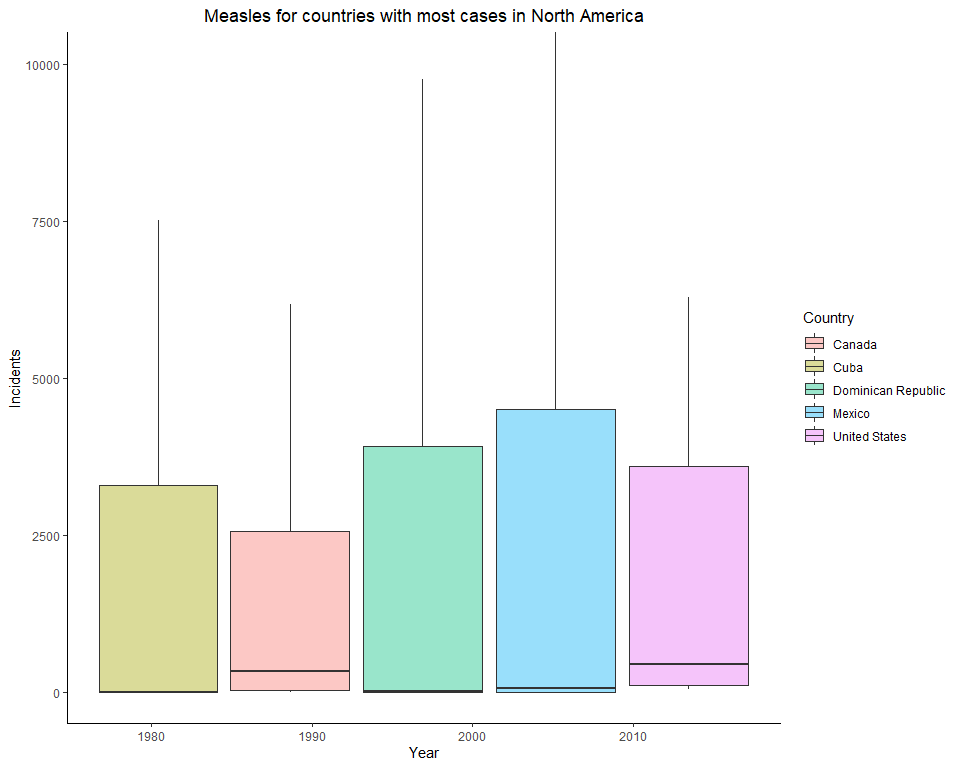
# Boxplot for Measles cases in SELECT countries in Africa  
Measles %>% filter(Continent == "Africa" & Country %in% c("Nigeria","Malawi","Kenya","Democratic Republic of Congo")) %>% ggplot(aes(x = Year, y = Incidence, fill = Country)) + geom\_boxplot(outlier.shape = NA, alpha = 0.4) + coord\_cartesian(ylim = c(0,200000)) + labs(title = 'Measles for countries with most cases in Africa', x = 'Year', y = 'Incidents')



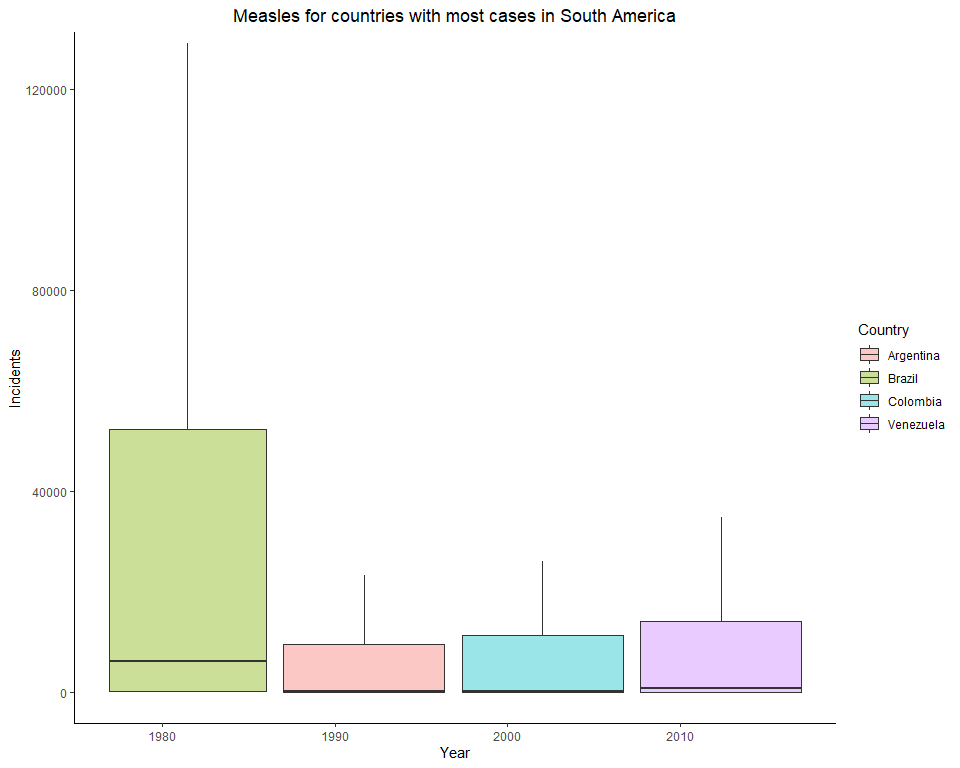
# Boxplot for Measles cases in SELECT countries in Europe  
Measles %>% filter(Continent == "Europe" & Country %in% c("Sapin","United Kingdom","Italy","Romania","Poland")) %>% ggplot(aes(x = Year, y = Incidence, fill = Country)) + geom\_boxplot(outlier.shape = NA, alpha = 0.4) + coord\_cartesian(ylim = c(0,150000)) + labs(title = 'Measles for countries with most cases in Europe', x = 'Year', y = 'Incidents')



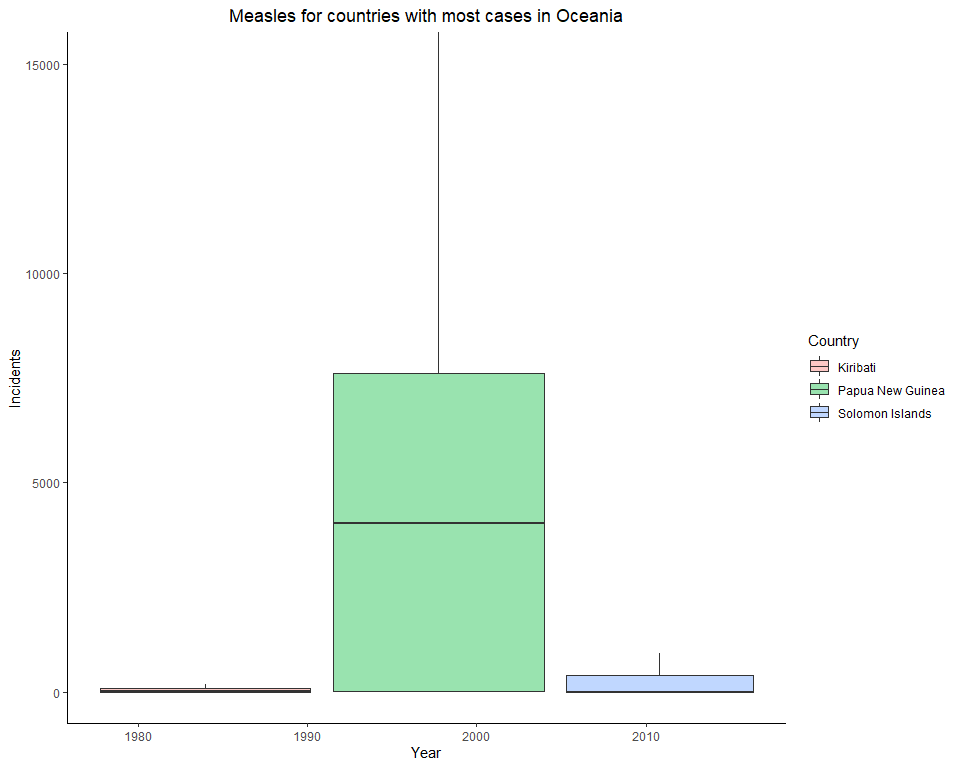
# Boxplot for Measles cases in SELECT countries in North America  
Measles %>% filter(Continent == "North America" & Country %in% c("United States","Mexico","Cuba","Canada","Dominican Republic")) %>% ggplot(aes(x = Year, y = Incidence, fill = Country)) + geom\_boxplot(outlier.shape = NA, alpha = 0.4) + coord\_cartesian(ylim = c(0,10000)) + labs(title = 'Measles for countries with most cases in North America', x = 'Year', y = 'Incidents')



# Boxplot for Measles cases in SELECT countries in South America  
Measles %>% filter(Continent == "South America" & Country %in% c("Brazil","Venezuela","Argentina","Colombia")) %>% ggplot(aes(x = Year, y = Incidence, fill = Country)) + geom\_boxplot(outlier.shape = NA, alpha = 0.4) + coord\_cartesian(ylim = c(0,125000)) + labs(title = 'Measles for countries with most cases in South America', x = 'Year', y = 'Incidents')



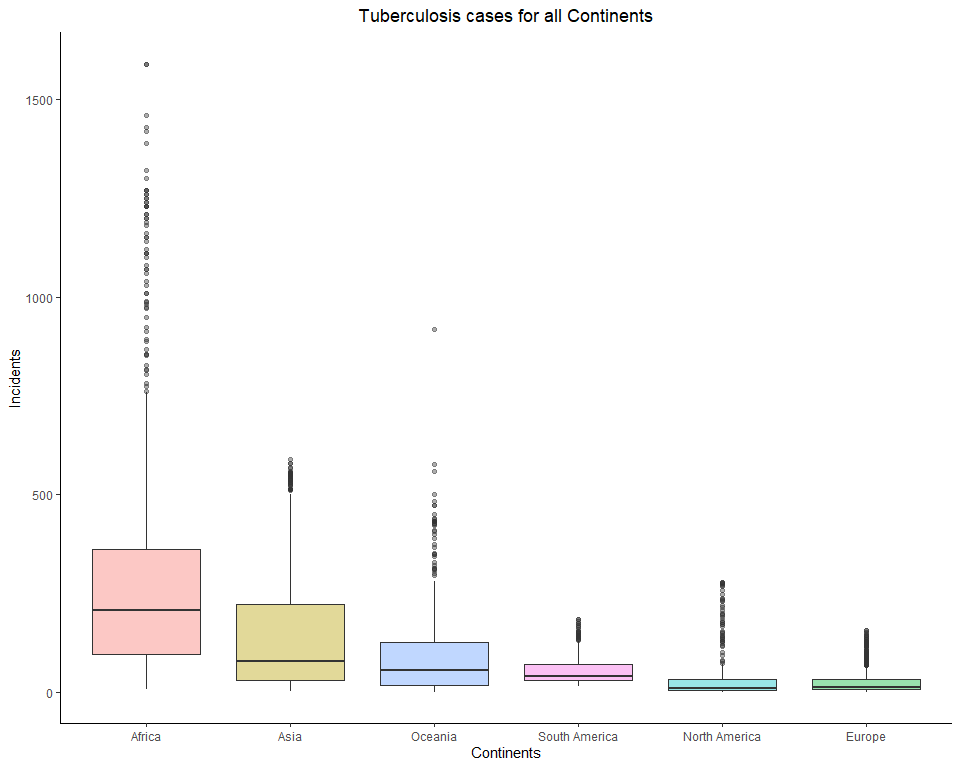
# Boxplot for Measles cases in SELECT countries in Oceania  
Measles %>% filter(Continent == "Oceania" & Country %in% c("Papua New Guinea","Solomon Islands","Kiribati")) %>% ggplot(aes(x = Year, y = Incidence, fill = Country)) + geom\_boxplot(outlier.shape = NA, alpha = 0.4) + coord\_cartesian(ylim = c(0,15000)) + labs(title = 'Measles for countries with most cases in Oceania', x = 'Year', y = 'Incidents')



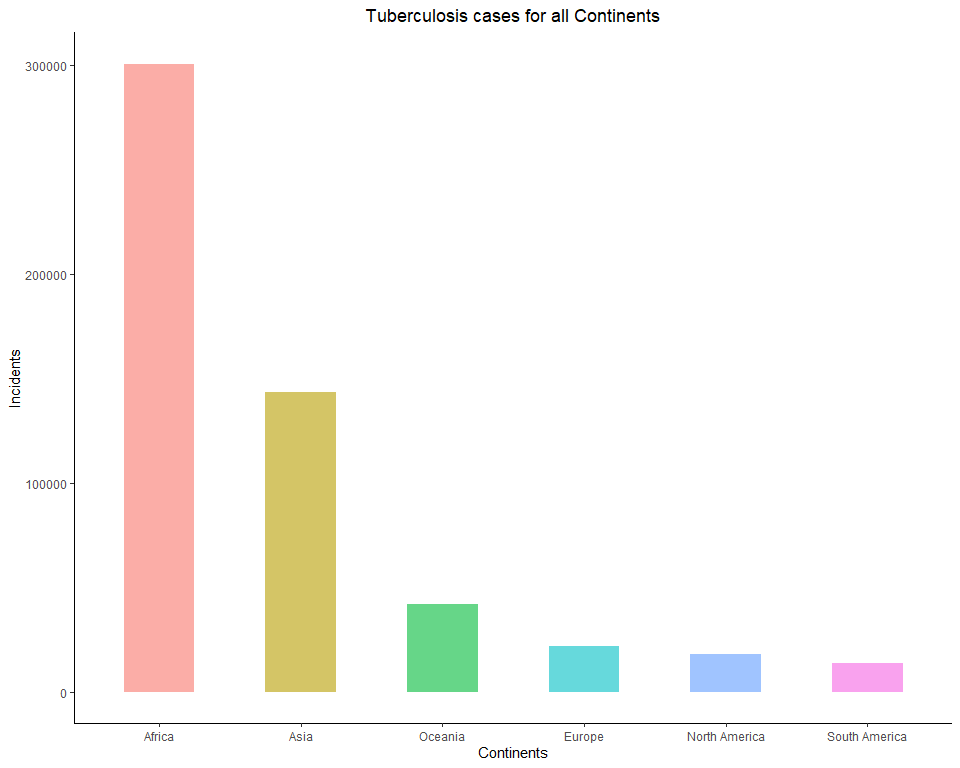
# Tuberculosis

# Tuberculosis cases among continents and regions

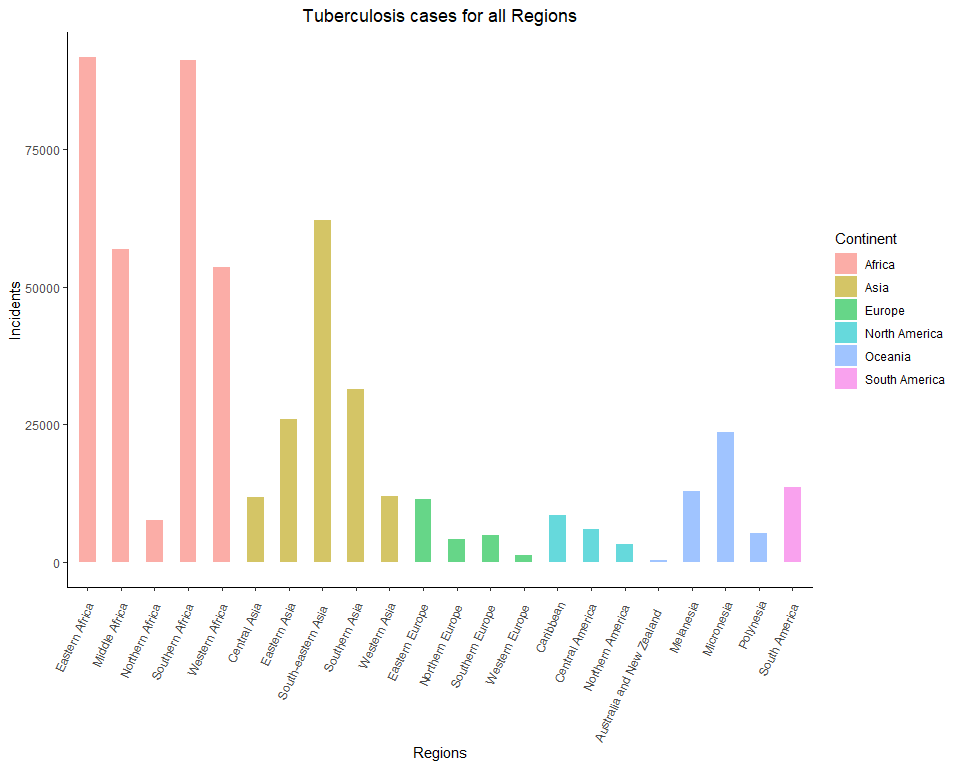
# Boxplot for Tuberculosis cases by all continents  
Tuberculosis %>% filter(Continent != "#N/A") %>% ggplot(aes(x = reorder(Continent, -Incidence), y = Incidence, fill = Continent)) + geom\_boxplot(alpha = 0.4) + labs(title = 'Tuberculosis cases for all Continents', x = 'Continents', y = 'Incidents') + theme(legend.position ="none")



# Barplot for Tuberculosis cases by all continents  
# Arrange (order) data by descending Total Cases  
Tuberculosis\_Cont = Tuberculosis %>% group\_by(Continent) %>% summarize(TotalCases = sum(Incidence)) %>% arrange(desc(TotalCases))  
# Reorder level of Continent factor based on descending Total Cases  
Tuberculosis\_Cont$Continent = factor(Tuberculosis\_Cont$Continent, level = Tuberculosis\_Cont$Continent[order(-Tuberculosis\_Cont$TotalCases)])  
  
Tuberculosis\_Cont %>% filter(Continent != "#N/A") %>% ggplot(aes(x = Continent, y = TotalCases, fill = Continent)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'Tuberculosis cases for all Continents', x = 'Continents', y = 'Incidents') + theme(legend.position = "none")

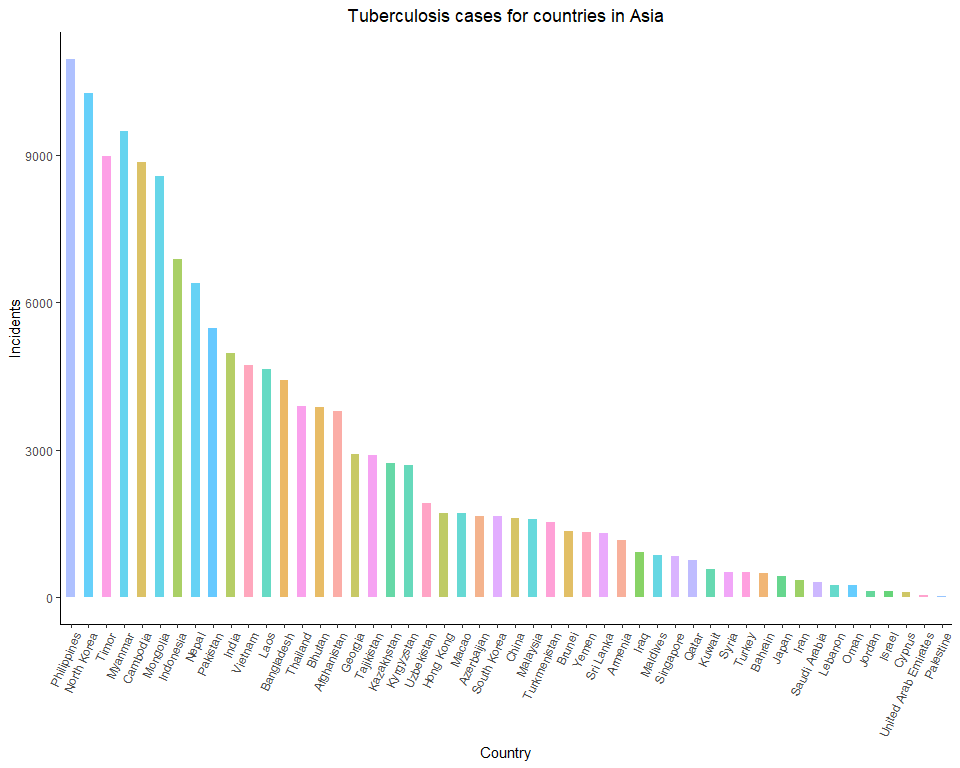


# Barplot for Tuberculosis cases by all regions  
Tuberculosis$Region <- factor(Tuberculosis$Region, levels=unique(Tuberculosis$Region[order(Tuberculosis$Continent,Tuberculosis$Region)]), ordered=TRUE)  
  
Tuberculosis %>% filter(Region != "#N/A") %>% ggplot(aes(x = Region, y = Incidence, fill = Continent)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'Tuberculosis cases for all Regions', x = 'Regions', y = 'Incidents') + theme(axis.text.x = element\_text(angle = 65, hjust = 1.1))

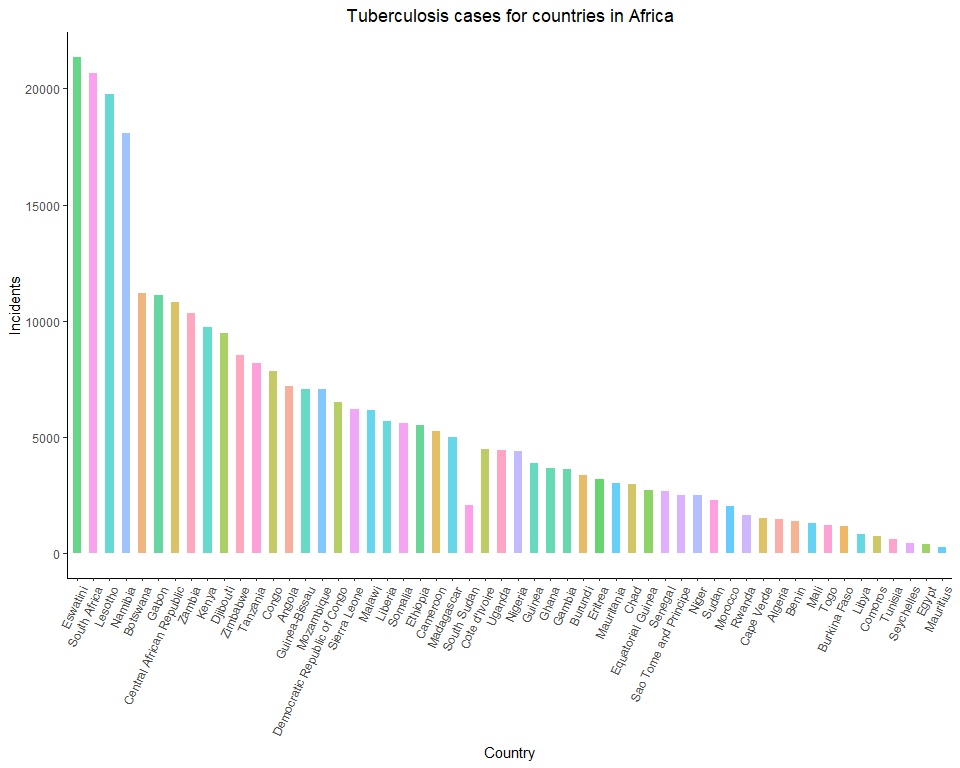


# Tuberculosis cases in continents each year by countries

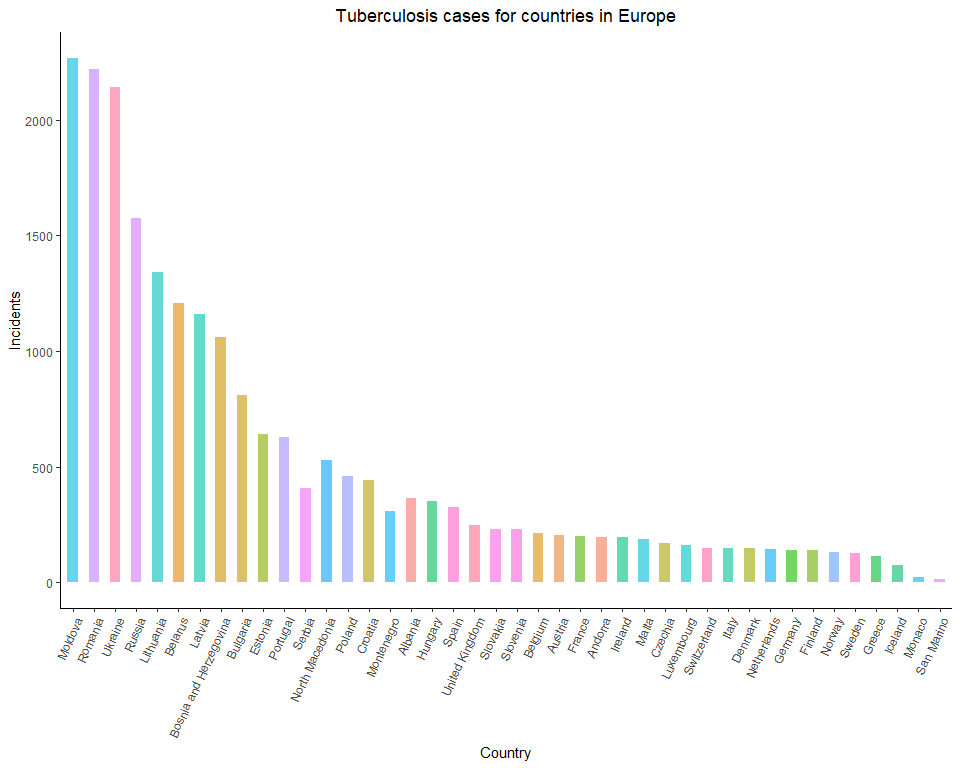
# # Arrange (order) data by descending Total Cases  
# TB\_Country = Tuberculosis %>% group\_by(Continent,Country) %>% summarize(TotalCases = sum(Incidence)) %>% arrange(desc(TotalCases))  
# # Reorder level of Continent factor based on descending Total Cases  
# TB\_Country$Country = factor(TB\_Country$Country, level = TB\_Country$Country[order(-TB\_Country$TotalCases)])  
  
# Barplot for Tuberculosis cases in Asia by Country  
Tuberculosis %>% filter(Continent == "Asia") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill = Country)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'Tuberculosis cases for countries in Asia', x = 'Country', y = 'Incidents') + theme(legend.position = "none", axis.text.x = element\_text(angle = 65, hjust = 1))



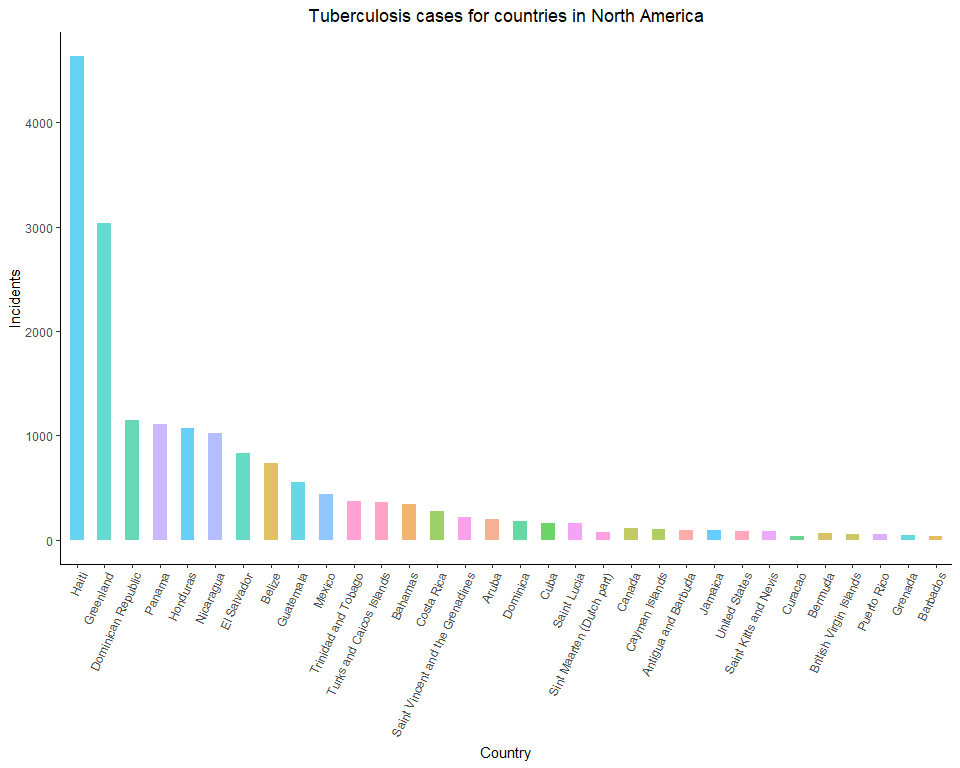
# TB\_Country %>% filter(Continent == "Asia") %>% ggplot(aes(x = Country, y = TotalCases, fill = Country)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'Tuberculosis cases for countries in Asia', x = 'Country', y = 'Incidents') + theme(legend.position = "none", axis.text.x = element\_text(angle = 65, hjust = 1))  
  
# Barplot for Tuberculosis cases in Africa by Country  
Tuberculosis %>% filter(Continent == "Africa") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill = Country)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'Tuberculosis cases for countries in Africa', x = 'Country', y = 'Incidents') + theme(legend.position = "none", axis.text.x = element\_text(angle = 65, hjust = 1))



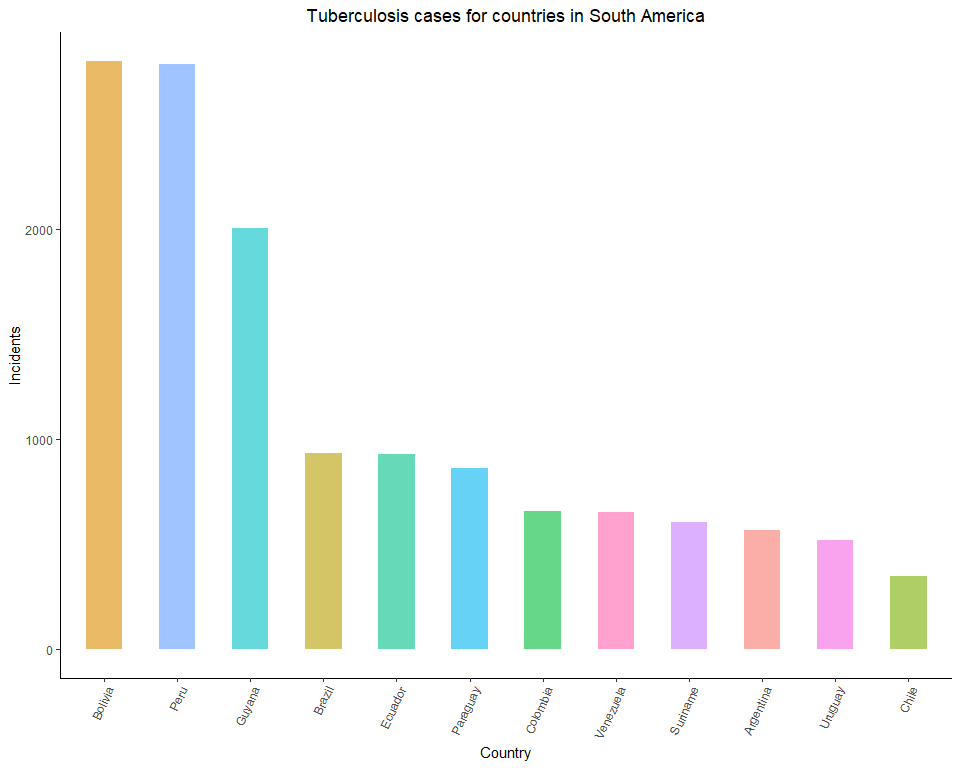
# Barplot for Tuberculosis cases in Europe by Country  
Tuberculosis %>% filter(Continent == "Europe") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill = Country)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'Tuberculosis cases for countries in Europe', x = 'Country', y = 'Incidents') + theme(legend.position = "none", axis.text.x = element\_text(angle = 65, hjust = 1))



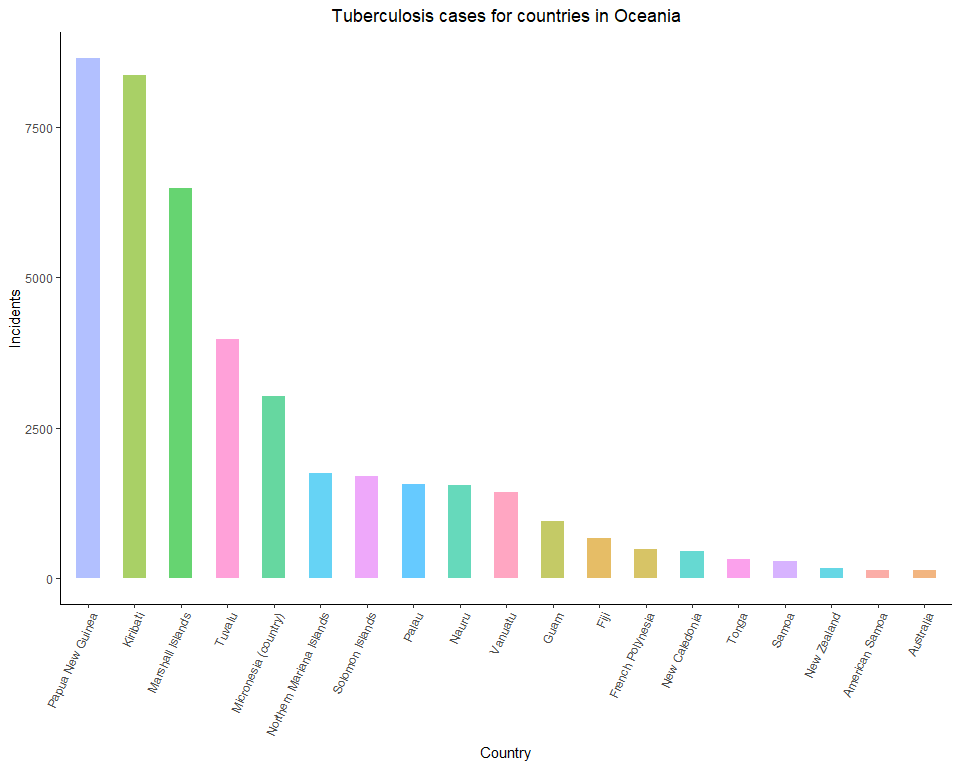
# Barplot for Tuberculosis cases in North America by Country  
Tuberculosis %>% filter(Continent == "North America") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill = Country)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'Tuberculosis cases for countries in North America', x = 'Country', y = 'Incidents') + theme(legend.position = "none", axis.text.x = element\_text(angle = 65, hjust = 1))



# Barplot for Tuberculosis cases in South America by Country  
Tuberculosis %>% filter(Continent == "South America") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill = Country)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'Tuberculosis cases for countries in South America', x = 'Country', y = 'Incidents') + theme(legend.position = "none", axis.text.x = element\_text(angle = 65, hjust = 1))

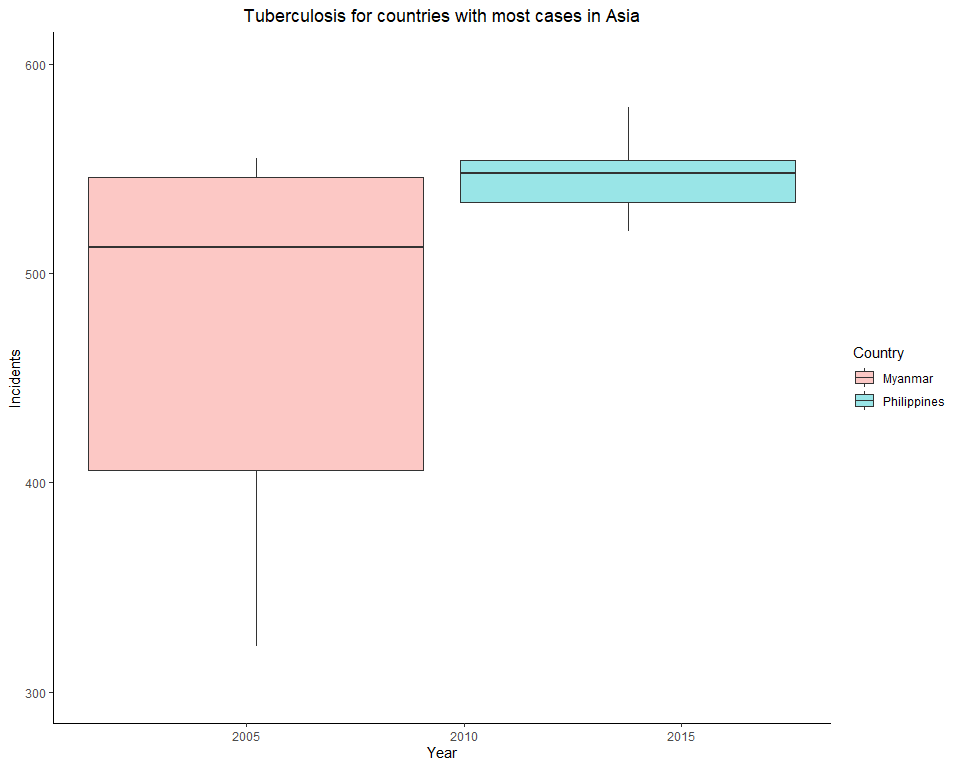


# Barplot for Tuberculosis cases in Oceania by Country  
Tuberculosis %>% filter(Continent == "Oceania") %>% ggplot(aes(x = reorder(Country, -Incidence), y = Incidence, fill = Country)) + geom\_bar(stat = "identity", width = 0.5, alpha = 0.6) + labs(title = 'Tuberculosis cases for countries in Oceania', x = 'Country', y = 'Incidents') + theme(legend.position = "none", axis.text.x = element\_text(angle = 65, hjust = 1))

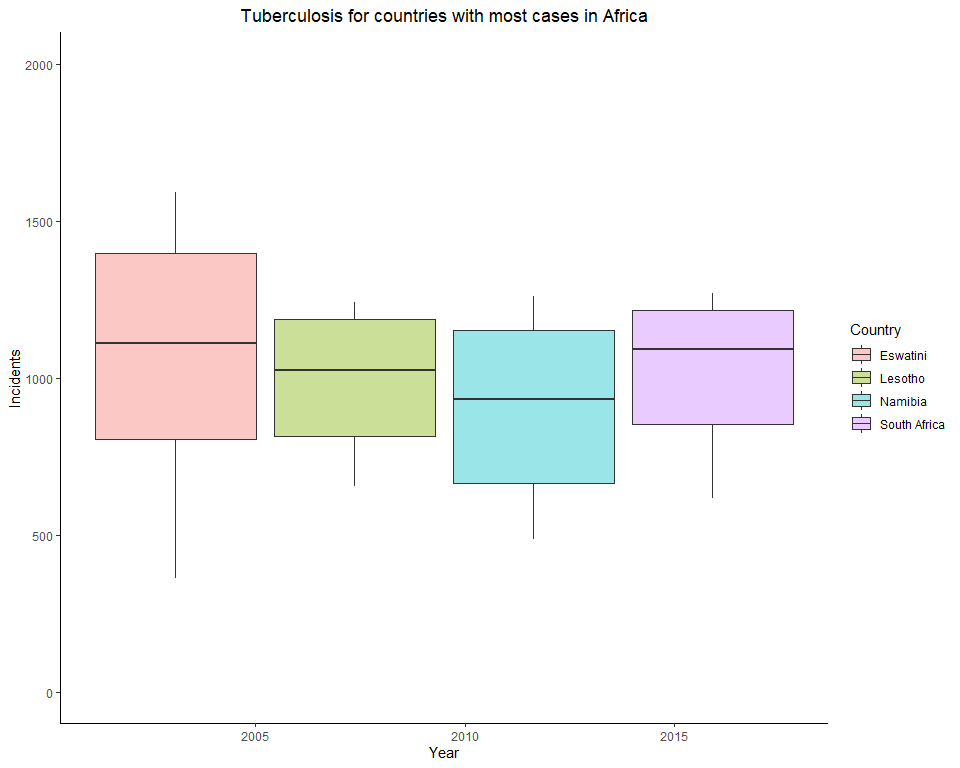


# Tuberculosis cases in SELECT top countries within each continent

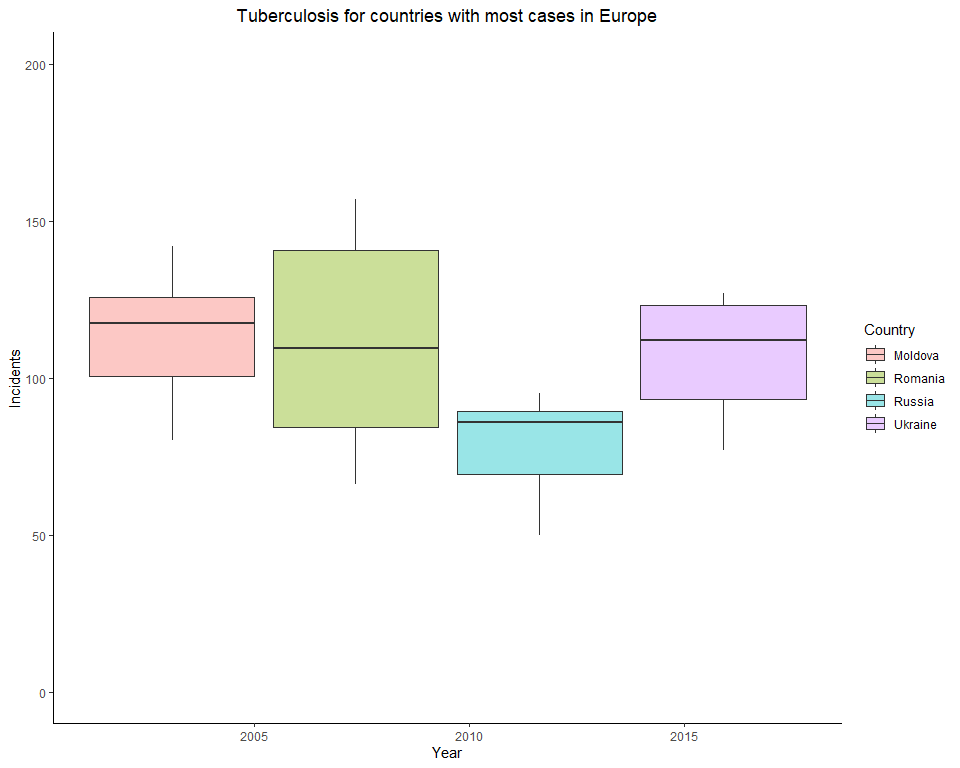
# Boxplot for Tuberculosis cases in SELECT countries in Asia  
Tuberculosis %>% filter(Continent == "Asia" & Country %in% c("Philippines","Myanmar")) %>% ggplot(aes(x = Year, y = Incidence, fill = Country)) + geom\_boxplot(outlier.shape = NA, alpha = 0.4) + coord\_cartesian(ylim = c(300,600)) + labs(title = 'Tuberculosis for countries with most cases in Asia', x = 'Year', y = 'Incidents')



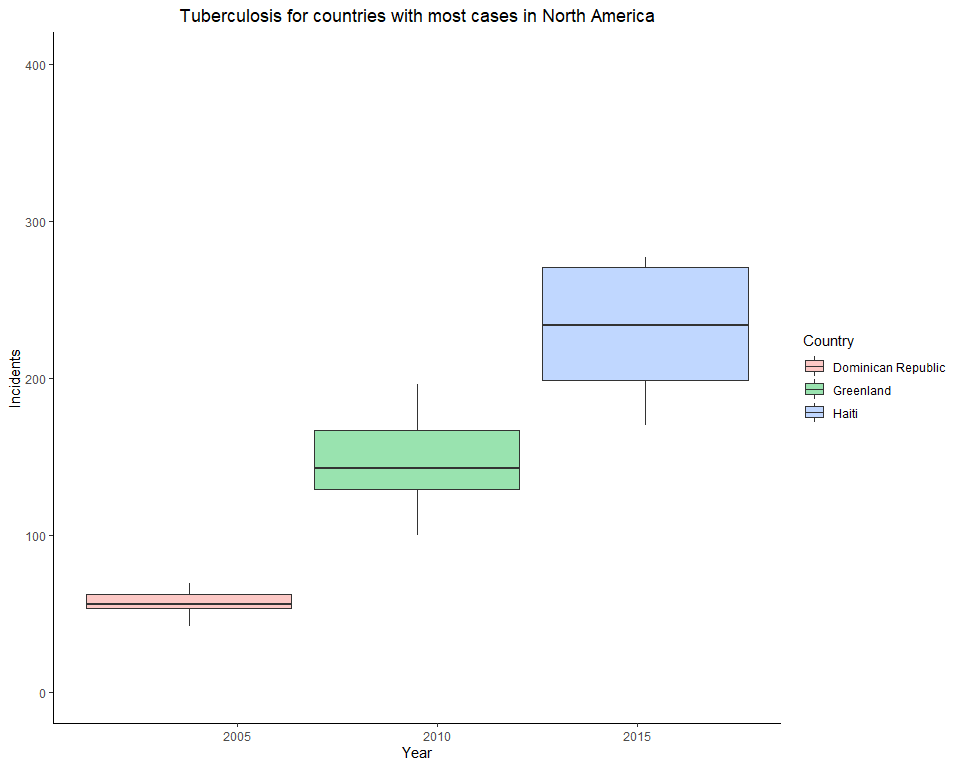
# Boxplot for Tuberculosis cases in SELECT countries in Africa  
Tuberculosis %>% filter(Continent == "Africa" & Country %in% c("Eswatini","South Africa","Lesotho","Namibia")) %>% ggplot(aes(x = Year, y = Incidence, fill = Country)) + geom\_boxplot(outlier.shape = NA, alpha = 0.4) + coord\_cartesian(ylim = c(0,2000)) + labs(title = 'Tuberculosis for countries with most cases in Africa', x = 'Year', y = 'Incidents')



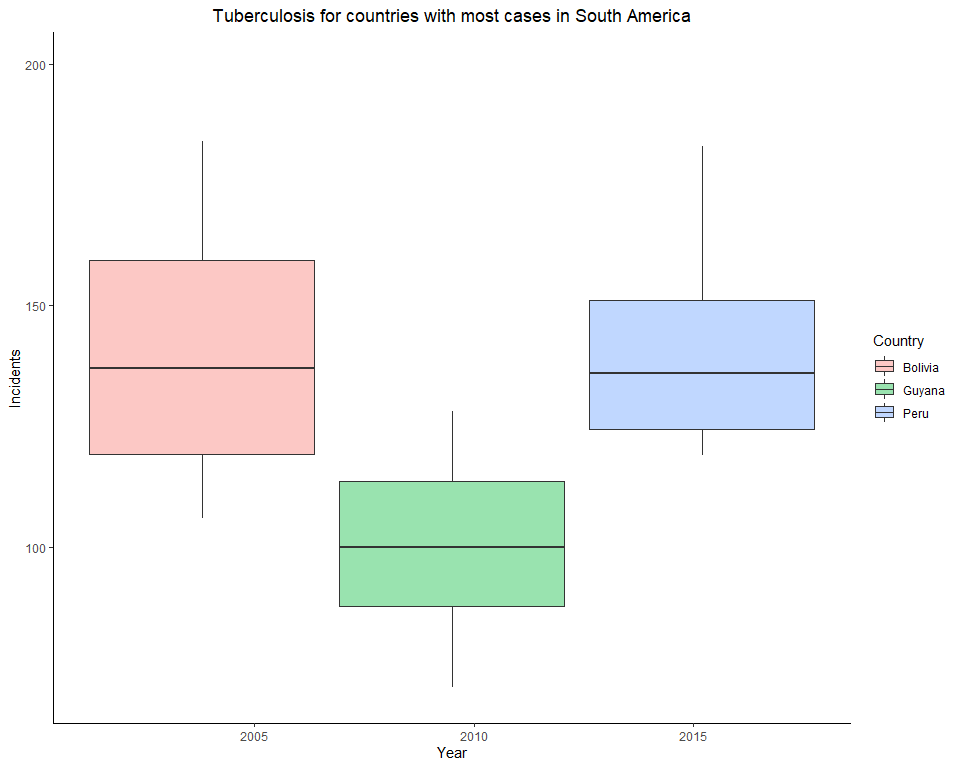
# Boxplot for Tuberculosis cases in SELECT countries in Europe  
Tuberculosis %>% filter(Continent == "Europe" & Country %in% c("Moldova","Romania","Ukraine","Russia")) %>% ggplot(aes(x = Year, y = Incidence, fill = Country)) + geom\_boxplot(outlier.shape = NA, alpha = 0.4) + coord\_cartesian(ylim = c(0,200)) + labs(title = 'Tuberculosis for countries with most cases in Europe', x = 'Year', y = 'Incidents')



# Boxplot for Tuberculosis cases in SELECT countries in North America  
Tuberculosis %>% filter(Continent == "North America" & Country %in% c("Haiti","Greenland","Dominican Republic")) %>% ggplot(aes(x = Year, y = Incidence, fill = Country)) + geom\_boxplot(outlier.shape = NA, alpha = 0.4) + coord\_cartesian(ylim = c(0,400)) + labs(title = 'Tuberculosis for countries with most cases in North America', x = 'Year', y = 'Incidents')



# Boxplot for Tuberculosis cases in SELECT countries in South America  
Tuberculosis %>% filter(Continent == "South America" & Country %in% c("Bolivia","Peru","Guyana")) %>% ggplot(aes(x = Year, y = Incidence, fill = Country)) + geom\_boxplot(outlier.shape = NA, alpha = 0.4) + coord\_cartesian(ylim = c(70,200)) + labs(title = 'Tuberculosis for countries with most cases in South America', x = 'Year', y = 'Incidents')



# !!!!!! Papua New Guinea DOESNT SHOW UP on boxplot !!!!!!!  
# Boxplot for Tuberculosis cases in SELECT countries in Oceania  
Tuberculosis %>% filter(Continent == "Oceania" & Country %in% c("Papua New Guinea","Kiribati","Marshall Islands")) %>% ggplot(aes(x = Year, y = Incidence, fill = Country)) + geom\_boxplot(outlier.shape = NA, alpha = 0.4) + coord\_cartesian(ylim = c(70,650)) + labs(title = 'Tuberculosis for countries with most cases in Oceania', x = 'Year', y = 'Incidents')

