Data Challenge for Natinal Data Managment Center

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2024-06-06

1. Preprocessing and EDA: Based on the given dataset(champs.csv) and the decoded variables in table 1, do the following preprocessing and Exploratory Data Analysis (EDA)

* **Ans:** First call or load necessary R packages from repository (CRAN)

library(dplyr)  
library(readr)  
require(corrplot)  
library(graphics)  
library(grDevices)  
library(caret)  
library(kernlab)  
library(randomForest)  
library(gbm)  
library(xgboost)  
library(e1071)  
library(pROC)  
library(ggplot2)  
library(pander)  
library(pandoc)  
library(tidyr)

A). read the dataset

**Ans:**

library(readr)  
df<- read\_csv("CHAMPS.csv")  
# View(CHAMPS)

B). How many rows and columns are they in the dataset?

**Ans:**

dimensions <- dim(df)  
num\_rows <- dimensions[1]  
num\_cols <- dimensions[2]  
dimensions

## [1] 444 381

rows <- nrow(df)  
rows

## [1] 444

cols <- ncol(df)

## The dataset has 444 rows and 381 columns.

C). Enumerate the columns of the dataset

**Ans:**

columns <- colnames(df)  
#columns

D). Rename the columns. Example: rename column dp\_013 to case\_type

**Ans:** Lets select only few columns to show these renaming challenges

df1 <- df %>% select(id\_ver\_nmb, champs\_id, dp\_013, dp\_108, dp\_118) %>%   
 rename(case\_type = dp\_013, underlying\_cause = dp\_108, maternal\_condition = dp\_118)  
head(df1,4)

## # A tibble: 4 × 5  
## id\_ver\_nmb champs\_id case\_type underlying\_cause maternal\_condition  
## <chr> <chr> <chr> <chr> <chr>   
## 1 2.0.0 ETAA00002 CH00716 Undetermined Undetermined   
## 2 2.0.0 ETAA00004 CH00716 Undetermined Undetermined   
## 3 2.0.0 ETAA00005 CH00716 Intrauterine hypoxia Fetus and newborn…  
## 4 2.0.0 ETAA00008 CH00719 Severe acute malnutrition -… <NA>

E). Rename values. Example: rename CH00716 to Stillbirth. Do the same for others too.

**Ans:** Lets check the levels of the variable exclusively

table(df1$case\_type)

##   
## CH00716 CH00718 CH00719 CH01404 CH01405 CH01406   
## 239 27 42 69 49 18

# Then using mutate we can recode as  
df2 <- df1 %>%  
 mutate(case\_type = recode(case\_type,  
 "CH00716" = "Stillbirth",  
 "CH01404" = "Death in the first 24 hours",  
 "CH01405" = "Early Neonate (1 to 6 days)",  
 "CH01406" = "Late Neonate (7 to 27 days)",  
 "CH00718" = "Infant (28 days to less than 12 months)",  
 "CH00719" = "Child (12 months to less than 60 months)"))  
# df2

* Rename error value Abruptio placenta under maternal\_condition(dp\_118) column

df2 <- df2 %>%  
 mutate(maternal\_condition = recode(maternal\_condition,  
 "Abruptio placenta" = "Abruption placenta"))

F). Show the proportion of null values in each column.

**Ans**: Calculate the proportion of null values in each column and summarize the proportions with rounded values and display only the first 5 or 6 results

pander(df2 %>%  
 summarise(across(everything(), ~ sum(is.na(.)) / nrow(df2))) %>%  
 gather(key = "variables", value = "Missing proportion") %>% head(10))

| variables | Missing proportion |
| --- | --- |
| id\_ver\_nmb | 0 |
| champs\_id | 0 |
| case\_type | 0 |
| underlying\_cause | 0 |
| maternal\_condition | 0.5563 |

## 2. Descriptive Data analysis: looking back to the dataset above

A). What are the magnitude and proportion of each of the infant underlying cause for child death?

Lets first remove missing value and then we should sorted by count/magnitude of underlying\_cause

underlying\_cause\_counts <- df2 %>%  
 filter(!is.na(underlying\_cause)) %>%  
 group\_by(underlying\_cause) %>%  
 summarize(count = n()) %>%  
 mutate(proportion = round((count / sum(count)) \* 100, 3)) %>%  
 arrange(desc(count))   
pander(head(underlying\_cause\_counts, 4))

| underlying\_cause | count | proportion |
| --- | --- | --- |
| Intrauterine hypoxia | 153 | 34.46 |
| Birth asphyxia | 33 | 7.432 |
| Undetermined | 28 | 6.306 |
| Severe acute malnutrition | 27 | 6.081 |

However the third top of proportion is the value of **undetermined** and is not underling cause while it is indicating missing values. So I strongly belive that I should remove it before going to any further analysis.

# Remove the third row  
underlying\_cause\_counts <- underlying\_cause\_counts[c(1, 2, 4:97), ]  
pander(head(underlying\_cause\_counts, 4))

| underlying\_cause | count | proportion |
| --- | --- | --- |
| Intrauterine hypoxia | 153 | 34.46 |
| Birth asphyxia | 33 | 7.432 |
| Severe acute malnutrition | 27 | 6.081 |
| Craniorachischisis | 17 | 3.829 |

## B. What are the proportion and magnitude of the maternal factors contributing for child death?

* To calculate proportion I first removed missing observation even not affected the result and show the first top count value by order counts in descending order.

sort\_maternal\_condition\_counts <- df2 %>%  
 filter(!is.na(maternal\_condition)) %>%  
 group\_by(maternal\_condition) %>%  
 summarize(count = n()) %>%  
 mutate(proportion = count / sum(count)) %>%  
 arrange(desc(count))   
pander(head(sort\_maternal\_condition\_counts, 4))

| maternal\_condition | count | proportion |
| --- | --- | --- |
| Preeclampsia | 36 | 0.1827 |
| Twin pregnancy | 12 | 0.06091 |
| Fetus and newborn affected by other forms of placental separation and hemorrhage (Abruption placenta) | 11 | 0.05584 |
| Eclampsia | 9 | 0.04569 |

## C. What are the proportion of the child death by the case type

chprop <- df2 %>%  
 filter(!is.na(case\_type)) %>%  
 group\_by(case\_type) %>%  
 summarize(count = n()) %>%  
 mutate(proportion = round((count / sum(count)) \* 100, 3)) %>%  
 arrange(desc(count))   
pander(head(chprop))

| case\_type | count | proportion |
| --- | --- | --- |
| Stillbirth | 239 | 53.83 |
| Death in the first 24 hours | 69 | 15.54 |
| Early Neonate (1 to 6 days) | 49 | 11.04 |
| Child (12 months to less than 60 months) | 42 | 9.459 |
| Infant (28 days to less than 12 months) | 27 | 6.081 |
| Late Neonate (7 to 27 days) | 18 | 4.054 |

1. Correlation analysis: Using correlation or Heat Maps, show how each of the infant under lying conditions and maternal factors are correlated to the top three causes of the child death identified above under 2(A)

to extract only top underlying cause and maternal factors

top\_3\_causes <- underlying\_cause\_counts[1:3, ]  
pander(top\_3\_causes)

| underlying\_cause | count | proportion |
| --- | --- | --- |
| Intrauterine hypoxia | 153 | 34.46 |
| Birth asphyxia | 33 | 7.432 |
| Severe acute malnutrition | 27 | 6.081 |

top\_factor<-sort\_maternal\_condition\_counts[1:3,]  
pander(top\_factor)

| maternal\_condition | count | proportion |
| --- | --- | --- |
| Preeclampsia | 36 | 0.1827 |
| Twin pregnancy | 12 | 0.06091 |
| Fetus and newborn affected by other forms of placental separation and hemorrhage (Abruption placenta) | 11 | 0.05584 |

top\_causes\_list <- top\_3\_causes$underlying\_cause  
pander(top\_causes\_list)

*Intrauterine hypoxia*, *Birth asphyxia* and *Severe acute malnutrition*

df\_top\_causes <- df2 %>%  
 filter(underlying\_cause %in% top\_causes\_list)  
df\_top\_causes\_numeric <- df\_top\_causes %>%  
 mutate(  
 case\_type = as.numeric(factor(case\_type)),  
 underlying\_cause = as.numeric(factor(underlying\_cause)),  
 maternal\_condition = as.numeric(factor(maternal\_condition)))

## correlation analysis

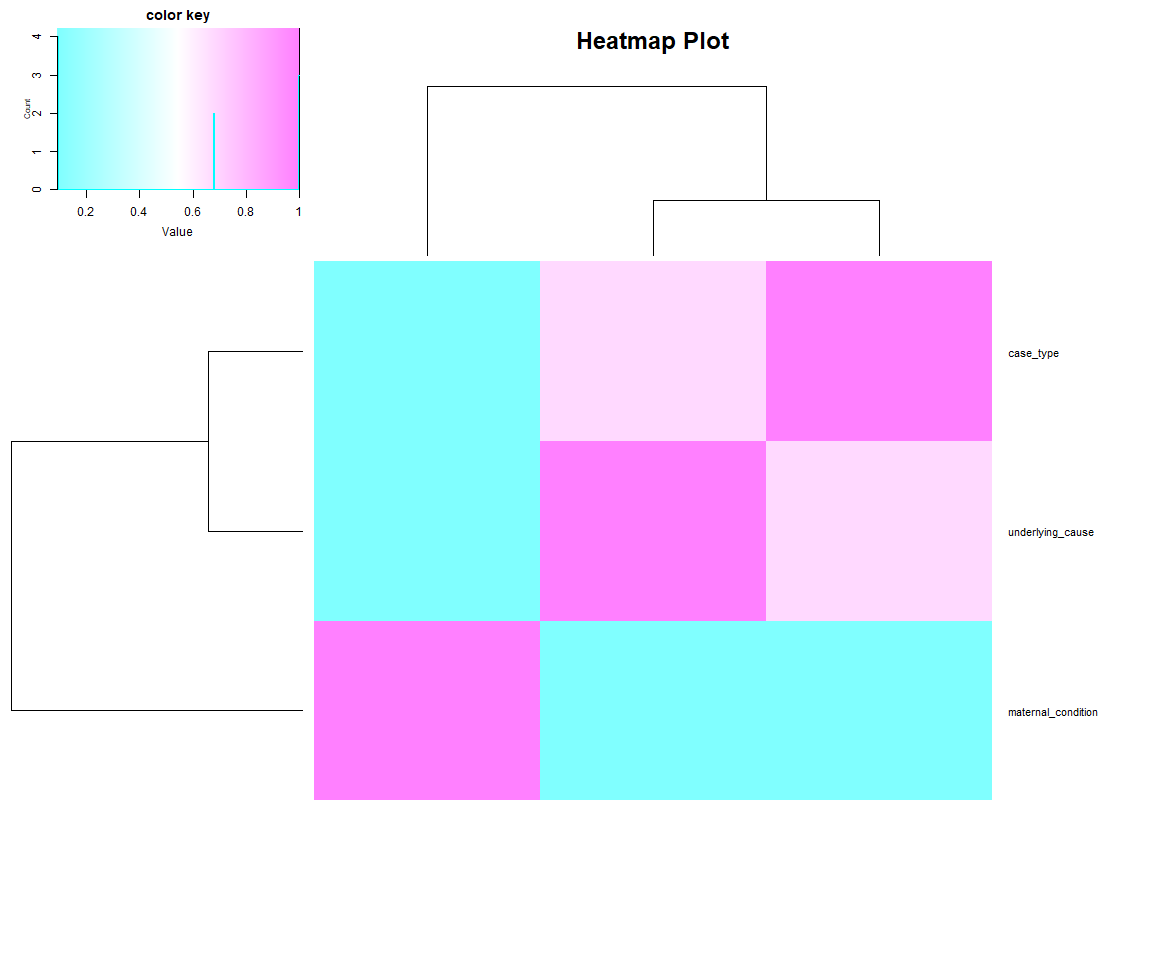
cor\_matrix <- cor(df\_top\_causes\_numeric[, c('case\_type', 'underlying\_cause', 'maternal\_condition')], use = "complete.obs")  
  
pander(print(cor\_matrix))

case\_type underlying\_cause maternal\_condition

case\_type 1.00000000 0.6783914 0.09447408 underlying\_cause 0.67839136 1.0000000 0.09277980 maternal\_condition 0.09447408 0.0927798 1.00000000

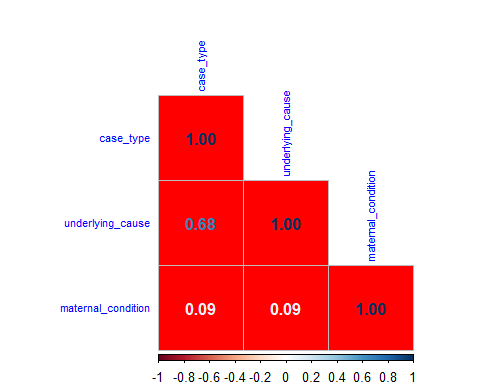
|  | case\_type | underlying\_cause | maternal\_condition |
| --- | --- | --- | --- |
| **case\_type** | 1 | 0.6784 | 0.09447 |
| **underlying\_cause** | 0.6784 | 1 | 0.09278 |
| **maternal\_condition** | 0.09447 | 0.09278 | 1 |

library(gplots)  
heatmap.2(cor\_matrix, col = cm.colors(256), margins = c(10, 10),   
 xlab = NULL, ylab = NULL, main = "Heatmap Plot", trace = "none",   
 key = TRUE, cexRow = 0.8, cexCol = 0.8, key.title = "color key", labCol = F)



## or

corrplot(cor\_matrix, method = "number", type = "lower", tl.cex = 0.7, tl.col = "blue",bg ="red" ,diag = TRUE,)



top\_infant\_causes<- head(underlying\_cause\_counts[order(-underlying\_cause\_counts$count),],6)

1. Feature engineering:
2. Select the classification models *Logistic Regression, Support Vector Machine, AdaBoostClassifier, Random Forest Classifier , Gradient Boosting Classifier and XGBOOST* and train each on the dataset
3. Import the appropriate package for each of the classification models above
4. Rank the features based on their importance for each of the top underlying causes of child death identified above under 2(A), for each of the classification algorithms under (A )

**Ans:** Here what we do is select the best features (infant underlying causes and maternal factors) that contribute to the top three causes of child death that we identified in step 2A. Therefore let us select variables and remove missing values completely.

# A. Import the appropriate package for each of the classification models  
library(caret)  
library(randomForest)  
library(gbm)  
library(xgboost)  
library(e1071)  
library(glmnet)  
library(pROC)  
  
# Prepare data  
df\_model <- df\_top\_causes\_numeric %>%  
 select(case\_type, underlying\_cause, maternal\_condition) %>%  
 na.omit()  
  
df\_model$case\_type <- as.factor(df\_model$case\_type)  
df\_model$underlying\_cause <- as.factor(df\_model$underlying\_cause)  
df\_model$maternal\_condition <- as.factor(df\_model$maternal\_condition)

classification data as train data (70%) and test data (30%)

set.seed(12345)  
trainIndex <- createDataPartition(df\_model$case\_type, p = 0.7, list = FALSE, times = 1)  
trainData <- df\_model[trainIndex, ]  
testData <- df\_model[-trainIndex, ]

Train classification models

# Define control  
control <- trainControl(method = "cv", number = 10)  
models <- list()  
  
# Logistic Regression  
models$logistic\_multinomial <- train(underlying\_cause ~ ., data = trainData,  
 method = "multinom", trControl = control)

## # weights: 183 (120 variable)  
## initial value 83.494534   
## iter 10 value 3.411747  
## iter 20 value 2.775335  
## iter 30 value 2.772593  
## final value 2.772589   
## converged  
## # weights: 183 (120 variable)  
## initial value 83.494534   
## iter 10 value 13.188116  
## final value 13.169485   
## converged  
## # weights: 183 (120 variable)  
## initial value 83.494534   
## iter 10 value 3.460893  
## iter 20 value 2.961297  
## iter 30 value 2.932773  
## iter 40 value 2.923729  
## iter 50 value 2.916974  
## iter 60 value 2.914077  
## iter 70 value 2.911490  
## iter 80 value 2.910702  
## iter 90 value 2.910003  
## iter 100 value 2.909865  
## final value 2.909865   
## stopped after 100 iterations  
## # weights: 183 (120 variable)  
## initial value 84.593146   
## iter 10 value 3.417234  
## iter 20 value 2.776119  
## iter 30 value 2.772594  
## final value 2.772589   
## converged  
## # weights: 183 (120 variable)  
## initial value 84.593146   
## iter 10 value 12.850822  
## final value 12.831802   
## converged  
## # weights: 183 (120 variable)  
## initial value 84.593146   
## iter 10 value 3.465317  
## iter 20 value 2.958435  
## iter 30 value 2.931043  
## iter 40 value 2.920987  
## iter 50 value 2.913106  
## iter 60 value 2.909641  
## iter 70 value 2.908852  
## iter 80 value 2.908210  
## iter 90 value 2.907679  
## iter 100 value 2.907589  
## final value 2.907589   
## stopped after 100 iterations  
## # weights: 183 (120 variable)  
## initial value 84.593146   
## iter 10 value 1.974309  
## iter 20 value 1.390814  
## iter 30 value 1.386301  
## final value 1.386294   
## converged  
## # weights: 183 (120 variable)  
## initial value 84.593146   
## iter 10 value 11.938667  
## iter 20 value 11.886836  
## final value 11.886836   
## converged  
## # weights: 183 (120 variable)  
## initial value 84.593146   
## iter 10 value 2.027098  
## iter 20 value 1.575700  
## iter 30 value 1.542402  
## iter 40 value 1.536798  
## iter 50 value 1.529630  
## iter 60 value 1.526397  
## iter 70 value 1.525207  
## iter 80 value 1.524724  
## iter 90 value 1.524010  
## iter 100 value 1.523822  
## final value 1.523822   
## stopped after 100 iterations  
## # weights: 183 (120 variable)  
## initial value 84.593146   
## iter 10 value 3.368649  
## iter 20 value 2.774808  
## iter 30 value 2.772592  
## final value 2.772589   
## converged  
## # weights: 183 (120 variable)  
## initial value 84.593146   
## iter 10 value 12.706833  
## final value 12.690968   
## converged  
## # weights: 183 (120 variable)  
## initial value 84.593146   
## iter 10 value 3.413769  
## iter 20 value 2.944795  
## iter 30 value 2.916012  
## iter 40 value 2.909522  
## iter 50 value 2.902100  
## iter 60 value 2.899881  
## iter 70 value 2.897714  
## iter 80 value 2.896944  
## iter 90 value 2.896220  
## iter 100 value 2.896095  
## final value 2.896095   
## stopped after 100 iterations  
## # weights: 183 (120 variable)  
## initial value 84.593146   
## iter 10 value 2.518530  
## iter 20 value 1.914797  
## iter 30 value 1.909549  
## final value 1.909543   
## converged  
## # weights: 183 (120 variable)  
## initial value 84.593146   
## iter 10 value 12.133221  
## final value 12.112734   
## converged  
## # weights: 183 (120 variable)  
## initial value 84.593146   
## iter 10 value 2.568387  
## iter 20 value 2.098466  
## iter 30 value 2.070515  
## iter 40 value 2.057272  
## iter 50 value 2.051511  
## iter 60 value 2.048420  
## iter 70 value 2.046098  
## iter 80 value 2.045329  
## iter 90 value 2.044721  
## iter 100 value 2.044595  
## final value 2.044595   
## stopped after 100 iterations  
## # weights: 61 (60 variable)  
## initial value 51.986039   
## iter 10 value 2.268458  
## iter 20 value 1.910258  
## iter 30 value 1.909543  
## final value 1.909543   
## converged  
## # weights: 61 (60 variable)  
## initial value 51.986039   
## iter 10 value 9.570115  
## final value 9.568037   
## converged  
## # weights: 61 (60 variable)  
## initial value 51.986039   
## iter 10 value 2.322696  
## iter 20 value 2.044814  
## iter 30 value 2.035815  
## iter 40 value 2.031253  
## iter 50 value 2.027833  
## iter 60 value 2.025412  
## iter 70 value 2.025252  
## iter 80 value 2.025201  
## final value 2.025181   
## converged  
## # weights: 183 (120 variable)  
## initial value 84.593146   
## iter 10 value 3.369928  
## iter 20 value 2.774749  
## iter 30 value 2.772592  
## final value 2.772589   
## converged  
## # weights: 183 (120 variable)  
## initial value 84.593146   
## iter 10 value 12.692492  
## final value 12.677391   
## converged  
## # weights: 183 (120 variable)  
## initial value 84.593146   
## iter 10 value 3.414877  
## iter 20 value 2.945500  
## iter 30 value 2.916587  
## iter 40 value 2.909831  
## iter 50 value 2.902028  
## iter 60 value 2.899833  
## iter 70 value 2.897660  
## iter 80 value 2.896897  
## iter 90 value 2.896160  
## iter 100 value 2.896039  
## final value 2.896039   
## stopped after 100 iterations  
## # weights: 183 (120 variable)  
## initial value 83.494534   
## iter 10 value 3.120712  
## iter 20 value 2.773972  
## iter 30 value 2.772591  
## final value 2.772589   
## converged  
## # weights: 183 (120 variable)  
## initial value 83.494534   
## iter 10 value 11.465518  
## iter 20 value 11.421273  
## iter 20 value 11.421273  
## iter 20 value 11.421273  
## final value 11.421273   
## converged  
## # weights: 183 (120 variable)  
## initial value 83.494534   
## iter 10 value 3.159784  
## iter 20 value 2.898821  
## iter 30 value 2.871782  
## iter 40 value 2.860481  
## iter 50 value 2.857046  
## iter 60 value 2.855085  
## iter 70 value 2.854386  
## iter 80 value 2.853899  
## iter 90 value 2.853755  
## iter 100 value 2.853689  
## final value 2.853689   
## stopped after 100 iterations  
## # weights: 183 (120 variable)  
## initial value 83.494534   
## iter 10 value 3.385640  
## iter 20 value 2.774441  
## iter 30 value 2.772592  
## final value 2.772589   
## converged  
## # weights: 183 (120 variable)  
## initial value 83.494534   
## iter 10 value 12.380090  
## final value 12.362171   
## converged  
## # weights: 183 (120 variable)  
## initial value 83.494534   
## iter 10 value 3.434699  
## iter 20 value 2.952829  
## iter 30 value 2.931546  
## iter 40 value 2.919660  
## iter 50 value 2.912396  
## iter 60 value 2.907229  
## iter 70 value 2.906732  
## iter 80 value 2.906078  
## iter 90 value 2.905709  
## iter 100 value 2.905509  
## final value 2.905509   
## stopped after 100 iterations  
## # weights: 183 (120 variable)  
## initial value 84.593146   
## iter 10 value 3.401799  
## iter 20 value 2.775484  
## iter 30 value 2.772593  
## final value 2.772589   
## converged  
## # weights: 183 (120 variable)  
## initial value 84.593146   
## iter 10 value 13.180080  
## final value 13.163130   
## converged  
## # weights: 183 (120 variable)  
## initial value 84.593146   
## iter 10 value 3.450895  
## iter 20 value 2.959214  
## iter 30 value 2.934048  
## iter 40 value 2.925553  
## iter 50 value 2.916735  
## iter 60 value 2.913466  
## iter 70 value 2.911096  
## iter 80 value 2.910509  
## iter 90 value 2.909747  
## iter 100 value 2.909556  
## final value 2.909556   
## stopped after 100 iterations  
## # weights: 183 (120 variable)  
## initial value 93.382045   
## iter 10 value 3.538674  
## iter 20 value 2.966966  
## iter 30 value 2.932529  
## iter 40 value 2.924327  
## iter 50 value 2.916249  
## iter 60 value 2.913962  
## iter 70 value 2.912020  
## iter 80 value 2.911323  
## iter 90 value 2.910553  
## iter 100 value 2.910428  
## final value 2.910428   
## stopped after 100 iterations

# Support Vector Machine  
models$svm <- train(underlying\_cause ~ ., data = trainData, method = "svmRadial", trControl = control)  
  
# Random Forest  
models$random\_forest <- train(underlying\_cause ~ ., data = trainData, method = "rf", trControl = control)  
  
# Gradient Boosting Classifier  
models$gbm <- train(underlying\_cause ~ ., data = trainData, method = "gbm", trControl = control, verbose = FALSE)  
  
# XGBoost  
models$xgboost <- train(underlying\_cause ~ ., data = trainData, method = "xgbTree", trControl = control)

## [14:29:59] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:29:59] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:00] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:00] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:00] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
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## [14:30:00] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:00] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:01] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:01] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:01] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:01] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:01] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:01] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:02] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:02] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
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## [14:30:02] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:03] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:03] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:03] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:03] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:04] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:04] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:04] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:04] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:05] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:30:05] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
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## [14:32:40] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.  
## [14:32:40] WARNING: src/c\_api/c\_api.cc:935: `ntree\_limit` is deprecated, use `iteration\_range` instead.

Rank features based on their importance

library(caret)  
library(gbm)  
library(xgboost)  
  
# Function to get feature importance  
get\_feature\_importance <- function(model) {  
 if (inherits(model$finalModel, "randomForest")) {  
 importance(model$finalModel)  
 } else if (inherits(model$finalModel, "gbm")) {  
 summary(model$finalModel, plotit = FALSE)$importance  
 } else if (inherits(model$finalModel, "xgb.Booster")) {  
 xgb.importance(model = model$finalModel)  
 } else if (inherits(model$finalModel, "glmnet")) {  
 coef(model$finalModel) # For glmnet (Lasso/Ridge) models  
 } else {  
 NULL # For models without feature importance  
 }  
}  
  
# Get feature importance for each model  
feature\_importance <- lapply(models, get\_feature\_importance)  
  
# Print feature importance  
 pander(head(feature\_importance))

* **logistic\_multinomial**:
* **svm**:
* **random\_forest**:

|  | MeanDecreaseGini |
| --- | --- |
| **case\_type3** | 3.162 |
| **case\_type4** | 0.7581 |
| **case\_type5** | 11.02 |
| **maternal\_condition2** | 0.3095 |
| **maternal\_condition3** | 0.7852 |
| **maternal\_condition4** | 0.0003091 |
| **maternal\_condition5** | 0.01594 |
| **maternal\_condition6** | 4.58e-05 |
| **maternal\_condition7** | 0 |
| **maternal\_condition8** | 0 |
| **maternal\_condition9** | 0 |
| **maternal\_condition10** | 0.8312 |
| **maternal\_condition11** | 0.1203 |
| **maternal\_condition12** | 0.6994 |
| **maternal\_condition13** | 0 |
| **maternal\_condition14** | 0 |
| **maternal\_condition15** | 0 |
| **maternal\_condition16** | 0 |
| **maternal\_condition17** | 0 |
| **maternal\_condition18** | 0.0003249 |
| **maternal\_condition19** | 0 |
| **maternal\_condition20** | 0 |
| **maternal\_condition21** | 2.237e-05 |
| **maternal\_condition22** | 0.0001503 |
| **maternal\_condition23** | 0 |
| **maternal\_condition24** | 1.481e-05 |
| **maternal\_condition25** | 1.389e-05 |
| **maternal\_condition26** | 0 |
| **maternal\_condition27** | 0.3993 |
| **maternal\_condition28** | 0.3881 |
| **maternal\_condition29** | 0 |
| **maternal\_condition30** | 0.0003713 |
| **maternal\_condition31** | 0.7907 |
| **maternal\_condition32** | 0.005734 |
| **maternal\_condition33** | 0 |
| **maternal\_condition34** | 0 |
| **maternal\_condition35** | 0 |
| **maternal\_condition36** | 0 |
| **maternal\_condition37** | 0 |
| **maternal\_condition38** | 0 |
| **maternal\_condition39** | 0.1747 |
| **maternal\_condition40** | 0 |
| **maternal\_condition41** | 6.977e-06 |
| **maternal\_condition42** | 0 |
| **maternal\_condition43** | 0 |
| **maternal\_condition44** | 0.08877 |
| **maternal\_condition45** | 0 |
| **maternal\_condition46** | 0 |
| **maternal\_condition47** | 0.769 |
| **maternal\_condition48** | 0 |
| **maternal\_condition49** | 0 |
| **maternal\_condition50** | 0 |
| **maternal\_condition51** | 0 |
| **maternal\_condition52** | 0.7339 |
| **maternal\_condition53** | 0 |
| **maternal\_condition54** | 0 |
| **maternal\_condition55** | 0 |
| **maternal\_condition56** | 4.237e-05 |
| **maternal\_condition57** | 0.2506 |

* **gbm**:
* **xgboost**:

| Feature | Gain | Cover | Frequency |
| --- | --- | --- | --- |
| case\_type5 | 0.796 | 0.5908 | 0.5333 |
| case\_type3 | 0.1556 | 0.1738 | 0.1333 |
| maternal\_condition52 | 0.04686 | 0.2121 | 0.32 |
| maternal\_condition32 | 0.001608 | 0.02332 | 0.01333 |

------------------------------------------------------  
 Feature Gain Cover Frequency  
---------------------- --------- --------- -----------  
 case\_type5 0.8226 0.659 0.58  
  
 case\_type3 0.1257 0.1224 0.14  
  
 maternal\_condition52 0.04242 0.1636 0.24  
  
 maternal\_condition32 0.00927 0.05498 0.04  
------------------------------------------------------

1. Model evaluation using the proper metrics

A. Import the appropriate evaluation metric packages

B. Using the appropriate n-fold cross validation and out of sample data, select the best preforming model from the candidate models under 4(A)

C. Ensemble the models and see the performance of the combination models on the data

D. Use Accuracy score metrics to evaluate the performance of the models above

E. Plot the AUC and ROC curve on the same graph to visualize and compare the performance of each of the models above

**Ans:**

# Import evaluation metric packages  
library(pROC)  
library(caret)  
# Predict and evaluate models  
results <- lapply(models, predict, newdata = testData)  
accuracy <- sapply(results, function(pred) {  
 mean(pred == testData$underlying\_cause)  
})  
  
# Print accuracy of individual models  
pander(accuracy)

| logistic\_multinomial | svm | random\_forest | gbm | xgboost |
| --- | --- | --- | --- | --- |
| 0.8824 | 0.8824 | 0.8824 | 0.8824 | 0.9118 |

# Ensemble the models using majority voting  
ensemble\_pred <- apply(do.call(cbind, results), 1, function(row) {  
 as.numeric(names(sort(table(row), decreasing = TRUE))[1])  
})  
ensemble\_accuracy <- mean(ensemble\_pred == testData$underlying\_cause)  
pander(ensemble\_accuracy)

*0.8824*

then we can ase Accuracy score metrics to evaluate the performance of the models above

accuracy\_metrics <- sapply(results, function(pred) {  
 confusionMatrix(pred, testData$underlying\_cause)$overall['Accuracy']  
})  
panderOptions('table.split.table', 120)  
pander(accuracy\_metrics)

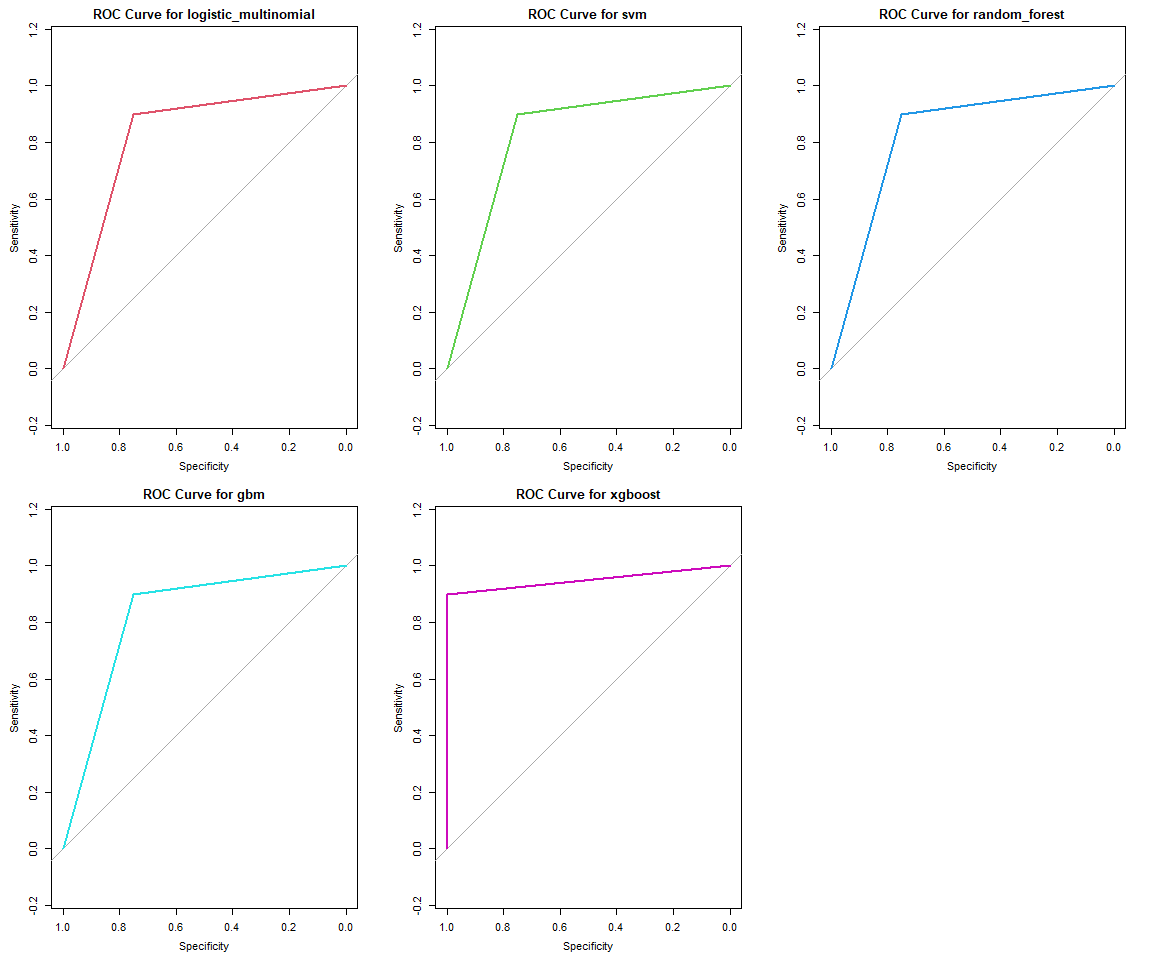
| logistic\_multinomial.Accuracy | svm.Accuracy | random\_forest.Accuracy | gbm.Accuracy | xgboost.Accuracy |
| --- | --- | --- | --- | --- |
| 0.8824 | 0.8824 | 0.8824 | 0.8824 | 0.9118 |

## Plot AUC and ROC curves

roc\_data <- lapply(results, function(pred) {  
 roc(testData$underlying\_cause, as.numeric(pred))  
})

## Plot ROC curves

par(mfrow = c(2, 3))  
for (i in 1:length(roc\_data)) {  
 plot(roc\_data[[i]], col = i + 1, main = paste("ROC Curve for", names(models)[i]))  
}



1. Result Visualization: Import the appropriate visualization package and:

A. Plot the feature importance in descending order for each of the models using horizontal bar chart

B. Plot the top five infant underlying causes of the child death

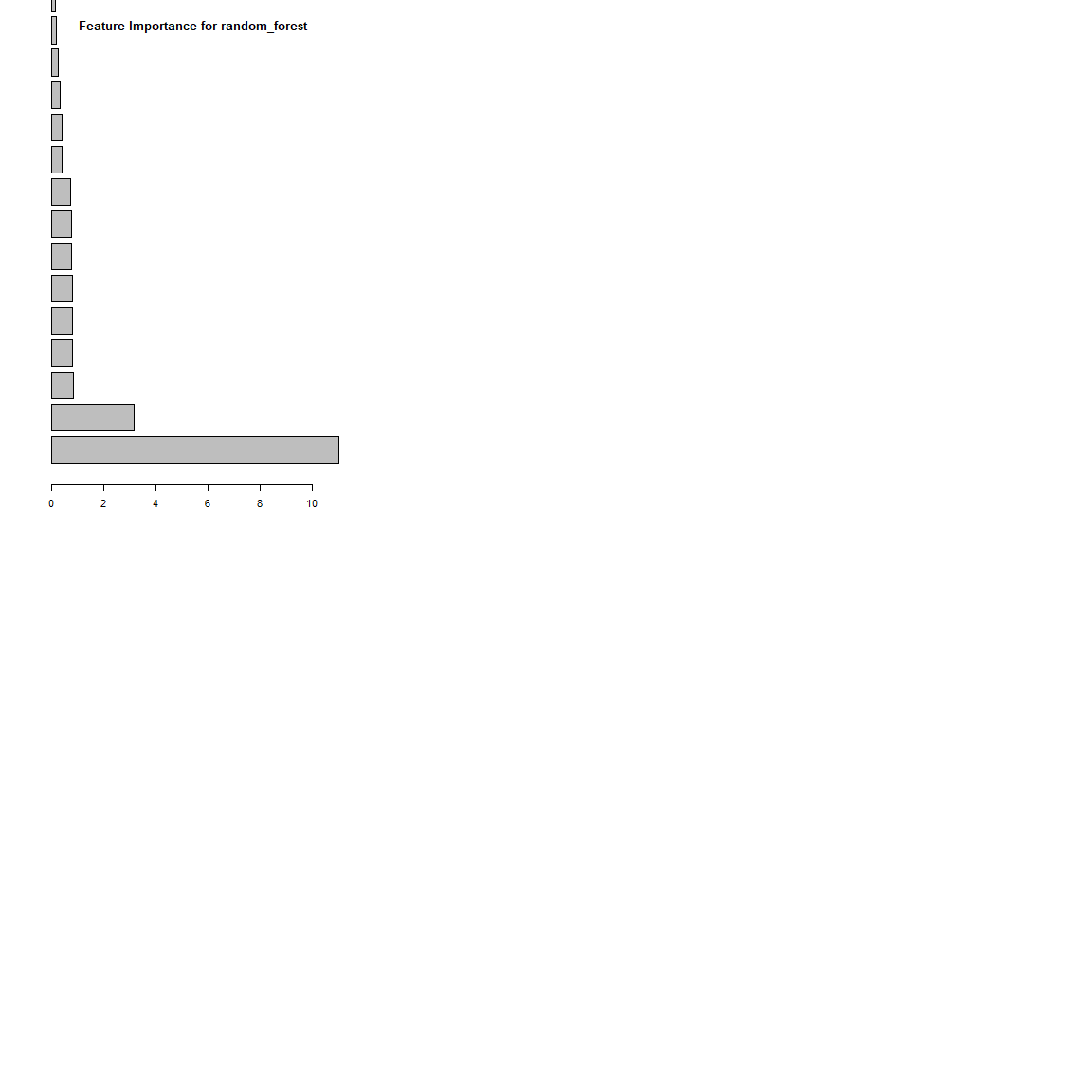
C. Plot the top five maternal factors contributing to the child death

D. Plot the child death based on the case types

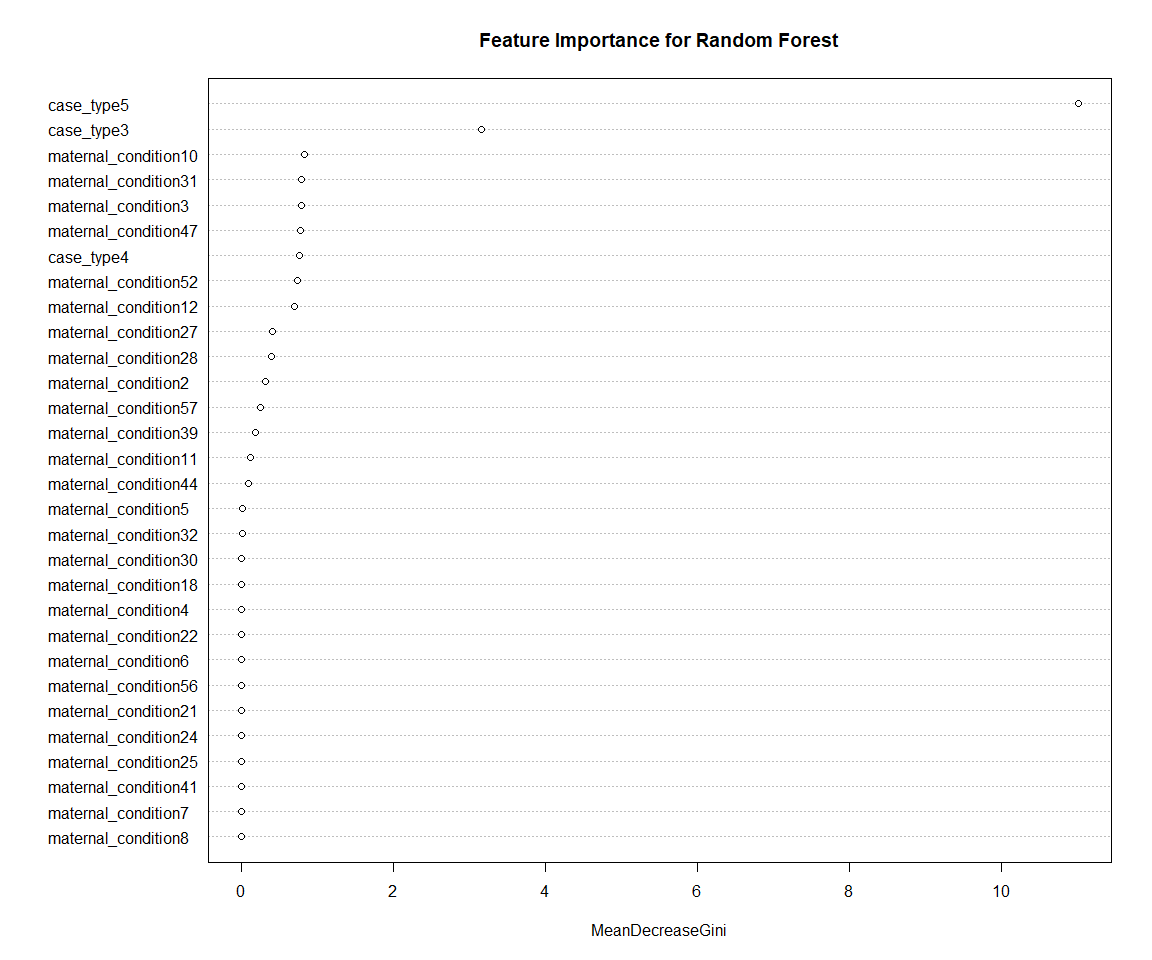
# Plot feature importance for each model  
par(mfrow = c(2, 3))  
for (model\_name in names(models)) {  
 importance <- feature\_importance[[model\_name]]  
 if (is.numeric(importance)) {  
 barplot(sort(importance, decreasing = TRUE), horiz = TRUE,ylim = c(0, 15), main = paste("Feature Importance for", model\_name))  
 } else {  
 print(paste())  
 }  
}

## character(0)  
## character(0)

## character(0)  
## character(0)



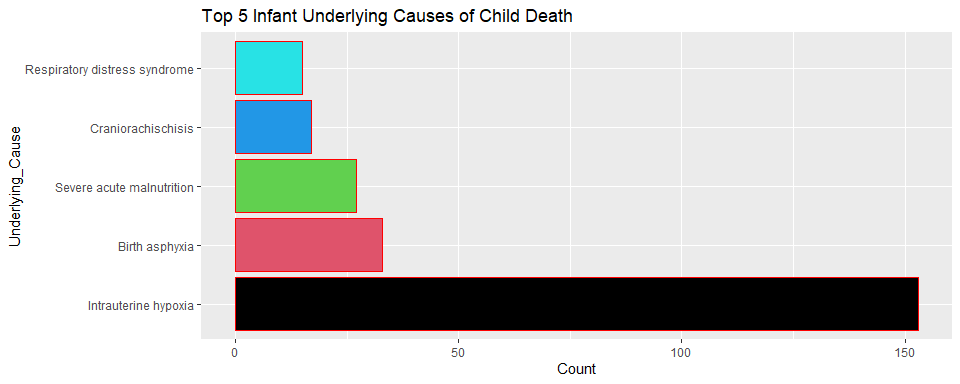
varImpPlot(models$random\_forest$finalModel, main = "Feature Importance for Random Forest")



## Plot top five infant underlying causes of child death

top\_infant\_causes<-top\_infant\_causes[1:5,]

ggplot(top\_infant\_causes, aes(x = reorder(underlying\_cause, -count) , y = count )) +  
 geom\_bar(stat = "identity", fill = 1:5 , colour = "red") +  
 coord\_flip() +   
 labs(title = "Top 5 Infant Underlying Causes of Child Death",  
 x = "Underlying\_Cause",  
 y = "Count")



## Plot top five maternal factors contributing to child death

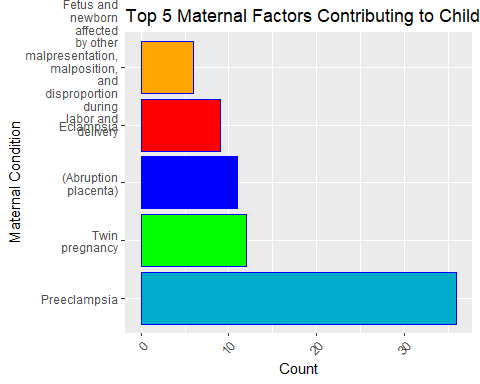
top\_maternal\_factors <- head(sort\_maternal\_condition\_counts[order(-sort\_maternal\_condition\_counts$count), ], 6)

top\_maternal\_factors<-top\_maternal\_factors[1:5,]

top\_maternal\_factors<- top\_maternal\_factors %>%  
 mutate(maternal\_condition = recode(maternal\_condition,  
 "Fetus and newborn affected by other forms of placental separation and hemorrhage (Abruption placenta)" =   
 "(Abruption placenta)"))

top\_maternal\_factors<- top\_maternal\_factors %>%  
 mutate(maternal\_condition = recode(maternal\_condition, "Fetus and newborn affected by other forms of placental separation and hemorrhage" = "(F & N affected by PSH)"))

library(ggplot2)  
library(stringr)  
  
ggplot(top\_maternal\_factors, aes(x = reorder(maternal\_condition, -count), y = count)) +  
 geom\_bar(stat = "identity", fill = c("#00abcc","green", "blue", "red", "orange"), colour = "blue") +  
 coord\_flip() +  
 labs(  
 title = "Top 5 Maternal Factors Contributing to Child Death",  
 x = "Maternal Condition",  
 y = "Count"  
 ) +  
 theme(axis.text.x = element\_text(angle = 45, hjust = 1)) +  
 scale\_x\_discrete(labels = function(x) str\_wrap(x, width = 10))



## Plot distribution of child deaths based on case types

ggplot(top\_infant\_causes, aes(x = reorder(underlying\_cause, -count), y = count)) +  
 geom\_bar(stat = "identity" , fill = c("#00abcc","green", "blue", "red", "orange") , colour = "red") +  
 coord\_flip() +  
 labs(title = "Distribution of Child Death by Case Type",  
 x = "Case Type",  
 y = "Count")

