MDRO

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title: “Irene Data analysis” author: “Mwaura Patrick” date: “1/27/2021” output: word\_document: default pdf\_document: default html\_document: default —

options( warn = -1 )  
library(tidyverse)

## -- Attaching packages --------------------------------------- tidyverse 1.3.0 --

## v ggplot2 3.3.3 v purrr 0.3.4  
## v tibble 3.0.5 v dplyr 1.0.3  
## v tidyr 1.1.2 v stringr 1.4.0  
## v readr 1.4.0 v forcats 0.5.0

## -- Conflicts ------------------------------------------ tidyverse\_conflicts() --  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag() masks stats::lag()

library(dplyr)  
library(readxl)  
library(here)

## here() starts at E:/RESULTS/Mwaura/mwaura/WORK1/Covid19

library(skimr)  
library(kableExtra)

##   
## Attaching package: 'kableExtra'

## The following object is masked from 'package:dplyr':  
##   
## group\_rows

library(AMR)  
library(scales)

##   
## Attaching package: 'scales'

## The following object is masked from 'package:purrr':  
##   
## discard

## The following object is masked from 'package:readr':  
##   
## col\_factor

library(pipeR)  
library(cleaner)

# Set the working directory and load the data

setwd("E:/RESULTS/Mwaura/mwaura/WORK1/Covid19/Irene Work")  
IRENE\_DATA\_ANALYSIS\_R <- read\_csv("IRENE DATA ANALYSIS R.csv")

##   
## -- Column specification --------------------------------------------------------  
## cols(  
## .default = col\_character(),  
## CAMEL\_ID\_NUMBER = col\_double(),  
## MDR = col\_double()  
## )  
## i Use `spec()` for the full column specifications.

# Explore the data

#skimr::skim(IRENE\_DATA\_ANALYSIS\_R)

# Brief summary

knitr::kable(IRENE\_DATA\_ANALYSIS\_R %>% select(mo,CAMEL\_ID\_NUMBER) %>% group\_by(mo) %>% summarize(Count=n()) %>% mutate(Percentage=paste0(round(Count/sum(Count)\*100,2),"%")),"pipe")

|  |  |  |
| --- | --- | --- |
| mo | Count | Percentage |
| enterobacter | 3 | 0.99% |
| Escherichia coli | 136 | 45.03% |
| no growth | 141 | 46.69% |
| non-Escherichia coli | 22 | 7.28% |

knitr::kable(IRENE\_DATA\_ANALYSIS\_R %>% freq(mo))

item

count

percent

cum\_count

cum\_percent

no growth

141

0.4668874

141

0.4668874

Escherichia coli

136

0.4503311

277

0.9172185

non-Escherichia coli

22

0.0728477

299

0.9900662

enterobacter

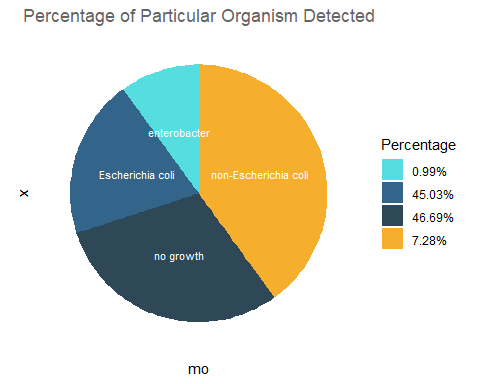
3

0.0099338

302

1.0000000

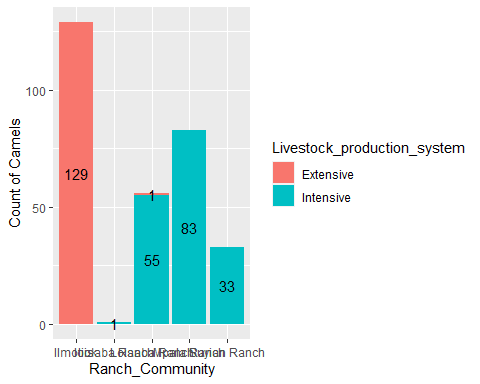
IRENE\_DATA\_ANALYSIS\_R %>% select(mo,CAMEL\_ID\_NUMBER) %>% group\_by(mo) %>% summarize(Count=n()) %>% mutate(Percentage=paste0(round(Count/sum(Count)\*100,2),"%")) %>% ggplot(aes(x="", y=mo, fill=Percentage)) + geom\_bar(stat="identity", width=1)+ coord\_polar("y", start=0) +theme\_classic()+labs( title = "Percentage of Particular Organism Detected")+scale\_fill\_manual(values=c("#55DDE0", "#33658A", "#2F4858", "#F6AE2D"))+theme(axis.line = element\_blank(),axis.text = element\_blank(),axis.ticks = element\_blank(), plot.title = element\_text(hjust = 0.5, color = "#666666"))+geom\_text(aes(y = mo, label = mo), position = position\_stack(vjust = .5),color = "white", size=3)

 # Cross tabulation by Ranch\_community vs the livestock production system

IRENE\_DATA\_ANALYSIS\_R %>% select(Ranch\_Community,Livestock\_production\_system) %>% pivot\_wider(names\_from = Livestock\_production\_system, values\_from= Livestock\_production\_system,values\_fn=list(Livestock\_production\_system=list))

## # A tibble: 5 x 3  
## Ranch\_Community Intensive Extensive   
## <chr> <list> <list>   
## 1 Mpala Ranch <chr [83]> <NULL>   
## 2 Ilmotiok <NULL> <chr [129]>  
## 3 Loisaba Ranch <chr [55]> <chr [1]>   
## 4 loisaba Ranch <chr [1]> <NULL>   
## 5 Suyian Ranch <chr [33]> <NULL>

IRENE\_DATA\_ANALYSIS\_R %>% select(Ranch\_Community,Livestock\_production\_system) %>% ggplot(aes(x=Ranch\_Community,fill=Livestock\_production\_system))+geom\_bar()+ylab("Count of Camels")+stat\_count(geom="text",aes(label=stat(count)), position = position\_stack(vjust = .5),color="black")

 # MDRO analysis

IRENE\_DATA\_ANALYSIS\_R %>% select(mo,Amoxicillin\_clavulanic\_acid:Norfloxacin) %>% mutate\_at(vars(Amoxicillin\_clavulanic\_acid:Norfloxacin), as.rsi)%>% mdro()%>% freq()

##   
##   
## \*\*Frequency table\*\*   
##   
## Class: factor > ordered (numeric)   
## Length: 302   
## Levels: 4: Negative < Multi-drug-resistant (MDR) < Extensively drug-resistant ...   
## Available: 158 (52.32%, NA: 144 = 47.68%)   
## Unique: 2  
##   
##   
## | |Item | Count| Percent| Cum. Count| Cum. Percent|  
## |:--|:--------------------------|-----:|-------:|----------:|------------:|  
## |1 |Negative | 152| 96.20%| 152| 96.20%|  
## |2 |Multi-drug-resistant (MDR) | 6| 3.80%| 158| 100.00%|

# Resistance

knitr::kable(IRENE\_DATA\_ANALYSIS\_R %>% select(mo,Amoxicillin\_clavulanic\_acid:Norfloxacin) %>% mutate\_at(vars(Amoxicillin\_clavulanic\_acid:Norfloxacin), as.rsi) %>% group\_by(mo) %>% summarise(amoxiclav = resistance(Amoxicillin\_clavulanic\_acid), Ampicillin = resistance(Ampicillin), Norflaxin = resistance(Norfloxacin)))

mo

amoxiclav

Ampicillin

Norflaxin

enterobacter

NA

NA

NA

Escherichia coli

0

0.0882353

0

no growth

NA

NA

NA

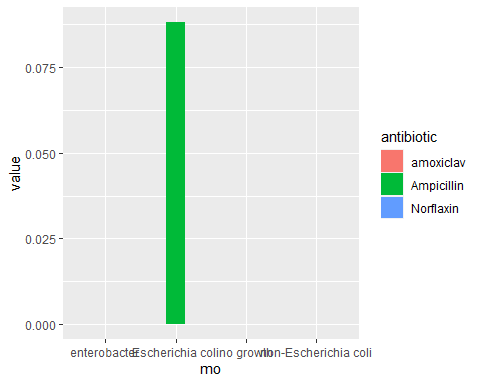
non-Escherichia coli

NA

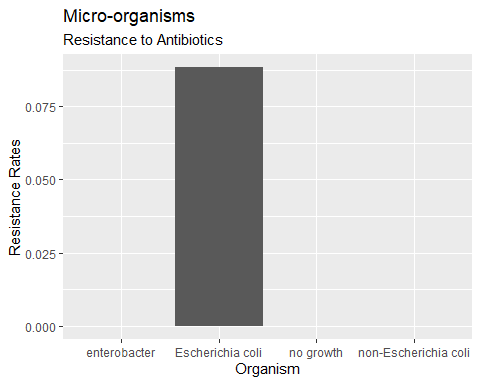
NA

NA

IRENE\_DATA\_ANALYSIS\_R %>% select(mo,Amoxicillin\_clavulanic\_acid:Norfloxacin) %>% mutate\_at(vars(Amoxicillin\_clavulanic\_acid:Norfloxacin), as.rsi) %>% group\_by(mo) %>% summarise(amoxiclav = resistance(Amoxicillin\_clavulanic\_acid), Ampicillin = resistance(Ampicillin), Norflaxin = resistance(Norfloxacin)) %>% tidyr::pivot\_longer(-mo, names\_to = "antibiotic") %>% ggplot(aes(x = mo,y = value,fill = antibiotic)) +geom\_col(position = "dodge2")



IRENE\_DATA\_ANALYSIS\_R %>% select(mo,Amoxicillin\_clavulanic\_acid:Norfloxacin) %>% mutate\_at(vars(Amoxicillin\_clavulanic\_acid:Norfloxacin), as.rsi) %>% group\_by(mo) %>% summarise(amoxiclav = resistance(Amoxicillin\_clavulanic\_acid), Ampicillin = resistance(Ampicillin), Norflaxin = resistance(Norfloxacin)) %>% tidyr::pivot\_longer(-mo, names\_to = "antibiotic") %>%ggplot(mapping = aes(x = mo,y = value)) +geom\_col() +labs(title = "Micro-organisms",subtitle = "Resistance to Antibiotics", x = "Organism",y = "Resistance Rates")

 # Conduct principal component analysis (PCA) for AMR

options(warn = -1)  
resistance\_data<-IRENE\_DATA\_ANALYSIS\_R %>% select(mo,Amoxicillin\_clavulanic\_acid:Norfloxacin) %>% mutate\_at(vars(Amoxicillin\_clavulanic\_acid:Norfloxacin), as.rsi) %>% group\_by(mo) %>% summarise\_if(is.rsi, resistance) %>% select(mo,Amoxicillin\_clavulanic\_acid:Norfloxacin)  
  
  
knitr::kable(resistance\_data)

mo

Amoxicillin\_clavulanic\_acid

Ampicillin

Ceftazidime

Cefotaxime

Ceftriaxone

Cefuroxime

Cefepime

Cefaclor

Tetracycline

Gentamicin

Spectinomycin

Chloramphenicol

Ciprofloxacin

Trimethoprim\_sulfamethoxazole

Norfloxacin

enterobacter

NA

NA

NA

NA

NA

NA

NA

NA

NA

NA

NA

NA

NA

NA

NA

Escherichia coli

0

0.0882353

0.0735294

0.1617647

0.0294118

0.0367647

0.0294118

0.2794118

0.0514706

0.0073529

0.0220588

0

0.0147059

0.0294118

0

no growth

NA

NA

NA

NA

NA

NA

NA

NA

NA

NA

NA

NA

NA

NA

NA

non-Escherichia coli

NA

NA

NA

NA

NA

NA

NA

NA

NA

NA

NA

NA

NA

NA

NA

resistant\_data\_2<-data.frame(na.omit(resistance\_data))  
  
knitr::kable(resistant\_data\_2)

mo

Amoxicillin\_clavulanic\_acid

Ampicillin

Ceftazidime

Cefotaxime

Ceftriaxone

Cefuroxime

Cefepime

Cefaclor

Tetracycline

Gentamicin

Spectinomycin

Chloramphenicol

Ciprofloxacin

Trimethoprim\_sulfamethoxazole

Norfloxacin

Escherichia coli

0

0.0882353

0.0735294

0.1617647

0.0294118

0.0367647

0.0294118

0.2794118

0.0514706

0.0073529

0.0220588

0

0.0147059

0.0294118

0

## R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

summary(cars)

## speed dist   
## Min. : 4.0 Min. : 2.00   
## 1st Qu.:12.0 1st Qu.: 26.00   
## Median :15.0 Median : 36.00   
## Mean :15.4 Mean : 42.98   
## 3rd Qu.:19.0 3rd Qu.: 56.00   
## Max. :25.0 Max. :120.00

## Including Plots

You can also embed plots, for example:



Note that the echo = FALSE parameter was added to the code chunk to prevent printing of the R code that generated the plot.