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Assignment 2 Task 3
May 13th , 2020

First of all here is my github link

Please check code on github instead of copy and paste from pdf.

Question 1
Part a,

The author tried to combine mi_counties into mi_census(left join) by using "country" from mi_census equal to "id" from mi_counties. That way, author could access all the information with countries in census_counties.

Part b,

The author tired to connect map with wdi database, using country code. that way, the author could showed all wdi information on a map.

Question 2, (question2.R on github)

Citation,
(*As_tibble Function | R Documentation*, n.d.)(*First Line of Every R Script?*, 2017)("Select & Rename R Functions of Dplyr Package (2 Examples)," n.d.)


```
# Assignment 2 Task 3
# BUSA8090
# Author, Zhengyu Pan
# May 13th, 2020

rm(list = ls(all = TRUE))  # clear all
                           # addtionally do shift + control+ F10
                           # to clean up the libraries
library(WDI) # assume that WDI is installed
library(ggplot2) # assume that ggplot2 is installed
library(dplyr)    # assume that dplyr is installed
```

```
library(maps)    # assume that maps is installed
                 # it seems that we don't need this library, but
                 # I will leave it here anyway
library(countrycode)  # assume that countrycode is installed
library(UserNetR)    # assume already did
                     # install_github("DougLuke/UserNetR")
                     # install.packages("UserNetR") will NOT work
library(sna)            # assume sna is installed


# question 2 part a
wdi_data    <-WDI(indicator=c("NY.GDP.PCAP.PP.KD",   "EN.ATM.CO2E.PC"),   start   =
2010, end   =   2010,   extra   =   TRUE)
wdi_data   =   as_tibble(wdi_data)
wdi   <-   wdi_data   %>%   rename(GDPpercap   =   NY.GDP.PCAP.PP.KD,
Emit_co2percap=EN.ATM.CO2E.PC)
dat_map<-map_data("world")
dat_map$ccode <- countrycode(dat_map$region,origin = "country.name",destination =
"wb")
wdi$ccode<- countrycode(wdi$country, origin = "country.name", destination = "wb")
merged <-full_join(dat_map, wdi, by="ccode")
ggplot(merged, aes(x=long,y =lat, group = group, fill= Emit_co2percap))+geom_polygon()

# question 2 part b

data(Bali)
op <- par(mar = c(0,0,0,0))
plot(Bali,displaylabels=TRUE,label.cex=0.8,pad=0.4,label.col="darkblue")


# question 2 part c

rolelab <- get.vertex.attribute(Bali,"role")
plot(Bali,usearrows=FALSE,label=rolelab,displaylabels=T,label.col="darkblue")
```
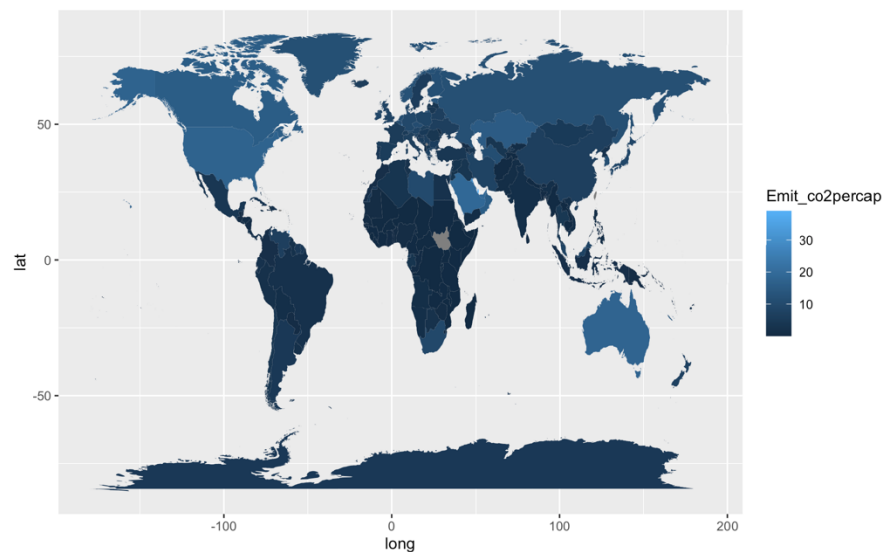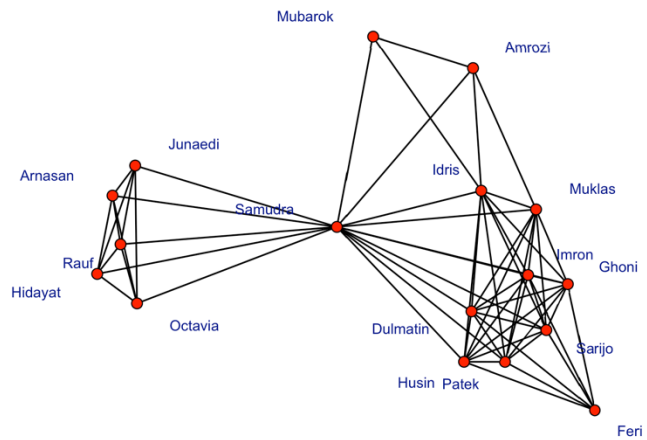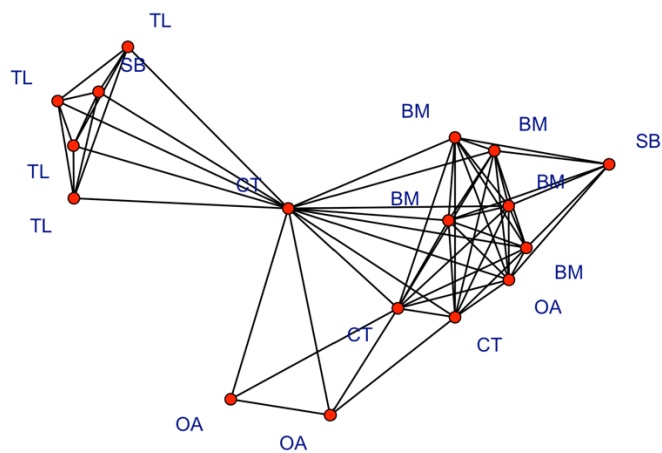
Part a

Part b

Mubarok

Amrozi

Junaedi

Arnasan

Idris

Muklas

Samudra

Imron

Ghoni

Rauf

Hidayat

Octavia

Dulmatin

Sarijo

Husin Patek

Feri

Part c

TL

SB

TL

BM

BM

SB

TL

CT

BM

BM

TL

BM

TL

BM
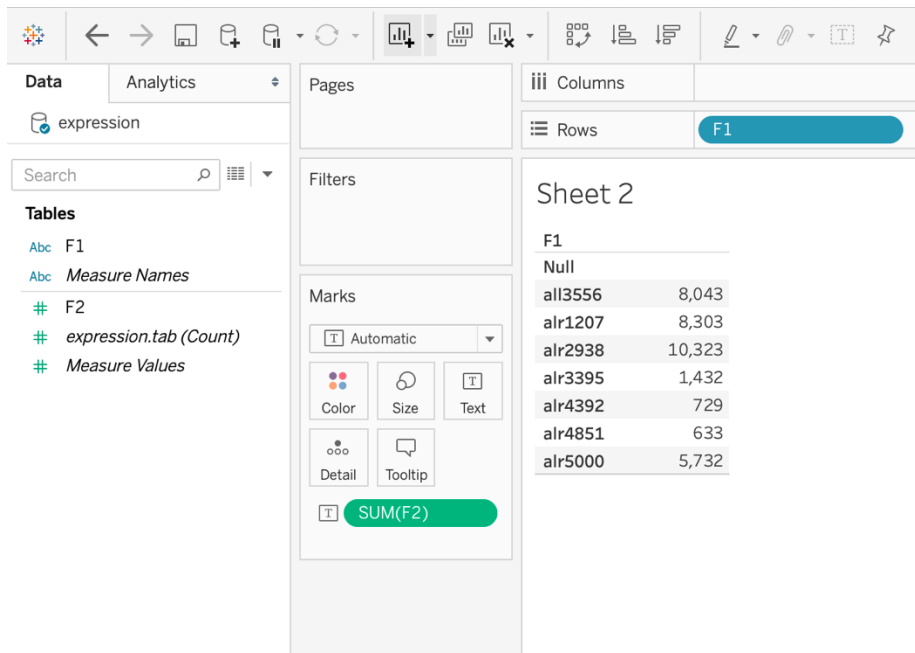
OA

CT

CT

OA

OA

Question 3 (question3a.twb   question3b.twb   question3c.twb)
Please use the data I upload on github to check, since annotation.tab I need manually add header to make it work

Citation,
(*Using "CONTAINS" Function to Filter for Certain... |Tableau Community Forums*, n.d.)

Part a,

Step 1,

Step 2 go to Filter
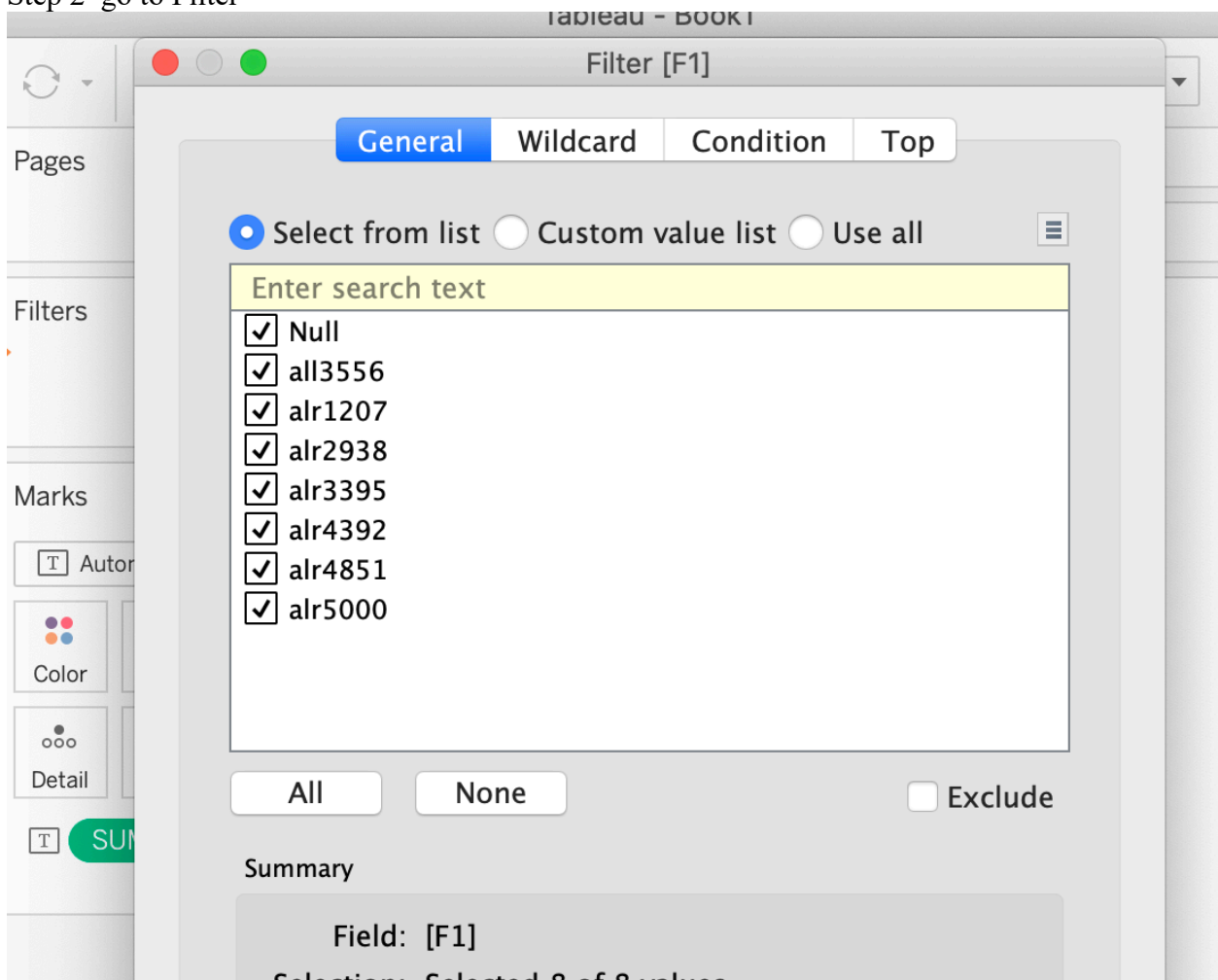
Step 3, set up conditions
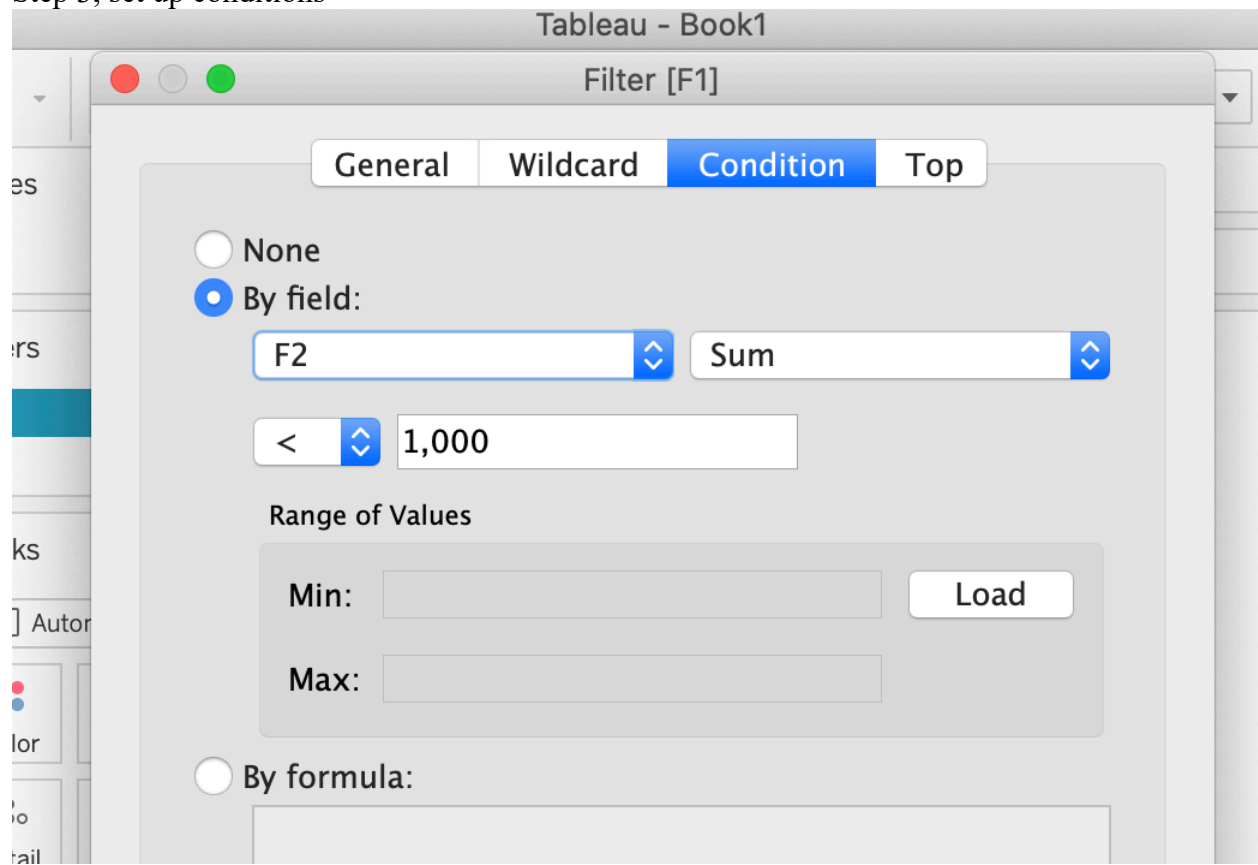
Step 4 result

Pages

iii Columns
☰ Rows	F1

Filters

F1

Sheet 2

F1	
alr4392	729
alr4851	633

Marks

T Automatic ▼

Color	Size	Text
Detail	Tooltip	

T SUM(F2)

Part b,
Step 1, I need add a header manually, so it won't use any real data as header

Columns

Rows | C1 | C2 | C3

Sheet 1

C1	C2	C3	
Null	Null	Null	Abc
all3556	succinate-dehydrogenase	TCA cycle	Abc
alr1207	uridylate kinase	Pyrimidine biosynthesis	Abc
alr2938	iron superoxide dismutase	Detoxification	Abc
alr3395	adenylosuccinate lyase	Purine biosynthesis	Abc
alr4392	nitrogen-responsive regul..	Nitrogen assimilation	Abc
alr4851	preprotein translocase su..	Protein and peptide secre..	Abc
alr5000	CTP synthetase	Pyrimidine biosynthesis	Abc

Text

Standard

Step 2

C1	C2 ▼	C3

		Filter...
	C3	Show Filter
	Null	Show Highlighter
ate-dehydrogenase	TCA	Sort...	Abc
te kinase	Pyri	Format...	Abc
peroxide dismutase	Det	✓ Show Header	Abc
osuccinate lyase	Puri	✓ Include in Tooltip	Abc
en-responsive regul..	Nitr		Abc
		Edit Aliases...	Abc

1234	6
368	3
2620	2
971	3

Step 3

Filter [C2]

General   Wildcard   **Condition**   Top

◯ None

◯ By field:

| C1 ⌄ | Count ⌄ |

| = ⌄ | 0 |

Range of Values

Min: [   ]   Load

Max: [   ]

◉ By formula:

CONTAINS([C2] ,"ase")

Step 4

C1	C2	C3	
alr3395	adenylosuccinate lyase	Purine biosynthesis	Abc
alr5000	CTP synthetase	Pyrimidine biosynthesis	Abc
alr2938	iron superoxide dismutase	Detoxification	Abc
alr4851	preprotein translocase su..	Protein and peptide secre..	Abc
all3556	succinate-dehydrogenase	TCA cycle	Abc
alr1207	uridylate kinase	Pyrimidine biosynthesis	Abc

Pages

Filters
C2

Marks
T Aut...
Co... Size Text
De... To...

iii Columns

≡ Rows   C1   C2   C3

Sheet 1

Part 3,

Step 1 after load data like part 2

C3

Filter...

Show Filter
Show Highlighter

Sort...
Format...
✓ Show Header

e biosynthesis

Step 2

General   Wildcard   Condition   Top

○ None
○ By field:

| C1 ◇ | Count ◇ |

| = ◇ | 0 |

Range of Values

Min: [   ]   Load

Max: [   ]

● By formula:

```
CONTAINS([C3], "Pyrimidine biosynthesis")
OR CONTAINS([C3], "Purine biosynthesis")
```

Step 3

Reference:

As_tibble function | R Documentation. (n.d.). Retrieved May 12, 2020, from

   https://www.rdocumentation.org/packages/tidyquant/versions/0.5.3/topics/as_tibble

First line of every R script? (2017, September 17). RStudio Community.

   https://community.rstudio.com/t/first-line-of-every-r-script/799

Select & rename R Functions of dplyr Package (2 Examples). (n.d.). *Statistics Globe*. Retrieved

   May 12, 2020, from https://statisticsglobe.com/r-select-rename-functions-dplyr-package/

Using "CONTAINS" function to filter for certain... |Tableau Community Forums. (n.d.).

   Retrieved May 12, 2020, from https://community.tableau.com/thread/122402