

Project 1

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Background

The World Health Organization has recently employed a new data science initiative, *CSIT-165*, that uses data science to characterize pandemic diseases. *CSIT-165* disseminates data driven analyses to global decision makers.

CSIT-165 is a conglomerate comprised of two fabricated entities: *Global Health Union (GHU)* and *Private Diagnostic Laboratories (PDL)*. Your and your partner's role is to play a data scientist from one of these two entities.

Data

2019 Novel Coronavirus COVID-19 (2019-nCoV) Data Repository by John Hopkins CSSE Data for 2019 Novel Coronavirus is operated by the John Hopkins University Center for Systems Science and Engineering (JHU CSSE). Data includes daily time series CSV summary tables, including confirmations, recoveries, and deaths. Country/region are countries/regions that conform to World Health Organization (WHO). Lat and Long refer to coordinates references for the user. Date fields are stored in MM/DD/YYYY format.

```
confirmed_download <- getURL("https://raw.githubusercontent.com/CSSEGISandData/COVID-19/master/csse_covid_19_data/csse_covid_19_data/daily_time_series/2019_nCoV_data/confirmed.csv")
confirmed <- read.csv(text=confirmed_download, stringsAsFactors = FALSE)

recovered_download <- getURL("https://raw.githubusercontent.com/CSSEGISandData/COVID-19/master/csse_covid_19_data/csse_covid_19_data/daily_time_series/2019_nCoV_data/recovered.csv")
recovered <- read.csv(text=recovered_download, stringsAsFactors = FALSE)

deaths_download <- getURL("https://raw.githubusercontent.com/CSSEGISandData/COVID-19/master/csse_covid_19_data/csse_covid_19_data/daily_time_series/2019_nCoV_data/deaths.csv")
deaths <- read.csv(text=deaths_download, stringsAsFactors = FALSE)
```

Project Objectives

Objective 1

```
confirmed_origin <- confirmed[which.max(confirmed$X1.22.20), c("Province.State", "Country.Region")]
confirmed_country <- as.character(confirmed_origin[[c("Country.Region")]])
```

```

confirmed_state <- as.character(confirmed_origin[[c("Province.State")]])

deaths_origin <- deaths[which.max(deaths$X1.22.20), c("Province.State", "Country.Region")]
deaths_country <- as.character(deaths_origin[[c("Country.Region")]])
deaths_state <- as.character(deaths_origin[[c("Province.State")]])

recovered_origin <- recovered[which.max(recovered$X1.22.20), c("Province.State", "Country.Region")]
recovered_country <- as.character(recovered_origin[[c("Country.Region")]])
recovered_state <- as.character(recovered_origin[[c("Province.State")]])

paste("Confirmed data indicates ", confirmed_state, ", ", confirmed_country, " as origin.", sep = "")

## [1] "Confirmed data indicates Hubei, China as origin."
paste("Death data indicates ", deaths_state, ", ", deaths_country, " as origin.", sep = "")

## [1] "Death data indicates Hubei, China as origin."
paste("Recovered data indicates ", recovered_state, ", ", recovered_country, " as origin.", sep = "")

## [1] "Recovered data indicates Hubei, China as origin."
if(identical(deaths_country, recovered_country) == identical(recovered_country, confirmed_country))
{
  paste(recovered_country, " is the origin country.", sep = "")
}else
{
  paste(recovered_country, "is NOT the origin country.", sep = "")
}

## [1] "China is the origin country."
if(identical(deaths_state, recovered_state) == identical(recovered_state, confirmed_state))
{
  paste(recovered_state, " is the origin state.", sep = "")
}else
{
  paste(recovered_state, " is NOT the origin state.", sep = "")
}

## [1] "Hubei is the origin state."

```

Confirmed cases, number deaths and number of recoveries data sets all suggest Hubei, China to be the origin of COVID-19. The max number of confirmed cases, deaths and recoveries occurred in Hubei, China on the first day data was recorded; 01/22/2021. We are unable to conclude Hubei, China to be the true origin of COVID-19 since no data is available from earlier dates. An ideal case to determine origin would include data where number confirmed cases in countries and states are in a close proximity to one another. Right now, we have multiple locations with occurrences of confirmed cases on 01/22/2021 that are not very close to each other.

Objective 2

```

ncol <- ncol(confirmed)
confirmed_ordered <- arrange(confirmed, confirmed[5:ncol])
recent_first <- as.character(head(confirmed_ordered$Country.Region, n = 1))

recent <- confirmed_ordered[1,-c(1:4)]

```

```
ncol_recent <- ncol(recent)

recent <- recent[,recent[,1:ncol_recent]!=0]

paste(recent_first, " had the most recent confirmed case on ", colnames(recent[1]), sep = "")

## [1] "Micronesia had the most recent confirmed case on X1.21.21"
```

The confirmed data set suggests Micronesia to have had the most recent first confirmed case of COVID-19 on 01/21/2021. No other countries appear to have had a first confirmed case on this same day. Interestingly, all countries in the data set have had confirmed cases of COVID-19 since the beginning of data collection.

Objective 3

```
nrow_origin <- as.numeric(which(grepl("Hubei", confirmed$Province.State)))
nrow_recent <- which(grepl("Micronesia", confirmed$Country.Region))

miles_between <- as.numeric(round(distm(as.numeric(confirmed[nrow_origin, 4:3]), as.numeric(confirmed[nrow_recent, 4:3])), 1))

data <- data.frame(Case=c("Origin", "Recent"),
                   Country.Region = c(confirmed[nrow_origin, 1], confirmed[nrow_recent, 1]),
                   State.Province = c(confirmed[nrow_origin, 2], confirmed[nrow_recent, 2]),
                   Lat = c(confirmed[nrow_origin, 4], confirmed[nrow_recent, 4]),
                   Long = c(confirmed[nrow_origin, 3], confirmed[nrow_recent, 3]))

paste(data[2,3], " is ", miles_between, " miles away from ", data[1,2], ", ", data[1,3], ".", sep = "")

## [1] "Micronesia is 2955 miles away from Hubei, China."
```

Micronesia is the only location to have had the most recent first confirmed case of COVID-19. Micronesia is 2955 miles away from the suggested origin for COVID-19 in Hubei, China. No Province/State is associated with Micronesia.

Objective 4

Objective 4.1

```
colnum_deaths <- ncol(deaths)
total_deaths <- subset(deaths, select = c(1, 2, colnum_deaths))
total_deaths$StateRegion <- do.call(paste0, total_deaths[1:2])
colnames(total_deaths) = c("Province.State", "Country.Region", "Total.Deaths", "StateRegion")

colnum_recovered <- ncol(recovered)
total_recovered <- subset(recovered, select = c(1, 2, colnum_recovered))
total_recovered$StateRegion <- do.call(paste0, total_recovered[1:2])
colnames(total_recovered) = c("Province.State", "Country.Region", "Total.Recovered", "StateRegion")

colnum_confirmed <- ncol(confirmed)
total_confirmed <- subset(confirmed, select = c(1, 2, colnum_confirmed))
total_confirmed$StateRegion <- do.call(paste0, total_confirmed[1:2])
colnames(total_confirmed) = c("Province.State", "Country.Region", "Total.Confirmed", "StateRegion")

risk_score <- merge(total_deaths, total_recovered, by = "StateRegion")
risk_score <- subset(risk_score, select = c(1:4, 7))
risk_score <- merge(risk_score, total_confirmed, by = "StateRegion")
```

```

risk_score <- subset(risk_score, select = c(2:5, 8))
risk_score$Risk.Score <- risk_score$Total.Deaths / risk_score$Total.Recovered
risk_score$Death.Burden <- risk_score$Risk.Score * risk_score$Total.Confirmed

GRS <- sum(risk_score$Total.Deaths) / sum(risk_score$Total.Recovered)

paste("Global risk score is ", GRS, sep = "")

```

```
## [1] "Global risk score is 0.0381312754337771"
```

```
head(risk_score[order(-risk_score$Risk.Score),], n = 8)
```

```

##      Province.State.x Country.Region.x Total.Deaths Total.Recovered
## 21                Belgium           23473             0
## 163              Netherlands           16771             0
## 165 New South Wales      Australia         54             0
## 201                Serbia           5735             0
## 223                Sweden          13621             0
## 242              United Kingdom        127087             0
## 244                US          562066             0
## 147      Martinique      France           59             98
##      Total.Confirmed Risk.Score Death.Burden
## 21           925476      Inf      Inf
## 163          1350665      Inf      Inf
## 165           5339      Inf      Inf
## 201          642208      Inf      Inf
## 223          857401      Inf      Inf
## 242          4369775      Inf      Inf
## 244          31197511      Inf      Inf
## 147           8887  0.6020408  5350.337

```

```
tail(risk_score[order(-risk_score$Risk.Score),], n = 23)
```

```

##      Province.State.x Country.Region.x
## 209                Singapore
## 6              Anguilla      United Kingdom
## 60                Dominica
## 70      Falkland Islands (Malvinas)      United Kingdom
## 86              Greenland      Denmark
## 101                Holy See
## 119              Jiangsu      China
## 129                Laos
## 139              Macau      China
## 146      Marshall Islands
## 152      Micronesia
## 164      New Caledonia      France
## 170              Ningxia      China
## 172      Northern Territory      Australia
## 184              Qinghai      China
## 191 Saint Helena, Ascension and Tristan da Cunha      United Kingdom
## 192                Saint Kitts and Nevis
## 194      Saint Pierre and Miquelon      France
## 196                Samoa
## 206              Shanxi      China
## 213      Solomon Islands

```

## 232			Tibet		China
## 246					Vanuatu
##	Total.Deaths	Total.Recovered	Total.Confirmed	Risk.Score	Death.Burden
## 209	30	60335	60653	0.0004972238	30.15812
## 6	0	22	25	0.0000000000	0.00000
## 60	0	159	165	0.0000000000	0.00000
## 70	0	54	60	0.0000000000	0.00000
## 86	0	31	31	0.0000000000	0.00000
## 101	0	15	27	0.0000000000	0.00000
## 119	0	708	716	0.0000000000	0.00000
## 129	0	47	51	0.0000000000	0.00000
## 139	0	48	49	0.0000000000	0.00000
## 146	0	4	4	0.0000000000	0.00000
## 152	0	1	1	0.0000000000	0.00000
## 164	0	58	121	0.0000000000	0.00000
## 170	0	75	75	0.0000000000	0.00000
## 172	0	107	112	0.0000000000	0.00000
## 184	0	18	18	0.0000000000	0.00000
## 191	0	4	4	0.0000000000	0.00000
## 192	0	44	44	0.0000000000	0.00000
## 194	0	24	24	0.0000000000	0.00000
## 196	0	2	3	0.0000000000	0.00000
## 206	0	240	248	0.0000000000	0.00000
## 213	0	18	19	0.0000000000	0.00000
## 232	0	1	1	0.0000000000	0.00000
## 246	0	1	3	0.0000000000	0.00000

There are 22 areas with a low risk score of 0. These areas include provinces and states in UK, Dominica, Denmark, Holy See, China, Laos, Marshall Islands, Micronesia, France, Australia, Saint Kitts and Nevis, Samoa, Solomon Islands and Vanuatu. A risk score of 0 is likely due to a lack of deaths data where total deaths is at 0. Singapore would be the first true low risk score at 0.00050, which is 0.13 almost 1/8 of the global risk score value.

Seven areas show a high risk score of "Inf". These areas include Belgium, Netherlands, Australia (New South Wales), Serbia, Sweden, United Kingdom, and US. However, a contributing discrepancy to the risk score assessment of the listed areas is likely due to a lack of recovered cases data. Having total deaths number divided by total recovered number of 0 results in Inf, which would not be representative of the true risk score for these areas. France (Martinique), is therefore the first listed area with a true high value risk score of 0.602. Compared to the global risk score of 0.038, Martinique's risk score is 15 times greater than the global risk score.

Death burden value of the least risky area (Singapore) is 178 times less when compared to the most risky area (Martinique). There is a large difference in death burden between these two areas with opposite risk scores.

Objective 4.2

```
total_deaths2 <- subset(deaths, select = c(2,colnum_deaths))
total_deaths2$Sum.total <- rowSums(total_deaths2[-1])
total_deaths2 <- aggregate(x = total_deaths2$Sum.total, by = list(total_deaths2$Country.Region), FUN = sum)
colnames(total_deaths2) = c("Country.Region", "Total.Deaths")

total_recovered2 <- subset(recovered, select = c(2,colnum_recovered))
total_recovered2$Sum.total <- rowSums(total_recovered2[-1])
total_recovered2 <- aggregate(x = total_recovered2$Sum.total, by = list(total_recovered2$Country.Region), FUN = sum)
colnames(total_recovered2) = c("Country.Region", "Total.Recovered")
```

```

total_confirmed2 <- subset(confirmed, select = c(2,colnum_confirmed))
total_confirmed2$Sum.total <- rowSums(total_confirmed2[-1])
total_confirmed2 <- aggregate(x = total_confirmed2$Sum.total, by = list(total_confirmed2$Country.Region,
colnames(total_confirmed2) = c("Country.Region", "Total.Confirmed")

risk_score2 <- merge(total_deaths2, total_recovered2, by = "Country.Region")
risk_score2 <- merge(risk_score2, total_confirmed2, by = "Country.Region")
risk_score2$Risk.Score <- risk_score2$Total.Deaths / risk_score2$Total.Recovered
risk_score2$Death.Burden <- risk_score2$Risk.Score * risk_score2$Total.Confirmed

#kable(head(total_confirmed2[order(-total_confirmed2$Total.Confirmed),], n = 5))

#kable(head(total_recovered2[order(-risk_score2$Total.Recovered),], n = 5))

#kable(head(total_deaths2[order(-risk_score2$Total.Deaths),], n = 5))

```

Note: I am unable to uninstall an old version of kableExtra package and can not knit my rmarkdown file without omitting the kable() functions.

GitHub Log

```
git log --pretty=format:"%nSubject: %s%nAuthor: %aN%nDate: %aD%nBody: %b"
```

```

##
## Subject: Updated pdf
## Author: mrgrabiel
## Date: Sun, 11 Apr 2021 18:38:14 -0700
## Body:
##
## Subject: Load final Markdown script
## Author: mrgrabiel
## Date: Sun, 11 Apr 2021 18:33:00 -0700
## Body:
##
## Subject: Final version by Marc with Objective 4 draft
## Author: mrgrabiel
## Date: Sun, 11 Apr 2021 18:25:38 -0700
## Body:
##
## Subject: Time to copy, paste, and format
## Author: Naycari De Luna
## Date: Sun, 11 Apr 2021 11:32:49 -0700
## Body:
##
## Subject: NDL attempt at Obj 3
## Author: Naycari De Luna
## Date: Sun, 11 Apr 2021 11:26:19 -0700
## Body:
##
## Subject: obj 2 without loop
## Author: Naycari De Luna
## Date: Sun, 11 Apr 2021 08:09:41 -0700

```

Body:

Subject: Obj 2 without loops
Author: Naycari De Luna
Date: Sun, 11 Apr 2021 08:05:13 -0700
Body:

Subject: Draft project file for submission. Up to obj. 3
Author: mrgrabiel
Date: Sat, 10 Apr 2021 16:54:34 -0700
Body:

Subject: Include all three absolute filepaths
Author: mrgrabiel
Date: Sat, 10 Apr 2021 14:15:40 -0700
Body:

Subject: update on obj 4
Author: Naycari De Luna
Date: Sat, 10 Apr 2021 10:34:19 -0700
Body:

Subject: Progress on obj 4
Author: Naycari De Luna
Date: Sat, 10 Apr 2021 09:37:22 -0700
Body:

Subject: complete object 1
Author: Naycari De Luna
Date: Thu, 8 Apr 2021 20:54:43 -0700
Body:

Subject: worked a bit on ob1 for deaths and recovery
Author: Naycari De Luna
Date: Wed, 7 Apr 2021 23:04:01 -0700
Body:

Subject: re-uploading correct data files
Author: Naycari De Luna
Date: Wed, 7 Apr 2021 21:23:16 -0700
Body:

Subject: adding covid recovered data
Author: Naycari De Luna
Date: Tue, 6 Apr 2021 23:29:04 -0700
Body:

Subject: adding covid death data
Author: Naycari De Luna
Date: Tue, 6 Apr 2021 23:27:23 -0700
Body:

Subject: Objective 3 code for distance between recent and origin
Author: mrgrabiel

Date: Sun, 4 Apr 2021 16:45:19 -0700
Body:

Subject: Share Objective 2 code for recent confirmed case
Author: mrgrabiel
Date: Sun, 4 Apr 2021 12:36:04 -0700
Body:

Subject: Share objective 1 code for confirmed cases
Author: mrgrabiel
Date: Sun, 4 Apr 2021 10:56:48 -0700
Body:

Subject: Add files via upload
Author: mrgrabiel
Date: Sat, 3 Apr 2021 18:10:22 -0700
Body:

Subject: Update README.md
Author: ndeluna-i
Date: Thu, 1 Apr 2021 21:54:50 -0700
Body:

Subject: Initial commit
Author: ndeluna-i
Date: Wed, 24 Mar 2021 19:03:15 -0700
Body: