## UCSF Stages Data - Prelim Analysis

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## Background

#### **Project**

MINDSCAPE: Modeling of infectious network dynamics for surveillance, control and prevention enhancement

#### Description

This file summarizes the data, creates descriptive tables for the continuous and categorical variables, and generates plots to show the distribution of length of stay (LOS) by admission stage.

#### Source Data

- Demographics and Daily Covid Stage Data (dm\_stg\_unique\_pt\_11.08.2021.csv)
  - ▶ This file contains data on patient demographics and COVID stage (based on WHO Clinical Progression Scale, which aims to capture patient clinical trajectory and resource usage over the course of the clinical illness in this case, COVID-19).
  - Each row contains a different patient as shown by their unique encounter ID.

# Load required packages

# Import and preview data

## Rows: 1117 Columns: 17

## -- Column specification -----## Delimiter: ","

## chr (7): ID, sex, zip, race, ethnicity, smoking, death
## dbl (7): age, BMI, LOS, stage, max\_stage, stage\_adm, stage\_adm

## date (3): date\_adm, date\_disc, DOD
##

## i Use 'spec()' to retrieve the full column specification
## i Specify the column types or set 'show\_col\_types = FALS

ID age sex zip

ID	age	sex	zip
0055f0c4-990c-44ce-911e-4b1784666eeb	53	Male	95382
00a80297-7016-4b06-8dfc-21a1490baafa	57	Male	94939
01abe61d-6df2-4f18-9a85-8b8d12f94f08	51	Male	93722
01b4c414 b32c 46dc 8c2a 20f300147f70	67	Mala	04001

# Create table one for categorical and continuous variables

```
# Define categorical and continuous variables
#cat_vars <- c("sex", "race", "ethnicity", "smoking", "dea
cat_vars <- c("sex", "race", "ethnicity", "smoking", "deatl
cont_vars <- c("age", "BMI", "LOS")

t1 <- CreateCatTable(data = df, cat_vars)
#print(t1, varLabels = T, showAllLevels = T, digits = 1)
kableone(t1)</pre>
```

	Overall
n	1117
sex = Male (%)	576 (51.6)
race (%)	
Asian	221 (19.8)
Black or African American	110 ( 9.8)
Native Hawaiian or Other Pacific Islander	18 ( 1.6)
Other	341 (30.5)
Unknown	33 ( 3.0)

#### Stage transition matrices

stage\_disc (%)

n

**L17** 

# Create categorical table of stage\_adm vs. stage\_disc
CreateCatTable(strata = 'stage\_adm', vars = 'stage\_disc', or other stage\_adm')

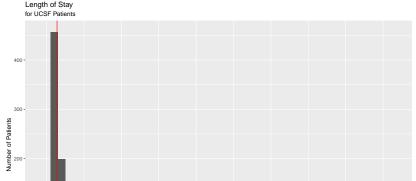
435 (84.1) 200 (50.4) 29 (36.7) 4 (36.4) 20 (4

EΛ

55 (10.6) 3 ( 0.6) 3 ( 0.6)	162 (40.8) 5 ( 1.3)	32 (40.5) 2 ( 2.5)	0 ( 0.0)	14 (2				
, ,	,	2 ( 2.5)	0 ( 0.0)	0 ( (				
3 ( 0 6)	4 ( 0 0)			, ,				
0 ( 0.0)	1 ( 0.3)	2 ( 2.5)	6 (54.5)	5 (10				
0 ( 0.0)	0 ( 0.0)	0 ( 0.0)	1 ( 9.1)	1 ( 2				
0 ( 0.0)	0 ( 0.0)	1 ( 1.3)	0 ( 0.0)	0 ( 0				
21 ( 4.1)	29 ( 7.3)	13 (16.5)	0 ( 0.0)	10 (2				
# Create categorical table of stage adm vs. max stage								
	0 ( 0.0)	0 ( 0.0)     0 ( 0.0)       21 ( 4.1)     29 ( 7.3)	0 ( 0.0)     0 ( 0.0)     1 ( 1.3)       21 ( 4.1)     29 ( 7.3)     13 (16.5)	0 ( 0.0)     0 ( 0.0)     1 ( 1.3)     0 ( 0.0)       21 ( 4.1)     29 ( 7.3)     13 (16.5)     0 ( 0.0)				

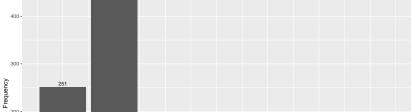
CreateCatTable(strata = 'stage\_adm', vars = 'max\_stage', data

# Create histogram of LOS



# Create barplot showing distribution of max stages

```
ggplot(df, aes(x = max_stage)) +
  geom_bar() +
  labs(title = 'Distribution of Max Stages',
       subtitle = 'at UCSF',
       x = 'WHO Clinical Progression Stage',
       y = 'Frequency') +
  scale_x_continuous(breaks = 4:10) +
  geom text(stat = 'count', aes(label = after stat(count))
  Distribution of Max Stages
  at UCSF
               476
 400 -
```



# Create proportional stacked bar chart to show proportion of max\_stage within stage\_adm

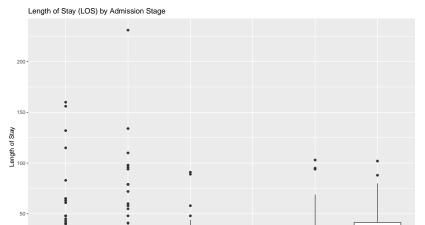
```
df %>%
  group_by(stage_adm, max_stage) %>%
  summarize(count = n()) %>%
  ggplot(aes(x = as.factor(stage_adm), y = count, fill = as
  geom_col(position = 'fill') +
  labs(title = 'Distribution of Max Stage by Admission Stage
       subtitle = 'at UCSF',
       x = 'Admission Stage',
       y = 'Proportion',
       fill = 'Max Stage') #+
```

## 'summarise()' has grouped output by 'stage\_adm'. You can

at UCSF

Distribution of Max Stage by Admission Stage

# Create boxplot of LOS grouped by admission stage



Re-run the proportional stacked bar chart and boxplot from above using stage

# categories (moderate, severe, dead)

```
# Proportional stacked bar chart showing which proportion
df %>%
  group_by(stgcat_adm, stgcat_max) %>%
  summarize(count = n()) %>%
  ggplot(aes(x = stgcat_adm, y = count, fill = stgcat_max))
  geom_col(position = 'fill') +
  labs(title = 'Distribution of Max Stage by Admission Stage
       subtitle = 'at UCSF',
       x = 'Admission Stage',
       y = 'Proportion',
       fill = 'Max Stage')
```

## 'summarise()' has grouped output by 'stgcat\_adm'. You ca

Distribution of Max Stage by Admission Stage at UCSF

# **End of Document**