

# Characterize a Given OMOP CDM Database

## Initial Set-Up

### Activating Project Environment

```
knitr::opts_chunk$set(echo = TRUE, message = F, results = 'hold')
options(scipen=999)
devtools::load_all()
```

```
## i Loading MentalHealthEquity
library(MentalHealthEquity)
```

### Packages Used in Analysis

DatabaseConnector

Package Description:

This package will be used to create connections to the database and execute queries to obtain characterizations about the cohorts in the database.

## Introduction

### Background

The intent of this report is to investigate the characterization statement:

**Characterization Statement 1:** Characterize the individuals being seen for mental health care services (related to depression, bipolar disorder, and suicidality) at least one time – including hospitalization events.

This characterization statement is founded on the central research topic for this study:

**Research Topic:** Based on [CLAIMS], we see X% of all persons with at least one claim indicating [DEPRESSION/BIPOLAR DISORDER/SUICIDALITY] are not seen again.

By which the phrases “... all persons...” refer to those seen by patient care provider, etc. and “...are not seen again.” implies lack of adherence to care.

## Data Analysis Preparation

### Creating Initial Connection

Defining connection details for connecting to a given database:

```
connectionDetails <- createConnectionDetails(
  dbms = "postgresql",
  server = "data.hdap.gatech.edu/synpuf_v5",
  user = keyring::key_list("synPUF")[1,2],
```

```
password = keyring::key_get("synPUF", keyring::key_list("synPUF")[1,2]),
port = 5434,
pathToDriver = "../utils"
)
```

## Creating Initial OMOP Tables

In this case, the schema follows the OMOP CDM v5 schema:

For this analysis, we will work with the following tables from the schema:

Per the [Book of OHDSI], here are the break downs for these tables:

- PERSON -
- LOCATION -
- OBSERVATION\_PERIOD -
- CONDITION\_OCCURRENCE -

## General Characterization of Data

```
sql <- "
SELECT @table.@concept_name, count(*)
FROM person
  LEFT JOIN (select LOCATION_ID, STATE FROM location) AS location ON
    person.location_id = location.location_id
  LEFT JOIN (select * FROM concept WHERE DOMAIN_ID = 'Race'
    AND STANDARD_CONCEPT = 'S') AS race ON
    person.race_concept_id = race.concept_id
  LEFT JOIN (select * FROM concept WHERE DOMAIN_ID = 'Ethnicity'
    AND STANDARD_CONCEPT = 'S') AS ethnicity ON
    person.ethnicity_concept_id = ethnicity.concept_id
  LEFT JOIN (select * FROM concept WHERE DOMAIN_ID = 'Gender'
    AND STANDARD_CONCEPT = 'S') AS gender ON
    person.gender_concept_id = gender.concept_id
GROUP BY @table.@concept_name
ORDER BY count(*) DESC
"
```

## Cohort Populations

### General Cohort

#### Overall Trends

```
conn <- connect(connectionDetails)
date_sql <- "
  SELECT MIN(visit.visit_end_date) as first_visit,
         MAX(visit.visit_end_date) as last_visit
  FROM visit_occurrence visit
"
dates <- renderTranslateQuerySql(conn, date_sql)
```

```
disconnect(conn)
dates
```

```
## FIRST_VISIT LAST_VISIT
## 1 2008-01-01 2010-12-31
```

The dates in the dataset range from 2008-01-01 and 2010-12-31

**Patient Spread** This calculates the number of patients in the dataset:

```
conn <- connect(connectionDetails)
count <- querySql(conn, sql = "SELECT COUNT(DISTINCT PERSON_ID) FROM PERSON")
disconnect(conn)
```

In this dataset, there are 2326856 patients. To further examine this data, we can break them down across the following axes:

- State
- Age
- Race
- Gender
- Care setting

```
conn <- connect(connectionDetails)
state <- renderTranslateQuerySql(conn, sql, table = "location", concept_name = "state")
disconnect(conn)
```

**State Breakdown** The top states are: CA, FL, TX, NY, PA, IL, OH, MI, NC, NJ

STATE	COUNT
CA	201651
FL	155040
TX	133809
NY	132059
PA	102191
IL	86557
OH	86325
MI	79556
NC	78912
NJ	63475

```
conn <- connect(connectionDetails)
age_sql <- "
  SELECT MIN(YEAR(visit.visit_end_date) - person.year_of_birth) as min_age,
         MAX(YEAR(visit.visit_end_date) - person.year_of_birth) as max_age
  FROM person
  JOIN visit_occurrence visit ON
    person.person_id = visit.person_id
"
age <- renderTranslateQuerySql(conn, age_sql)
disconnect(conn)
age
```

## Age Breakdown

```
##   MIN_AGE MAX_AGE
## 1      25     101
```

The age of the patient at the time of visit ranged from years of age to years of age.

```
conn <- connect(connectionDetails)
race <- renderTranslateQuerySql(conn, sql, table = "race", concept_name= "concept_name")
disconnect(conn)
race
```

## Racial Breakdown

```
##           CONCEPT_NAME  COUNT
## 1                White 1926708
## 2 Black or African American 247723
## 3                  <NA> 152425
```

In the dataset, there are 1926708 White persons, 247723 Black or African American persons, 152425 NA persons

CONCEPT_NAME	COUNT
White	1926708
Black or African American	247723
NA	152425

```
conn <- connect(connectionDetails)
gender <- renderTranslateQuerySql(conn, sql, table = "gender", concept_name = "concept_name")
disconnect(conn)
gender
```

## Gender Breakdown

```
##   CONCEPT_NAME  COUNT
## 1          FEMALE 1292861
## 2           MALE 1033995
```

In the dataset, there are 1292861 FEMALE persons, 1033995 MALE persons

CONCEPT_NAME	COUNT
FEMALE	1292861
MALE	1033995

```
conn <- connect(connectionDetails)
caresite_sql <- "
  SELECT concept.concept_name, count(*)
  FROM visit_occurrence visit
  JOIN (SELECT CONCEPT_NAME , CONCEPT_ID
        FROM concept
        WHERE DOMAIN_ID = 'Visit'
        AND STANDARD_CONCEPT = 'S') concept ON
```

```

        visit.visit_concept_id = concept.concept_id
    GROUP BY concept.concept_name
    ORDER BY count(*) DESC
"
care_site <- renderTranslateQuerySql(conn, caresite_sql)
disconnect(conn)
care_site

```

### Care Site Breakdown

```
##      CONCEPT_NAME      COUNT
## 1 Inpatient Visit 111637582
```

In the dataset, the care site setting Inpatient Visit had 111637582 visits