

# Project Notebook

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## Project Objectives

Create a predictive model for identifying patients with Diabetes

See Capstone Proposal for details.

## Project Dataset

Practice Fusion De-Identified Data Set containing EHR data for approximately 10,000 de-identified patients, including data points for diagnoses, medication, transcript data, and lab observations. See the Data Dictionary for details.

## General Notes

### Working with SQLite

The dataset is contained within an SQLite database file (420.7MB). To load the data into R requires installation and loading of **RSQLite** and **DBI** R packages. One of the dependencies is the tibble package. During the install, I was asked whether to install the binary version (1.3.4) or the source version (1.4.1), which would need compilation. I wasn't comfortable enough to explore compiling R package code yet, so I went with the 1.3.4 version.

I found this brief example of how to connect to and query an SQLite database file to be very helpful in getting up and going quickly.

```
#Connect to SQLite file
con <- dbConnect(SQLite(), dbname="data.db")

#Define query and store it in my_query
my_query <- dbSendQuery(con, "SELECT name from person_table")
#Fetch data using query and store it in my_data
my_data <- dbFetch(my_query)

#Clear the results cache from my_query
dbClearResult(my_query)

#Perform additional queries

#Disconnect from the database file
dbDisconnect(con)
```

dplyr also has sqlite functions

## Project Notes

### R Packages

The following packages are needed to work on the project.

Note that dbplyr is required to make database connections using dplyr functions.

```
library(tidyr)
library(dplyr)

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

library(dbplyr)

##
## Attaching package: 'dbplyr'

## The following objects are masked from 'package:dplyr':
##
##   ident, sql

library(readr)
```

### Connect to database

Note that dbplyr library is required in order for this command to work

```
# Connect to database
my_db <- src_sqlite("compData.db")
```

### Load relevant tables

The tables of interest are:

- *training\_diagnosis* contains diagnosis information (we need this in order to identify the patients diagnosed with diabetes)
- *training\_allergy* contains allergy information for patient
- *training\_medication* contains medication information for patient
- *training\_patient* contains gender and year of birth
- *training\_smoke* combines patient info with smoking statuses
- *lab tables* contain lab results
  - *training\_labResult* contains a record of lab results for a particular transcript
  - *training\_labPanel* links *training\_labResult* and *training\_labObservation*
  - *training\_labObservation* contains details regarding lab tests

```
diagnosis_tbl <- tbl(my_db, sql("SELECT DiagnosisGuid, PatientGuid, ICD9Code, StartYear, StopYear, Acute"))
```

```

allergy_tbl <- tbl(my_db, sql("SELECT AllergyGuid, PatientGuid, AllergyType, StartYear as AllergyStartYear, StopYear as AllergyStopYear, AllergyMedicationNdcCode as AllergyMedicationNdcCode, AllergyMedicationName as AllergyMedicationName FROM training_allergy"))
medication_tbl <- tbl(my_db, sql("SELECT MedicationGuid, PatientGuid, MedicationNdcCode, MedicationName, StartYear as MedicationStartYear, StopYear as MedicationStopYear FROM training_medication"))
patient_tbl <- tbl(my_db, sql("SELECT PatientGuid, Gender, YearOfBirth FROM training_patient"))
transcript_tbl <- tbl(my_db, sql("SELECT TranscriptGuid, PatientGuid, VisitYear, Height, Weight, BMI, SmokingStatus, SmokeEffectiveYear FROM training_transcript"))
smoke_tbl <- tbl(my_db, sql("SELECT PatientGuid, SmokeEffectiveYear, SmokingStatus_Description, SmokingStatus FROM training_smoke"))
# to get a single table that links the observation data back to the patient,
# join training_labResult, training_labPanel, and training_labObservation
lab_tbl <- left_join(left_join(tbl(my_db, sql("SELECT LabResultGuid, PatientGuid FROM training_labResult")), training_labPanel), training_labObservation)

```

## Identify target population

All Type 1 Diabetes diagnoses have an ICD9Code that starts with 205. We have a table with all of the diagnoses and one with only the diabetes diagnoses.

```

diabetes_tbl <- tbl(my_db, sql("SELECT DiagnosisGuid, PatientGuid, ICD9Code, StartYear, StopYear, Acute FROM training_diagnosis WHERE ICD9Code LIKE '205%'"))

## Observations: ??

## Warning in rsqLite_fetch(res@ptr, n = n): Column `StopYear`: mixed type,
## first seen values of type string, coercing other values of type integer

## Variables: 6
## $ DiagnosisGuid <chr> "AC80E20C-EEF2-4AA4-B9C8-00661EF88886", "43EA46E...
## $ PatientGuid <chr> "D76FC581-580A-4988-B13F-D4E9BD6763EA", "F6E5C45...
## $ ICD9Code <chr> "250.71", "250.61", "250.03", "250.61", "250.03"...
## $ StartYear <int> 0, 2010, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 2011, 0, ...
## $ StopYear <chr> "NULL", "NULL", "NULL", "NULL", "NULL", "NULL", ...
## $ Acute <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...

```

## Identify allergy data for target population

```

# join allergy_tbl to diabetes_tbl to get allergy data for diabetic patients
diabetes_allergy_tbl <- as_tibble(left_join(diabetes_tbl, allergy_tbl, by = c("PatientGuid")) %>%
  select(PatientGuid, AllergyGuid, AllergyType, ReactionName, SeverityName, AllergyMedicationNdcCode = AllergyMedicationNdcCode))

# add has_allergy to diabetes_allergy_tbl to indicate whether diabetic patient has allergies
diabetes_allergy_tbl <- diabetes_allergy_tbl %>%
  mutate(has_allergy = as.integer(!is.na(diabetes_allergy_tbl$AllergyGuid)))

glimpse(diabetes_allergy_tbl)

## Observations: 219
## Variables: 7
## $ PatientGuid <chr> "D76FC581-580A-4988-B13F-D4E9BD6763EA..."
## $ AllergyGuid <chr> NA, NA, NA, NA, NA, "2CDB164D-4AB8-4B..."
## $ AllergyType <chr> NA, NA, NA, NA, NA, "Medication", "Me..."
## $ ReactionName <chr> NA, NA, NA, NA, NA, "Shortness of bre..."
## $ SeverityName <chr> NA, NA, NA, NA, NA, "Modest", "Mild",..."
## $ AllergyMedicationNdcCode <chr> NA, NA, NA, NA, NA, "68462033905", "6..."
## $ has_allergy <int> 0, 0, 0, 0, 0, 1, 1, 1, 0, 0, 0, 0, 0, 0, 0, ...

```

## Identify medication data for target population

Exclude medication specifically given in response to diabetes diagnosis (?)

```
# join medication_tbl to diabetes_tbl to get medication data for diabetic patients
# filter out medication that is linked to the diabetes diagnosis
diabetes_medication_tbl <- as_tibble(left_join(diabetes_tbl, medication_tbl, by = c("PatientGuid"))) %>%
  filter(DiagnosisGuid.x != DiagnosisGuid.y) %>%
  select(PatientGuid, MedicationGuid, MedicationNdcCode)

# add has_meds to diabetes_medication_tbl to indicate whether diabetic patient has medication
diabetes_medication_tbl <- diabetes_medication_tbl %>%
  mutate(has_meds = as.integer(!is.na(diabetes_medication_tbl$MedicationGuid)))

glimpse(diabetes_medication_tbl)

## Observations: 1,099
## Variables: 4
## $ PatientGuid      <chr> "D76FC581-580A-4988-B13F-D4E9BD6763EA", "D76...
## $ MedicationGuid    <chr> "18D1EC29-6EB4-48C0-AF06-95E7F74D1270", "2D0...
## $ MedicationNdcCode <chr> "49483022110", "00247200674", "38245067973",...
## $ has_meds          <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,...
```

## Identify patient information for target population

```
# join patient_tbl to diabetes_tbl to get gender & age data for diabetic patients
diabetes_patient_tbl <- as_tibble(left_join(diabetes_tbl, patient_tbl, by = c("PatientGuid"))) %>%
  select(PatientGuid, Gender, YearOfBirth) %>% glimpse()

## Observations: 188
## Variables: 3
## $ PatientGuid <chr> "D76FC581-580A-4988-B13F-D4E9BD6763EA", "F6E5C45F-...
## $ Gender      <chr> "M", "F", "F", "M", "F", "F", "F", "M", "F", "M", ...
## $ YearOfBirth <int> 1927, 1960, 1959, 1947, 1968, 1934, 1987, 1949, 19...
```

## Identify smoking information for target population

Need to parse through results to identify smokers, former smokers, etc. How should these be grouped?

```
# join smoke_tbl to diabetes_tbl to get smoking data for diabetic patients
diabetes_smoke_tbl <- as_tibble(left_join(diabetes_tbl, smoke_tbl, by = c("PatientGuid"))) %>%
  select(PatientGuid, SmokeEffectiveYear, SmokingStatus_Description, SmokingStatus_NISTCode) %>%
  arrange(SmokingStatus_NISTCode) %>%
  glimpse()

## Observations: 191
## Variables: 4
## $ PatientGuid      <chr> "83706824-EF87-4916-ACEE-4727FF3A1C1...
## $ SmokeEffectiveYear <int> 2011, 2012, 2012, 2011, 2011, 2011, ...
## $ SmokingStatus_Description <chr> "Not a current tobacco user", "Not a...
## $ SmokingStatus_NISTCode    <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
```

## Identify lab information for target population

```
# join lab_tbl to diabetes_tbl to get lab results data for diabetic patients
diabetes_lab_tbl <- as_tibble(left_join(diabetes_tbl, lab_tbl, by = c("PatientGuid"))) %>%
  select(PatientGuid, LabObservationGuid, HL7Identifier, HL7Text, HL7CodingSystem, ObservationValue, Units)

# add has_labs to diabetes_lab_tbl to indicate whether diabetic patient has lab results
diabetes_lab_tbl <- diabetes_lab_tbl %>%
  mutate(has_labs = as.integer(!is.na(diabetes_lab_tbl$LabObservationGuid)))

glimpse(diabetes_lab_tbl)
```

```
## Observations: 312
## Variables: 12
## $ PatientGuid      <chr> "D76FC581-580A-4988-B13F-D4E9BD6763EA", "F6...
## $ LabObservationGuid <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ HL7Identifier     <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ HL7Text           <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ HL7CodingSystem   <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ ObservationValue   <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ Units             <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ ReferenceRange     <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ AbnormalFlags      <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ ResultStatus       <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ ObservationYear    <int> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ has_labs           <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0...
```

## disconnect from database

This is getting an error. May have to use a different method to connect

```
dbDisconnect(my_db)
```

## Revised process for loading and organizing data

Read the data files into R. Use select statements to pre-filter the desired columns.

```
patient <- read_csv("db/training_patient.csv")

diagnosis <- read_csv("db/training_diagnosis.csv") %>%
  select(DiagnosisGuid, PatientGuid, ICD9Code, StartYear, StopYear, Acute)

allergy <- read_csv("db/training_allergy.csv") %>%
  select(AllergyGuid, PatientGuid, AllergyType, AllergyStartYear = StartYear, ReactionName, SeverityName)

allergy <- transform(allergy, MedicationNdcCode = as.character(MedicationNdcCode))
medication <- read_csv("db/training_medication.csv") %>%
  select(MedicationGuid, PatientGuid, MedicationNdcCode, MedicationName, MedicationStrength, Schedule, Units)

immunization <- read_csv("db/training_immunization.csv") %>%
  select(ImmunizationGuid, PatientGuid, VaccineName, AdministeredYear, CvxCode)

# read in lab observations joined to include PatientGuid and PanelName
```

```

labs <- left_join(
  left_join(
    read_csv("db/training_labResult.csv") %>%
      select(LabResultGuid, PatientGuid, TranscriptGuid),
    read_csv("db/training_labPanel.csv") %>%
      select(LabResultGuid, LabPanelGuid, PanelName),
    by="LabResultGuid"
  ),
  read_csv("db/training_labObservation.csv"),
  by="LabPanelGuid"
)

# read in transcript table
transcript <- read_csv("db/training_transcript.csv") %>%
  select(TranscriptGuid, PatientGuid, VisitYear, Height, Weight, BMI, SystolicBP, DiastolicBP, Respirat

# read in smoke table
smoke <- read_csv("db/training_smoke.csv") %>%
  select(PatientGuid, SmokeEffectiveYear, SmokingStatus_Description, SmokingStatus_NISTCode)

#read in join tables
transDiag <- read_csv("db/training_transcriptDiagnosis.csv")
transMed <- read_csv("db/training_transcriptMedication.csv")
transAllergy <- read_csv("db/training_transcriptAllergy.csv")

```

join tables that link on transcript

```

#join diagnosis and transcript
diagJoin <- left_join(diagnosis, transDiag) %>% select(-TranscriptDiagnosisGuid)
diagTran <- left_join(diagJoin, transcript)
diagTran$TranscriptGuid[is.na(diagTran$TranscriptGuid)] <- "DIAG"

#join medication and transcript
medJoin <- left_join(medication, transMed) %>% select(-TranscriptMedicationGuid)
medTran <- left_join(medJoin, transcript)
medTran$TranscriptGuid[is.na(medTran$TranscriptGuid)] <- "MED"

# join allergy and transcript
allerJoin <- left_join(allergy, transAllergy) %>% select(-TranscriptAllergyGuid)
allerTran <- left_join(allerJoin, transcript)
allerTran$TranscriptGuid[is.na(allerTran$TranscriptGuid)] <- "ALLERGY"

# join medTran, diagTran, allerTran, and rest of transcript
allerDiagMedTran <- full_join(full_join(full_join(allerTran, diagTran), medTran), transcript)

```

give non-transcript tables TranscriptGuid column so that they join without causing cartesian products

```

smoke <- smoke %>% mutate(TranscriptGuid = "SMOKE")
immunization <- immunization %>% mutate(TranscriptGuid = "IMMUNIZATION")

```

join remaining tables

```

admts <- full_join(allerDiagMedTran, smoke)
admtsi <- full_join(admts, immunization)
admtsil <- full_join(admtsi, labs)
patient_pop_data <- left_join(patient, admtsil)

```

```
isolate diabetes patients
```

```
diabetes_pop_data <- patient_pop_data %>% filter(dmIndicator == 1)
```

```
glimpse(patient_pop_data)
```

```
## Observations: 462,414
## Variables: 53
## $ PatientGuid      <chr> "FB6EFC3D-1A20-4497-9CBD-00027CC5D22..."
## $ dmIndicator      <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ Gender           <chr> "M", "M", "M", "M", "M", "M", "M", "M", "...
## $ YearOfBirth      <int> 1929, 1929, 1929, 1929, 1929, 1929, ...
## $ State            <chr> "SD", "SD", "SD", "SD", "SD", "SD", ...
## $ PracticeGuid     <chr> "7BF4DAD8-5F67-4985-B911-20C9E89A373..."
## $ AllergyGuid      <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ AllergyType      <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ AllergyStartYear <int> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ ReactionName     <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ SeverityName     <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ MedicationNdcCode <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ TranscriptGuid    <chr> "5D30ACC4-1D99-482B-964A-8A80DE1F048..."
## $ VisitYear        <int> 2009, 2009, 2011, 2011, 2011, 2009, ...
## $ Height           <chr> "69", "69", "NULL", "NULL", "NULL", ...
## $ Weight           <dbl> 128, 128, 0, 137, 141, 128, 0, 137, ...
## $ BMI              <dbl> 18.900, 18.900, 0.000, 0.000, 0.000, ...
## $ SystolicBP       <chr> "NULL", "134", "136", "142", "132", ...
## $ DiastolicBP      <chr> "NULL", "72", "86", "71", "80", "72"...
## $ RespiratoryRate  <chr> "NULL", "NULL", "NULL", "NULL", "NUL...
## $ HeartRate        <chr> "NULL", "NULL", "NULL", "NULL", "NUL...
## $ Temperature     <chr> "NULL", "NULL", "NULL", "NULL", "NUL...
## $ DiagnosisGuid    <chr> "CF8EC250-BF6D-4C1C-84E3-489F349C007..."
## $ ICD9Code         <chr> "V58.69", "V58.69", "805.4", "805.4"...
## $ StartYear        <int> 0, 0, 2011, 2011, 2009, 2009, 2009, ...
## $ StopYear         <chr> "NULL", "NULL", "2011", "2011", "NUL...
## $ Acute            <int> 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, ...
## $ MedicationGuid   <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ MedicationName   <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ MedicationStrength <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ Schedule         <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ SmokeEffectiveYear <int> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ SmokingStatus_Description <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ SmokingStatus_NISTCode <int> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ ImmunizationGuid <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ VaccineName      <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ AdministeredYear <int> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ CvxCode          <int> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ LabResultGuid    <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ LabPanelGuid     <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ PanelName        <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ HL7Identifier    <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ HL7Text          <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ LabObservationGuid <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ HL7CodingSystem  <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
```

```
## $ ObservationValue <dbl> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ Units <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ ReferenceRange <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ AbnormalFlags <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ ResultStatus <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ ObservationYear <int> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ UserGuid <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ IsAbnormalValue <int> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
```

```
glimpse(diabetes_pop_data)
```

```
## Observations: 113,027
## Variables: 53
## $ PatientGuid <chr> "D2516A79-B6E2-4830-B637-002B16BA942..."
## $ dmIndicator <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, ...
## $ Gender <chr> "F", "F", "F", "F", "F", "F", "F", "F", "..."
## $ YearOfBirth <int> 1951, 1951, 1951, 1951, 1951, 1951, ...
## $ State <chr> "OK", "OK", "OK", "OK", "OK", "OK", ...
## $ PracticeGuid <chr> "444D72AC-4F3C-4571-81DF-FFB9B5F1601..."
## $ AllergyGuid <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ AllergyType <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ AllergyStartYear <int> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ ReactionName <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ SeverityName <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ MedicationNdcCode <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ TranscriptGuid <chr> "BF10ED38-3DAD-478D-A34A-682490ACD19..."
## $ VisitYear <int> 2010, 2011, 2009, 2010, 2011, 2010, ...
## $ Height <chr> "64", "NULL", "NULL", "NULL", "NULL", ...
## $ Weight <dbl> 255, 252, 0, 0, 252, 255, 250, 0, 0, ...
## $ BMI <dbl> 43.766, 0.000, 0.000, 0.000, 0.000, ...
## $ SystolicBP <chr> "132", "198", "NULL", "NULL", "198", ...
## $ DiastolicBP <chr> "75", "82", "NULL", "NULL", "82", "7..."
## $ RespiratoryRate <chr> "16", "NULL", "NULL", "NULL", "NULL", ...
## $ HeartRate <chr> "NULL", "NULL", "NULL", "NULL", "NUL..."
## $ Temperature <chr> "97.9", "97.9", "95.5", "NULL", "97..."
## $ DiagnosisGuid <chr> "6A20D092-EF35-41FE-93E0-2CE7B8A8CD8..."
## $ ICD9Code <chr> "787.0", "729.5", "465.9", "272.0", ...
## $ StartYear <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ StopYear <chr> "NULL", "NULL", "NULL", "NULL", "NUL..."
## $ Acute <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ MedicationGuid <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ MedicationName <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ MedicationStrength <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ Schedule <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ SmokeEffectiveYear <int> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ SmokingStatus_Description <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ SmokingStatus_NISTCode <int> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ ImmunizationGuid <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ VaccineName <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ AdministeredYear <int> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ CvxCode <int> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ LabResultGuid <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ LabPanelGuid <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ PanelName <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## $ HL7Identifier <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
```



## \$ HL7Text	<chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## \$ LabObservationGuid	<chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## \$ HL7CodingSystem	<chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## \$ ObservationValue	<dbl> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## \$ Units	<chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## \$ ReferenceRange	<chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## \$ AbnormalFlags	<chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## \$ ResultStatus	<chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## \$ ObservationYear	<int> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## \$ UserGuid	<chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...
## \$ IsAbnormalValue	<int> NA, NA, NA, NA, NA, NA, NA, NA, NA, ...