

EHR Vignette for Structured Data

Introduction

The **EHR** package provides several modules to perform diverse medication-related studies using data from electronic health record (EHR) databases. Especially, the package includes modules to perform pharmacokinetic/pharmacodynamic (PK/PD) analyses using EHRs, as outlined in Choi *et al.*¹, and additional modules will be added in the future. This vignette describes four modules for processing data (*Pro-Demographic*, *Pro-Med-Str*, *Pro-Drug Level*, *Pro-Laboratory*) and one module for PK data building (*Build-PK-IV*) for intravenously administered medications, when data are typically obtained from a structured database. The *Pro-Med-Str* module consists of two parts for processing structured medication data, one for intravenous (IV) infusion or bolus dose given to inpatients, one for electronic (e)-prescription medication data.

The process starts with structured data extracted by Structured Query Language (SQL) from EHRs or provided by a user, then moves through two phases: data processing which standardizes and combines the input data (*Pro-Med-Str*, *Pro-Drug Level*, etc.) and data building which creates the final PK data (*Build-PK-IV*).

The vignette has two examples. The first example demonstrates how to build PK data without using the data processing modules when cleaned concentration, drug dose, demographic and laboratory datasets are available in an appropriate data form. The second example shows how to use several data processing modules to standardize and combine more complex datasets, and build PK data using *Build-PK-IV*.

To begin we load the **EHR** package, the **pkdata** package, and the **lubridate** package.

```
# load EHR package and dependencies
library(EHR)
library(pkdata)
library(lubridate)
```

Example 1: Quick Data Building with Processed Datasets

The data for example 1 includes a demographic file, a concentration file, an IV dosing file, and a laboratory file, which are all cleaned and formatted appropriately. We also define a directory for the raw data and a directory for interactive checking output files.

```
# define directories
td <- tempdir()
checkDir <- file.path(td, 'check1')
rawDataDir <- system.file("examples", "str_ex1", package="EHR")
dir.create(checkDir)

# pre-processed demographic data
demo <- read.csv(file.path(rawDataDir, "Demographics_DATA_simple.csv"))
head(demo)
```

```
##   patient_id patient_visit_id gender weight height surgery_date ageatsurgery stat_sts cpb_sts
## 1           2                2.1      1  62.99 179.72   6/20/2015         6245      2      80
## 2           3                3.1      0   7.71  72.99  12/15/2018         574      3      67
```

```
## 3      4      4.1      1 12.00 92.02    1/12/2018      1214      1      70
## 4      5      5.1      0  5.89 56.13    5/13/2018      102      1     151
## 5      6      6.2      1  7.90 63.31    9/24/2018      343      2      50
## 6      6      6.1      1  6.16 60.89    5/26/2018      222      4      99
```

```
##   date_icu_dc time_fromor length_of_icu_stay  surgery_date_time
## 1   6/22/2015      NA           2              <NA>
## 2  12/16/2018      NA           1              <NA>
## 3   1/13/2018      NA           1              <NA>
## 4   5/14/2018    1427           1 2018-05-13 14:27:00
## 5   10/6/2018      NA          12              <NA>
## 6   8/13/2018    1958          79 2018-05-26 19:58:00
```

```
conc.data <- read.csv(file.path(rawDataDir,"Concentration_DATA_simple.csv"))
head(conc.data)
```

```
##   patient_id patient_visit_id event conc.level      date.time
## 1          10              10.1     4      0.17 2019-02-02 05:30:00
## 2          10              10.1     2      4.05 2019-02-24 14:00:00
## 3          10              10.1     3      0.64 2019-02-25 03:30:00
## 4          10              10.1     5      0.33 2019-02-27 02:45:00
## 5          10              10.1     6      0.07 2019-02-28 03:30:00
## 6          10              10.1     7      0.05 2019-03-01 02:35:00
```

```
ivdose.data <- read.csv(file.path(rawDataDir,"IVDose_DATA_simple.csv"))
head(ivdose.data)
```

```
##   patient_id date.dose   infuse.time.real      infuse.time infuse.dose bolus.time bolus.dose
## 1          1 2009-10-18 2009-10-18 11:35:00 2009-10-18 12:00:00      8.8      <NA>      NA
## 2          1 2009-10-18 2009-10-18 12:00:00 2009-10-18 12:00:00      8.8      <NA>      NA
## 3          1 2009-10-18 2009-10-18 13:00:00 2009-10-18 13:00:00      8.8      <NA>      NA
## 4          1 2009-10-18 2009-10-18 14:00:00 2009-10-18 14:00:00      8.8      <NA>      NA
## 5          1 2009-10-18 2009-10-18 15:00:00 2009-10-18 15:00:00      8.8      <NA>      NA
## 6          1 2009-10-18 2009-10-18 16:00:00 2009-10-18 16:00:00      8.8      <NA>      NA
```

```
##   given.dose maxint weight
## 1          0     60    4.4
## 2          0     60    4.4
## 3          0     60    4.4
## 4          0     60    4.4
## 5          0     60    4.4
## 6          0     60    4.4
```

```
creat.data <- read.csv(file.path(rawDataDir,"Creatinine_DATA_simple.csv"))
head(creat.data)
```

```
##   patient_id      date.time creat
## 1          2 2015-06-23 04:35:00 0.75
## 2          2 2015-06-22 04:00:00 0.69
## 3          2 2015-06-21 01:55:00 0.78
## 4          2 2015-06-24 03:45:00 0.64
## 5          2 2015-06-14 15:11:00 0.71
## 6          2 2015-06-20 20:14:00 0.58
```

The EHR package modules use a standardized naming convention for patient identification (ID) variables. We rename the unique patient-level ID from `patient_id` to `mod_id` and the visit-level ID from `patient_visit_id` to `mod_id_visit`. The visit-level ID can be used to distinguish different visits (i.e., occasions) when the same patient has multiple hospitalizations. If there is only a single visit per subject the unique patient-level ID and visit-level ID can be the same.

```
names(conc.data)[1:2] <- names(demo)[1:2] <- c("mod_id", "mod_id_visit")
names(creat.data)[1] <- names(ivdose.data)[1] <- "mod_id"
```

Using the four datasets, we can build a final PK dataset with the function `run_Build_PK_IV()`. Additional details for this function are provided below in the *Build-PK-IV* subsection of Example 2: Complete Data Processing and Building from Raw Extracted Data to PK Data.

```
simple_pk_dat <- run_Build_PK_IV(
  conc=conc.data,
  conc.columns = list(id = 'mod_id', datetime = 'date.time', druglevel = 'conc.level',
                      idvisit = 'mod_id_visit'),
  dose=ivdose.data,
  dose.columns = list(id = 'mod_id', date = 'date.dose', infuseDatetime = 'infuse.time',
                      infuseDose = 'infuse.dose', infuseTimeExact = 'infuse.time.real',
                      bolusDatetime = 'bolus.time', bolusDose = 'bolus.dose',
                      gap = 'maxint', weight = 'weight'),
  demo.list = demo,
  demo.columns = list(id = 'mod_id', idvisit = 'mod_id_visit'),
  lab.list = list(creat.data),
  lab.columns = list(id = 'mod_id', datetime = 'date.time'),
  drugname='fent',
  check.path=checkDir)
```

```
## 0 duplicated rows
## The dimension of the PK data before merging with demographics: 149 x 9
## The number of subjects in the PK data before merging with demographics: 10
## The number of subjects in the demographic file, who meet the exclusion
## criteria: 0
## check NA frequency in demographics, see file /tmp/Rtmp3Nbb0L/check1/
## fent-missing-demo.csv
## Some demographic variables are missing and will be excluded:
## The list of final demographic variables: gender
## weight
## height
## surgery_date
## ageatsurgery
## stat_sts
## cpb_sts
## date_icu_dc
## time_fromor
## length_of_icu_stay
## surgery_date_time
## weight_demo
## Checked: there are no missing creat
## The dimension of the final PK data exported with the key demographics:
## 149 x 20 with 10 distinct subjects (mod_id)
```

```
head(simple_pk_dat,15)
```

	mod_id_visit	time	amt	dv	rate	mdv	evid	gender	weight	height	surgery_date	ageatsurgery
## 1	1.2	0.00	50	NA	0	1	1	1	25.04	114.39	1/8/2016	2295
## 2	1.2	0.75	100	NA	0	1	1	1	25.04	114.39	1/8/2016	2295
## 3	1.2	1.65	100	NA	0	1	1	1	25.04	114.39	1/8/2016	2295
## 4	1.2	1.77	250	NA	0	1	1	1	25.04	114.39	1/8/2016	2295
## 5	1.2	2.05	250	NA	0	1	1	1	25.04	114.39	1/8/2016	2295

```

## 6      1.2  3.72 250   NA    0  1  1      1 25.04 114.39      1/8/2016      2295
## 7      1.2  5.23 100   NA    0  1  1      1 25.04 114.39      1/8/2016      2295
## 8      1.2  6.25  NA 2.83   NA  0  0      1 25.04 114.39      1/8/2016      2295
## 9      1.2 20.68  NA 0.41   NA  0  0      1 25.04 114.39      1/8/2016      2295
## 10     1.2 70.90  NA 0.04   NA  0  0      1 25.04 114.39      1/8/2016      2295
## 11     1.2 95.25  NA 0.01   NA  0  0      1 25.04 114.39      1/8/2016      2295
## 12     10.1 0.00  25   NA    0  1  1      0  6.06  63.20      2/24/2019      209
## 13     10.1 0.52 100   NA    0  1  1      0  6.06  63.20      2/24/2019      209
## 14     10.1 1.42  25   NA    0  1  1      0  6.06  63.20      2/24/2019      209
## 15     10.1 2.77  50   NA    0  1  1      0  6.06  63.20      2/24/2019      209
##      stat_sts  cpb_sts  date_icu_dc  time_fromor  length_of_icu_stay  surgery_date_time  weight_demo
## 1           2        79    1/9/2016      2020                1 2016-01-08 20:20:00      25.04
## 2           2        79    1/9/2016      2020                1 2016-01-08 20:20:00      25.04
## 3           2        79    1/9/2016      2020                1 2016-01-08 20:20:00      25.04
## 4           2        79    1/9/2016      2020                1 2016-01-08 20:20:00      25.04
## 5           2        79    1/9/2016      2020                1 2016-01-08 20:20:00      25.04
## 6           2        79    1/9/2016      2020                1 2016-01-08 20:20:00      25.04
## 7           2        79    1/9/2016      2020                1 2016-01-08 20:20:00      25.04
## 8           2        79    1/9/2016      2020                1 2016-01-08 20:20:00      25.04
## 9           2        79    1/9/2016      2020                1 2016-01-08 20:20:00      25.04
## 10          2        79    1/9/2016      2020                1 2016-01-08 20:20:00      25.04
## 11          2        79    1/9/2016      2020                1 2016-01-08 20:20:00      25.04
## 12          1       195    3/1/2019      2016                5 2019-02-24 20:16:00      6.06
## 13          1       195    3/1/2019      2016                5 2019-02-24 20:16:00      6.06
## 14          1       195    3/1/2019      2016                5 2019-02-24 20:16:00      6.06
## 15          1       195    3/1/2019      2016                5 2019-02-24 20:16:00      6.06
##      creat
## 1     0.60
## 2     0.60
## 3     0.60
## 4     0.60
## 5     0.60
## 6     0.60
## 7     0.60
## 8     0.60
## 9     0.50
## 10    0.54
## 11    0.57
## 12    0.64
## 13    0.64
## 14    0.64
## 15    0.64

```

Example 2: Complete Data Processing and Building from Raw Extracted Data to PK Data

To begin example 2 we define directories for the raw data, the processed data, and files used for interactive checking. If a file path for interactive checking is not provided, the interactive checking will not be performed.

```

dataDir <- file.path(td, 'data2')
checkDir <- file.path(td, 'check2')
rawDataDir <- system.file("examples", "str_ex2", package="EHR")

```

```
dir.create(dataDir)
dir.create(checkDir)
```

Pre-Processing for Raw Extracted Data

The raw data for example 2 includes a demographic file for use with the *Pro-Demographic* module; two files for the *Pro-Drug Level* module; two dosing files for the *Pro-Med-Str* module; and two lab files for use with the *Pro-Laboratory* module.

The structured datasets extracted by SQL must go through a pre-processing stage which creates new ID variables and datasets that can be used by the data processing modules. The following annotated example demonstrates the three main steps of pre-processing: (1) read and clean raw data; (2) merge raw data to create new ID variables; (3) make new data for use with modules.

Each raw dataset should contain a subject unique ID, a subject visit ID, or both ids. In this example the subject unique ID is called `subject_uid` and the subject visit ID is called `subject_id`. The subject visit ID is a combination of subject and visit/course – e.g., `subject_id` 14.0 is the first course for subject 14, `subject_id` 14.1 is the second course for subject 14, and so on. `subject_uid` is a unique ID that is the same for all subject records. The integer part of `subject_id` has a 1-to-1 correspondence with `subject_uid` – for this example, `subject_uid` 62734832 is associated with both `subject_id` 14.0 and `subject_id` 14.1. If there is only a single visit/course per subject only the subject unique ID is needed.

(1) Read and clean raw data

The demographics data file contains ID variables `subject_id` and `subject_uid`, in addition to demographic variables such as gender, date of birth, height, weight, etc. The `Demographics_DATA.csv` file is read in using the `readTransform()` function.

```
# demographics data
demo.in <- readTransform(file.path(rawDataDir, "Demographics_DATA.csv"))
head(demo.in)
```

```
##  subject_id subject_uid gender weight height surgery_date ageatsurgery stat_sts cpb_sts
## 1      1106      34364670      0   5.14  59.18    6/28/2014          141      3    133
## 2      1444      36792472      1   5.67  62.90    1/10/2016          292      1     65
## 3      1465      36292449      0  23.67 118.02    3/19/2016         2591      2    357
## 4      1520      34161967      0  14.07  97.04    7/18/2016         1320      5     93
## 5      1524      37857374      1  23.40 102.80    7/23/2016         1561      3     87
## 6      1550      37826262      1   6.21  62.03    9/4/2016          208      1    203
##  in_hospital_mortality add_ecmo date_icu_dc time_fromor
## 1                      0      0    7/2/2014         1657
## 2                      0      0    1/12/2016         1325
## 3                      0      0    3/20/2016           NA
## 4                      0      0    7/19/2016         1745
## 5                      1      0    7/30/2016         1847
## 6                      0      0    9/11/2016         1210
```

The example concentration data consists of two files, `SampleTimes_DATA.csv` and `SampleConcentration_DATA.csv` containing the concentration sampling times and values, respectively.

The sampling times data csv file is read in with `read.csv()`. Then the function `dataTransformation()` is used to rename the variable `Study.ID` to `subject_id` and to create a new variable called `samp`, which indexes the sample number, using the `modify=` argument.

```

# concentration sampling times data
# read in raw data
samp.raw <- read.csv(file.path(rawDataDir, "SampleTimes_DATA.csv"))
head(samp.raw)

##   Study.ID Event.Name Sample.Collection.Date.and.Time
## 1    466.1   Sample 1           2/3/2017 10:46
## 2    466.1   Sample 2           2/4/2017 20:30
## 3   1106.0   Sample 1           6/28/2014 13:40
## 4   1106.0   Sample 2           6/29/2014 03:10
## 5   1106.0   Sample 3           6/30/2014 03:35
## 6   1106.0   Sample 4           7/1/2014 03:45

# transform data
samp.in0 <- dataTransformation(samp.raw,
  rename = c('Study.ID' = 'subject_id'),
  modify = list(samp = expression(as.numeric(sub('Sample ', '', Event.Name)))))
head(samp.in0)

##   subject_id Event.Name Sample.Collection.Date.and.Time samp
## 1    466.1   Sample 1           2/3/2017 10:46      1
## 2    466.1   Sample 2           2/4/2017 20:30      2
## 3   1106.0   Sample 1           6/28/2014 13:40      1
## 4   1106.0   Sample 2           6/29/2014 03:10      2
## 5   1106.0   Sample 3           6/30/2014 03:35      3
## 6   1106.0   Sample 4           7/1/2014 03:45      4

```

Equivalently, the function `readTransform()` can be used to read in and transform the data with a single function call.

```

# read in and transform data
samp.in <- readTransform(file.path(rawDataDir, "SampleTimes_DATA.csv"),
  rename = c('Study.ID' = 'subject_id'),
  modify = list(samp = expression(as.numeric(sub('Sample ', '', Event.Name)))))
head(samp.in)

##   subject_id Event.Name Sample.Collection.Date.and.Time samp
## 1    466.1   Sample 1           2/3/2017 10:46      1
## 2    466.1   Sample 2           2/4/2017 20:30      2
## 3   1106.0   Sample 1           6/28/2014 13:40      1
## 4   1106.0   Sample 2           6/29/2014 03:10      2
## 5   1106.0   Sample 3           6/30/2014 03:35      3
## 6   1106.0   Sample 4           7/1/2014 03:45      4

```

The same steps can be used for the sample values data csv file. It is read in using `read.csv()`. Then using `dataTransformation()` the `subject_id` variable is created from the `name` variable using a call to the helper function `sampId()` in the `modify=` argument.

```

# concentration sample values data
# read in raw data
conc.raw <- read.csv(file.path(rawDataDir, "SampleConcentration_DATA.csv"))
head(conc.raw)

##   record_id   name fentanyl_calc_conc
## 1         1 466.1_1         0.01413622
## 2         2 466.1_2         0.27982075
## 3         3 1106_1         6.11873679

```

```
## 4      4  1106_2      0.59161716
## 5      5  1106_3      0.11280471
## 6      6  1106_4      0.02112153

# helper function used to make subject_id
sampId <- function(x) {
  # remove leading zeroes or trailing periods
  subid <- gsub('^0*|\\.$', '', x)
  # change _ to .
  gsub('_([0-9]+[_.]*)$', '\\1', subid)
}

# transform data
conc.in0 <- dataTransformation(conc.raw,
                               modify = list(
                                 subid = expression(sampId(name)),
                                 subject_id = expression(as.numeric(sub('[_].*', '', subid))),
                                 samp = expression(sub('[^_]*[_]', '', subid)),
                                 name = NULL,
                                 data_file = NULL,
                                 subid = NULL
                               )
                             )
head(conc.in0)
```

```
##   record_id fentanyl_calc_conc subject_id samp
## 1         1         0.01413622        466.1   1
## 2         2         0.27982075        466.1   2
## 3         3         6.11873679       1106.0   1
## 4         4         0.59161716       1106.0   2
## 5         5         0.11280471       1106.0   3
## 6         6         0.02112153       1106.0   4
```

Again, we can perform the same two steps with a single call to `readTransform()`.

```
# equivalent using readTransform()
conc.in <- readTransform(file.path(rawDataDir, "SampleConcentration_DATA.csv"),
                        modify = list(
                          subid = expression(sampId(name)),
                          subject_id = expression(as.numeric(sub('[_].*', '', subid))),
                          samp = expression(sub('[^_]*[_]', '', subid)),
                          name = NULL,
                          data_file = NULL,
                          subid = NULL
                        )
                      )
head(conc.in)
```

```
##   record_id fentanyl_calc_conc subject_id samp
## 1         1         0.01413622        466.1   1
## 2         2         0.27982075        466.1   2
## 3         3         6.11873679       1106.0   1
## 4         4         0.59161716       1106.0   2
## 5         5         0.11280471       1106.0   3
## 6         6         0.02112153       1106.0   4
```

The example drug dosing data consists of files `FLOW_DATA.csv` and `MAR_DATA.csv` containing two

sources of IV dose information (for details about these data sources, see *Pro-Med-Str* module below). The FLOW data csv file contains aliases for both ID variables; it is read in with the `readTransform()` function which renames the variables `Subject.Id` to `subject_id` and `Subject.Uniq.Id` to `subject_uid`, and creates the required `date.time`, `unit`, and `rate` variables.

```
# FLOW dosing data
flow.in <- readTransform(file.path(rawDataDir, "FLOW_DATA.csv"),
  rename = c('Subject.Id' = 'subject_id',
             'Subject.Uniq.Id' = 'subject_uid'),
  modify=list(
    date.time = expression(pkdata::parse_dates(EHR:::fixDates(Perform.Date))),
    unit = expression(sub('.*[ ]', '', Final.Rate..NFR.units)),
    rate = expression(as.numeric(sub('[0-9.]+.*', '\\1', Final.Rate..NFR.units)))
  )
)
head(flow.in)
```

```
##   subject_id subject_uid   Perform.Date FOCUS_MEDNAME Final.Wt..kg. Final.Rate..NFR.units.
## 1      1596    38340814   12/4/2016 5:30      Fentanyl         6.75             1 mcg/kg/hr
## 2      1596    38340814   12/4/2016 6:00      Fentanyl         6.75             1 mcg/kg/hr
## 3      1596    38340814   12/4/2016 7:00      Fentanyl         6.75             1 mcg/kg/hr
## 4      1596    38340814   12/4/2016 7:40      Fentanyl         6.75             0 mcg/kg/hr
## 5      1607    38551767  12/24/2016 19:30      Fentanyl         2.60             2 mcg/kg/hr
## 6      1607    38551767  12/24/2016 20:00      Fentanyl         2.60             2 mcg/kg/hr
##   Final.Units Flow      date.time      unit rate
## 1      3.375   NA 2016-12-04 05:30:00 mcg/kg/hr    1
## 2      6.750   0.1 2016-12-04 06:00:00 mcg/kg/hr    1
## 3      4.500   0.1 2016-12-04 07:00:00 mcg/kg/hr    1
## 4      0.000   NA 2016-12-04 07:40:00 mcg/kg/hr    0
## 5      2.600   NA 2016-12-24 19:30:00 mcg/kg/hr    2
## 6      5.200   0.2 2016-12-24 20:00:00 mcg/kg/hr    2
```

The MAR data csv file contains several variables with a colon (:) character. To preserve the colon in these variable names, the data can be read in without checking for syntactically valid R variable names. The data is read in using `read.csv()` with the argument `check.names = FALSE` and then passed to the `dataTransformation()` function which renames `Uniq.Id` to `subject_uid`.

```
# MAR dosing data
mar.in0 <- read.csv(file.path(rawDataDir, "MAR_DATA.csv"), check.names = FALSE)
mar.in <- dataTransformation(mar.in0, rename = c('Uniq.Id' = 'subject_uid'))
head(mar.in)
```

```
##   subject_uid   Date   Time      med:mDrug med:dosage med:route med:freq med:given
## 1    28579217 2017-02-04 19:15      Nicardipine 3 mcg/kg/min      IV      <NA>      Given
## 2    28579217 2011-10-02 22:11      Famotidine    4.5 mg      IV    q12hrs      Given
## 3    28579217 2011-10-02 20:17      Morphine sulfate    1 mg      IV    q2h prn      Given
## 4    28579217 2011-10-03 02:28 Diphenhydramine injection    12 mg      IV      now      Given
## 5    28579217 2011-10-02 22:11      Cefazolin    225 mg      IV    q8hrs      Given
## 6    28579217 2011-10-02 23:30      Morphine sulfate    1 mg      IV    q2h prn      Given
```

The example laboratory data consists of files `Creatinine_DATA.csv` and `Albumin_DATA.csv`. Both files are read in using the `readTransform()` function and `Subject.uniq` is renamed to `subject_uid`.

```
# Serum creatinine lab data
creat.in <- readTransform(file.path(rawDataDir, "Creatinine_DATA.csv"),
  rename = c('Subject.uniq' = 'subject_uid'))
head(creat.in)
```



```
##      subject_uid      date time creat
## 1      28579217 02/05/17 4:00  0.52
## 2      28579217 02/06/17 5:00  0.53
## 3      28579217 10/03/11 4:28  0.42
## 4      28579217 10/04/11 4:15  0.35
## 5      28579217 10/06/11 4:25  0.29
## 6      28579217 10/09/11 4:45  0.28

# Albumin lab data
alb.in <- readTransform(file.path(rawDataDir, "Albumin_DATA.csv"),
  rename = c('Subject.uniq' = 'subject_uid'))
head(alb.in)

##      subject_uid      date  time alb
## 1      35885929 07/30/20   5:23 2.9
## 2      35885929 07/28/20   3:12 2.0
## 3      35885929 07/29/20   1:39 2.7
## 4      35885929 08/21/20  10:35 4.1
## 5      36292449 06/13/15  17:20 4.1
## 6      37857374 07/25/16   8:35 2.3
```

(2) Merge data to create new ID variables

The function `idCrosswalk()` merges all of the cleaned input datasets and creates new IDs. The `data=` argument of this function accepts a list of input datasets and the `idcols=` argument accepts a list of vectors or character strings that identify the ID variables in the corresponding input dataset.

The output of `idCrosswalk()` is a crosswalk dataset between the original ID variables (`subject_id`, `subject_uid`) and the new ID variables (`mod_id`, `mod_visit`, and `mod_id_visit`). The new variable `mod_id_visit` has a 1-to-1 correspondence to variable `subject_id` and uniquely identifies each subjects' visit/course; the new variable `mod_id` has a 1-to-1 correspondence to variable `subject_uid` and uniquely identifies each subject.

```
# merge all ID datasets
data <- list(demo.in,
  samp.in,
  conc.in,
  flow.in,
  mar.in,
  creat.in,
  alb.in)

idcols <- list(c('subject_id', 'subject_uid'), # id vars in demo.in
  'subject_id', # id var in samp.in
  'subject_id', # id var in conc.in
  c('subject_id', 'subject_uid'), # id vars in flow.in
  'subject_uid', # id var in mar.in
  'subject_uid', # id var in creat.in
  'subject_uid') # id var in creat.in

mod.id <- idCrosswalk(data, idcols, visit.id="subject_id", uniq.id="subject_uid")
saveRDS(mod.id, file=file.path(dataDir, "Fentanyl_module_id.rds"))

mod.id

##      subject_id subject_uid mod_visit mod_id mod_id_visit
```

## 1	466.0	28579217	1	1	1.1
## 2	466.1	28579217	2	1	1.2
## 3	1106.0	34364670	1	2	2.1
## 4	1444.0	36792472	1	3	3.1
## 5	1465.0	36292449	1	4	4.1
## 6	1520.0	34161967	1	5	5.1
## 7	1524.0	37857374	1	6	6.1
## 8	1550.0	37826262	1	7	7.1
## 9	1566.0	35885929	1	8	8.1
## 10	1566.1	35885929	2	8	8.2
## 11	1596.0	38340814	1	9	9.1
## 12	1607.0	38551767	1	10	10.1
## 13	1607.1	38551767	2	10	10.2
## 14	1724.0	39087607	1	11	11.1
## 15	1770.0	39418554	1	12	12.1
## 16	1770.1	39418554	2	12	12.2
## 17	2157.0	42023523	1	13	13.1
## 18	2162.0	42044808	1	14	14.1
## 19	2164.0	41221120	1	15	15.1

(3) Make new data for use with modules

The function `pullFakeId()` replaces the original IDs – `subject_id` and `subject_uid` – with new IDs – `mod_id`, `mod_visit`, and `mod_id_visit` – to create datasets which can be used by the data processing modules. Generally, the function call to `pullFakeId()` is

```
pullFakeId(dat, xwalk, firstCols = NULL, orderBy = NULL)
```

The `dat=` argument should contain the cleaned input data.frame from pre-processing step (1) and the `xwalk=` argument should contain the crosswalk data.frame produced in step (2). Additional arguments `firstCols=` and `orderBy=` control which variables are in the first columns of the output and the sort order, respectively. The cleaned structured data are saved as R objects for use with the modules.

```
## demographics data
demo.cln <- pullFakeId(demo.in, mod.id,
  firstCols = c('mod_id', 'mod_visit', 'mod_id_visit'),
  uniq.id = 'subject_uid')
head(demo.cln)
```

##	mod_id	mod_visit	mod_id_visit	gender	weight	height	surgery_date	ageatsurgery	stat_sts	cpb_sts
## 1	2	1	2.1	0	5.14	59.18	6/28/2014	141	3	133
## 2	3	1	3.1	1	5.67	62.90	1/10/2016	292	1	65
## 3	4	1	4.1	0	23.67	118.02	3/19/2016	2591	2	357
## 4	5	1	5.1	0	14.07	97.04	7/18/2016	1320	5	93
## 5	6	1	6.1	1	23.40	102.80	7/23/2016	1561	3	87
## 6	7	1	7.1	1	6.21	62.03	9/4/2016	208	1	203

##	in_hospital_mortality	add_ecmo	date_icu_dc	time_fromor
## 1		0	7/2/2014	1657
## 2		0	1/12/2016	1325
## 3		0	3/20/2016	NA
## 4		0	7/19/2016	1745
## 5		1	7/30/2016	1847
## 6		0	9/11/2016	1210

```
saveRDS(demo.cln, file=file.path(dataDir,"Fentanyl_demo_mod_id.rds"))
```

```
## drug level data
```

```
# sampling times
```

```
samp.cln <- pullFakeId(samp.in, mod.id,
  firstCols = c('mod_id', 'mod_visit', 'mod_id_visit', 'samp'),
  orderBy = c('mod_id_visit','samp'),
  uniq.id = 'subject_uid')
head(samp.cln)
```

```
##   mod_id mod_visit mod_id_visit samp Event.Name Sample.Collection.Date.and.Time
## 1      1          2          1.2   1 Sample 1           2/3/2017 10:46
## 2      1          2          1.2   2 Sample 2           2/4/2017 20:30
## 3     10          1         10.1   1 Sample 1          12/23/2016 05:15
## 4     10          1         10.1   2 Sample 2          12/24/2016 18:00
## 5     10          1         10.1   3 Sample 3          12/25/2016 03:00
## 6     10          1         10.1   4 Sample 4          12/26/2016 04:00
```

```
saveRDS(samp.cln, file=file.path(dataDir,"Fentanyl_samp_mod_id.rds"))
```

```
# sampling concentrations
```

```
conc.cln <- pullFakeId(conc.in, mod.id,
  firstCols = c('record_id', 'mod_id', 'mod_visit', 'mod_id_visit', 'samp'),
  orderBy = 'record_id',
  uniq.id = 'subject_uid')
head(conc.cln)
```

```
##   record_id mod_id mod_visit mod_id_visit samp fentanyl_calc_conc
## 1          1      1          2          1.2   1      0.01413622
## 2          2      1          2          1.2   2      0.27982075
## 3          3      2          1          2.1   1      6.11873679
## 4          4      2          1          2.1   2      0.59161716
## 5          5      2          1          2.1   3      0.11280471
## 6          6      2          1          2.1   4      0.02112153
```

```
saveRDS(conc.cln, file=file.path(dataDir,"Fentanyl_conc_mod_id.rds"))
```

```
## dosing data
```

```
# flow
```

```
flow.cln <- pullFakeId(flow.in, mod.id,
  firstCols = c('mod_id', 'mod_visit', 'mod_id_visit'),
  uniq.id = 'subject_uid')
head(flow.cln)
```

```
##   mod_id mod_visit mod_id_visit Perform.Date FOCUS_MEDNAME Final.Wt..kg. Final.Rate..NFR.units.
## 1      9          1          9.1 12/4/2016 5:30      Fentanyl           6.75           1 mcg/kg/hr
## 2      9          1          9.1 12/4/2016 6:00      Fentanyl           6.75           1 mcg/kg/hr
## 3      9          1          9.1 12/4/2016 7:00      Fentanyl           6.75           1 mcg/kg/hr
## 4      9          1          9.1 12/4/2016 7:40      Fentanyl           6.75           0 mcg/kg/hr
## 5     10          1         10.1 12/24/2016 19:30      Fentanyl           2.60           2 mcg/kg/hr
## 6     10          1         10.1 12/24/2016 20:00      Fentanyl           2.60           2 mcg/kg/hr
##   Final.Units Flow      date.time      unit rate
## 1      3.375   NA 2016-12-04 05:30:00 mcg/kg/hr    1
## 2      6.750   0.1 2016-12-04 06:00:00 mcg/kg/hr    1
## 3      4.500   0.1 2016-12-04 07:00:00 mcg/kg/hr    1
```

```
## 4      0.000    NA 2016-12-04 07:40:00 mcg/kg/hr    0
## 5      2.600    NA 2016-12-24 19:30:00 mcg/kg/hr    2
## 6      5.200    0.2 2016-12-24 20:00:00 mcg/kg/hr    2

saveRDS(flow.cln, file=file.path(dataDir,"Fentanyl_flow_mod_id.rds"))

# mar
mar.cln <- pullFakeId(mar.in, mod.id, firstCols = 'mod_id', uniq.id = 'subject_uid')
head(mar.cln)

##   mod_id      Date   Time                med:mDrug  med:dosage med:route med:freq med:given
## 1      1 2017-02-04 19:15             Nicardipine 3 mcg/kg/min          IV    <NA>      Given
## 2      1 2011-10-02 22:11             Famotidine      4.5 mg          IV   q12hrs      Given
## 3      1 2011-10-02 20:17      Morphine sulfate        1 mg          IV   q2h prn      Given
## 4      1 2011-10-03 02:28 Diphenhydramine injection    12 mg          IV     now      Given
## 5      1 2011-10-02 22:11             Cefazolin     225 mg          IV    q8hrs      Given
## 6      1 2011-10-02 23:30      Morphine sulfate        1 mg          IV   q2h prn      Given

saveRDS(mar.cln, file=file.path(dataDir,"Fentanyl_mar_mod_id.rds"))

## laboratory data
creat.cln <- pullFakeId(creat.in, mod.id, 'mod_id',uniq.id = 'subject_uid')
head(creat.cln)

##   mod_id      date time creat
## 1      1 02/05/17 4:00 0.52
## 2      1 02/06/17 5:00 0.53
## 3      1 10/03/11 4:28 0.42
## 4      1 10/04/11 4:15 0.35
## 5      1 10/06/11 4:25 0.29
## 6      1 10/09/11 4:45 0.28

alb.cln <- pullFakeId(alb.in, mod.id, 'mod_id', uniq.id = 'subject_uid')
head(alb.cln)

##   mod_id      date   time alb
## 1      8 07/30/20  5:23 2.9
## 2      8 07/28/20  3:12 2.0
## 3      8 07/29/20  1:39 2.7
## 4      8 08/21/20 10:35 4.1
## 5      4 06/13/15 17:20 4.1
## 6      6 07/25/16  8:35 2.3

saveRDS(creat.cln, file=file.path(dataDir,"Fentanyl_creat_mod_id.rds"))
saveRDS(alb.cln, file=file.path(dataDir,"Fentanyl_alb_mod_id.rds"))
```

Before running the processing modules, it is necessary to define several options and parameters. Using `options(pkxwalk =)` allows the modules to access the crosswalk file. We also create a `drugname` stub and define the lower limit of quantification (LLOQ) for the drug of interest, which is optional.

```
# set crosswalk option
xwalk <- readRDS(file.path(dataDir, "Fentanyl_module_id.rds"))
oldxwalk <- options(pkxwalk = 'xwalk')

# define parameters
drugname <- 'fent'
LLOQ <- 0.05
```

Pro-Demographic

The *Pro-Demographic* module accepts the cleaned structured demographic dataset and a user-defined set of exclusion criteria and returns a formatted list with the demographic data and records meeting the exclusion criteria suitable for integration with the other modules. For this example, we exclude subjects with a value of 1 for `in_hospital_mortality` or `add_ecmo` and create a new variable called `length_of_icu_stay`.

The demographic data can be processed by the `run_Demo()` function using:

```
# helper function
exclude_val <- function(x, val=1) { !is.na(x) & x == val }

demo.out <- run_Demo(demo.path = file.path(dataDir, "Fentanyl_demo_mod_id.rds"),
  demo.columns = list(id = 'mod_id_visit'),
  toexclude = expression(exclude_val(in_hospital_mortality) | exclude_val(add_ecmo)),
  demo.mod.list = list(length_of_icu_stay =
    expression(daysDiff(surgery_date, date_icu_dc))))
```

```
## The number of subjects in the demographic data, who meet the exclusion criteria: 2
```

```
head(demo.out$demo)
```

```
##   mod_id mod_visit mod_id_visit gender weight height surgery_date ageatsurgery stat_sts cpb_sts
## 1      2         1          2.1     0   5.14  59.18   6/28/2014          141         3      133
## 2      3         1          3.1     1   5.67  62.90   1/10/2016          292         1       65
## 3      4         1          4.1     0  23.67 118.02   3/19/2016         2591         2     357
## 4      5         1          5.1     0  14.07  97.04   7/18/2016         1320         5       93
## 5      6         1          6.1     1  23.40 102.80   7/23/2016         1561         3       87
## 6      7         1          7.1     1   6.21  62.03   9/4/2016          208         1     203
##   in_hospital_mortality add_ecmo date_icu_dc time_fromor length_of_icu_stay
## 1                      0         0   7/2/2014          1657             4
## 2                      0         0  1/12/2016           1325             2
## 3                      0         0  3/20/2016              NA             1
## 4                      0         0  7/19/2016           1745             1
## 5                      1         0  7/30/2016           1847             7
## 6                      0         0  9/11/2016           1210             7
```

```
demo.out$exclude
```

```
## [1] "6.1" "13.1"
```

- The `run_Demo` function arguments are as follows:
 - `demo.path`: file name of demographic file (CSV, RData, RDS) or data.frame
 - `demo.columns`: a named list that should specify columns in demo data; `id` is required
 - `toexclude`: (optional) a set of user-defined expressions to set exclusion rules to be applied to the demographic dataset within the module
 - `demo.mod.list`: (optional) a list of user defined expressions to set modification rules within the module

See the `run_Demo()` function documentation for more examples.

- The output of `run_Demo()` is a list with two components: `demo`, a dataframe containing a demographic information and `exclude`, vector of excluded visit IDs.

Pro-Med-Str

The *Pro-Med-Str* module processes structured medication data. Part I handles IV dose data and Part II handles e-prescription dose data.

Part I: IV dose data

Part I handles IV dose data from two sources, Flow data and Medication Administration Records (MAR) data. In this example, the Flow data are patient flow sheets which record infusion rates and changes outside of the operating room, while the MAR data record all bolus and infusion doses administered in the operating room before 11/01/2017. After 11/01/2017 when a new EHR system – *Epic* – was implemented, MAR data recorded all types of medications for inpatients. Thus, while MAR data is required, the use of Flow sheet data is optional for this module. The module can be semi-interactive for data checking (although it is not required, we recommend using this feature); if `check.path` is provided (the default is `NULL`), it can generate several files to check potential data errors and get feedback from an investigator. If corrected information ('fix' files) are provided, the module should be re-run to incorporate the corrections. The major functions of this module are:

- Process MAR data using the given medications in the `medchk.path` file, infusion units, bolus units, and bolus rate threshold. If there are data rows containing units other than those specified, a file listing these records will be produced using the `failunit_fn` stub appended with drugname.
 - e.g., if `failunit_fn` is 'Unit' the file 'failUnit-fent.csv' will be created in the `check.path` directory. The corrected file should replace 'fail' with 'fix' (e.g., 'fixUnit-fent.csv'), and include an additional variable called 'flag' with the value 'keep' for the records to be retained.
- Process and clean Flow data, which remove duplicate records, including invalid duplicate rows with `final.units` of 0, rate missing, one rate or unit missing, one unit of 0, or additional discrepancy.
- Check for records with a unit containing 'kg' (e.g., 'mcg/kg/hr') but missing weight in flow data. These records will result in a calculated rate of NA when producing standardized rates (see step below). If there are records with missing weight, a file listing these records will be produced using the `failnowgt_fn` stub appended with drugname. A 'fix' file can be added to correct these records.
- Combine Flow and MAR infusion data and produce standardized rate (dose per unit time). Infusion rates with dose per weight per unit time (e.g., 'mcg/kg/hr') and dose per unit time ('mcg/hr') can both be handled. For infusion rates of dose per weight per unit time, weight is imputed using the closest available Flow weight (if possible) and the rate is multiplied by weight to get dose per unit time. Infusion rates of dose per unit time are assumed to be formatted correctly.
- Merge infusion dose data and bolus dose data and conform doses. See the `pkdata::conformDoses()` documentation for additional details.

The IV dose data can be processed by the `run_MedStrI()` function using:

```
ivdose.out <- run_MedStrI(
  mar.path=file.path(dataDir,"Fentanyl_mar_mod_id.rds"),
  mar.columns = list(id = 'mod_id', datetime = c('Date','Time'), dose = 'med:dosage',
    drug = 'med:mDrug', given = 'med:given'),
  medGivenReq = TRUE,
  flow.path=file.path(dataDir,"Fentanyl_flow_mod_id.rds"),
  flow.columns = list(id = 'mod_id', datetime = 'date.time', finalunits = 'Final.Units',
    unit = 'unit', rate = 'rate', weight = 'Final.Wt..kg.'),
  medchk.path = file.path(rawDataDir, sprintf('medChecked-%s.csv', drugname)),
  demo.list = NULL,
  demo.columns = list(),
  missing.wgt.path = NULL,
  wgt.columns = list(),
  check.path = checkDir,
  failflow_fn = 'FailFlow',
  failunit_fn = 'Unit',
  failnowgt_fn = 'NoWgt',
  infusion.unit = 'mcg/kg/hr',
```

```

bolus.unit = 'mcg',
bol.rate.thresh = Inf,
rateunit = 'mcg/hr',
ratewtunit = 'mcg/kg/hr',
weightunit = 'kg',
drugname = drugname)

```

```

## The number of rows in the original data          124
## The number of rows after removing the duplicates 124
## no units other than mcg/kg/hr or mcg, file /tmp/Rtmp3Nbb0L/check2/
##      failUnit-fent.csv not created
## #####
## 33 rows from 1 subjects with "kg" in infusion unit but missing weight,
##      see file /tmp/Rtmp3Nbb0L/check2/failNoWgt-fent.csv AND create /tmp/
##      Rtmp3Nbb0L/check2/fixNoWgt-fent.csv
## #####
## #####
## censor dates created, please see /tmp/Rtmp3Nbb0L/check2/CensorTime-fent.csv
## #####

```

```
head(ivdose.out)
```

```

##   mod_id  date.dose  infuse.time.real  infuse.time  infuse.dose      bolus.time  bolus.dose
## 1      1  2011-10-02                <NA>         <NA>         NA  2011-10-02  15:35:00         25
## 2      1  2011-10-02                <NA>         <NA>         NA  2011-10-02  17:26:00         25
## 3      1  2017-02-04                <NA>         <NA>         NA  2017-02-04  16:15:00         50
## 4      1  2017-02-04                <NA>         <NA>         NA  2017-02-04  16:30:00         20
## 5      1  2017-02-04                <NA>         <NA>         NA  2017-02-04  20:57:00         20
## 6      2  2014-06-28                <NA>         <NA>         NA  2014-06-28  08:15:00         20
##   given.dose maxint  weight
## 1          NA      0      NA
## 2          NA      0      NA
## 3          NA      0      NA
## 4          NA      0      NA
## 5          NA      0      NA
## 6          NA      0      NA

```

- The `run_MedStrI` function arguments are as follows:
 - `mar.path`: filename of MAR data (CSV, RData, RDS), or `data.frame`
 - `mar.columns`: a named list that should specify columns in MAR data; 'id', 'datetime' and 'dose' are required. 'drug', 'weight', 'given' may also be specified. 'datetime' is date and time for data measurement, which can refer to a single date-time variable (`datetime = 'date_time'`) or two variables holding date and time separately (e.g., `datetime = c('Date', 'Time')`). 'dose' can also be given as a single variable or two variables. If given as a single column, the column's values should contain dose and units such as '25 mcg'. If given as two column names, the dose column should come before the unit column (e.g., `dose = c('doseamt', 'unit')`). If 'drug' is present, the 'medchk.path' argument should also be provided. The 'given' variable should be used in conjunction with the 'medGivenReq' argument.
 - `medGivenReq`: indicator if values in the MAR given column should equal "Given"; if this is FALSE (the default), NA values are also acceptable.
 - `flow.path`: (optional) file name of flow data (CSV, RData, RDS), or `data.frame`
 - `flow.columns`: a named list that should specify columns in flow data; 'id', 'datetime', 'finalunits', 'unit', 'rate', 'weight' are required. 'idvisit' may also be specified. 'datetime' is date and time for data measurement, which can refer to a single date-time variable (`datetime = 'date_time'`) or two variables holding date and time separately (e.g., `datetime = c('Date', 'Time')`).

- **medchk.path**: (optional) file name containing data set (CSV, RData, RDS), or data.frame; should have the column ‘medname’ with list of acceptable drug names used to filter MAR data.
- **demo.list**: (optional) demographic data; if available, the output from `run_Demo` or a correctly formatted data.frame, which can be used to impute weight when missing
- **demo.columns**: a named list that should specify columns in demographic data; ‘id’, ‘datetime’, and ‘weight’ are required. ‘datetime’ is the date and time when the demographic data were obtained, which can refer to a single date-time variable (datetime = ‘date_time’) or two variables holding date and time separately (e.g., datetime = c(‘Date’, ‘Time’)).
- **missing.wgt.path**: (optional) filename containing additional weight data (CSV, RData, RDS), or data.frame. The variables in this file should be defined in the ‘wgt.columns’ argument.
- **wgt.columns**: a named list that should specify columns in weight data; ‘id’, ‘datetime’, and ‘weight’ are required. ‘datetime’ is date and time for weight measurement, which can refer to a single date-time variable (datetime = ‘date_time’) or two variables holding date and time separately (e.g., datetime = c(‘Date’, ‘Time’)).
- **check.path**: (optional) file path where the generated files for data checking are stored, and the corresponding data files with fixed data exist. The default (NULL) will not produce any check files.
- **failflow_fn**: filename stub for invalid duplicate rows in the Flow data with rate of 0 check file. The stub will be prepended with the string ‘fail’ to create a .csv with the invalid data. The corrected data with failures replaced should use the same filename stub prepended with the string ‘fix’.
 - * e.g., if **failflow_fn** is ‘FailFlow’, the file ‘failFailFlow.csv’ with invalid duplicate rows will be created in the directory specified by **check.path**. The corrected version named ‘fixFailFlow.csv’ should be placed in the same directory.
- **failunit_fn**: filename stub for records with units other than those specified with **infusion.unit** and **bolus.unit**
- **failnowgt_fn**: filename stub for records with missing weight in the Flow data and unit involving ‘kg’
- **infusion.unit**: string specifying units for infusion doses (default: ‘mcg/kg/hr’)
- **bolus.unit**: string specifying units for bolus doses (default: ‘mcg’)
- **bol.rate.thresh**: upper bound for retaining bolus doses. Bolus units with a rate above the threshold are dropped (default: Inf; i.e., keep all bolus doses)
- **rateunit**: string specifying units for hourly rate (default: ‘mcg/hr’)
- **ratewgtunit**: string specifying units for hourly rate by weight (default: ‘mcg/kg/hr’)
- **weightunit**: string specifying units for weight (default: ‘kg’)
- **drugname**: drug name of interest (e.g., dex, fent)
- The output of the `run_MedStrI` function is a dataset with processed IV dosing data with the following variables:
 - user provided identification numbers for further merging with the output from other modules (e.g., `mod_id` in this example data)
 - `date.dose`: date of dose administration
 - `infuse.time.real`: actual infusion dosing time
 - `infuse.time`: infusion dose time processed (rounded time) based on continuous infusion time
 - `infuse.dose`: infusion dose amount (e.g., calculated by rate \times weight if the unit includes weight)
 - `bolus.time`: bolus dose time
 - `bolus.dose`: bolus dose amount
 - `given.dose`: the raw dose given is preserved from the flow sheet data when available (identified as “finalunits” in `flow.columns`)
 - `maxint`: infusion recording interval (e.g., default: `maxint` = 15 min for MAR data; `maxint` = 60 min for flow data). In a typical setting this variable should be unused but it may be specified as the “gap” variable in the “dose.columns” argument of the `run_Build_PK_IV` function (see *Build-PK-IV* below for details).
 - `weight`: subject body weight recorded near infusion time, which will be used in dose calculation

Part II: e-prescription data

Part II handles e-prescription data. To use this module, all prescriptions must be for only one drug. Different names, such as brand names and generic names, for the same drug are allowed (e.g., Lamictal and lamotrigine). The data used in this module must include columns for ID, date, strength, dose amount, and frequency. The major tasks the module performs are as follows:

- Creating numeric variables for strength, dose, and frequency
- Calculating daily dose
- Removing duplicate daily doses for a patient

There are two underlying functions used in this module. `processErx` performs the basic cleaning described above. `processErxAdd1` performs some additional processing for more complicated dose expressions.

Below is example e-prescription data including columns for ID, drug name, dose, frequency, date, strength, and description.

```
(erX <- read.csv(file.path(rawDataDir,"e-rx_DATA.csv"),stringsAsFactors = FALSE))
```

```
##  GRID    MED_NAME  RX_DOSE          FREQUENCY ENTRY_DATE STRENGTH_AMOUNT
## 1  ID1 lamotrigine      1             bid 2009-02-24           100
## 2  ID2 lamotrigine      2             bid 2006-12-30           100
## 3  ID2  Lamictal       1             bid 2006-12-30           200
## 4  ID3 Lamictal XR      3             bid 2004-08-24
## 5  ID4 lamotrigine      1       twice a day 2010-05-22       200 mg
## 6  ID5 lamotrigine    2 tabs             qam 2007-06-13           200
## 7  ID6 lamotrigine 1.5+1+1.5 brkfst, lunch, dinner 2015-03-14           100
##                                     DESCRIPTION
## 1 lamotrigine 100 mg tablet (Also Known As Lamictal)
## 2 lamotrigine 100 mg tablet (Also Known As Lamictal)
## 3                                     LaMictal 200 mg tablet
## 4                                     Lamictal XR 100 mg 24 hr Tab
## 5 lamotrigine 200 mg tablet (Also Known As Lamictal)
## 6                                     LaMictal XR 200 mg tablet,extended release
## 7 lamoTRigine 100 mg tablet (Also Known As Lamictal)
```

The e-prescription data can be processed by the `run_MedStrII` function using:

```
erX.out <- run_MedStrII(file.path(rawDataDir,"e-rx_DATA.csv"),
  dat.columns = list(id = 'GRID', dose = 'RX_DOSE', freq = 'FREQUENCY', date = 'ENTRY_DATE',
    str = 'STRENGTH_AMOUNT', desc = 'DESCRIPTION')
)
```

erX.out

```
##  GRID    MED_NAME  RX_DOSE          FREQUENCY ENTRY_DATE STRENGTH_AMOUNT
## 1  ID1 lamotrigine      1             bid 2009-02-24           100
## 2  ID2 lamotrigine      2             bid 2006-12-30           100
## 4  ID3 Lamictal XR      3             bid 2004-08-24
## 5  ID4 lamotrigine      1       twice a day 2010-05-22       200 mg
## 6  ID5 lamotrigine    2 tabs             qam 2007-06-13           200
## 7  ID6 lamotrigine 1.5+1+1.5 brkfst, lunch, dinner 2015-03-14           100
##                                     DESCRIPTION strength freq.standard freq.num dose
## 1 lamotrigine 100 mg tablet (also known as lamictal)      100      bid          2      1
## 2 lamotrigine 100 mg tablet (also known as lamictal)      100      bid          2      2
## 4                                     lamictal xr 100 mg 24 hr tab      100      bid          2      3
## 5 lamotrigine 200 mg tablet (also known as lamictal)      200      bid          2      1
```

```
## 6          lamictal xr 200 mg tablet,extended release      200          am          1      2
## 7 lamotrigine 100 mg tablet (also known as lamictal)      100          tid          3      4
##   daily.dose num_doses num_freqs
## 1         200         NA         NA
## 2         400         NA         NA
## 4         600         NA         NA
## 5         400         NA         NA
## 6         400         NA         NA
## 7         400          3          3
```

The following arguments are used in the `run_MedStrII` function:

- **file:** file name of prescription data (CSV, RData, RDS), or data.frame
- **dat.columns:** a named list that should specify columns in data; 'id', 'dose', 'freq', 'date', and 'str' are required. 'desc' may also be specified.

In the above example, daily dose was calculated for the first 5 patients by multiplying strength \times dose \times freq.num, and a redundant daily dose was removed for the patient with ID2. In order to calculate a daily dose for the patient with ID3, the strength of 100 from the description was used because STRENGTH_AMOUNT was missing. For the patient with ID6, the dose amounts of 1.5, 1, and 1.5 are added together to get a dose of 4, and the daily dose is calculated as strength \times dose.

Pro-Drug Level

Pro-Drug Level module processes drug concentration data that can be merged with medication dose data and other types of data. This module can be semi-interactive for data checking (although it is not required, we recommend using this feature); if `check.path` is provided (the default is NULL), the module will generate several files to check missing data and potential data errors, and get feedback from an investigator. If corrected information ('fix' files) are provided, the module should be re-run to incorporate the corrections. The major functions of this module are:

- Combine drug concentration data with sampling time: This step is necessary only if the drug concentration data file does not contain the sampling time (i.e., the time when blood samples were drawn for drug concentration measurements). When this is the case, the sampling time should be obtained from a separate data file.
- Check missing date-time for drug level measurements. If there are any missing dates, a file listing these records will be produced using the `failmiss_fn` stub appended with drugname. A 'fix' file can be added to correct these records. If no 'fix' file is provided, records with missing dates will be removed.
 - e.g., if `failmiss_fn` is 'MissingConcDate-', the file 'failMissingConcDate-dex.csv' will be created in the `check.path` directory. The file with corrected dates and times should replace 'fail' with 'fix' (e.g., 'fixMissingConcDate-dex.csv'), and be placed in the same `check.path` directory.
- Check for multiple sets of concentration data for the same subject, and keep the set of concentration data with the most drug concentration records above a lower limit of quantification (LLOQ). Data for subjects with multiple records, if any, is included in a file produced with the `multsets_fn` stub appended with the drugname and date.
 - e.g., if `multsets_fn` is 'multipleSetsConc-', the file such as 'multipleSetsConc-dex2020-07-15.csv' will be created in the `check.path` directory.
- Check duplicate concentration records on the same date-time. If there are any records with multiple concentrations on the same date-time, a file listing these records will be produced using the `faildup_fn` stub appended with drugname. A 'fix' file can be added to correct these records. If no 'fix' file is found, all duplicates are retained.

- e.g., if faildup_fn is 'DuplicateConc-', the file 'failDuplicateConc-dex.csv' will be created in the check.path directory. The corrected file should replace 'fail' with 'fix', e.g. 'fixDuplicateConc-dex.csv', and include an additional variable called 'flag' with the value 'keep' for the records to be retained.

The drug concentration data can be processed by the run_DrugLevel function using:

```
conc.out <- run_DrugLevel(conc.path=file.path(dataDir,"Fentanyl_conc_mod_id.rds"),
  conc.columns = list(
    id = 'mod_id', conc = 'conc.level',
    idvisit = 'mod_id_visit', samplinkid = 'mod_id_event'
  ),
  conc.select=c('mod_id','mod_id_visit','samp','fentanyl_calc_conc'),
  conc.rename=c(fentanyl_calc_conc = 'conc.level', samp= 'event'),
  conc.mod.list=list(mod_id_event = expression(paste(mod_id_visit, event, sep = '_'))),
  samp.path=file.path(dataDir,"Fentanyl_samp_mod_id.rds"),
  samp.columns = list(
    conclinkid = 'mod_id_event', datetime = 'Sample.Collection.Date.and.Time'
  ),
  samp.mod.list=list(mod_id_event = expression(paste(mod_id_visit, samp, sep = '_'))),
  check.path=checkDir,
  failmiss_fn = 'MissingConcDate-',
  multsets_fn = 'multipleSetsConc-',
  faildup_fn = 'DuplicateConc-',
  drugname = drugname,
  LLOQ = LLOQ,
  demo.list = demo.out,
  demo.columns = list(id = 'mod_id', idvisit = 'mod_id_visit'))
```

```
## #####
```

```
## 3 rows need review, see file /tmp/Rtmp3Nbb0L/check2/failMissingConcDate-fent.csv AND create /tmp/Rtmp3Nbb0L/check2/failMissingConcDate-fent.csv
```

```
## #####
```

```
## subjects with concentration missing from sample file
```

```
## 1 subjects have multiple sets of concentration data
```

```
## 16 total unique subjects ids (including multiple visits) currently in the concentration data
```

```
## 15 total unique subjects in the concentration data
```

```
## #####
```

```
## 15 rows need review, see file /tmp/Rtmp3Nbb0L/check2/multipleSetsConc-fent2022-10-11.csv
```

```
## #####
```

```
## 15 total unique subjects ids (after excluding multiple visits) in the concentration data
```

```
## 15 total unique subjects in the concentration data
```

```
## mod_id mod_id_event
```

```
##      8      8.1_1
```

```
##      8      8.1_2
```

```
##      8      8.1_3
```

```
head(conc.out)
```

```
##      mod_id mod_id_visit event  conc.level mod_id_event      date.time eid
## 1         1           1.2    1 0.014136220      1.2_1 2017-02-03 10:46:00    1
```

```
## 2      1      1.2      2 0.279820752      1.2_2 2017-02-04 20:30:00 1
## 55     10     10.1      2 3.136047304      10.1_2 2016-12-24 18:00:00 1
## 56     10     10.1      9 0.004720171      10.1_9 2017-01-01 04:20:00 1
## 57     10     10.1     10 0.017136367      10.1_10 2017-01-02 04:42:00 1
## 58     10     10.1     12 0.006335571      10.1_12 2017-01-04 03:40:00 1
```

The output provides a message that 3 rows are missing concentration date. The file 'failMissingConcDate-fent.csv' contains the 3 records with missing values for the `date.time` variable.

```
( fail.miss.conc.date <- read.csv(file.path(checkDir,"failMissingConcDate-fent.csv")) )
```

```
##  subject_id subject_uid mod_id_event datetime
## 1      1566    35885929      8.1_1      NA
## 2      1566    35885929      8.1_2      NA
## 3      1566    35885929      8.1_3      NA
```

We can correct the missing dates by providing an updated file called 'fixMissingConcDate-fent.csv' that contains the missing data.

```
fail.miss.conc.date[, "datetime"] <- c("9/30/2016 09:32", "10/1/2016 19:20", "10/2/2016 02:04")
fail.miss.conc.date
```

```
##  subject_id subject_uid mod_id_event      datetime
## 1      1566    35885929      8.1_1 9/30/2016 09:32
## 2      1566    35885929      8.1_2 10/1/2016 19:20
## 3      1566    35885929      8.1_3 10/2/2016 02:04
```

```
write.csv(fail.miss.conc.date, file.path(checkDir,"fixMissingConcDate-fent.csv"))
```

After providing the updated file, the same `run_DrugLevel()` function should be re-run. The output now contains an additional message below the first message saying "fixMissingConcDate-fent.csv read with failures replaced". The `conc.out` data.frame also contains 3 additional rows with the corrected data.

```
conc.out <- run_DrugLevel(conc.path=file.path(dataDir,"Fentanyl_conc_mod_id.rds"),
  conc.columns = list(
    id = 'mod_id', conc = 'conc.level',
    idvisit = 'mod_id_visit', samplinkid = 'mod_id_event'
  ),
  conc.select=c('mod_id','mod_id_visit','samp','fentanyl_calc_conc'),
  conc.rename=c(fentanyl_calc_conc = 'conc.level', samp = 'event'),
  conc.mod.list=list(mod_id_event = expression(paste(mod_id_visit, event, sep = '_'))),
  samp.path=file.path(dataDir,"Fentanyl_samp_mod_id.rds"),
  samp.columns = list(
    conclinkid = 'mod_id_event', datetime = 'Sample.Collection.Date.and.Time'
  ),
  samp.mod.list=list(mod_id_event = expression(paste(mod_id_visit, samp, sep = '_'))),
  check.path=checkDir,
  failmiss_fn = 'MissingConcDate-',
  multsets_fn = 'multipleSetsConc-',
  faildup_fn = 'DuplicateConc-',
  drugname = drugname,
  LLOQ = LLOQ,
  demo.list = demo.out,
  demo.columns = list(id = 'mod_id', idvisit = 'mod_id_visit'))
```

```
## #####
```

```
## 3 rows need review, see file /tmp/Rtmp3Nbb0L/check2/failMissingConcDate-fent.csv AND create /tmp/Rtmp
```

```
## #####
## file /tmp/Rtmp3Nbb0L/check2/fixMissingConcDate-fent.csv read with failures replaced
## subjects with concentration missing from sample file
## 1 subjects have multiple sets of concentration data
## 16 total unique subjects ids (including multiple visits) currently in the concentration data
## 15 total unique subjects in the concentration data
## #####
## 15 rows need review, see file /tmp/Rtmp3Nbb0L/check2/multipleSetsConc-fent2022-10-11.csv
## #####
## 15 total unique subjects ids (after excluding multiple visits) in the concentration data
## 15 total unique subjects in the concentration data
## [1] mod_id      mod_id_event
## <0 rows> (or 0-length row.names)
```

Before discussing the function arguments, we should first describe the expected data: either a single concentration data set, or concentration data plus sampling time data. If the concentration data set includes a date-time variable, then sampling time data is not necessary.

Concentration data should include the following columns specified in `conc.columns`:

1. id: patient-level ID
2. idvisit: visit-level ID
3. conc: drug concentration level
4. datetime (unless provided with sampling time): date-time of concentration sample
5. samplinkid: unique identifier for subject, visit, and event number. This will be used to link sampling data when necessary.

If sampling time is provided, it should include the following columns in `samp.columns`:

1. conclinkid: unique identifier for subject, visit, and event number
2. datetime: date-time of sample collection

The `conc.select`, `conc.rename`, `conc.mod.list`, and `samp.mod.list` arguments can usually be ignored (and set to `NULL`). Otherwise they should be used to help create the proper format. For example, the subject/visit/event identifier may need to be created.

- The `run_DrugLevel` function arguments are as follows:
 - `conc.path`: (required) file name of concentration data (CSV, RData, RDS), or `data.frame`
 - `conc.columns`: (required) a named list that should specify columns in concentration data; `id`, and `conc` are required. `idvisit` may also be specified. If linking with sampling data, `samplinkid` is required. Otherwise `datetime` is required. This is the date and time for concentration measurement, which can refer to a single date-time variable (`datetime = date_time`) or two variables holding date and time separately (e.g., `datetime = c('Date', 'Time')`).
 - `conc.select`: list of variables in the drug concentration data, which are used for processing; `id` (e.g., `'mod_id'`), sample event id within each subject id (e.g., `'samp'`), and drug concentration (e.g., `'fentanyl_calc_conc'`) are required to be selected if the data are not in an appropriate form.
 - `conc.rename`: rename variables for the variables in `conc.select`; the selected variables should be renamed using `'conc.level'` for drug concentration and `'event'` for sample event name (e.g., `fentanyl_calc_conc = 'conc.level'`, `samp = 'event'`)
 - `conc.mod.list`: list containing modifications to variables in the drug concentration data

- **samp.path**: (optional) file name of data with sampling time (CSV, RData, RDS), or data.frame; if provided, 'conc.mod.list' and 'samp.mod.list' should be provided to create 'mod_id_event' as shown above (unless provided in each dataset), which will be used to connect the concentration data and the sample data to generate the date-time variable for concentration data
- **samp.columns**: a named list that should specify columns in sampling data. **conclinkid** and **datetime** are required to link sampling data to concentration data. **conclinkid** should match the id variable provided as **samplinkid** in the **conc.columns** argument. **datetime** is the date and time when blood samples were obtained.
- **samp.mod.list**: list containing modifications to variables in the sampling time data
- **check.path**: file path to **check** directory, where the generated files for data checking are stored, and the corresponding data files with fixed data exist. The default (NULL) will not produce any check files.
- **failmiss_fn**: filename stub for missing concentration date check file
- **multsets_fn**: filename stub for multiple sets of concentration data check file
- **faildup_fn**: filename stub for duplicate concentration check file
- **drugname**: drug name of interest (e.g., dex, fent)
- **LLOQ**: lower limit of quantification (LLOQ)
 - * e.g., dexmedetomidine 0.005 ng/mL, fentanyl 0.05 ng/mL
- **demo.list**: file name for processed demographic file that is used to exclude subjects based on exclusion criteria
- **demo.columns**: a named list that should specify columns in demographic data; **id**, is required. If **idvisit** is present in the concentration data, then it is required here too.
- The output of the **run_DrugLevel** function is a dataset for processed drug concentration levels (**conc.level**) matched with date-time (**date.time**), as well as necessary identification numbers for further merging with the output from other modules.

Pro-Laboratory

The Pro-Laboratory module processes laboratory data that can be merged with data from other modules. The laboratory data can be processed using:

```
creat.out <- run_Labs(lab.path=file.path(dataDir,"Fentanyl_creat_mod_id.rds"),
  lab.select = c('mod_id','date.time','creat'),
  lab.mod.list = list(date.time = expression(parse_dates(fixDates(paste(date, time))))))

alb.out <- run_Labs(lab.path=file.path(dataDir,"Fentanyl_alb_mod_id.rds"),
  lab.select = c('mod_id','date.time','alb'),
  lab.mod.list = list(date.time = expression(parse_dates(fixDates(paste(date, time))))))

lab.out <- list(creat.out, alb.out)

str(lab.out)
```

```
## List of 2
## $ : 'data.frame': 266 obs. of 3 variables:
## ..$ mod_id : int [1:266] 1 1 1 1 1 1 1 1 1 1 ...
## ..$ date.time: POSIXct[1:266], format: "2017-02-05 04:00:00" "2017-02-06 05:00:00" "2011-10-03 04:00:00" ...
## ..$ creat : num [1:266] 0.52 0.53 0.42 0.35 0.29 0.28 0.34 0.59 0.54 0.26 ...
## $ : 'data.frame': 44 obs. of 3 variables:
## ..$ mod_id : int [1:44] 8 8 8 8 4 6 6 9 10 10 ...
## ..$ date.time: POSIXct[1:44], format: "2020-07-30 05:23:00" "2020-07-28 03:12:00" "2020-07-29 01:30:00" ...
## ..$ alb : num [1:44] 2.9 2 2.7 4.1 4.1 2.3 2.6 3 3.1 4.2 ...
```

- The **run_Labs** function arguments are as follows:

- **lab.path**: filename of a lab file (CSV, RData, RDS), or data.frame
- **lab.select**: list of variables in the laboratory data to be retained
- **lab.mod.list**: list of expressions giving modifications to make to variables in the laboratory data; passed to **dataTransformation**

Build-PK-IV

The Build-PK-IV module creates PK data for IV medications. Both dose data from the *Pro-Med-Str1* module and concentration data from the *Pro-DrugLevel* module are required. Demographic data from the *Pro-Demographic* module and laboratory data from the *Pro-Laboratory* module may optionally be included. Each dataset including dose and concentration datasets can be provided by users without being generated by our modules as long as they are a correctly formatted data.frame. This module can be semi-interactive for data checking (although it is not required, we recommend using this feature); if **check.path** is provided (the default is NULL), it can generate several files to check potential data errors, and get feedback from an investigator. If corrected information ('fix' files) are provided, the module should be re-run to incorporate the corrections. The major functions this module performs are:

- Determine whether each IV dose is valid by comparing to concentration data. Doses outside the time frame window defined by concentration data (by default seven days before first concentration through last concentration) are dropped. See **pkdata::trimDoses()** for more information.
- Resolve duplicate doses. A file with duplicate bolus dose records, if any, will be produced using the **faildupbol_fn** stub appended with drugname. A 'fix' file can be added to correct these records.
 - e.g., if **faildupbol_fn** is 'DuplicateBolus-', the file 'failDuplicateBolus-fent.csv' will be created in the **check.path** directory. The corrected file should replace 'fail' with 'fix' (e.g., 'fixDuplicateBolus-fent.csv'), and include an additional variable called 'flag' with the value 'keep' for the records to be retained.
- Add zero dose values (i.e., impute stopping time for a continuous infusion) and (conceptually) impute missing records if 'gap' is provided in **dose.columns**. This allows a continuous infusion given when there are missing records between infusion dosing records. For example, suppose that 'gap' = 60 is defined (which is typical gap size when infusion dosing is supposed to be recorded hourly for inpatients) and time between two records (i.e., gap) are greater than 1 hour (i.e., missing record). If the gap between the two records is less or equal to twice of the gap (i.e., $2 \times 60 = 120$ min), a continuous infusion is assumed until the 2nd dose record; otherwise, the first infusion is assumed to be stopped (i.e., add zero doses) after 60 min (i.e., equal to the gap size) and a new infusion (the 2nd record) starts at its recorded time. Both **infuse.time.real** and **infuse.time** are used to impute stopping time for a continuous infusion based on 'gap' if it is provided in the dose data, while **infuse.time.real** is used to generate 'time' variable in the processed data. Note that if no **gap** variable is set, no additional (zero dose) rows will be created (as **addZeroDose** is the function (internal function) that adds a stopping dose).

Often the gap variable will be defined by the previous function, **run_MedStr1**. The user may also choose to set their own gap variable with appropriate recording interval. In most settings, the gap variable is unnecessary. For example of Vanderbilt University Medical Center, after *Epic* EHR system was implemented, only MAR data are collected without flow sheet data, which have infusion data recorded with any time intervals, and hence **maxint** should not be set for 'gap' in **dose.columns** argument of **run_Build_PK_IV** function.

- Combine dose and concentration data into PK data format.
- If laboratory data is provided, merge onto PK data based on ID and time.
- If demographic data is provided, merge onto PK data. Demographic weight is used to impute records with missing dose weight. In addition, subjects who meet the exclusion criteria and those with no demographic data are removed. A file showing the missingness frequency and percent for each variable is produced using the **misssdemo_fn** stub appended with drugname.

- e.g., if `missdemo_fn` is ‘-missing-demo’, the file ‘dex-missing-demo.csv’ will be created in the `check.path` directory.
- The final PK data includes ID and standard NONMEM formatted variables:
 - `time` - time of dosing or concentration event
 - `amt` - dose amount administered (NA for concentration records)
 - `dv` - dependent variable; i.e., observed concentration (NA for dosing records)
 - `rate` - rate of drug administration (e.g., `rate=0` for bolus doses)
 - `mdv` - missing dependent variable (`dv`) indicator (e.g., 0 = not missing `dv`, 1 = missing `dv`)
 - `evid` - event indicator (e.g., 0 = observation, 1 = dose event)

If demographic data is provided, the demographic variables will also be included.

If `pk.vars` includes ‘`date`’, the output generates its original date-time to which the ‘`time`’ is mapped. Users can use `pk.vars` to include variables for demographics or labs that are already merged with the concentration dataset when they prefer to provide a single concentration data file (required). But a separate dose data file is still required.

PK data with IV dosing can be built by the `run_Build_PK_IV` function using:

```
pk_dat <- run_Build_PK_IV(
  conc=conc.out,
  conc.columns = list(id = 'mod_id', datetime = 'date.time', druglevel = 'conc.level',
                      idvisit = 'mod_id_visit'),
  dose=ivdose.out,
  dose.columns = list(id = 'mod_id', date = 'date.dose', infuseDatetime = 'infuse.time',
                      infuseDose = 'infuse.dose', infuseTimeExact= 'infuse.time.real',
                      bolusDatetime = 'bolus.time', bolusDose = 'bolus.dose',
                      gap = 'maxint', weight = 'weight'),
  demo.list = demo.out,
  demo.columns = list(id = 'mod_id', idvisit = 'mod_id_visit'),
  lab.list = lab.out,
  lab.columns = list(id = 'mod_id', datetime = 'date.time'),
  pk.vars=c('date'),
  drugname=drugname,
  check.path=checkDir,
  missdemo_fn='-missing-demo',
  faildupbol_fn='DuplicateBolus-',
  date.format="%m/%d/%y %H:%M:%S",
  date.tz="America/Chicago")
```

```
## 0 duplicated rows
## The dimension of the PK data before merging with demographics: 234 x 9
## The number of subjects in the PK data before merging with demographics: 15
## The number of subjects in the demographic file, who meet the exclusion
##   criteria: 2
## check NA frequency in demographics, see file /tmp/Rtmp3Nbb0L/check2/
##   fent-missing-demo.csv
## Some demographic variables are missing and will be excluded:
## The list of final demographic variables: mod_visit
## gender
## weight
## height
## surgery_date
## ageatsurgery
## stat_sts
```



```
## cpb_sts
## in_hospital_mortality
## add_ecmo
## date_icu_dc
## time_fromor
## length_of_icu_stay
## weight_demo
## Checked: there are no missing creat
## List of IDs missing at least 1 alb: 1.2
## 11.1
## 15.1
## 2.1
## 3.1
## 4.1
## 5.1
## 7.1
## 8.1
## The dimension of the final PK data exported with the key demographics:
##      197 x 24 with 13 distinct subjects (mod_id)
```

The function `pullRealId()` appends the original IDs – `subject_id` and `subject_uid` to the data. The parameter `remove.mod.id=TRUE` can be used to also remove any module IDs – `mod_id`, `mod_visit`, and `mod_id_visit`.

```
# convert id back to original IDs
pk_dat <- pullRealId(pk_dat, remove.mod.id=TRUE)

head(pk_dat)
```

```
##      subject_id subject_uid time    amt      dv rate mdv evid      date gender weight
## 2      466.1      28579217 0.00   50.0      NA  0.0  1    1 02/04/17 16:15:00    0  21.99
## 2.1    466.1      28579217 0.25   20.0      NA  0.0  1    1 02/04/17 16:30:00    0  21.99
## 2.2    466.1      28579217 4.25    NA 0.2798208  NA  0    0 02/04/17 20:30:00    0  21.99
## 12     1607.0     38551767 0.00  109.2      NA 10.4  1    1 12/24/16 07:15:00    0   2.60
## 12.1   1607.0     38551767 0.00   10.0      NA  0.0  1    1 12/24/16 07:15:00    0   2.60
## 12.2   1607.0     38551767 1.25   15.0      NA  0.0  1    1 12/24/16 08:30:00    0   2.60
##      height surgery_date ageatsurgery stat_sts cpb_sts in_hospital_mortality add_ecmo date_icu_dc
## 2     116.90    2/4/2017      2451         1     107              0          0    2/5/2017
## 2.1    116.90    2/4/2017      2451         1     107              0          0    2/5/2017
## 2.2    116.90    2/4/2017      2451         1     107              0          0    2/5/2017
## 12      45.94   12/24/2016         23         3     110              0          0    1/5/2017
## 12.1    45.94   12/24/2016         23         3     110              0          0    1/5/2017
## 12.2    45.94   12/24/2016         23         3     110              0          0    1/5/2017
##      time_fromor length_of_icu_stay weight_demo creat alb
## 2           1322           1      21.99  0.54  NA
## 2.1          1322           1      21.99  0.54  NA
## 2.2          1322           1      21.99  0.54  NA
## 12            NA           12      2.76  0.66  1.6
## 12.1           NA           12      2.76  0.66  1.6
## 12.2           NA           12      2.76  0.66  1.6
```

- The `run_Build_PK_IV` function arguments are as follows:
 - `conc`: (required) drug concentration data output from `run_DrugLevel`, or a correctly formatted data.frame
 - `conc.columns`: (required) a named list that should specify columns in concentration data; 'id', 'datetime', 'druglevel' are required. 'idvisit' may also be specified. 'datetime' is date and time for

concentration measurement, which can refer to a single date-time variable (`datetime = 'date_time'`) or two variables holding date and time separately (e.g., `datetime = c('Date', 'Time')`). `'idvisit'` can be used when there are multiple visits (i.e., several occasions) for the same subject. If both `'id'` and `'idvisit'` are provided, `'idvisit'` will be generated.

- **dose**: (required) IV dose data output from `run_MedStrI`, or a correctly formatted `data.frame`
- **dose.columns**: (required) a named list that should specify columns in dose data; `'id'` is required. `'infuseDatetime'` and `'infuseDose'` should be set if infusion dose data is present. `'infuseTimeExact'` may also be specified for infusion data – this variable represents a precise time, if for example the `'infuseDatetime'` variable is rounded. `'bolusDatetime'` and `'bolusDose'` should be set if bolus dose data is present. A generic `'date'` variable may be provided, agnostic to either infusion or bolus dosing. `'gap'` and `'weight'` column names may also be set. Any of the date-time variables can be specified as a single date-time variable (`infuseDatetime = 'date_time'`) or two variables holding date and time separately (e.g., `infuseDatetime = c('Date', 'Time')`). For details of the utility for `'gap'`, see above.
- **demo.list**: (optional) demographic data, containing processed output from `run_Demo`, or a correctly formatted `data.frame`
- **demo.columns**: a named list that should specify columns in demographic data; `'id'` is required. `'weight'` and `'idvisit'` may also be used to specify columns for weight or the unique `idvisit`. `'idvisit'` can be used when there are multiple visits (i.e., several occasions) for the same subject. Any other columns present in the demographic data are treated as covariates.
- **lab.list**: (optional) laboratory data, containing processed output from `run_Labs`, or a correctly formatted list
- **lab.columns**: a named list that should specify columns in lab data; `'id'`, and `'datetime'` are required. `'datetime'` is the date and time when the lab data was obtained, which can refer to a single date-time variable (`datetime = 'date_time'`) or two variables holding date and time separately (e.g., `datetime = c('Date', 'Time')`). Any other columns present in lab data are treated as lab values.
- **pk.vars**: (optional) variables to include in the returned PK data. The variable `'date'` is a special case; when included, it maps the `'time'` offset to its original date-time. Other named variables will be merged from the concentration data set. For example, rather than being separate data sets, labs or demographics may already be present in the concentration data. These columns should be named here.
- **drugname**: (optional) drug name stub (e.g., `fent`)
- **check.path**: (optional) file path where the generated files for data checking are stored, and the corresponding data files with fixed data exist
- **missdemo_fn**: filename stub for report of missingness frequency and percent for variables
- **faildupbol_fn**: filename stub for duplicate bolus dose records
- **date.format**: date and time format (e.g., `"%m/%d/%y %H:%M:%S"`)
- **date.tz**: date timezone (e.g., `"America/Chicago"`)
- The output of the `run_MedStrI` function is a dataset with NONMEM formatted PK variables and (optionally) demographic and laboratory data.

References

1. Choi L, Beck C, McNeer E, Weeks HL, Williams ML, James NT, Niu X, Abou-Khalil BW, Birdwell KA, Roden DM, Stein CM. Development of a System for Post-marketing Population Pharmacokinetic and Pharmacodynamic Studies using Real-World Data from Electronic Health Records. *Clinical Pharmacology & Therapeutics*. 2020 Apr; 107(4): 934-943.