

Create DM table as csv file

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Introduction

This is a somewhat convoluted script. The idea is to take an existing cube structure and derive the results. That was usefull initially to extend a cube. Now, it is not as usefull. So the script may seem pointless. TODO(mja): fix it.

Create DM sample table as CSV file and other files

This script creates the result and codelist for a simple DM table.

```
library(rrdfancillary)
devtools::load_all(pkg="../..")
```

```
## Loading rrdfqbcindex
```

Get the data and prepare for derivation of summary statistics

```
library(foreign)
library(sqldf)

fnadsl<- system.file("extdata/sample-xpt", "adsl.xpt", package="rrdfqbcindex")
print(fnadsl)
```

```
## [1] "/home/ma/projects/rrdfqbcindex0/rrdfqbcindex/inst/extdata/sample-xpt/adsl.xpt"
```

```

if (!file.exists(fnadsl)) {
  fnadsl<- file.path("../", "extdata/sample-xpt", "adsl.xpt")
}
if (!file.exists(fnadsl)) {
  stop("File does not exist - ",fnadsl)
}
adsl<- read.xport(fnadsl)
adsl$TRT01A<- as.character(adsl$TRT01A)
adsl$RACE<- as.character(adsl$RACE)
adsl$SAFFL<- as.character(adsl$SAFFL)
adsl$SEX<- as.character(adsl$SEX)

## SASxport package maps characters and dates etc into more R like data type
## install.packages("SASxport")
## library(SASxport)
## adsl<- as.data.frame(read.xport(fnadsl,as.is=TRUE))
## str(adsl)

```

Create frame for cube from an existing RDF data cube

The code input a turtle file with an RDF data cube. SQL statements for calculating the measurements are derived from the cube, and used to derive the summary statistics. Note: the SQL statements does not show records where the combination of values lead to 0 observations. This is handled below, in a not so clever way. A better approach would be to include the concept of a skeleton in the SQL statements.

ToDo(MJA): move this to rrdqbcbrndcheck or move to another package, like rrdqbcbrnd0

```

library(rrdfqbcbrndcheck)

dataCubeFile<- system.file("extdata/sample-rdf", "DC-DM-sample.ttl", package="rrdfqbcbrndcheck")
checkCube <- new.rdf(ontology=FALSE) # Initialize
load.rdf(dataCubeFile, format="TURTLE", appendTo= checkCube)
summarize.rdf(checkCube)

stmtSQL<- GetSQLFromCube(checkCube)

cat(stmtSQL$summStatSQL)

adsl.summ.stat.res<- sqldf( stmtSQL$summStatSQL)
names(adsl.summ.stat.res)<- tolower(gsub("(a|b)\\."," ", names(adsl.summ.stat.res)))

```

Store the SQL statements to a file

```

res.text<- stmtSQL$summStatSQL

cr.text<- paste0("create table qbframe ", "(", paste(names(stmtSQL$qbframe), "TEXT", collapse=", "), ")")

in.text<- paste0(
  paste(
    paste0("insert into qbframe ", "(", paste0(names(stmtSQL$qbframe),collapse=", "), ")\\n" ),
    "values\\n",

```

```

paste0( "(", apply(stmtSQL$qbframe,1,function(x) {paste0("'",x,"'", collapse=",")}), ")", collapse="
collapse="\n"
),";\n")

se.text<- "select * from qbframe;"

tempfile<- file.path(tempdir(),"temp-code.R")
cat(paste('res.text<- "', res.text,'"\\n',collapse="\n"), file=tempfile)
cat(paste("cr.text<- '", cr.text,'"\\n",collapse="\n"), file=tempfile,append=TRUE)
cat(paste("in.text<- '", in.text,'"\\n",collapse="\n"), file=tempfile,append=TRUE)
cat(paste("se.text<- '", se.text,'"\\n",collapse="\n"), file=tempfile,append=TRUE)
print(tempfile)

```

Define SQL statements directly

The statements below are inserted from the file generated above.

Work-around: add SELECT statments below corresponding to the desired statistics. Update the .csv file, and re-create the cube. Repeat until done. This is of course not the ideal way; waiting to the formular interface to the cube.

```

res.text<- "
SELECT a.TRT01A, '_ALL_' as RACE, a.SEX, a.SAFFL, 'count' as procedure, 'quantity' as factor, '_ALL_' as
UNION
SELECT a.TRT01A, '_ALL_' as RACE, '_ALL_' as SEX, a.SAFFL, 'mean' as procedure, 'WEIGHTBL' as factor, '_ALL_' as
UNION
SELECT a.TRT01A, '_ALL_' as RACE, '_ALL_' as SEX, a.SAFFL, 'max' as procedure, 'WEIGHTBL' as factor, '_ALL_' as
UNION
SELECT a.TRT01A, '_ALL_' as RACE, '_ALL_' as SEX, a.SAFFL, 'max' as procedure, 'AGE' as factor, '_NULL_' as
UNION
SELECT a.TRT01A, '_ALL_' as RACE, '_ALL_' as SEX, a.SAFFL, 'median' as procedure, 'WEIGHTBL' as factor, '_ALL_' as
UNION
SELECT a.TRT01A, a.RACE, '_ALL_' as SEX, a.SAFFL, 'count' as procedure, 'quantity' as factor, '_ALL_' as
UNION
SELECT a.TRT01A, b.RACE, '_ALL_' as SEX, a.SAFFL, 'percent' as procedure, 'proportion' as factor, 'RACE' as
UNION
SELECT a.TRT01A, '_ALL_' as RACE, '_ALL_' as SEX, a.SAFFL, 'stdev' as procedure, 'AGE' as factor, '_NULL_' as
UNION
SELECT a.TRT01A, '_ALL_' as RACE, '_ALL_' as SEX, a.SAFFL, 'min' as procedure, 'AGE' as factor, '_NULL_' as
UNION
SELECT a.TRT01A, '_ALL_' as RACE, b.SEX, a.SAFFL, 'percent' as procedure, 'proportion' as factor, 'SEX' as
UNION
SELECT a.TRT01A, '_ALL_' as RACE, '_ALL_' as SEX, a.SAFFL, 'min' as procedure, 'WEIGHTBL' as factor, '_ALL_' as
UNION
SELECT '_ALL_' as TRT01A, a.RACE, '_ALL_' as SEX, a.SAFFL, 'count' as procedure, 'quantity' as factor, '_ALL_' as
UNION
SELECT a.TRT01A, '_ALL_' as RACE, '_ALL_' as SEX, a.SAFFL, 'mean' as procedure, 'AGE' as factor, '_NULL_' as
UNION
SELECT '_ALL_' as TRT01A, '_ALL_' as RACE, a.SEX, a.SAFFL, 'count' as procedure, 'quantity' as factor, '_ALL_' as
UNION
SELECT a.TRT01A, '_ALL_' as RACE, '_ALL_' as SEX, a.SAFFL, 'median' as procedure, 'AGE' as factor, '_NULL_' as
UNION
SELECT a.TRT01A, '_ALL_' as RACE, '_ALL_' as SEX, a.SAFFL, 'count' as procedure, 'quantity' as factor, '_ALL_' as

```

```

UNION
SELECT a.TRTO1A, '_ALL_' as RACE, '_ALL_' as SEX, a.SAFFL, 'stdev' as procedure, 'WEIGHTBL' as factor,
"

cr.text<- '
create table qbframe (trt01a TEXT, race TEXT, factor TEXT, procedure TEXT, sex TEXT, saffl TEXT, unit TEXT,
,

in.text<- '
insert into qbframe (trt01a,race,factor,procedure,sex,saffl,unit,denominator)
values
("Xanomeline High Dose","AMERICAN INDIAN OR ALASKA NATIVE","proportion","percent","_ALL_","Y","_NULL_","_ALL_"),
("Xanomeline Low Dose","AMERICAN INDIAN OR ALASKA NATIVE","proportion","percent","_ALL_","Y","_NULL_","_ALL_"),
("Xanomeline Low Dose","BLACK OR AFRICAN AMERICAN","proportion","percent","_ALL_","Y","_NULL_","RACE"),
("Placebo","_ALL_","quantity","count","F","Y","_NULL_","_ALL_"),
("_ALL_","WHITE","quantity","count","_ALL_","Y","_NULL_","_ALL_"),
("Xanomeline Low Dose","_ALL_","AGE","min","_ALL_","Y","YEARS","_NULL_"),
("Xanomeline High Dose","_ALL_","AGE","stdev","_ALL_","Y","YEARS","_NULL_"),
("Xanomeline Low Dose","_ALL_","proportion","percent","M","Y","_NULL_","SEX"),
("Placebo","_ALL_","AGE","stdev","_ALL_","Y","YEARS","_NULL_"),
("Xanomeline High Dose","WHITE","quantity","count","_ALL_","Y","_NULL_","_ALL_"),
("Xanomeline Low Dose","WHITE","quantity","count","_ALL_","Y","_NULL_","_ALL_"),
("Xanomeline High Dose","_ALL_","AGE","max","_ALL_","Y","YEARS","_NULL_"),
("Xanomeline High Dose","AMERICAN INDIAN OR ALASKA NATIVE","quantity","count","_ALL_","Y","_NULL_","_ALL_"),
("Placebo","BLACK OR AFRICAN AMERICAN","quantity","count","_ALL_","Y","_NULL_","_ALL_"),
("Placebo","_ALL_","AGE","max","_ALL_","Y","YEARS","_NULL_"),
("Placebo","AMERICAN INDIAN OR ALASKA NATIVE","proportion","percent","_ALL_","Y","_NULL_","RACE"),
("Placebo","BLACK OR AFRICAN AMERICAN","proportion","percent","_ALL_","Y","_NULL_","RACE"),
("Xanomeline Low Dose","_ALL_","quantity","count","_ALL_","Y","_NULL_","_ALL_"),
("Placebo","_ALL_","quantity","count","M","Y","_NULL_","_ALL_"),
("Placebo","_ALL_","proportion","percent","F","Y","_NULL_","SEX"),
("Xanomeline High Dose","_ALL_","quantity","count","_ALL_","Y","_NULL_","_ALL_"),
("Xanomeline Low Dose","_ALL_","quantity","count","M","Y","_NULL_","_ALL_"),
("Xanomeline High Dose","_ALL_","proportion","percent","F","Y","_NULL_","SEX"),
("Xanomeline Low Dose","_ALL_","quantity","count","F","Y","_NULL_","_ALL_"),
("Placebo","_ALL_","AGE","mean","_ALL_","Y","YEARS","_NULL_"),
("Xanomeline High Dose","_ALL_","AGE","median","_ALL_","Y","YEARS","_NULL_"),
("Placebo","_ALL_","AGE","min","_ALL_","Y","YEARS","_NULL_"),
("_ALL_","BLACK OR AFRICAN AMERICAN","quantity","count","_ALL_","Y","_NULL_","_ALL_"),
("Placebo","_ALL_","AGE","median","_ALL_","Y","YEARS","_NULL_"),
("Xanomeline Low Dose","_ALL_","AGE","stdev","_ALL_","Y","YEARS","_NULL_"),
("Xanomeline Low Dose","AMERICAN INDIAN OR ALASKA NATIVE","quantity","count","_ALL_","Y","_NULL_","_ALL_"),
("Xanomeline Low Dose","BLACK OR AFRICAN AMERICAN","quantity","count","_ALL_","Y","_NULL_","_ALL_"),
("Xanomeline Low Dose","_ALL_","AGE","max","_ALL_","Y","YEARS","_NULL_"),
("Xanomeline High Dose","BLACK OR AFRICAN AMERICAN","proportion","percent","_ALL_","Y","_NULL_","RACE"),
("Xanomeline High Dose","WHITE","proportion","percent","_ALL_","Y","_NULL_","RACE"),
("Xanomeline Low Dose","WHITE","proportion","percent","_ALL_","Y","_NULL_","RACE"),
("_ALL_","_ALL_","quantity","count","M","Y","_NULL_","_ALL_"),
("Xanomeline High Dose","_ALL_","quantity","count","M","Y","_NULL_","_ALL_"),
("_ALL_","_ALL_","quantity","count","F","Y","_NULL_","_ALL_"),
("Xanomeline High Dose","_ALL_","quantity","count","F","Y","_NULL_","_ALL_"),
("Placebo","_ALL_","proportion","percent","M","Y","_NULL_","SEX"),

```

```

("Xanomeline Low Dose", "_ALL_", "proportion", "percent", "F", "Y", "_NULL_", "SEX"),
("Xanomeline Low Dose", "_ALL_", "AGE", "mean", "_ALL_", "Y", "YEARS", "_NULL_"),
("Xanomeline High Dose", "_ALL_", "proportion", "percent", "M", "Y", "_NULL_", "SEX"),
("Placebo", "AMERICAN INDIAN OR ALASKA NATIVE", "quantity", "count", "_ALL_", "Y", "_NULL_", "_ALL_"),
("Xanomeline High Dose", "_ALL_", "AGE", "mean", "_ALL_", "Y", "YEARS", "_NULL_"),
("Xanomeline High Dose", "BLACK OR AFRICAN AMERICAN", "quantity", "count", "_ALL_", "Y", "_NULL_", "_ALL_"),
("Placebo", "WHITE", "quantity", "count", "_ALL_", "Y", "_NULL_", "_ALL_"),
("Xanomeline Low Dose", "_ALL_", "AGE", "median", "_ALL_", "Y", "YEARS", "_NULL_"),
("Xanomeline High Dose", "_ALL_", "AGE", "min", "_ALL_", "Y", "YEARS", "_NULL_"),
("_ALL_", "AMERICAN INDIAN OR ALASKA NATIVE", "quantity", "count", "_ALL_", "Y", "_NULL_", "_ALL_"),
("Placebo", "WHITE", "proportion", "percent", "_ALL_", "Y", "_NULL_", "RACE"),
("Placebo", "_ALL_", "quantity", "count", "_ALL_", "Y", "_NULL_", "_ALL_"),
("Xanomeline Low Dose", "_ALL_", "WEIGHTBL", "min", "_ALL_", "Y", "KG", "_NULL_"),
("Xanomeline High Dose", "_ALL_", "WEIGHTBL", "stdev", "_ALL_", "Y", "KG", "_NULL_"),
("Placebo", "_ALL_", "WEIGHTBL", "stdev", "_ALL_", "Y", "KG", "_NULL_"),
("Xanomeline High Dose", "_ALL_", "WEIGHTBL", "max", "_ALL_", "Y", "KG", "_NULL_"),
("Placebo", "_ALL_", "WEIGHTBL", "max", "_ALL_", "Y", "KG", "_NULL_"),
("Placebo", "_ALL_", "WEIGHTBL", "mean", "_ALL_", "Y", "KG", "_NULL_"),
("Xanomeline High Dose", "_ALL_", "WEIGHTBL", "median", "_ALL_", "Y", "KG", "_NULL_"),
("Placebo", "_ALL_", "WEIGHTBL", "min", "_ALL_", "Y", "KG", "_NULL_"),
("Placebo", "_ALL_", "WEIGHTBL", "median", "_ALL_", "Y", "KG", "_NULL_"),
("Xanomeline Low Dose", "_ALL_", "WEIGHTBL", "stdev", "_ALL_", "Y", "KG", "_NULL_"),
("Xanomeline Low Dose", "_ALL_", "WEIGHTBL", "max", "_ALL_", "Y", "KG", "_NULL_"),
("Xanomeline Low Dose", "_ALL_", "WEIGHTBL", "mean", "_ALL_", "Y", "KG", "_NULL_"),
("Xanomeline High Dose", "_ALL_", "WEIGHTBL", "mean", "_ALL_", "Y", "KG", "_NULL_"),
("Xanomeline Low Dose", "_ALL_", "WEIGHTBL", "median", "_ALL_", "Y", "KG", "_NULL_"),
("Xanomeline High Dose", "_ALL_", "WEIGHTBL", "min", "_ALL_", "Y", "KG", "_NULL_")
;
;
se.text<- '
select * from qbframe;
,

```

Evaluate the SQL code

```

adsl.summ.stat.res<- sqldf( res.text )
# adsl.summ.stat$unit<- "_NULL_"
names(adsl.summ.stat.res)<- tolower(gsub("(a|b)\\.", "", names(adsl.summ.stat.res)))

rm(qbframe)
sqldf()

```

<SQLiteConnection>

```
sqldf(cr.text )
```

NULL

```
sqldf(in.text )
```

```
## NULL
```

```
qbframe<- sqldf(se.text)
sqldf()
```

```
## NULL
```

```
# str(qbframe)
```

Combine generated results with the cube frame and write CSV file

```
adsl.summ.stat<- merge(qbframe,adsl.summ.stat.res,by=names(qbframe),all=TRUE)
# adsl.summ.stat<- merge(stmtSQL$qbframe,adsl.summ.stat.res,all=TRUE)
adsl.summ.stat$measure[ is.na(adsl.summ.stat$measure) & adsl.summ.stat$procedure=="count" ] <- 0
adsl.summ.stat
```

```
##          trt01a          race      factor
## 1          _ALL_          _ALL_    quantity
## 2          _ALL_          _ALL_    quantity
## 3          _ALL_ AMERICAN INDIAN OR ALASKA NATIVE    quantity
## 4          _ALL_          BLACK OR AFRICAN AMERICAN    quantity
## 5          _ALL_          WHITE    quantity
## 6      Placebo          _ALL_          AGE
## 7      Placebo          _ALL_          AGE
## 8      Placebo          _ALL_          AGE
## 9      Placebo          _ALL_          AGE
## 10     Placebo          _ALL_          AGE
## 11     Placebo          _ALL_ proportion
## 12     Placebo          _ALL_ proportion
## 13     Placebo          _ALL_    quantity
## 14     Placebo          _ALL_    quantity
## 15     Placebo          _ALL_    quantity
## 16     Placebo          _ALL_ WEIGHTBL
## 17     Placebo          _ALL_ WEIGHTBL
## 18     Placebo          _ALL_ WEIGHTBL
## 19     Placebo          _ALL_ WEIGHTBL
## 20     Placebo          _ALL_ WEIGHTBL
## 21     Placebo AMERICAN INDIAN OR ALASKA NATIVE proportion
## 22     Placebo AMERICAN INDIAN OR ALASKA NATIVE    quantity
## 23     Placebo          BLACK OR AFRICAN AMERICAN proportion
## 24     Placebo          BLACK OR AFRICAN AMERICAN    quantity
## 25     Placebo          WHITE proportion
## 26     Placebo          WHITE    quantity
## 27 Xanomeline High Dose          _ALL_          AGE
## 28 Xanomeline High Dose          _ALL_          AGE
## 29 Xanomeline High Dose          _ALL_          AGE
## 30 Xanomeline High Dose          _ALL_          AGE
## 31 Xanomeline High Dose          _ALL_          AGE
## 32 Xanomeline High Dose          _ALL_ proportion
## 33 Xanomeline High Dose          _ALL_ proportion
## 34 Xanomeline High Dose          _ALL_    quantity
```

## 35	Xanomeline High Dose	_ALL_	quantity
## 36	Xanomeline High Dose	_ALL_	quantity
## 37	Xanomeline High Dose	_ALL_	WEIGHTBL
## 38	Xanomeline High Dose	_ALL_	WEIGHTBL
## 39	Xanomeline High Dose	_ALL_	WEIGHTBL
## 40	Xanomeline High Dose	_ALL_	WEIGHTBL
## 41	Xanomeline High Dose	_ALL_	WEIGHTBL
## 42	Xanomeline High Dose	AMERICAN INDIAN OR ALASKA NATIVE	proportion
## 43	Xanomeline High Dose	AMERICAN INDIAN OR ALASKA NATIVE	quantity
## 44	Xanomeline High Dose	BLACK OR AFRICAN AMERICAN	proportion
## 45	Xanomeline High Dose	BLACK OR AFRICAN AMERICAN	quantity
## 46	Xanomeline High Dose	WHITE	proportion
## 47	Xanomeline High Dose	WHITE	quantity
## 48	Xanomeline Low Dose	_ALL_	AGE
## 49	Xanomeline Low Dose	_ALL_	AGE
## 50	Xanomeline Low Dose	_ALL_	AGE
## 51	Xanomeline Low Dose	_ALL_	AGE
## 52	Xanomeline Low Dose	_ALL_	AGE
## 53	Xanomeline Low Dose	_ALL_	proportion
## 54	Xanomeline Low Dose	_ALL_	proportion
## 55	Xanomeline Low Dose	_ALL_	quantity
## 56	Xanomeline Low Dose	_ALL_	quantity
## 57	Xanomeline Low Dose	_ALL_	quantity
## 58	Xanomeline Low Dose	_ALL_	WEIGHTBL
## 59	Xanomeline Low Dose	_ALL_	WEIGHTBL
## 60	Xanomeline Low Dose	_ALL_	WEIGHTBL
## 61	Xanomeline Low Dose	_ALL_	WEIGHTBL
## 62	Xanomeline Low Dose	_ALL_	WEIGHTBL
## 63	Xanomeline Low Dose	AMERICAN INDIAN OR ALASKA NATIVE	proportion
## 64	Xanomeline Low Dose	AMERICAN INDIAN OR ALASKA NATIVE	quantity
## 65	Xanomeline Low Dose	BLACK OR AFRICAN AMERICAN	proportion
## 66	Xanomeline Low Dose	BLACK OR AFRICAN AMERICAN	quantity
## 67	Xanomeline Low Dose	WHITE	proportion
## 68	Xanomeline Low Dose	WHITE	quantity
##	procedure	sex	saffl unit denominator measure
## 1	count	F	Y _NULL_ _ALL_ 143.000000
## 2	count	M	Y _NULL_ _ALL_ 111.000000
## 3	count	_ALL_	Y _NULL_ _ALL_ 1.000000
## 4	count	_ALL_	Y _NULL_ _ALL_ 23.000000
## 5	count	_ALL_	Y _NULL_ _ALL_ 230.000000
## 6	max	_ALL_	Y YEARS _NULL_ 89.000000
## 7	mean	_ALL_	Y YEARS _NULL_ 75.209302
## 8	median	_ALL_	Y YEARS _NULL_ 76.000000
## 9	min	_ALL_	Y YEARS _NULL_ 52.000000
## 10	stdev	_ALL_	Y YEARS _NULL_ 8.590167
## 11	percent	F	Y _NULL_ SEX 61.627907
## 12	percent	M	Y _NULL_ SEX 38.372093
## 13	count	_ALL_	Y _NULL_ _ALL_ 86.000000
## 14	count	F	Y _NULL_ _ALL_ 53.000000
## 15	count	M	Y _NULL_ _ALL_ 33.000000
## 16	max	_ALL_	Y KG _NULL_ 86.200000
## 17	mean	_ALL_	Y KG _NULL_ 62.759302
## 18	median	_ALL_	Y KG _NULL_ 60.550000
## 19	min	_ALL_	Y KG _NULL_ 34.000000

## 20	stdev	_ALL_	Y	KG	_NULL_	12.771544
## 21	percent	_ALL_	Y	_NULL_	RACE	0.000000
## 22	count	_ALL_	Y	_NULL_	_ALL_	0.000000
## 23	percent	_ALL_	Y	_NULL_	RACE	9.302326
## 24	count	_ALL_	Y	_NULL_	_ALL_	8.000000
## 25	percent	_ALL_	Y	_NULL_	RACE	90.697674
## 26	count	_ALL_	Y	_NULL_	_ALL_	78.000000
## 27	max	_ALL_	Y	YEARS	_NULL_	88.000000
## 28	mean	_ALL_	Y	YEARS	_NULL_	74.380952
## 29	median	_ALL_	Y	YEARS	_NULL_	76.000000
## 30	min	_ALL_	Y	YEARS	_NULL_	56.000000
## 31	stdev	_ALL_	Y	YEARS	_NULL_	7.886094
## 32	percent	F	Y	_NULL_	SEX	47.619048
## 33	percent	M	Y	_NULL_	SEX	52.380952
## 34	count	_ALL_	Y	_NULL_	_ALL_	84.000000
## 35	count	F	Y	_NULL_	_ALL_	40.000000
## 36	count	M	Y	_NULL_	_ALL_	44.000000
## 37	max	_ALL_	Y	KG	_NULL_	108.000000
## 38	mean	_ALL_	Y	KG	_NULL_	70.004762
## 39	median	_ALL_	Y	KG	_NULL_	69.200000
## 40	min	_ALL_	Y	KG	_NULL_	41.700000
## 41	stdev	_ALL_	Y	KG	_NULL_	14.653433
## 42	percent	_ALL_	Y	_NULL_	RACE	1.190476
## 43	count	_ALL_	Y	_NULL_	_ALL_	1.000000
## 44	percent	_ALL_	Y	_NULL_	RACE	10.714286
## 45	count	_ALL_	Y	_NULL_	_ALL_	9.000000
## 46	percent	_ALL_	Y	_NULL_	RACE	88.095238
## 47	count	_ALL_	Y	_NULL_	_ALL_	74.000000
## 48	max	_ALL_	Y	YEARS	_NULL_	88.000000
## 49	mean	_ALL_	Y	YEARS	_NULL_	75.666667
## 50	median	_ALL_	Y	YEARS	_NULL_	77.500000
## 51	min	_ALL_	Y	YEARS	_NULL_	51.000000
## 52	stdev	_ALL_	Y	YEARS	_NULL_	8.286051
## 53	percent	F	Y	_NULL_	SEX	59.523810
## 54	percent	M	Y	_NULL_	SEX	40.476190
## 55	count	_ALL_	Y	_NULL_	_ALL_	84.000000
## 56	count	F	Y	_NULL_	_ALL_	50.000000
## 57	count	M	Y	_NULL_	_ALL_	34.000000
## 58	max	_ALL_	Y	KG	_NULL_	106.100000
## 59	mean	_ALL_	Y	KG	_NULL_	67.279518
## 60	median	_ALL_	Y	KG	_NULL_	64.900000
## 61	min	_ALL_	Y	KG	_NULL_	45.400000
## 62	stdev	_ALL_	Y	KG	_NULL_	14.123599
## 63	percent	_ALL_	Y	_NULL_	RACE	0.000000
## 64	count	_ALL_	Y	_NULL_	_ALL_	0.000000
## 65	percent	_ALL_	Y	_NULL_	RACE	7.142857
## 66	count	_ALL_	Y	_NULL_	_ALL_	6.000000
## 67	percent	_ALL_	Y	_NULL_	RACE	92.857143
## 68	count	_ALL_	Y	_NULL_	_ALL_	78.000000

```

dmtableFile<- file.path( system.file("extdata/sample-cfg", package="rrdfqbcindex"), "dm.AR.csv" )
## dmtableFile<- file.path(tempdir(),"temp-dm.AR.csv")

write.csv(adsl.summ.stat, file=dmtableFile, row.names=FALSE)

```



```
cat("Written to ", dhtableFile, "\n")
```

```
## Written to /home/ma/projects/rrdfqbcrrnd0/rrdfqbcrrndex/inst/extdata/sample-cfg/dm.AR.csv
```