

# R documentation

of  
'C:/Users/BDG/Documents/000\_github/DIDSR.iMRMC.trunk/Rpackage/viperData'

December 31, 2018

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viperSummary

*viperSummaries*

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## Description

The VIPER summary files contain summary statistics of the VIPER observations

## Usage

viperSummary365

viperSummary455

## Format

An object of class `list` of length 5.

## Details

Each element of the list pertains to one of the VIPER sub-studies:

- screeningLowP [list] Screening population, per reader prevalence ~ 10%
- screeningMedP [list] Screening population, per reader prevalence ~ 30%
- screeningHighP [list] Screening population, per reader prevalence ~ 50%
- challengeMedP [list] Challenge population, per reader prevalence ~ 30%
- challengeHighP [list] Challenge population, per reader prevalence ~ 50%

Each substudy list element is a list object of length 4.

- desc [string] Sub-study label. This is the same as the sub-study list element name.
- studyDesign [list] This list object contains several ways to summarize the distribution of cases in the study according to case type.
  - nObs [num] The number of observations in the sub-study.
  - readers [char] The reader IDs in the sub-study.
  - nR [num] The number of readers in the sub-study.

- nC [data frame] The number of cases in the sub-study by case type. One row of birads0ffdm, birads0sfm, birads12ffdm, birads12sfm, cancer, noncancer.
- perReader [list] This list contains two data frames: FFDM and SFM. Each of these data frames includes the number of cases evaluated by each reader by case type. 20 readers == 20 Rows of birads0ffdm, birads0sfm, birads12ffdm, birads12sfm, cancer, noncancer.
- perReader.summary [list] This list contains two data frames: FFDM and SFM. Each of these data frames includes the total number of cases evaluated by all readers by case type. One row of birads0ffdm, birads0sfm, birads12ffdm, birads12sfm, cancer, noncancer.
- iMRMC [list] This list object contains the MRMC analysis results for auc, tpf, and tnf. There are four groups of results: perReader, Ustat, MLEstat, ROC, and varDecomp The analysis results are produced by a command line version of iMRMC called by R: <https://github.com/DIDSR/iMRMC/releases>, <https://github.com/DIDSR/iMRMC/tree/master/Rpackage>, <https://cran.r-project.org/web/packages/iMRMC/index.html>

**viperSummary365:** This summary is based on [viperObs365](#) the dataset based on cancer at 365 days.

**viperSummary455:** This summary is based on [viperObs455](#) the dataset based on cancer at 455 days.

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