vignette PlasmodeSim

2022-10-19

Welcome to the vignette about the R package PlasmodeSim. This package is still under development.

installing plasmodeSim using remotes

To install using `remotes` run:

```
#install.packages("remotes")
remotes::install_github("GidiusVanDeKamp/PlasmodeSim")
```

```
## Skipping install of 'PlasmodeSim' from a github remote, the SHA1 (644fb4c2) has not changed since las
##   Use 'force = TRUE' to force installation
```

Setting up

This documents skips some parts, we have skipped the steps to obtain the plpResults and the plpData.

```
library(dplyr)

modelSettings <- PatientLevelPrediction::setLassoLogisticRegression()

plpResultLogistic <- PatientLevelPrediction::loadPlpResult("~/R/internshipErasmusMC/simulate-new-patien

plpData<- PatientLevelPrediction::loadPlpData("~/R/internshipErasmusMC/simulate-new-patients-outcomes/pl
```

Example 1

In this example we obtain new outcomes of a fitted logistic model.

```
plpModelLog <- plpResultLogistic$model
probabilites <- PlasmodeSim::newPropsParametersPlpModel(plpModelLog, plpData, plpData$cohorts)
```

```
## Removing infrequent and redundant covariates and normalizing
## Removing infrequent and redundant covariates covariates and normalizing took 0.189 secs
## Prediction took 0.18 secs
```

The function predictPlp returned this information.

```
newOut <- PlasmodeSim::newOutcomes(200, probabilites)
head(newOut)
```

```
##   rowId newOutcomes
## 1  1900           1
## 2  2134           0
## 3  1051           0
## 4    77           0
## 5  1533           0
## 6  2617           1
```

In the output of newOut patients are drawed randomly with the same chance, the patients could be drawed multiple times. If this happens they can have a different outcome. The function `newOutcomes` needs a data set where the column that contains the probabilities is called `value`.

Example 2

We here we show how to simulate new outcomes from an unfitted logistic model.

```
Parameters <- plpModelLog$model$coefficients
UnfittedParameters <- Parameters
UnfittedParameters[1,1] <- -0.4
UnfittedParameters[2:4,1] <- 0.4
head(UnfittedParameters)
```

```
##     betas covariateIds
## 1 -0.4000  (Intercept)
## 2  0.4000         6003
## 3  0.4000         8003
## 4  0.4000         9003
## 5  0.0226      8507001
## 6  0.0000     28060210
```

For the logistic model it is necessary that the parameters are stored in a dataset with a column called `betas` and a column called `covariateIds`.

```
plpModelunfitted <- PlasmodeSim::makeLogisticModel(UnfittedParameters)
newprobs <- PatientLevelPrediction::predictPlp(plpModelunfitted, plpData,plpData$cohorts)
```

```
## Removing infrequent and redundant covariates and normalizing
## Removing infrequent and redundant covariates covariates and normalizing took 0.184 secs
## Prediction took 0.167 secs
```

```
newOut <- PlasmodeSim::newOutcomes(200, newprobs)
head(newOut)
```

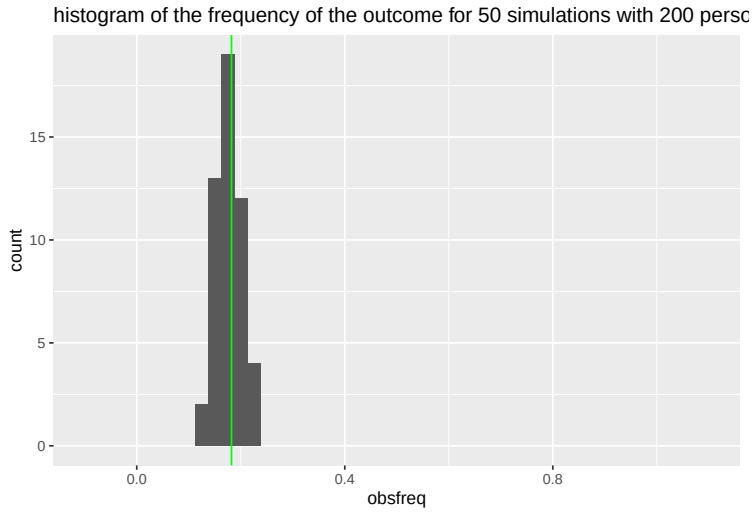
```
##   rowId newOutcomes
## 1  1147           1
## 2  2066           1
## 3  1085           0
## 4  1108           0
## 5   224           0
## 6  1123           0
```

Visual simulations

The function `visualOutcome` simulated new data and then plots the frequency of the outcome. Right now the function `visualOutcome` only works for a logistic model. The green line in the plots is the average outcome in the original dataset.

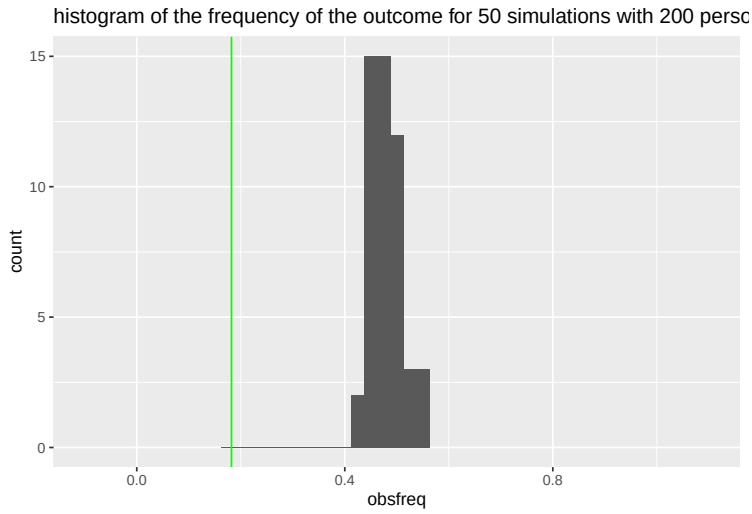
```
PlasmodeSim::visualOutcome(plpData,50,200,Parameters)
```

```
## Removing infrequent and redundant covariates and normalizing
## Removing infrequent and redundant covariates covariates and normalizing took 0.173 secs
## Prediction took 0.171 secs
```




```
PlasmodeSim::visualOutcome(plpData,50,200,UnfittedParameters)
```

```
## Removing infrequent and redundant covariates and normalizing
## Removing infrequent and redundant covariates covariates and normalizing took 0.184 secs
## Prediction took 0.167 secs
```



Here we have plotted 50 times the frequency of the outcome for a simulated dataset with 200 people.

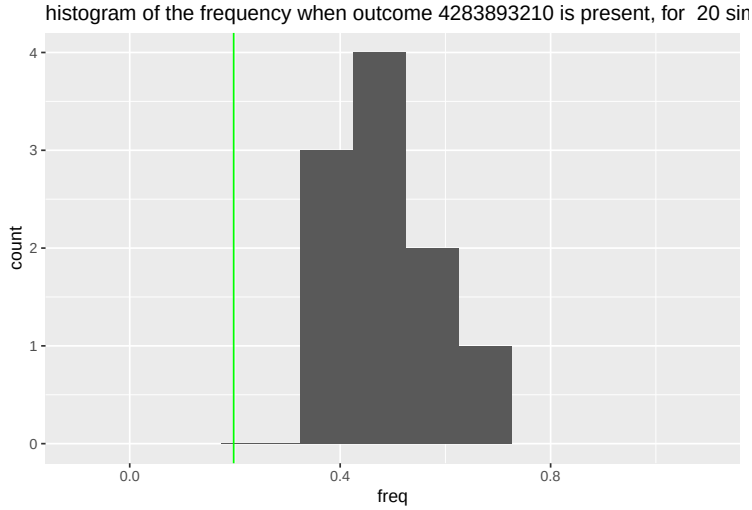
Visual of a specific covariate

```
covariateIdToStudy<- plpResultLogistic$covariateSummary$covariateId[3]
UnfittedParameters[3,]
```

```
##   betas covariateIds
## 3   0.4         8003
```

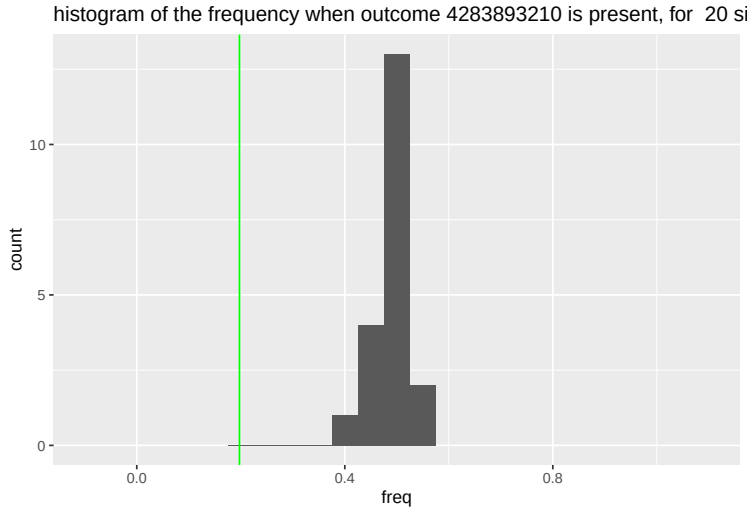
```
PlasmodeSim::visualOutcomeCovariateId(plpData, covariateIdToStudy, 20, 200, UnfittedParameters)
```

```
## Removing infrequent and redundant covariates and normalizing
## Removing infrequent and redundant covariates covariates and normalizing took 0.188 secs
## Prediction took 0.169 secs
```




```
PlasmodeSim::visualOutcomeCovariateId2(plpData, covariateIdToStudy, 20, 200, UnfittedParameters)
```

```
## Removing infrequent and redundant covariates and normalizing
## Removing infrequent and redundant covariates covariates and normalizing took 0.173 secs
## Prediction took 0.167 secs
```



As one can see `visualOutcomeCovariateId` and `visualOutcomeCovariateId2` are very similiar, they both calculate and plot the frequency for a group with a specific covariate present. The small difference is that `visualOutcomeCovariateId` filters a newly simulated dataset set to only keep the patients where the covariate is present, and `visualOutcomeCovariateId2` only simulates new outcomes for patients that have the covariate present. We see they are almost the identical only `visualOutcomeCovariateId2` is spread out less because the groups for calculating the frequency with are bigger.

survival times outcomes.

For simulating new survival times we need more than one probability, we use the baselinehazard, stored in the plpModel.

```
modelSettings <- PatientLevelPrediction::setCoxModel()
plpResult <- PatientLevelPrediction::loadPlpResult("~/R/internshipErasmusMC/simulate-new-patients-outcor
plpModel<- plpResult$model


# function that simulates uncensored data,  simulateSurvivaltimes(plpModel, plpData, 20)
```

simulation censored survival data

first we have to set some settings.

```
populationSettings <- PatientLevelPrediction::createStudyPopulationSettings(
  binary = TRUE,
  includeAllOutcomes = FALSE,
  firstExposureOnly = FALSE,
  washoutPeriod = 180,
  removeSubjectsWithPriorOutcome = FALSE,
  priorOutcomeLookback = 99999,
  requireTimeAtRisk = TRUE,
  minTimeAtRisk = 1,
  riskWindowStart = 1,
  startAnchor = 'cohort start',
  riskWindowEnd = 7300,
  endAnchor = 'cohort start'
)
executeSettings <- PatientLevelPrediction::createExecuteSettings(
  runSplitData = TRUE,
  runSampleData = FALSE,
  runfeatureEngineering = FALSE,
  runPreprocessData = TRUE,
  runModelDevelopment = TRUE,
  runCovariateSummary = TRUE
)
splitSettings <- PatientLevelPrediction::createDefaultSplitSetting(
  testFraction = 0.25,
  trainFraction = 0.75,
  splitSeed = 123,
  nfold = 3,
  type = 'stratified'
)
```

```
sampleSettings <- PatientLevelPrediction::createSampleSettings(
  type = 'none'
)
featureEngineeringSettings <- PatientLevelPrediction::createFeatureEngineeringSettings(
  type = 'none'
)
preprocessSettings <- PatientLevelPrediction::createPreprocessSettings(
  minFraction = 0,
  normalize = TRUE,
  removeRedundancy = TRUE
)
modelSettings <- PatientLevelPrediction::setCoxModel()
```

now that we have out settings. We define a training set and fit the model. The model acctually consist of two plpModels stored in a list.

```
TrainingSet <- PlasmodeSim::MakeTraingSet(plpData, executeSettings, populationSettings, splitSettings, s
```

```
## Outcome is 0 or 1
## seed: 123
## Creating a 25% test and 75% train (into 3 folds) random stratified split by class
## Data split into 656 test cases and 1974 train cases (658, 658, 658)
## Train Set:
## Fold 1 658 patients with 120 outcomes - Fold 2 658 patients with 120 outcomes - Fold 3 658 patients w
## 103 covariates in train data
## Test Set:
## 656 patients with 119 outcomes
## Removing 2 redundant covariates
## Normalizing covariates
## Tidying covariates took 0.496 secs
## Train Set:
## Fold 1 658 patients with 120 outcomes - Fold 2 658 patients with 120 outcomes - Fold 3 658 patients w
## 101 covariates in train data
## Test Set:
## 656 patients with 119 outcomes
```

```
fitcensor<-  PlasmodeSim::fitCensoring(TrainingSet$Train, modelSettings)
```

```
## Running Cyclops
## Done.
## GLM fit status:  OK
## Creating variable importance data frame
## Prediction took 0.135 secs
## Running Cyclops
## Done.
## GLM fit status:  OK
## Creating variable importance data frame
## Prediction took 0.136 secs
```

```
head(fitcensor$outcomesModel$prediction$value)
```

```
## [1] 0.2673806 0.1793623 0.1819307 0.1819307 0.1819307 0.1819307
```

```
NewOutcomes <- PlasmodeSim::simulateSurvivaltimesWithCensoring(fitcensor, plpData, populationSettings, 1
```

```
## Outcome is 0 or 1
## Removing infrequent and redundant covariates and normalizing
## Removing infrequent and redundant covariates covariates and normalizing took 0.181 secs
## Prediction took 0.264 secs
## Removing infrequent and redundant covariates and normalizing
## Removing infrequent and redundant covariates covariates and normalizing took 0.171 secs
## Prediction took 0.263 secs
```

```
head(NewOutcomes)
```

```
##   rowId outcomeCount outcomes
## 1  1290            1       54
## 2   500            1        7
## 3  1864            1       26
## 4   428            0      185
## 5   315            0     7300
## 6   392            0     5863
```