Package ‘analysisPipelines’

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Title Compose Interoperable Analysis Pipelines & Put Them in Production

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Description Enables data scientists to compose pipelines of analysis which consist of data manipulation, exploratory analysis & reporting, as well as modeling steps. Data scientists can use tools of their choice through an R interface, and compose interoperable pipelines between R, Spark, and Python. Credits to Mu Sigma for supporting the development of the package.

Note - To enable pipelines involving Spark tasks, the package uses the 'SparkR' package. The SparkR package needs to be installed to use Spark as an engine within a pipeline. SparkR is distributed natively with Apache Spark and is not distributed on CRAN. The SparkR version needs to directly map to the Spark version (hence the native distribution), and care needs to be taken to ensure that this is configured properly.

To install SparkR from Github, run the following command if you know the Spark version: 'devtools::install_github('apache/spark@v2.x.x', subdir='R/pkg')'. The other option is to install SparkR by running the following terminal commands if Spark has already been installed: `$ export SPARK_HOME=/path/to/spark/directory && cd $SPARK_HOME/R/lib/SparkR/ && R -e "`devtools::install('.')"`".

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AnalysisPipeline-class

Class for constructing Analysis Pipelines for batch/one-time analyses

Description

Class for constructing Analysis Pipelines for batch/one-time analyses

Details

Inherits the base class BaseAnalysisPipeline class which holds the metadata including the registry of available functions, the data on which the pipeline is to be applied, as well as the pipeline itself. Additionally, this class is meant to be used for batch/one-time processing. Contains additional slots to hold the data frame to be used for the pipeline and associated schema.

Slots

input The input dataset on which analysis is to be performed
originalSchemaDf Empty data frame representing the schema of the input
See Also

Other Package core functions for batch/one-time analyses: `checkSchema`, `generateReport`, `initialize`, `BaseAnalysisPipeline`

---

**assessEngineSetUp**

Assesses engine (R, Spark, Python, Spark Structured Streaming) set up

**Usage**

```r
assessEngineSetUp(object)
```

```r
## S4 method for signature 'BaseAnalysisPipeline'
assessEngineSetUp(object)
```
BaseAnalysisPipeline-class

Arguments

object A Pipeline object

Details

Assesses whether engines required for executing functions in an AnalysisPipeline or StreamingAnalysisPipeline object have been set up

This method is implemented on the base class as it is a shared functionality across Pipeline objects

Value

Tibble containing the details of available engines, whether they are required for a pipeline, a logical value reporting whether the engine has been set up, and comments.

See Also

Other Package core functions: BaseAnalysisPipeline-class, MetaAnalysisPipeline-class, checkSchemaMatch, createPipelineInstance, exportAsMetaPipeline, generateOutput, genericPipelineException, getInput, getILoggerDetails, getOutputById, getPipelinePrototype, getPipeline, getRegistry, initDfBasedOnType, initialize, BaseAnalysisPipeline-method, loadMetaPipeline, loadPipeline, loadPredefinedFunctionRegistry, loadRegistry, prepExecution, registerFunction, savePipeline, saveRegistry, setInput, setILoggerDetails, updateObject, visualizePipeline

Examples

```r
## Not run:
library(analysisPipelines)
pipelineObj <- AnalysisPipeline(input = iris)
pipelineObj %>>% univarCatDistPlots(uniCol = "Species", priColor = "blue", optionalPlots = 0) %>>% assessEngineSetUp

## End(Not run)
```

BaseAnalysisPipeline-class

Base class for AnalysisPipeline and StreamingAnalysisPipeline objects

Description

Base class for AnalysisPipeline and StreamingAnalysisPipeline objects
Details

The class which holds the metadata including the registry of available functions, the data on which
the pipeline is to be applied, as well as the pipeline itself, and serves as the base class for various
types of Pipeline objects such as Batch and Streaming.

This base class which contains the slots related to the registry, pipeline and output can be extended
to create custom class for specific scenarios if required.

In the documentation, objects of classes which are subclasses of this class are referred to as 'Pipeline'
objects

Slots

pipeline  A tibble which holds functions to be called
pipelineExecutor  A list containing details of the execution, such as topological ordering of func-
tions to be executed, dependency map of functions, as well as logger configuration
output  A list which holds all the functions output

See Also

Other Package core functions: MetaAnalysisPipeline-class, assessEngineSetUp, checkSchemaMatch,
createPipelineInstance, exportAsMetaPipeline, generateOutput, genericPipelineException,
getInput, getLoggerDetails, getOutputById, getPipelinePrototype, getPipeline, getRegistry,
initDfBasedOnType, initialize,BaseAnalysisPipeline-method, loadMetaPipeline, loadPipeline,
loadPredefinedFunctionRegistry, loadRegistry, prepExecution, registerFunction, savePipeline,
saveRegistry, setInput, setLoggerDetails, updateObject, visualizePipeline

bivarPlots  

bivarPlots  

Bi-Variate Plot

Bi-Variate Plot

Usage

bivarPlots(dataset, select_var_name_1, select_var_name_2,
   priColor = "blue", secColor = "black")

Arguments

dataset  the dataframe that needs to be loaded
select_var_name_1  the name of first column on which the plot needs to be generated
select_var_name_2  the name of second column on which the plot needs to be generated
priColor  the primary color for the plots
secColor  A secondary color for the plots
**castKafkaStreamAsString**

**Details**
A bivariate distribution graph on the selected columns from the dataframe. Selected two columns are on two axis’ and a plot is generated

**Value**
Bivariate plot

**See Also**
Other Package EDA Utilites functions: `CheckColumnType, correlationMatPlot, getDatatype, ignoreCols, multiVarOutlierPlot, outlierPlot, univarCatDistPlots`

**Examples**
```r
bivarPlots(dataset = iris, select_var_name_1 = "Sepal.Length", select_var_name_2 = "Sepal.Width")
```

---

**castKafkaStreamAsString**

_Connect to a Spark session_

**Description**
Connect to a Spark session

**Usage**
```r
castKafkaStreamAsString(streamObj)
```

**Arguments**
- `streamObj` Spark Structured Streaming DataFrame returned by `read.stream` function with source = 'kafka'

**Details**
Takes in a Structured Stream from Kafka created from `read.stream(source = 'kafka',...)` and returns a Structured Streaming DataFrame where the key and value from the Kafka stream are cast to string

**Value**
Updated Spark Structured Streaming DataFrame with key, value, topic and timestamp from the Kafka stream

**See Also**
Other Spark utilities: `convertKafkaValueFromJson, sparkRSessionCreateIfNotPresent`
CheckColumnType

Description
Check for type of column

Usage
CheckColumnType(dataVector)

Arguments
dataVector a data vector of a column

Details
Checking for type of columns in the datavector

Value
column Type

See Also
Other Package EDA Utilites functions: bivarPlots, correlationMatPlot, getDatatype, ignoreCols, multiVarOutlierPlot, outlierPlot, univarCatDistPlots

Examples
CheckColumnType(iris$Sepal.Length)

checkSchemaMatch

Description
Checks the schema of the input to a Pipeline object against the original

Usage
checkSchemaMatch(object, newData)

## S4 method for signature 'AnalysisPipeline'
checkSchemaMatch(object, newData)
convertKafkaValueFromJson

Arguments

object A Pipeline object
newData The newData that the pipeline is to be initialized with

Details

Checks the schema of the new data frame that the pipeline is to be initialized with against the original schema that the pipeline was saved with. Provides a detailed comparison

Value

Returns a list with details on added columns, removed columns, comparison between column classes, and a logical whether the schema has remained the same from the old dataframe to the new one

See Also

Other Package core functions: BaseAnalysisPipeline-class, MetaAnalysisPipeline-class, assessEngineSetUp, createPipelineInstance, exportAsMetaPipeline, generateOutput, genericPipelineException, getInput, getILoggerDetails, getOutputByld, getPipelinePrototype, getPipeline, getRegistry, initDfBasedOnType, initialize, BaseAnalysisPipeline-method, loadMetaPipeline, loadPipeline, loadPredefinedFunctionRegistry, loadRegistry, prepExecution, registerFunction, savePipeline, saveRegistry, setInput, setILoggerDetails, updateObject, visualizePipeline

connectKafkaValueFromJson

Connect to a Spark session

Description

Connect to a Spark session

Usage

convertKafkaValueFromJson(streamObj, schema)

Arguments

streamObj Spark Structured Streaming DataFrame which is returned by the castKafkaStreamAsString function
schema A structType object created from SparkR specifying the schema of the json data present in the value attribute of the incoming Kafka stream

Details

Takes in a Structured Stream from Kafka created from read.stream(source = 'kafka',...) and returns a Structured Streaming DataFrame where the key and value from the Kafka stream are cast to string
correlationMatPlot

Description

A correlation matrix is created and plotted across all the columns in the dataset

Usage

correlationMatPlot(dataset, methodused = "everything")

Arguments

dataset the dataset that needs to be loaded
methodused methods to be used for computing correlation

Value

Correlation Matrix graph

See Also

Other Package EDA Utilites functions: CheckColumnType, bivarPlots, getDatatype, ignoreCols, multiVarOutlierPlot, outlierPlot, univarCatDistPlots

Examples

correlationMatPlot(dataset = iris)
createPipelineInstance

Create a Pipeline object from a meta-pipeline

Description

Create a Pipeline object from a meta-pipeline

Usage

createPipelineInstance(metaPipelineObj, newParams)

## S4 method for signature 'MetaAnalysisPipeline'
createPipelineInstance(metaPipelineObj, newParams)

Arguments

metaPipelineObj

A MetaAnalysisPipeline object

newParams

Either a nested named list containing all the functions in the pipeline, their arguments and corresponding values (OR) an object of class proto which is a pipeline prototype, with the new values of the arguments set. Refer the getPipelinePrototype method.

Details

This method instantiates a Pipeline object (both AnalysisPipeline and StreamingAnalysisPipeline) from a meta-pipeline as well as an object containing the new set of values for the arguments of all the functions in the pipeline.

Value

A Pipeline object

See Also

Other Package core functions: BaseAnalysisPipeline-class, MetaAnalysisPipeline-class, assessEngineSetUp, checkSchemaMatch, exportAsMetaPipeline, generateOutput, genericPipelineException, getInput, getILoggerDetails, getOutputById, getPipelinePrototype, getPipeline, getRegistry, initDfBasedOnType, initialize, BaseAnalysisPipeline-method, loadMetaPipeline, loadPipeline, loadPredefinedFunctionRegistry, loadRegistry, prepExecution, registerFunction, savePipeline, saveRegistry, setInput, setILoggerDetails, updateObject, visualizePipeline
exportAsMetaPipeline

Method to export a meta-pipeline

Description

Method to export a meta-pipeline

Usage

exportAsMetaPipeline(object)

## S4 method for signature 'BaseAnalysisPipeline'
exportAsMetaPipeline(object)

Arguments

object A Pipeline object

Details

This method exports a Pipeline object i.e. of the classes AnalysisPipeline or StreamingAnalysisPipeline as a meta-pipeline

Value

an object of class "MetaAnalysisPipeline"

See Also

Other Package core functions: BaseAnalysisPipeline-class, MetaAnalysisPipeline-class, assessEngineSetUp, checkSchemaMatch, createPipelineInstance, generateOutput, genericPipelineException, getInput, getLoggerDetails, getOutputById, getPipelinePrototype, getPipeline, getRegistry, initDfBasedOnType, initialize, BaseAnalysisPipeline-method, loadMetaPipeline, loadPipeline, loadPredefinedFunctionRegistry, loadRegistry, prepExecution, registerFunction, savePipeline, saveRegistry, setInput, setLoggerDetails, updateObject, visualizePipeline

Examples

## Not run:
pipelineObj <- AnalysisPipeline(input = iris)
pipelineObj %>% univarCatDistPlots(uniCol = "Species") %>% pipelineObj
pipelineObj %>% exportAsMetaPipeline -> exportedMetaPipeline
exportedMetaPipeline %>%
createPipelineInstance(newParams = exportedMetaPipeline %>%
getPipelinePrototype)

## End(Not run)
Examples

```r
## Not run:
' pipelineObj <- AnalysisPipeline(input = iris)
pipelineObj %>>% univarCatDistPlots(uniCol = "Species") %>>%
exportAsMetaPipeline -> exportedMetaPipeline

## End(Not run)
```

---

### generateOutput

Generate a list of outputs from Pipeline objects

#### Description

Generate a list of outputs from Pipeline objects

#### Usage

```r
generateOutput(object)
```

#### Arguments

- `object`: object that contains input, pipeline, registry and output

#### Details

generateOutput is a generic function that is implemented for various types of pipeline objects such as `AnalysisPipeline` and `StreamingAnalysisPipeline`

The sequence of operations stored in the pipeline object are run and outputs generated, stored in a list

#### Value

Updated Pipeline object with the outputs at each step stored in the output slot.

Specific outputs can be obtained by using the `getOutputById` function
generateReport

## Description

Generate a HTML report from an `AnalysisPipeline` object

## Usage

```r
generateReport(object, path)
```

```r
## S4 method for signature 'AnalysisPipeline,character'
generateReport(object, path = ".")
```

## Arguments

- `object` object that contains input, pipeline, registry and output
- `path` path on the file system, where the generated html report should be stored

## Details

The sequence of operations stored in the `AnalysisPipeline` object are run, outputs generated, and a HTML report is generated with outputs in the same sequence as the pipeline created by the user

## Value

Updated `AnalysisPipeline` object

## See Also

Other Package core functions for batch/one-time analyses: `AnalysisPipeline-class, checkSchema, initialize,BaseAnalysisPipeline-method`
## Examples

```r
## Not run:
pipelineObj <- AnalysisPipeline(input = iris)
pipelineObj %>>% univarCatDistPlots(uniCol = "Species", storeOutput = T) -> pipelineObj
pipelineObj %>>% generateReport(path = ".")
## End(Not run)
```

---

### genericPipelineException

**Default exception for pipeline functions**

---

### Description

Default exception for pipeline functions

### Usage

```r
genericPipelineException(error)
```

### Arguments

- **error**
  Error encountered during the execution of a particular pipeline function

### Details

This function defines the default function which will be called in case of an exception occurring while executing any of the pipeline functions. While a function is registered, a custom function to deal with exceptions incurred during the call of the function being registered can be passed by the user. If passed, the custom function will be called instead of this function

### See Also

Other Package core functions: `BaseAnalysisPipeline-class`, `MetaAnalysisPipeline-class`, `assessEngineSetUp`, `checkSchemaMatch`, `createPipelineInstance`, `exportAsMetaPipeline`, `generateOutput`, `getInput`, `getLoggerDetails`, `getOutputById`, `getPipelinePrototype`, `getPipeline`, `getRegistry`, `initDfBasedOnType`, `initialize`, `BaseAnalysisPipeline-method`, `loadMetaPipeline`, `loadPipeline`, `loadPredefinedFunctionRegistry`, `loadRegistry`, `prepExecution`, `registerFunction`, `savePipeline`, `saveRegistry`, `setInput`, `setLoggerDetails`, `updateObject`, `visualizePipeline`
**getDatatype**  
*Get Data Type*

**Description**  
Get Data Type

**Usage**  
`getDatatype(dataset)`

**Arguments**  
- `dataset`: a dataset which needs to be loaded

**Details**  
Based on the datatype the columns are separated into categorical and numerical columns

**Value**  
list with `numeric_cols` and `cat_cols`

**See Also**  
Other Package EDA Utilities functions: `CheckColumnType, bivarPlots, correlationMatPlot, ignoreCols, multiVarOutlierPlot, outlierPlot, univarCatDistPlots`

**Examples**  
`getDatatype(iris)`

---

**getFeaturesForPyClassification**  
*Extracts selected columns from a data frame as a Python array*

**Description**  
Extracts selected columns from a data frame as a Python array

**Usage**  
`getFeaturesForPyClassification(dataset, featureNames)`
Arguments

- `dataset` - an R data frame
- `featureNames` - Column names to be extracted from the R data frame. A character vector.

Details

Helper function, which when provided an R data frame and a set of column/feature names, extracts them from the R data frame as a matrix and converts them to the equivalent Python array.

Typically this function can be used when providing a feature matrix to a Python machine learning function.

See Also

Other R helper utilities for Python: `getTargetForPyClassification`, `setPythonEnvir`

Examples

```r
## Not run:
getFeaturesForPyClassification(dataset = iris,
featureNames = c("Sepal.Length", "Sepal.Width"))
## End(Not run)
```

---

getInput

Obtains the initializedInput

Description

Obtains the initializedInput

Usage

```r
getInput(object)
```

## S4 method for signature 'BaseAnalysisPipeline'

```r
getInput(object)
```

Arguments

- `object` - The AnalysisPipeline or StreamingAnalysisPipeline object

Details

Obtains the input from the AnalysisPipeline or StreamingAnalysisPipeline object

This method is implemented on the base class as it is a shared functionality types of Analysis Pipelines which extend this class
**getLoggerDetails**

**Value**

Dataframe for an AnalysisPipeline & SparkDataFrame for a StreamingAnalysisPipeline

**See Also**

Other Package core functions: `BaseAnalysisPipeline-class`, `MetaAnalysisPipeline-class`, `assessEngineSetUp`, `checkSchemaMatch`, `createPipelineInstance`, `exportAsMetaPipeline`, `generateOutput`, `genericPipelineException`, `getLoggerDetails`, `getOutputById`, `getPipelinePrototype`, `getPipeline`, `getRegistry`, `initDfBasedOnType`, `initialize`, `BaseAnalysisPipeline-method`, `loadMetaPipeline`, `loadPipeline`, `loadPredefinedFunctionRegistry`, `loadRegistry`, `prepExecution`, `registerFunction`, `savePipeline`, `saveRegistry`, `setInput`, `setLoggerDetails`, `updateObject`, `visualizePipeline`

**Examples**

```r
library(analysisPipelines)
pipelineObj <- AnalysisPipeline(input = iris)
pipelineObj %>% getInput
```

---

**getLoggerDetails**  
*Obtains the logger configuration for the pipeline*

**Description**

Obtains the logger configuration for the pipeline

**Usage**

```r
c.getLoggerDetails(object)
```

## S4 method for signature 'BaseAnalysisPipeline'

c.getLoggerDetails(object)

**Arguments**

- `object`  
  A Pipeline object

**Details**

This function obtains the logger configuration for the pipeline.

**Value**

Logger configuration as a list
getOutputById

See Also

Other Package core functions: `BaseAnalysisPipeline-class`, `MetaAnalysisPipeline-class`, `assessEngineSetUp`, `checkSchemaMatch`, `createPipelineInstance`, `exportAsMetaPipeline`, `generateOutput`, `genericPipelineException`, `getInput`, `getOutputById`, `getPipelinePrototype`, `getPipeline`, `getRegistry`, `initDfBasedOnType`, `initialize`, `BaseAnalysisPipeline-method`, `loadMetaPipeline`, `loadPipeline`, `loadPredefinedFunctionRegistry`, `loadRegistry`, `prepExecution`, `registerFunction`, `savePipeline`, `saveRegistry`, `setInput`, `setLoggerDetails`, `updateObject`, `visualizePipeline`

Examples

```r
library(analysisPipelines)
pipelineObj <- AnalysisPipeline(input = iris)
pipelineObj %>% getLoggerDetails
```

<table>
<thead>
<tr>
<th>getOutputById</th>
<th>Obtains a specific output</th>
</tr>
</thead>
</table>

Description

Obtains a specific output

Usage

```r
getOutputById(object, reqId, includeCall = F)
```

## S4 method for signature 'BaseAnalysisPipeline'
```r
getOutputById(object, reqId, 
includeCall = F)
```

Arguments

- **object**: The `AnalysisPipeline` or `StreamingAnalysisPipeline` object
- **reqId**: The position of the function for which the output is desired in the sequence of operations in the pipeline.
- **includeCall**: Logical which defines whether the call used to generate the output should be returned. By default this is false

Details

Obtains a specific output from the `AnalysisPipeline` or `StreamingAnalysisPipeline` object by passing the position of the function for which the output is desired, in the sequence of operations in the pipeline. This can be obtained by passing the number under the 'id' column in the pipeline table corresponding to the required function

This method is implemented on the base class as it is a shared functionality types of Analysis Pipelines which extend this class
Value

If includeCall = F, the output object generated by the function is returned.

If includeCall = T, it is a list containing two elements - call: tibble with 1 row containing the function call for the output desired - output: output generated.

See Also

Other Package core functions: BaseAnalysisPipeline-class, MetaAnalysisPipeline-class, assessEngineSetUp, checkSchemaMatch, createPipelineInstance, exportAsMetaPipeline, generateOutput, genericPipelineException, getInput, getILoggerDetails, getPipelinePrototype, getPipeline, getRegistry, initDfBasedOnType, initialize, BaseAnalysisPipeline-method, loadMetaPipeline, loadPipeline, loadPredefinedFunctionRegistry, loadRegistry, prepExecution, registerFunction, savePipeline, saveRegistry, setInput, setLoggerDetails, updateObject, visualizePipeline.

Examples

## Not run:
library(analysisPipelines)
pipelineObj <- AnalysisPipeline(input = iris)
getNumRows <- function(dataset){
  return(nrow(dataset))
}
registerFunction("getNumRows")
pipelineObj %>>% getNumRows(storeOutput = TRUE) -> pipelineObj
pipelineObj %>>% generateOutput %>>% getOutputById("1")

## End(Not run)
getPipelinePrototype

Details
Obtains the pipeline from the AnalysisPipeline or StreamingAnalysisPipeline object as a tibble
This method is implemented on the base class as it is a shared functionality types of Analysis Pipelines which extend this class

Value
Tibble describing the pipeline

See Also
Other Package core functions: BaseAnalysisPipeline-class, MetaAnalysisPipeline-class, assessEngineSetUp, checkSchemaMatch, createPipelineInstance, exportAsMetaPipeline, generateOutput, genericPipelineException, getInput, getLogDetails, getOutputById, getPipelinePrototype, getRegistry, initDfBasedOnType, initialize, BaseAnalysisPipeline-method, loadMetaPipeline, loadPipeline, loadPredefinedFunctionRegistry, loadRegistry, prepExecution, registerFunction, savePipeline, saveRegistry, setInput, setLogDetails, updateObject, visualizePipeline

Examples
## Not run:
library(analysisPipelines)
pipelineObj <- AnalysisPipeline(input = iris)
getNumRows <- function(dataset){
  return(nrow(dataset))
}
registerFunction("getNumRows")
pipelineObj %>>% getNumRows %>>% getPipeline

## End(Not run)
getRegistry

Arguments

metaPipelineObj
A MetaAnalysisPipeline object

Details

This method returns the prototype of functions in the pipeline and their respective arguments as proto object. Functions in the pipeline can be accessed easily by using the '$' operator, and within the functions the arguments can be accessed the same way. These can be accessed and set to new values. This pipeline prototype can then be passed to the createPipelineInstance method which will instantiate an executable pipeline with the inputs set in the prototype

Value

An object of class proto from the 'proto' package

See Also

Other Package core functions: BaseAnalysisPipeline-class, MetaAnalysisPipeline-class, assessEngineSetUp, checkSchemaMatch, createPipelineInstance, exportAsMetaPipeline, generateOutput, genericPipelineException, getInput, getLoggerDetails, getOutputById, getPipeline, getRegistry, initDfBasedOnType, initialize, BaseAnalysisPipeline-method, loadMetaPipeline, loadPipeline, loadPredefinedFunctionRegistry, loadRegistry, prepExecution, registerFunction, savePipeline, saveRegistry, setInput, setLoggerDetails, updateObject, visualizePipeline

Examples

## Not run:
pipelineObj <- AnalysisPipeline(input = iris)
pipelineObj %>% univarCatDistPlots(uniCol = "Species") %>%
exportAsMetaPipeline %>% getPipelinePrototype

## End(Not run)

getRegistry Obtains the function registry

Description

Obtains the function registry

Usage

getRegistry()

Details

Obtains the function registry as a tibble, including both predefined and user defined functions
getResponse

Value

Tibble describing the registry

See Also

Other Package core functions: BaseAnalysisPipeline-class, MetaAnalysisPipeline-class, assessEngineSetUp, checkSchemaMatch, createPipelineInstance, exportAsMetaPipeline, generateOutput, genericPipelineException, getInput, getLoggerDetails, getOutputById, getPipelinePrototype, getPipeline, initDfBasedOnType, initialize, BaseAnalysisPipeline-method, loadMetaPipeline, loadPipeline, loadPredefinedFunctionRegistry, loadRegistry, prepExecution, registerFunction, savePipeline, saveRegistry, setInput, setLoggerDetails, updateObject, visualizePipeline

Examples

getResponse()

library(analysisPipelines)
getResponse(y ~ x1 + x2)
getTargetForPyClassification

Extracts selected column from a data frame a binary class Python array

Description

Extracts selected column from a data frame a binary class Python array

Usage

getTargetForPyClassification(dataset, targetVarName, positiveClass)

Arguments

dataset an R data frame
targetVarName Name of the target variable for classification. Should be a categorical variable.
positiveClass Name of the class of the target variable which should be coded as '1'

Details

Helper function, which when provided an R dataframe and a binary categorical column, extracts it from the R data frame, converts it to 1/0 class coding, and converts it to a Python array

Typically this function can be used to extract a target variable for a classifier to be provided to a Python machine learning function

See Also

Other R helper utilities for Python: getFeaturesForPyClassification, setPythonEnvir

Examples

```r
## Not run:
getTargetForPyClassification(dataset = iris, 
targetVarName = "Species", positiveClass = "setosa")
## End(Not run)
```
**getTerm**

*Obtains the dependency term from the formula*

**Description**
Obtains the dependency term from the formula

**Usage**
`getTerm(f)`

**Arguments**
- `f`  
  formula from which term is to be extracted.

**Details**
This is a helper function to extract the terms from a formula

**Value**
String with the terms

**Examples**
```r
library(analysisPipelines)
getTerm(y ~ x)
```

---

**ignoreCols**

*Ignores the columns in the loaded dataframe object*

**Description**
Ignores the columns in the loaded dataframe object

**Usage**
`ignoreCols(data, columns)`

**Arguments**
- `data`  
  the dataframe object that needs to be loaded
- `columns`  
  the names of columns to be ignored from dataframe object

**Details**
The columns selected are removed from the object
isDependencyParam

Value

Updated dataframe object

See Also

Other Package EDA Utilities functions: CheckColumnType, bivarPlots, correlationMatPlot, getDatatype, multiVarOutlierPlot, outlierPlot, univarCatDistPlots

Examples

ignoreCols(data = iris, columns = "Species")

library(analysisPipelines)

isDependencyParam(~f1)
loadMetaPipeline

Load a meta-pipeline

Description

Load a meta-pipeline

Usage

loadMetaPipeline(path)

Arguments

path

the path at which the .Rds file containing the pipeline is located

Details

This function loads a meta-pipeline from a file system, and returns the meta-pipeline object, which can be assigned to an object in the environment.

Note - When a meta-pipeline is loaded, the existing registry is overwritten with the registry saved with the meta-pipeline

Value

An MetaAnalysisPipeline object

See Also

Other Package core functions: BaseAnalysisPipeline-class, MetaAnalysisPipeline-class, assessEngineSetUp, checkSchemaMatch, createPipelineInstance, exportAsMetaPipeline, generateOutput, genericPipelineException, getInput, getLoggerDetails, getOutputById, getPipelinePrototype, getPipeline, getRegistry, initDfBasedOnType, initialize, BaseAnalysisPipeline-method, loadPipeline, loadPredefinedFunctionRegistry, loadRegistry, prepExecution, registerFunction, savePipeline, saveRegistry, setInput, setLoggerDetails, updateObject, visualizePipeline

Examples

## Not run:
loadMetaPipeline(path = "./metaPipeline.RDS")

## End(Not run)
loadPipeline

---

**loadPipeline**

*Loads the AnalysisPipeline or StreamingAnalysisPipeline object from the file system*

---

**Description**

Loads the AnalysisPipeline or StreamingAnalysisPipeline object from the file system

**Usage**

```r
loadPipeline(path, input = data.frame(), filePath = "")
```

**Arguments**

- **path**: the path at which the .Rds file containing the pipeline is located
- **input**: (optional) data frame with which the pipeline object should be initialized
- **filePath**: (optional) path where a dataset in .CSV format is present which is to be loaded

**Details**

The AnalysisPipeline or StreamingAnalysisPipeline object is loaded into the file system from the file system based on the path specified.

Optionally, the input parameter can be provided to initialize the AnalysisPipeline or StreamingAnalysisPipeline object with an R data frame or Streaming Spark DataFrame (in case of StreamingAnalysisPipeline object) present in the R session.

Another provided option, is to specify a filePath where the input dataset is present (in a .CSV format) and the object will be initialized with this data frame. The filePath parameter takes precedence over input parameter. This is applicable only from AnalysisPipeline objects

Note - When a pipeline is loaded, the existing registry is overwritten with the registry saved with the pipeline

**Value**

An AnalysisPipeline or StreamingAnalysisPipeline object, optionally initialized with the data frame provided

**See Also**

Other Package core functions: `BaseAnalysisPipeline-class`, `MetaAnalysisPipeline-class`, `assessEngineSetUp`, `checkSchemaMatch`, `createPipelineInstance`, `exportAsMetaPipeline`, `generateOutput`, `genericPipelineException`, `getInput`, `getLoggerDetails`, `getOutputById`, `getPipelinePrototype`, `getPipeline`, `getRegistry`, `initDfBasedOnType`, `initialize`, `BaseAnalysisPipeline-method`, `loadMetaPipeline`, `loadPredefinedFunctionRegistry`, `loadRegistry`, `prepExecution`, `registerFunction`, `savePipeline`, `saveRegistry`, `setInput`, `setLoggerDetails`, `updateObject`, `visualizePipeline`
Examples

```r
## Not run:
library(analysisPipelines)
loadPipeline(path = "/pipeline.RDS")

## End(Not run)
```

---

`loadPredefinedFunctionRegistry`

*Loading the registry of predefined functions*

Description

Loading the registry of predefined functions

Usage

```
loadPredefinedFunctionRegistry()
```

Details

Loads the registry of predefined functions

See Also

Other Package core functions: `BaseAnalysisPipeline-class`, `MetaAnalysisPipeline-class`, `assessEngineSetUp`, `checkSchemaMatch`, `createPipelineInstance`, `exportAsMetaPipeline`, `generateOutput`, `genericPipelineException`, `getInput`, `getLoggerDetails`, `getOutputById`, `getPipelinePrototype`, `getPipeline`, `getRegistry`, `initDfBasedOnType`, `initialize`, `BaseAnalysisPipeline-method`, `loadMetaPipeline`, `loadPipeline`, `loadRegistry`, `prepExecution`, `registerFunction`, `savePipeline`, `saveRegistry`, `setInput`, `setLoggerDetails`, `updateObject`, `visualizePipeline`

Examples

```r
## Not run:
library(analysisPipelines)
loadPredefinedFunctionRegistry()

## End(Not run)
```
loadRegistry  Loads a function registry from a file

Description

Loads a function registry from a file

Usage

loadRegistry(path)

Arguments

path  path on the file system, where the registry is to be loaded from

Details

This function loads a function registry and associated function definition stored in an RDS file into the environment. The existing registry is overwritten with the newly loaded registry

See Also

Other Package core functions: BaseAnalysisPipeline-class, MetaAnalysisPipeline-class, assessEngineSetUp, checkSchemaMatch, createPipelineInstance, exportAsMetaPipeline, generateOutput, genericPipelineException, getInput, getLoggerrDetails, getOutputById, getPipelinePrototype, getPipeline, getRegistry, initDfBasedOnType, initialize, BaseAnalysisPipeline-method, loadMetaPipeline, loadPipeline, loadPredefinedFunctionRegistry, prepExecution, registerFunction, savePipeline, saveRegistry, setInput, setLoggerDetails, updateObject, visualizePipeline

Examples

## Not run:
library(analysisPipelines)
loadRegistry(path = "./registry.RDS")

## End(Not run)
multiVarOutlierPlot

Details

This class works with the AnalysisPipeline and StreamingAnalysisPipeline classes, and allows the pipeline to be exported as meta-pipeline. A meta-pipeline is a construct, where the input dataset as well as the arguments to functions in the pipeline are not defined. Only the analysis flow and dependencies are stored.

Slots

pipeline A tibble which holds functions to be called in the pipeline
pipelinePrototype An object of class proto from the 'proto' package which maintains the prototype of the functions in the pipeline and their respective arguments
type A string defining whether it is a batch or streaming pipeline. Acceptable values are 'batch' & 'streaming'

See Also

Other Package core functions: BaseAnalysisPipeline-class, assessEngineSetUp, checkSchemaMatch, createPipelineInstance, exportAsMetaPipeline, generateOutput, genericPipelineException, getInput, getLoggerDetails, getOutputById, getPipelinePrototype, getPipeline, getRegistry, initDfBasedOnType, initialize, BaseAnalysisPipeline-method, loadMetaPipeline, loadPipeline, loadPredefinedFunctionRegistry, loadRegistry, prepExecution, registerFunction, savePipeline, saveRegistry, setInput, setLoggerDetails, updateObject, visualizePipeline

multiVarOutlierPlot  Multi-Variate Outlier Plot

Description

Multi-Variate Outlier Plot

Usage

multiVarOutlierPlot(data, depCol, indepCol, sizeCol, priColor = "blue", optionalPlots = 0, cutoffValue = 0.05)

Arguments

data the dataframe that needs to be loaded
depCol the name of column which is to be identified as dependent column
indepCol the name of an independent column
sizeCol the name of column used to define the size of point in plots
priColor the primary color for the plots
optionalPlots A Flag for optional plots
cutoffValue A p-value cutoff for detecting outliers
Details

Multivariate outlier plot using the selected columns from the dataframe

Value

Outliers plot

See Also

Other Package EDA Utilities functions: CheckColumnType, bivarPlots, correlationMatPlot, getDatatype, ignoreCols, outlierPlot, univarCatDistPlots

Examples

```r
## Not run:
multiVarOutlierPlot(data = iris, depCol = "Sepal.Length",
        indepCol = "Sepal.Width", sizeCol = "Petal.Length")
## End(Not run)
```

---

**outlierPlot**  
*Outlier detection plot*

Description

Outlier detection plot

Usage

```r
outlierPlot(data, method = "iqr", columnName, cutoffValue = 0.05,
        priColor = "blue", optionalPlots = 0)
```

Arguments

- `data`  
The dataframe that needs to be loaded
- `method`  
The method on which outliers are to be identified
- `columnName`  
The name of column for which the outliers are identified
- `cutoffValue`  
The cut off value to define the threshold for outliers
- `priColor`  
The primary color for the plots
- `optionalPlots`  
A Flag for optional plots

Details

Outlier are to be identified on the selected column from the dataframe
prepExecution

Description

Prepare the pipeline for execution

Usage

prepExecution(object)

## S4 method for signature 'BaseAnalysisPipeline'
prepExecution(object)

Arguments

object A Pipeline object

Details

The pipeline is prepared for execution by identifying the graph of the pipeline as well as its topological ordering, and dependency map in order to prepare for execution

Value

Updated AnalysisPipeline StreamingAnalysisPipeline object

See Also

Other Package core functions: BaseAnalysisPipeline-class, MetaAnalysisPipeline-class, assessEngineSetUp, checkSchemaMatch, createPipelineInstance, exportAsMetaPipeline, generateOutput, genericPipelineException, getInput, getLoggerDetails, getOutputById, getPipelinePrototype, getPipeline, getRegistry, initDFBasedOnType, initialize, BaseAnalysisPipeline-method, loadMetaPipeline, loadPipeline, loadPredefinedFunctionRegistry, loadRegistry, registerFunction, savePipeline, saveRegistry, setInput, setLoggerDetails, updateObject, visualizePipeline
### Examples

```r
## Not run:
library(analysisPipelines)
pipelineObj <- AnalysisPipeline(input = iris)
pipelineObj %>>% univarCatDistPlots(uniCol = "Species",
priColor = "blue", optionalPlots = 0, storeOutput = T) %>>%
prepExecution -> pipelineObj

## End(Not run)
```

---

**registerFunction**

Register a user-defined function to be used with a AnalysisPipeline or StreamingAnalysisPipeline object

### Description

Register a user-defined function to be used with a AnalysisPipeline or StreamingAnalysisPipeline object

### Usage

```r
registerFunction(functionName, heading = "", functionType = "batch",
engine = "r",
exceptionFunction = as.character(substitute(genericPipelineException)),
isDataFunction = T, firstArgClass = "", loadPipeline = F,
userDefined = T)
```

### Arguments

- **functionName**: name of function to be registered
- **heading**: heading of that section in report
- **functionType**: type of function - 'batch' for AnalysisPipeline objects, 'streaming' for StreamingAnalysisPipeline objects
- **engine**: specifies which engine the function is to be run on. Available engines include "r", "spark", and "python"
- **exceptionFunction**: R object corresponding to the exception function
- **isDataFunction**: logical parameter which defines whether the function to be registered operates on data i.e. the first parameter is a dataframe
- **firstArgClass**: character string with the class of the first argument to the function, if it is a non-data function
- **loadPipeline**: logical parameter to see if function is being used in loadPipeline or not. This is for internal working
- **userDefined**: logical parameter defining whether the function is user defined. By default, set to true
Details

The specified operation along with the heading and engine details is stored in the registry, after which it can be added to a pipeline.

If the function already exists in the registry, registration will be skipped. In order to change the definition, the function needs to be reassigned in the Global Environment and then the `registerFunction` called again.

See Also

Other Package core functions: `BaseAnalysisPipeline-class`, `MetaAnalysisPipeline-class`, `assessEngineSetUp`, `checkSchemaMatch`, `createPipelineInstance`, `exportAsMetaPipeline`, `generateOutput`, `genericPipelineException`, `getInput`, `getLoggerDetails`, `getOutputById`, `getPipelinePrototype`, `getPipeline`, `getRegistry`, `initDfBasedOnType`, `initialize`, `BaseAnalysisPipeline-method`, `loadMetaPipeline`, `loadPipeline`, `loadPredefinedFunctionRegistry`, `loadRegistry`, `prepExecution`, `savePipeline`, `saveRegistry`, `setInput`, `setLoggerDetails`, `updateObject`, `visualizePipeline`

Examples

```r
## Not run:
library(analysisPipelines)
getNumRows <- function(dataset){
  return(nrow(dataset))
}

registerFunction("getNumRows")

## End(Not run)
```

**savePipeline** Saves the AnalysisPipeline or StreamingAnalysisPipeline object to the file system without outputs

Description

Saves the AnalysisPipeline or StreamingAnalysisPipeline object to the file system without outputs

Usage

```r
savePipeline(object, path)
```

## S4 method for signature 'BaseAnalysisPipeline'
```r
savePipeline(object, path)
```

## S4 method for signature 'MetaAnalysisPipeline'
```r
savePipeline(object, path)
```
saveRegistry

Arguments

object  object that contains input, pipeline, registry and output
path    the path at which the .Rda file containing the pipeline should be stored, along
        with the name of the file including a .Rda extension

Details

The AnalysisPipeline or StreamingAnalysisPipeline object is saved to the file system in the
paths specified

This method is implemented on the base class as it is a shared functionality types of Analysis
Pipelines which extend this class

Value

Does not return a value

See Also

Other Package core functions: BaseAnalysisPipeline-class, MetaAnalysisPipeline-class,
assessEngineSetUp, checkSchemaMatch, createPipelineInstance, exportAsMetaPipeline,
generateOutput, genericPipelineException, getInput, getLogDetails, getOutputById,
getPipelinePrototype, getPipeline, getRegistry, initDfBasedOnType, initialize, BaseAnalysisPipeline-method,
loadMetaPipeline, loadPipeline, loadPredefinedFunctionRegistry, loadRegistry, prepExecution,
registerFunction, saveRegistry, setInput, setLogDetails, updateObject, visualizePipeline

Examples

## Not run:
library(analysisPipelines)
pipelineObj <- AnalysisPipeline(input = iris)
pipelineObj %>>% savePipeline(path = "./test.RDS")

## End(Not run)
**setInput**

Details

This function saves the existing function registry and associated function definition loaded in the environment into a file.

See Also

Other Package core functions: `BaseAnalysisPipeline-class`, `MetaAnalysisPipeline-class`, `assessEngineSetUp`, `checkSchemaMatch`, `createPipelineInstance`, `exportAsMetaPipeline`, `generateOutput`, `genericPipelineException`, `getInput`, `getLoggerDetails`, `getOutputByld`, `getPipelinePrototype`, `getPipeline`, `getRegistry`, `initDfBasedOnType`, `initialize`, `BaseAnalysisPipeline-method`, `loadMetaPipeline`, `loadPipeline`, `loadPredefinedFunctionRegistry`, `loadRegistry`, `prepExecution`, `registerFunction`, `savePipeline`, `setInput`, `setLoggerDetails`, `updateObject`, `visualizePipeline`

Examples

```r
## Not run:
library(analysisPipelines)
saveRegistry(path = "./registry.RDS")
## End(Not run)
```

---

**setInput**  
Sets the input for an AnalysisPipeline or StreamingAnalysisPipeline object

Description

Sets the input for an AnalysisPipeline or StreamingAnalysisPipeline object

Usage

```r
setInput(object, input, filePath = "")
```

## S4 method for signature 'BaseAnalysisPipeline'
```r
setInput(object, input, filePath = "")
```

Arguments

- `object`: object that contains input, pipeline, registry and output
- `input`: the input data frame
- `filePath`: path to the file which needs to be read (currently supports .csv files)

Details

Assigns the input to the pipeline for an AnalysisPipeline or StreamingAnalysisPipeline object

This method is implemented on the base class as it is a shared functionality types of Analysis Pipelines which extend this class
Value

Updated AnalysisPipeline StreamingAnalysisPipeline object

See Also

Other Package core functions: BaseAnalysisPipeline-class, MetaAnalysisPipeline-class, assessEngineSetUp, checkSchemaMatch, createPipelineInstance, exportAsMetaPipeline, generateOutput, genericPipelineException, getInput, getLoggnerDetails, getOutputById, getPipelinePrototype, getPipeline, getRegistry, initDfBasedOnType, initialize, BaseAnalysisPipeline-method, loadMetaPipeline, loadPipeline, loadPredefinedFunctionRegistry, loadRegistry, prepExecution, registerFunction, savePipeline, saveRegistry, setLoggerDetails, updateObject, visualizePipeline

Examples

library(analysisPipelines)
pipelineObj <- AnalysisPipeline()
pipelineObj %>>% setInput(input = iris) -> pipelineObj

Arguments

object A Pipeline object
target A string value, 'console' for appending to console, 'file' for appending to a file, or 'console&file' for both
targetFile File name of the log file in case the target is 'file'
layout Specify the layout according to 'futile.logger' package convention

Details

This function sets the logger configuration for the pipeline.
setPythonEnvir

See Also

Other Package core functions: BaseAnalysisPipeline-class, MetaAnalysisPipeline-class, assessEngineSetUp, checkSchemaMatch, createPipelineInstance, exportAsMetaPipeline, generateOutput, genericPipelineException, getInput, getLoggerDetails, getOutputById, getPipelinePrototype, getPipeline, getRegistry, initDbasedOnType, initialize, BaseAnalysisPipeline-method, loadMetaPipeline, loadPipeline, loadPredefinedFunctionRegistry, loadRegistry, prepExecution, registerFunction, savePipeline, saveRegistry, setInput, updateObject, visualizePipeline

Examples

library(analysisPipelines)
pipelineObj <- AnalysisPipeline(input = iris)
pipelineObj %>%% setLoggerDetails(target = "file", targetFile = "pipeline.out") -> pipelineObj

Description

Sets the python environment to be used

Usage

setPythonEnvir(type = "conda", pathOrEnvirName = "base")

Arguments

type

Type of python environment. Takes three possible values - 'conda' for Anaconda environments, 'virtualenv' for Virtual environments, and 'python' to manually set the python path to use

pathOrEnvirName

Name of the environment for Anaconda and Virtual environments, or the Python path when type is 'python'

Details

Wrapper function over reticulate functions to set a python environment to be used

See Also

Other R helper utilities for Python: getFeaturesForPyClassification, getTargetForPyClassification

Examples

## Not run:
setPythonEnvir()

## End(Not run)
sparkRSessionCreateIfNotPresent

Connect to a Spark session

Description

Connect to a Spark session

Usage

sparkRSessionCreateIfNotPresent(...)

Arguments

... Arguments to sparkR.session

Details

Loads the SparkR package and initializes a Spark session from R

See Also

Other Spark utilities: castKafkaStreamAsString, convertKafkaValueFromJson

Examples

## Not run:
sparkHome <- "/Users/naren/softwares/spark-2.3.1-bin-hadoop2.7/
sparkMaster <- "local[1]"
sparkPackages <- c("org.apache.spark:spark-sql-kafka-0-10_2.11:2.3.1")
sparkRSessionCreateIfNotPresent(master = sparkMaster,
sparkPackages = sparkPackages)

## End(Not run)

StreamingAnalysisPipeline-class

Class for constructing Analysis Pipelines for streaming analyses

Description

Class for constructing Analysis Pipelines for streaming analyses
Details
Inherits the base class `BaseAnalysisPipeline` class which holds the metadata including the registry of available functions, the data on which the pipeline is to be applied, as well as the pipeline itself. This class currently only supports Apache Spark Structured Streaming, implemented through the SparkR interface.

Slots
- **input**: The input Spark DataFrame on which analysis is to be performed.
- **originalSchemaDf**: Empty Spark DataFrame representing the schema of the input.

---

### `univarCatDistPlots`  
**Univariate Categoric Distribution**

**Description**
Univariate Categoric Distribution

**Usage**
```
univarCatDistPlots(data, uniCol, priColor = "blue", optionalPlots = 0)
```

**Arguments**
- **data**: the dataset where the column on which the plot is to be generated is present.
- **uniCol**: the name of column on which the plot needs to be generated.
- **priColor**: the primary color for the plots.
- **optionalPlots**: A Flag for optional plots.

**Details**
A univariate distribution graph on the selected categorical columns from the dataframe.

**Value**
A univariate categoric distribution plot.

**See Also**
Other Package EDA Utilities functions: `CheckColumnType`, `bivarPlots`, `correlationMatPlot`, `getDatatype`, `ignoreCols`, `multiVarOutlierPlot`, `outlierPlot`.

**Examples**
```
univarCatDistPlots(data = iris, uniCol = "Species")
```
updateObject

### Description
Update the `AnalysisPipeline` or `StreamingAnalysisPipeline` object by adding an operation to the pipeline

### Usage
```r
updateObject(object, operation, heading = "", parameters, outAsIn = F, storeOutput = F)
```

### Arguments
- `object`: object that contains input, pipeline, registry and output
- `operation`: function name to be updated in tibble
- `heading`: heading of that section in report
- `parameters`: parameters passed to that function
- `outAsIn`: whether to use original input or output from previous function
- `storeOutput`: whether the output of this operation is to be stored

### Details
The specified operation along with the heading and parameters is updated in the pipeline slot of the `AnalysisPipeline` or `StreamingAnalysisPipeline` object, where the sequence of operations to be performed is stored.

This method is implemented on the base class as it is a shared functionality types of `AnalysisPipelines` which extend this class.

### Value
Updated `AnalysisPipeline` `StreamingAnalysisPipeline` object

### See Also
Other Package core functions: `BaseAnalysisPipeline-class`, `MetaAnalysisPipeline-class`, `assessEngineSetUp`, `checkSchemaMatch`, `createPipelineInstance`, `exportAsMetaPipeline`, `generateOutput`, `genericPipelineException`, `getInput`, `getLoggerDetails`, `getOutputById`, `getPipelinePrototype`, `getPipeline`, `getRegistry`, `initDfBasedOnType`, `initialize`, `BaseAnalysisPipeline-method`, `loadMetaPipeline`, `loadPipeline`, `loadPredefinedFunctionRegistry`, `loadRegistry`, `prepExecution`, `registerFunction`, `savePipeline`, `saveRegistry`, `setInput`, `setLoggerDetails`, `visualizePipeline`
visualizePipeline  Visualizes the pipeline as a graph

Description
Visualizes the pipeline as a graph

Usage
visualizePipeline(object)

## S4 method for signature 'BaseAnalysisPipeline'
visualizePipeline(object)

## S4 method for signature 'MetaAnalysisPipeline'
visualizePipeline(object)

Arguments
object The AnalysisPipeline or StreamingAnalysisPipeline object

Details
Indicates dependencies amongst functions as well as functions for which output needs to be stored

Value
A graph object which can be printed (or) plotted to visualize the pipeline

See Also
Other Package core functions: BaseAnalysisPipeline-class, MetaAnalysisPipeline-class,
assessEngineSetUp, checkSchemaMatch, createPipelineInstance, exportAsMetaPipeline,
generateOutput, genericPipelineException, getInput, getLoggerDetails, getOutputById,
getPipelinePrototype, getPipeline, getRegistry, initDfBasedOnType, initialize,
BaseAnalysisPipeline-method, loadMetaPipeline, loadPipeline, loadPredefinedFunctionRegistry,
loadRegistry, prepExecution, registerFunction, savePipeline, saveRegistry, setInput,
setLoggerDetails, updateObject

Examples
## Not run:
library(analysisPipelines)
pipelineObj <- AnalysisPipeline(input = iris)
pipelineObj %>% univarCatDistPlots(uniCol = "Species",
  priColor = "blue", optionalPlots = 0, storeOutput = T) %>%
visualizePipeline

## End(Not run)
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