

# Package ‘OhdsiShinyModules’

January 19, 2024

**Type** Package

**Title** Repository of Shiny Modules for OHDSI Result Viewers

**Version** 2.1.1

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**Description** Install this package to access useful shiny modules for building shiny apps to explore results using the OHDSI tools .

**License** Apache License 2.0

**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 3.3.0)

**VignetteBuilder** knitr

**Language** EN-US

**Imports** checkmate,  
 CirceR,  
 cowplot,  
 DatabaseConnector,  
 dplyr,  
 DT,  
 ggplot2,  
 gridExtra,  
 htmltools,  
 lubridate,  
 methods,  
 ParallelLogger,  
 plotly,  
 purrr,  
 reactable,  
 readr,  
 RJSONIO,  
 rlang,  
 rmarkdown,  
 scales,  
 shiny,  
 shinycssloaders,  
 shinydashboard,

shinyWidgets,  
 SqlRender,  
 stringi,  
 stringr,  
 tibble,  
 tidyr,  
 tidysselect,  
 tippy,  
 RColorBrewer,  
 markdown

**Suggests** kableExtra,  
 knitr,  
 ResultModelManager,  
 RSQLite,  
 testthat,  
 withr

**Remotes** ohdsi/CirceR,  
 ohdsi/ResultModelManager

**RoxygenNote** 7.2.3

## R topics documented:

aboutHelperFile . . . . .	4
aboutServer . . . . .	5
aboutViewer . . . . .	5
characterizationAggregateFeaturesServer . . . . .	6
characterizationAggregateFeaturesViewer . . . . .	6
characterizationDechallengeRechallengeServer . . . . .	7
characterizationDechallengeRechallengeViewer . . . . .	8
characterizationHelperFile . . . . .	8
characterizationIncidenceServer . . . . .	9
characterizationIncidenceViewer . . . . .	9
characterizationServer . . . . .	10
characterizationTableServer . . . . .	10
characterizationTableViewer . . . . .	11
characterizationTimeToEventServer . . . . .	12
characterizationTimeToEventViewer . . . . .	12
characterizationViewer . . . . .	13
cohortCountsModule . . . . .	13
cohortCountsView . . . . .	14
cohortDefinitionsModule . . . . .	14
cohortDefinitionsView . . . . .	15
cohortDiagCharacterizationView . . . . .	15
cohortDiagnosticsHelperFile . . . . .	16
cohortDiagnosticsServer . . . . .	16
cohortDiagnosticsView . . . . .	17
cohortGeneratorHelperFile . . . . .	17
cohortGeneratorServer . . . . .	18
cohortGeneratorViewer . . . . .	18
cohortMethodAttritionServer . . . . .	19
cohortMethodAttritionViewer . . . . .	19

cohortMethodCovariateBalanceServer . . . . .	20
cohortMethodCovariateBalanceViewer . . . . .	20
cohortMethodDiagnosticsSummaryServer . . . . .	21
cohortMethodDiagnosticsSummaryViewer . . . . .	21
cohortMethodHelperFile . . . . .	22
cohortMethodKaplanMeierServer . . . . .	22
cohortMethodKaplanMeierViewer . . . . .	23
cohortMethodPopulationCharacteristicsServer . . . . .	23
cohortMethodPopulationCharacteristicsViewer . . . . .	24
cohortMethodPowerServer . . . . .	24
cohortMethodPowerViewer . . . . .	25
cohortMethodPropensityModelServer . . . . .	25
cohortMethodPropensityModelViewer . . . . .	26
cohortMethodPropensityScoreDistServer . . . . .	26
cohortMethodPropensityScoreDistViewer . . . . .	27
cohortMethodResultSummaryServer . . . . .	27
cohortMethodResultSummaryViewer . . . . .	28
cohortMethodServer . . . . .	28
cohortMethodSystematicErrorServer . . . . .	29
cohortMethodSystematicErrorViewer . . . . .	29
cohortMethodViewer . . . . .	30
cohortOverlapView . . . . .	30
compareCohortCharacterizationView . . . . .	30
conceptsInDataSourceView . . . . .	31
createCdDatabaseDataSource . . . . .	31
createCustomColDefList . . . . .	32
createLargeSqlQueryDt . . . . .	33
databaseInformationView . . . . .	33
dataDiagnosticDrillServer . . . . .	34
dataDiagnosticDrillViewer . . . . .	34
dataDiagnosticHelperFile . . . . .	35
dataDiagnosticServer . . . . .	35
dataDiagnosticSummaryServer . . . . .	36
dataDiagnosticSummaryViewer . . . . .	36
dataDiagnosticViewer . . . . .	37
datasourcesHelperFile . . . . .	37
datasourcesServer . . . . .	38
datasourcesViewer . . . . .	38
evidenceSynthesisHelperFile . . . . .	39
evidenceSynthesisServer . . . . .	39
evidenceSynthesisViewer . . . . .	40
getCirceRenderedExpression . . . . .	40
getEnabledCdReports . . . . .	41
getLogoImage . . . . .	41
incidenceRatesView . . . . .	41
inclusionRulesView . . . . .	42
indexEventBreakdownView . . . . .	42
LargeDataTable . . . . .	42
largeTableServer . . . . .	44
largeTableView . . . . .	45
makeButtonLabel . . . . .	45
OhdsiShinyModules . . . . .	46

orphanConceptsView . . . . .	46
patientLevelPredictionCalibrationServer . . . . .	46
patientLevelPredictionCalibrationViewer . . . . .	47
patientLevelPredictionCovariateSummaryServer . . . . .	47
patientLevelPredictionCovariateSummaryViewer . . . . .	48
patientLevelPredictionCutOffServer . . . . .	49
patientLevelPredictionCutOffViewer . . . . .	49
patientLevelPredictionDesignSummaryServer . . . . .	50
patientLevelPredictionDesignSummaryViewer . . . . .	51
patientLevelPredictionDiagnosticsServer . . . . .	51
patientLevelPredictionDiagnosticsViewer . . . . .	52
patientLevelPredictionDiscriminationServer . . . . .	52
patientLevelPredictionDiscriminationViewer . . . . .	53
patientLevelPredictionHelperFile . . . . .	54
patientLevelPredictionModelSummaryServer . . . . .	54
patientLevelPredictionModelSummaryViewer . . . . .	55
patientLevelPredictionNbServer . . . . .	55
patientLevelPredictionNbViewer . . . . .	56
patientLevelPredictionServer . . . . .	57
patientLevelPredictionSettingsServer . . . . .	57
patientLevelPredictionSettingsViewer . . . . .	58
patientLevelPredictionValidationServer . . . . .	59
patientLevelPredictionValidationViewer . . . . .	60
patientLevelPredictionViewer . . . . .	60
phevaluatorHelperFile . . . . .	61
phevaluatorServer . . . . .	61
phevaluatorViewer . . . . .	62
resultTableServer . . . . .	62
resultTableViewer . . . . .	63
sccsHelperFile . . . . .	63
sccsServer . . . . .	64
sccsView . . . . .	64
timeDistributionsView . . . . .	65
visitContextView . . . . .	65

---

aboutHelperFile	<i>The location of the about module helper file</i>
-----------------	-----------------------------------------------------

---

## Description

The location of the about module helper file

## Usage

aboutHelperFile()

## Details

Returns the location of the about helper file

## Value

string location of the about helper file

---

**aboutServer***The module server for the shiny app home*

---

**Description**

The module server for the shiny app home

**Usage**

```
aboutServer(  
  id = "homepage",  
  connectionHandler = NULL,  
  resultDatabaseSettings = NULL  
)
```

**Arguments**

<b>id</b>	the unique reference id for the module
<b>connectionHandler</b>	a connection to the database with the results
<b>resultDatabaseSettings</b>	a list containing the characterization result schema, dbms, tablePrefix, databaseTable and cgTablePrefix

**Details**

The user specifies the id for the module

**Value**

The server for the shiny app home

---

**aboutViewer***The module viewer for the shiny app home*

---

**Description**

The module viewer for the shiny app home

**Usage**

```
aboutViewer(id = "homepage")
```

**Arguments**

<b>id</b>	the unique reference id for the module
-----------	----------------------------------------

**Details**

The user specifies the id for the module

**Value**

The user interface to the home page module

---

characterizationAggregateFeaturesServer

*The module server for exploring aggregate features results*

---

**Description**

The module server for exploring aggregate features results

**Usage**

```
characterizationAggregateFeaturesServer(
    id,
    connectionHandler,
    resultDatabaseSettings
)
```

**Arguments**

`id` the unique reference id for the module

`connectionHandler` the connection to the prediction result database

`resultDatabaseSettings` a list containing the characterization result schema, dbms, tablePrefix, databaseTable and cgTablePrefix

**Details**

The user specifies the id for the module

**Value**

The server to the description aggregate features module

---

characterizationAggregateFeaturesViewer

*The module viewer for exploring aggregate feature results*

---

**Description**

The module viewer for exploring aggregate feature results

**Usage**

```
characterizationAggregateFeaturesViewer(id)
```

## Arguments

`id` the unique reference id for the module

## Details

The user specifies the id for the module

## Value

The user interface to the description aggregate feature module

---

characterizationDechallengeRechallengeServer

*The module server for exploring Dechallenge Rechallenge results*

---

## Description

The module server for exploring Dechallenge Rechallenge results

## Usage

```
characterizationDechallengeRechallengeServer(
  id,
  connectionHandler,
  resultDatabaseSettings
)
```

## Arguments

`id` the unique reference id for the module

`connectionHandler`

the connection to the prediction result database

`resultDatabaseSettings`

a list containing the characterization result schema, dbms, tablePrefix, databaseTable and cgTablePrefix

## Details

The user specifies the id for the module

## Value

The server to the Dechallenge Rechallenge module

---

`characterizationDechallengeRechallengeViewer`*The module viewer for exploring Dechallenge Rechallenge results*

---

**Description**

The module viewer for exploring Dechallenge Rechallenge results

**Usage**`characterizationDechallengeRechallengeViewer(id)`**Arguments**

`id` the unique reference id for the module

**Details**

The user specifies the id for the module

**Value**

The user interface to the description Dechallenge Rechallenge module

---

`characterizationHelperFile`*The location of the characterization module helper file*

---

**Description**

The location of the characterization module helper file

**Usage**`characterizationHelperFile()`**Details**

Returns the location of the characterization helper file

**Value**

string location of the characterization helper file



---

characterizationIncidenceServer

*The module server for exploring incidence results*

---

### Description

The module server for exploring incidence results

### Usage

characterizationIncidenceServer(id, connectionHandler, resultDatabaseSettings)

### Arguments

id                      the unique reference id for the module  
 connectionHandler      the connection to the prediction result database  
 resultDatabaseSettings   a list containing the characterization result schema, dbms, tablePrefix,  
                              databaseTable and cgTablePrefix

### Details

The user specifies the id for the module

### Value

The server to the prediction incidence module

---

characterizationIncidenceViewer

*The module viewer for exploring incidence results*

---

### Description

The module viewer for exploring incidence results

### Usage

characterizationIncidenceViewer(id)

### Arguments

id                      the unique reference id for the module

### Details

The user specifies the id for the module

### Value

The user interface to the description incidence module

characterizationServer

*The module server for exploring characterization studies*

---

### Description

The module server for exploring characterization studies

### Usage

```
characterizationServer(  
  id,  
  connectionHandler,  
  resultDatabaseSettings = list(port = 1)  
)
```

### Arguments

**id** the unique reference id for the module

**connectionHandler**  
a connection to the database with the results

**resultDatabaseSettings**  
a list containing the characterization result schema, dbms, tablePrefix,  
databaseTable and cgTablePrefix

### Details

The user specifies the id for the module

### Value

The server for the characterization module

---

characterizationTableServer

*The module server for exploring 1 or more cohorts features*

---

### Description

The module server for exploring 1 or more cohorts features

### Usage

```
characterizationTableServer(id, connectionHandler, resultDatabaseSettings)
```

## Arguments

id	the unique reference id for the module
connectionHandler	the connection to the prediction result database
resultDatabaseSettings	a list containing the characterization result schema, dbms, tablePrefix, databaseTable and cgTablePrefix

## Details

The user specifies the id for the module

## Value

The server to the cohorts features server

---

characterizationTableView

*The module viewer for exploring 1 or more cohorts features*

---

## Description

The module viewer for exploring 1 or more cohorts features

## Usage

characterizationTableView(id)

## Arguments

id	the unique reference id for the module
----	----------------------------------------

## Details

The user specifies the id for the module

## Value

The user interface to the description cohorts features

---

`characterizationTimeToEventServer`*The module server for exploring time to event results*

---

**Description**

The module server for exploring time to event results

**Usage**

```
characterizationTimeToEventServer(  
    id,  
    connectionHandler,  
    resultDatabaseSettings  
)
```

**Arguments**

`id` the unique reference id for the module

`connectionHandler` the connection to the prediction result database

`resultDatabaseSettings` a list containing the characterization result schema, dbms, tablePrefix, databaseTable and cgTablePrefix

**Details**

The user specifies the id for the module

**Value**

The server to the prediction time to event module

---

`characterizationTimeToEventViewer`*The module viewer for exploring time to event results*

---

**Description**

The module viewer for exploring time to event results

**Usage**

```
characterizationTimeToEventViewer(id)
```

**Arguments**

`id` the unique reference id for the module

## Details

The user specifies the id for the module

## Value

The user interface to the characterization time to event module

---

characterizationViewer

*The module viewer for exploring characterization studies*

---

## Description

The module viewer for exploring characterization studies

## Usage

```
characterizationViewer(id = 1)
```

## Arguments

**id** the unique reference id for the module

## Details

The user specifies the id for the module

## Value

The user interface to the characterization viewer module

---

cohortCountsModule

*Shiny module for cohort counts*

---

## Description

Shiny module for cohort counts. Displays reactable table of cohort counts

## Usage

```
cohortCountsModule(
  id,
  dataSource,
  cohortTable = dataSource$cohortTable,
  databaseTable = dataSource$dbTable,
  selectedCohorts,
  selectedDatabaseIds,
  cohortIds
)
```

**Arguments**

id	namespace id
dataSource	Backend Data source (DatabaseConnection)
cohortTable	data.frame of all cohorts
databaseTable	data.frame of all databases
selectedCohorts	shiny::reactive - should return cohorts selected or NULL
selectedDatabaseIds	shiny::reactive - should return cohorts selected or NULL
cohortIds	shiny::reactive - should return cohorts selected integers or NULL

---

cohortCountsView	<i>Cohort Counts View</i>
------------------	---------------------------

---

**Description**

Shiny view for cohort counts module

**Usage**

```
cohortCountsView(id)
```

**Arguments**

id	Namespace id
----	--------------

---

cohortDefinitionsModule	<i>Cohort Definition module</i>
-------------------------	---------------------------------

---

**Description**

cohort defintion conceptsets, json etc

**Usage**

```
cohortDefinitionsModule(
  id,
  dataSource,
  cohortDefinitions,
  cohortTable = dataSource$cohortTable,
  cohortCountTable = dataSource$cohortCountTable,
  databaseTable = dataSource$dbTable
)
```

**Arguments**

id	Namespace id
dataSource	DatabaseConnection
cohortDefinitions	reactive of cohort definitions to display
cohortTable	data.frame of cohorts, cohortId, cohortName
cohortCountTable	data.frame of cohortCounts, cohortId, subjects records
databaseTable	data.frame of databases, databaseId, name

---

cohortDefinitionsView *Cohort Definitions View*

---

**Description**

Outputs cohort definitions

**Usage**

cohortDefinitionsView(id)

**Arguments**

id	Namespace id for module
----	-------------------------

---

cohortDiagCharacterizationView  
*characterization*

---

**Description**

Use for customizing UI

**Usage**

cohortDiagCharacterizationView(id)

**Arguments**

id	Namespace Id - use namespaced id ns("characterization") inside diagnosticsExplorer module
----	-------------------------------------------------------------------------------------------

cohortDiagnosticsHelperFile

*The location of the description module helper file*

---

### Description

The location of the description module helper file

### Usage

```
cohortDiagnosticsHelperFile()
```

### Details

Returns the location of the description helper file

### Value

string location of the description helper file

---

cohortDiagnosticsServer

*Cohort Diagnostics Explorer main module*

---

### Description

Cohort Diagnostics Explorer main module

### Usage

```
cohortDiagnosticsServer(  
    id,  
    connectionHandler,  
    resultDatabaseSettings,  
    dataSource = NULL  
)
```

### Arguments

id	module Id
connectionHandler	ResultModelManager ConnectionHandler instance
resultDatabaseSettings	results database settings
dataSource	dataSource optionally created with createCdDatabaseDataSource



---

cohortDiagnosticsView    *View for cohort diagnostics module*

---

**Description**

View for cohort diagnostics module

**Usage**

```
cohortDiagnosticsView(id = "DiagnosticsExplorer")
```

**Arguments**

id                      the unique reference id for the module

**Details**

The user specifies the id for the module

**Value**

The user interface to the cohort diagnostics viewer module

---

cohortGeneratorHelperFile  
                          *The location of the cohort-generator module helper file*

---

**Description**

The location of the cohort-generator module helper file

**Usage**

```
cohortGeneratorHelperFile()
```

**Details**

Returns the location of the cohort-generator helper file

**Value**

string location of the cohort-generator helper file

---

`cohortGeneratorServer`    *The module server for the main cohort generator module*

---

**Description**

The module server for the main cohort generator module

**Usage**

```
cohortGeneratorServer(id, connectionHandler, resultDatabaseSettings)
```

**Arguments**

<code>id</code>	the unique reference id for the module
<code>connectionHandler</code>	a connection to the database with the results
<code>resultDatabaseSettings</code>	a named list containing the cohort generator results database details (schema, table prefix)

**Value**

the cohort generator results viewer main module server

---

`cohortGeneratorViewer`    *The viewer of the main cohort generator module*

---

**Description**

The viewer of the main cohort generator module

**Usage**

```
cohortGeneratorViewer(id)
```

**Arguments**

<code>id</code>	the unique reference id for the module
-----------------	----------------------------------------

**Value**

The user interface to the cohort generator results viewer

---

`cohortMethodAttritionServer`*The module server for rendering the PLE attrition results*

---

**Description**

The module server for rendering the PLE attrition results

**Usage**

```
cohortMethodAttritionServer(  
    id,  
    selectedRow,  
    connectionHandler,  
    resultDatabaseSettings  
)
```

**Arguments**

<code>id</code>	the unique reference id for the module
<code>selectedRow</code>	the selected row from the main results table
<code>connectionHandler</code>	the connection to the PLE results database
<code>resultDatabaseSettings</code>	a list containing the result schema and prefixes

**Value**

the PLE attrition results content server

---

`cohortMethodAttritionViewer`*The module viewer for rendering the PLE attrition results*

---

**Description**

The module viewer for rendering the PLE attrition results

**Usage**

```
cohortMethodAttritionViewer(id)
```

**Arguments**

<code>id</code>	the unique reference id for the module
-----------------	----------------------------------------

**Value**

The user interface to the cohort method attrition

---

cohortMethodCovariateBalanceServer

*The module server for rendering the covariate balance plot*

---

### Description

The module server for rendering the covariate balance plot

### Usage

```
cohortMethodCovariateBalanceServer(
  id,
  selectedRow,
  connectionHandler,
  resultDatabaseSettings,
  metaAnalysisDbIds = NULL
)
```

### Arguments

id	the unique reference id for the module
selectedRow	the selected row from the main results table
connectionHandler	the connection to the PLE results database
resultDatabaseSettings	a list containing the result schema and prefixes
metaAnalysisDbIds	metaAnalysisDbIds

### Value

the PLE covariate balance content server

---

cohortMethodCovariateBalanceViewer

*The module viewer for rendering the PLE covariate balance analysis*

---

### Description

The module viewer for rendering the PLE covariate balance analysis

### Usage

```
cohortMethodCovariateBalanceViewer(id)
```

### Arguments

id	the unique reference id for the module
----	----------------------------------------

**Value**

The user interface to the cohort method covariate balance results

---

cohortMethodDiagnosticsSummaryServer

*The module server for rendering the PLE diagnostics summary*

---

**Description**

The module server for rendering the PLE diagnostics summary

**Usage**

```
cohortMethodDiagnosticsSummaryServer(
  id,
  connectionHandler,
  resultDatabaseSettings,
  inputSelected
)
```

**Arguments**

id	the unique reference id for the module
connectionHandler	the connection to the PLE results database
resultDatabaseSettings	a list containing the result schema and prefixes
inputSelected	The target id, comparator id, outcome id and analysis id selected by the user

**Value**

the PLE diagnostics summary results

---

cohortMethodDiagnosticsSummaryViewer

*The module viewer for rendering the PLE diagnostics results*

---

**Description**

The module viewer for rendering the PLE diagnostics results

**Usage**

```
cohortMethodDiagnosticsSummaryViewer(id)
```

**Arguments**

id	the unique reference id for the module
----	----------------------------------------

**Value**

The user interface to the cohort method diagnostics viewer

---

cohortMethodHelperFile

*The location of the cohort method module helper file*

---

**Description**

The location of the cohort method module helper file

**Usage**

cohortMethodHelperFile()

**Details**

Returns the location of the cohort method helper file

**Value**

string location of the cohort method helper file

---

cohortMethodKaplanMeierServer

*The module server for rendering the Kaplan Meier curve*

---

**Description**

The module server for rendering the Kaplan Meier curve

**Usage**

```
cohortMethodKaplanMeierServer(
  id,
  selectedRow,
  connectionHandler,
  resultDatabaseSettings
)
```

**Arguments**

id	the unique reference id for the module
selectedRow	the selected row from the main results table
connectionHandler	the connection to the PLE results database
resultDatabaseSettings	a list containing the result schema and prefixes

**Value**

the PLE Kaplan Meier content server

---

`cohortMethodKaplanMeierViewer`*The module viewer for rendering the PLE Kaplan Meier curve*

---

**Description**

The module viewer for rendering the PLE Kaplan Meier curve

**Usage**

```
cohortMethodKaplanMeierViewer(id)
```

**Arguments**

`id` the unique reference id for the module

**Value**

The module viewer for Kaplan Meier objects

---

`cohortMethodPopulationCharacteristicsServer`*The module server for rendering the population characteristics*

---

**Description**

The module server for rendering the population characteristics

**Usage**

```
cohortMethodPopulationCharacteristicsServer(  
  id,  
  selectedRow,  
  connectionHandler,  
  resultDatabaseSettings  
)
```

**Arguments**

`id` the unique reference id for the module  
`selectedRow` the selected row from the main results table  
`connectionHandler` the connection to the PLE results database  
`resultDatabaseSettings` a list containing the result schema and prefixes

**Value**

the PLE population characteristics content server

---

cohortMethodPopulationCharacteristicsViewer

*The module viewer for rendering the PLE population characteristics*

---

### Description

The module viewer for rendering the PLE population characteristics

### Usage

```
cohortMethodPopulationCharacteristicsViewer(id)
```

### Arguments

id                      the unique reference id for the module

### Value

The user interface to the cohort method population characteristics objects

---

cohortMethodPowerServer

*The module server for rendering the PLE power analysis results*

---

### Description

The module server for rendering the PLE power analysis results

### Usage

```
cohortMethodPowerServer(
  id,
  selectedRow,
  connectionHandler,
  resultDatabaseSettings
)
```

### Arguments

id                      the unique reference id for the module

selectedRow          the selected row from the main results table

connectionHandler    the connection to the PLE results database

resultDatabaseSettings  
                        a list containing the result schema and prefixes

### Value

the PLE systematic error power server



---

`cohortMethodPowerViewer`*The module viewer for rendering the PLE power analysis*

---

**Description**

The module viewer for rendering the PLE power analysis

**Usage**

```
cohortMethodPowerViewer(id)
```

**Arguments**

`id` the unique reference id for the module

**Value**

The user interface to the cohort method power calculation results

---

`cohortMethodPropensityModelServer`*The module server for rendering the propensity score model*

---

**Description**

The module server for rendering the propensity score model

**Usage**

```
cohortMethodPropensityModelServer(  
  id,  
  selectedRow,  
  connectionHandler,  
  resultDatabaseSettings  
)
```

**Arguments**

`id` the unique reference id for the module  
`selectedRow` the selected row from the main results table  
`connectionHandler` the connection to the PLE results database  
`resultDatabaseSettings` a list containing the result schema and prefixes

**Value**

the PLE propensity score model

---

cohortMethodPropensityModelViewer

*The module viewer for rendering the PLE propensity score model covariates/coefficients*

---

### Description

The module viewer for rendering the PLE propensity score model covariates/coefficients

### Usage

```
cohortMethodPropensityModelViewer(id)
```

### Arguments

id                      the unique reference id for the module

### Value

The user interface to the cohort method propensity score model covariates/coefficients

---

cohortMethodPropensityScoreDistServer

*The module server for rendering a PLE propensity score distribution*

---

### Description

The module server for rendering a PLE propensity score distribution

### Usage

```
cohortMethodPropensityScoreDistServer(
  id,
  selectedRow,
  connectionHandler,
  resultDatabaseSettings,
  metaAnalysisDbIds = F
)
```

### Arguments

id                      the unique reference id for the module

selectedRow          the selected row from the main results table

connectionHandler    the connection to the PLE results database

resultDatabaseSettings   a list containing the result schema and prefixes

metaAnalysisDbIds     metaAnalysisDbIds

**Value**

the PLE propensity score distribution content server

---

cohortMethodPropensityScoreDistViewer

*The module viewer for rendering the propensity score distribution*

---

**Description**

The module viewer for rendering the propensity score distribution

**Usage**

```
cohortMethodPropensityScoreDistViewer(id)
```

**Arguments**

id                      the unique reference id for the module

**Value**

The user interface to the cohort method propensity score distribution

---

cohortMethodResultSummaryServer

*The module server for rendering the PLE diagnostics summary*

---

**Description**

The module server for rendering the PLE diagnostics summary

**Usage**

```
cohortMethodResultSummaryServer(
  id,
  connectionHandler,
  resultDatabaseSettings,
  inputSelected
)
```

**Arguments**

id                      the unique reference id for the module

connectionHandler      the connection to the PLE results database

resultDatabaseSettings   a list containing the result schema and prefixes

inputSelected          The target id, comparator id, outcome id and analysis id selected by the user

**Value**

the PLE diagnostics summary results

---

cohortMethodResultSummaryViewer	<i>The module viewer for rendering the cohort method results</i>
---------------------------------	------------------------------------------------------------------

---

**Description**

The module viewer for rendering the cohort method results

**Usage**

cohortMethodResultSummaryViewer(id)

**Arguments**

id                      the unique reference id for the module

**Value**

The user interface to the cohort method diagnostics viewer

---

cohortMethodServer	<i>The module server for the main cohort method module</i>
--------------------	------------------------------------------------------------

---

**Description**

The module server for the main cohort method module

**Usage**

cohortMethodServer(id, connectionHandler, resultDatabaseSettings)

**Arguments**

id                      the unique reference id for the module  
connectionHandler      a connection to the database with the results  
resultDatabaseSettings   a named list containing the PLE results database connection details

**Value**

the PLE results viewer main module server

---

cohortMethodSystematicErrorServer

*The module server for rendering the systematic error objects*


---

**Description**

The module server for rendering the systematic error objects

**Usage**

```
cohortMethodSystematicErrorServer(
    id,
    selectedRow,
    connectionHandler,
    resultDatabaseSettings
)
```

**Arguments**

id	the unique reference id for the module
selectedRow	the selected row from the main results table
connectionHandler	the connection handler to the result databases
resultDatabaseSettings	a list containing the result schema and prefixes

**Value**

the PLE systematic error content server

---

cohortMethodSystematicErrorViewer

*The module viewer for rendering the PLE systematic error objects*


---

**Description**

The module viewer for rendering the PLE systematic error objects

**Usage**

```
cohortMethodSystematicErrorViewer(id)
```

**Arguments**

id	the unique reference id for the module
----	----------------------------------------

**Value**

The user interface to the cohort method systematic error module

---

cohortMethodViewer	<i>The viewer of the main cohort method module</i>
--------------------	----------------------------------------------------

---

**Description**

The viewer of the main cohort method module

**Usage**

```
cohortMethodViewer(id)
```

**Arguments**

id	the unique reference id for the module
----	----------------------------------------

**Value**

The user interface to the cohort method results viewer

---

cohortOverlapView	<i>Cohort Overlap View</i>
-------------------	----------------------------

---

**Description**

Use for customizing UI

**Usage**

```
cohortOverlapView(id)
```

**Arguments**

id	Namespace Id - use namespaced id ns("cohortOverlap") inside diagnosticsExplorer module
----	----------------------------------------------------------------------------------------

---

compareCohortCharacterizationView	<i>compare characterization view</i>
-----------------------------------	--------------------------------------

---

**Description**

Use for customizing UI

**Usage**

```
compareCohortCharacterizationView(  
  id,  
  title = "Compare cohort characterization"  
)
```

## Arguments

id	Namespace Id - use namespaced id ns("compareCohortCharacterization") inside diagnosticsExplorer module
title	Optional string title field

---

conceptsInDataSourceView

*concepts In DataSource View*


---

## Description

Use for customizing UI

## Usage

```
conceptsInDataSourceView(id)
```

## Arguments

id	Namespace Id - use namespaced id ns("conceptsInDataSource") inside diagnosticsExplorer module
----	-----------------------------------------------------------------------------------------------

---

createCdDatabaseDataSource

*Create a CD data source from a database*


---

## Description

use this to create an interface to cohort diagnostics results data NOTE: I think this would make a good R6 class for other objects in this package so you could query them outside of a shiny app. E.g. if you wanted to make a custom R markdown template

## Usage

```
createCdDatabaseDataSource(
  connectionHandler,
  resultDatabaseSettings,
  dataModelSpecificationsPath = system.file("cohort-diagnostics-ref",
    "resultsDataModelSpecification.csv", package = utils::packageName()),
  dataMigrationsRef = system.file("cohort-diagnostics-ref", "migrations.csv", package =
    utils::packageName()),
  displayProgress = FALSE
)
```

**Arguments**

connectionHandler	An instance of a ResultModelManager::connectionHandler - manages a connection to a database.
resultDatabaseSettings	a list containing the result schema and prefixes
dataModelSpecificationsPath	The path to a file containing specifications for the data model used by the database.
dataMigrationsRef	The path to a file listing all migrations for the data model that should have been applied
displayProgress	display a progress message (can only be used inside a shiny reactive context)

**Value**

An object of class ‘CdDataSource’.

---

createCustomColDefList

*Creating a list of custom column definitions for use in reactables*

---

**Description**

Creating a list of custom column definitions for use in reactables

**Usage**

```
createCustomColDefList(
  rawColNames,
  niceColNames = NULL,
  tooltipText = NULL,
  case = NULL,
  customColDefOptions = NULL
)
```

**Arguments**

rawColNames	The raw column names taken directly from the source data table that are to be overwritten in the reactable
niceColNames	The formatted column names that will appear as-specified in the reactable
tooltipText	The text to be displayed in a toolTip when hovering over the column in the reactable
case	Optional argument to convert raw column names to snake or camel case. Defaults to NULL and preserves whatever raw column names are passed in
customColDefOptions	A list of lists, where the inner lists are any custom options from reactable::colDef for each column



**Value**

A named list of reactable::colDef objects

---

createLargeSqlQueryDt *Create Large Sql Query Data Table*

---

**Description**

Construct an instance of a LargeDataTable R6 instance for use inside largeTableServer

This should pass a parameterized sql query that can be used to iteratively return data from a table rather than returning the entire object.

**Usage**

```
createLargeSqlQueryDt(
  connectionHandler = NULL,
  connectionDetails = NULL,
  baseQuery,
  countQuery = NULL
)
```

**Arguments**

connectionHandler	ResultModelManager connectionHandler instance
connectionDetails	DatabaseConnector connectionDetails instance
baseQuery	base sql query
countQuery	count query string (should match query). Can be auto generated with sub query (default) but this will likely result in slow results

---

databaseInformationView  
*database Information View*

---

**Description**

Use for customizing UI

**Usage**

```
databaseInformationView(id)
```

**Arguments**

id	Namespace Id - use namespaced id ns("databaseInformation") inside diagnosticsExplorer module
----	----------------------------------------------------------------------------------------------

---

`dataDiagnosticDrillServer`*The module server for exploring prediction summary results*

---

**Description**

The module server for exploring prediction summary results

**Usage**

```
dataDiagnosticDrillServer(id, connectionHandler, resultDatabaseSettings)
```

**Arguments**

<code>id</code>	the unique reference id for the module
<code>connectionHandler</code>	the connection to the prediction result database
<code>resultDatabaseSettings</code>	a list containing the result schema and prefixes

**Details**

The user specifies the id for the module

**Value**

The server to the summary module

---

`dataDiagnosticDrillViewer`*The module viewer for exploring data-diagnostic results in more detail*

---

**Description**

The module viewer for exploring data-diagnostic results in more detail

**Usage**

```
dataDiagnosticDrillViewer(id)
```

**Arguments**

<code>id</code>	the unique reference id for the module
-----------------	----------------------------------------

**Details**

The user specifies the id for the module

**Value**

The user interface to the summary module

---

`dataDiagnosticHelperFile`*The location of the data-diagnostic module helper file*

---

**Description**

The location of the data-diagnostic module helper file

**Usage**

```
dataDiagnosticHelperFile()
```

**Details**

Returns the location of the data-diagnostic helper file

**Value**

string location of the data-diagnostic helper file

---

`dataDiagnosticServer`    *The module server for exploring data-diagnostic*

---

**Description**

The module server for exploring data-diagnostic

**Usage**

```
dataDiagnosticServer(  
  id = "dataDiag",  
  connectionHandler,  
  resultDatabaseSettings = list(port = 1)  
)
```

**Arguments**

<code>id</code>	the unique reference id for the module
<code>connectionHandler</code>	a connection to the database with the results
<code>resultDatabaseSettings</code>	a list containing the data-diagnostic result schema

**Details**

The user specifies the id for the module

**Value**

The server for the data-diagnostic module

---

`dataDiagnosticSummaryServer`*The module server for exploring prediction summary results*

---

**Description**

The module server for exploring prediction summary results

**Usage**

```
dataDiagnosticSummaryServer(id, connectionHandler, resultDatabaseSettings)
```

**Arguments**

<code>id</code>	the unique reference id for the module
<code>connectionHandler</code>	the connection to the prediction result database
<code>resultDatabaseSettings</code>	a list containing the result schema and prefixes

**Details**

The user specifies the id for the module

**Value**

The server to the summary module

---

`dataDiagnosticSummaryViewer`*The module viewer for exploring data-diagnostic summary results*

---

**Description**

The module viewer for exploring data-diagnostic summary results

**Usage**

```
dataDiagnosticSummaryViewer(id)
```

**Arguments**

<code>id</code>	the unique reference id for the module
-----------------	----------------------------------------

**Details**

The user specifies the id for the module

**Value**

The user interface to the summary module

---

dataDiagnosticViewer	<i>The module viewer for exploring data-diagnostic</i>
----------------------	--------------------------------------------------------

---

**Description**

The module viewer for exploring data-diagnostic

**Usage**

```
dataDiagnosticViewer(id = "dataDiag")
```

**Arguments**

id	the unique reference id for the module
----	----------------------------------------

**Details**

The user specifies the id for the module

**Value**

The user interface to the data-diagnostic viewer module

---

datasourcesHelperFile	<i>Define the helper file for the module</i>
-----------------------	----------------------------------------------

---

**Description**

Define the helper file for the module

**Usage**

```
datasourcesHelperFile()
```

**Value**

The helper html file for the datasources module

---

datasourcesServer	<i>The server function for the datasources module</i>
-------------------	-------------------------------------------------------

---

**Description**

The server function for the datasources module

**Usage**

```
datasourcesServer(id, connectionHandler, resultDatabaseSettings)
```

**Arguments**

id	The unique id for the datasources server namespace
connectionHandler	A connection to the database with the results
resultDatabaseSettings	A named list containing the cohort generator results database details (schema, table prefix)

**Value**

The server for the datasources module

---

datasourcesViewer	<i>The viewer function for hte datasources module</i>
-------------------	-------------------------------------------------------

---

**Description**

The viewer function for hte datasources module

**Usage**

```
datasourcesViewer(id)
```

**Arguments**

id	The unique id for the datasources viewer namespace
----	----------------------------------------------------

**Value**

The UI for the datasources module

---

evidenceSynthesisHelperFile

*The location of the evidence synthesis module helper file*


---

**Description**

The location of the evidence synthesis module helper file

**Usage**

```
evidenceSynthesisHelperFile()
```

**Details**

Returns the location of the evidence synthesis helper file

**Value**

string location of the evidence synthesis helper file

---

evidenceSynthesisServer

*The module server for exploring PatientLevelPrediction*


---

**Description**

The module server for exploring PatientLevelPrediction

**Usage**

```
evidenceSynthesisServer(
  id,
  connectionHandler,
  resultDatabaseSettings = list(port = 1)
)
```

**Arguments**

**id** the unique reference id for the module

**connectionHandler** a connection to the database with the results

**resultDatabaseSettings** a list containing the result schema and prefixes

**Details**

The user specifies the id for the module

**Value**

The server for the PatientLevelPrediction module

---

evidenceSynthesisViewer

*The module viewer for exploring evidence-synthesis*

---

### Description

The module viewer for exploring evidence-synthesis

### Usage

```
evidenceSynthesisViewer(id = 1)
```

### Arguments

**id** the unique reference id for the module

### Details

The user specifies the id for the module

### Value

The user interface to the evidence-synthesis viewer module

---

getCirceRenderedExpression

*Returns list with circe generated documentation*

---

### Description

Returns list with circe generated documentation

### Usage

```
getCirceRenderedExpression(
  cohortDefinition,
  cohortName = "Cohort Definition",
  includeConceptSets = FALSE
)
```

### Arguments

**cohortDefinition** An R object (list) with a list representation of the cohort definition expression, that may be converted to a cohort expression JSON using RJ-SONIO::toJSON(x = cohortDefinition, digits = 23, pretty = TRUE)

**cohortName** Name for the cohort definition

**includeConceptSets** Do you want to included concept set in the documentation

### Value

list object



---

getEnabledCdReports	<i>Get enable cd reports from available data</i>
---------------------	--------------------------------------------------

---

**Description**

Get enable cd reports from available data

**Usage**

```
getEnabledCdReports(dataSource)
```

**Arguments**

dataSource	C
------------	---

---

getLogoImage	<i>The location of the OHDSI logo</i>
--------------	---------------------------------------

---

**Description**

The location of the OHDSI logo

**Usage**

```
getLogoImage()
```

**Details**

Returns the location of the OHDSI logo

**Value**

string location of the OHDSI logo

---

incidenceRatesView	<i>incidence Rates View</i>
--------------------	-----------------------------

---

**Description**

Use for customizing UI

**Usage**

```
incidenceRatesView(id)
```

**Arguments**

id	Namespace Id - use namespaced id ns("incidenceRates") inside diagnosticsExplorer module
----	-----------------------------------------------------------------------------------------

---

inclusionRulesView	<i>inclusion Rules View</i>
--------------------	-----------------------------

---

**Description**

Use for customizing UI

**Usage**

inclusionRulesView(id)

**Arguments**

id	Namespace Id - use namespaced id ns("inclusionRules") inside diagnosticsExplorer module
----	-----------------------------------------------------------------------------------------

---

indexEventBreakdownView	<i>Index event breakdown view</i>
-------------------------	-----------------------------------

---

**Description**

Use for customizing UI

**Usage**

indexEventBreakdownView(id)

**Arguments**

id	Namespace Id - use namespaced id ns("indexEvents") inside diagnosticsExplorer module
----	--------------------------------------------------------------------------------------

---

LargeDataTable	<i>Large Data Table</i>
----------------	-------------------------

---

**Description**

Large data table R6 class.

Uses ResultModelManager::ConnectionHandler class to create paginating tables

NOTE Only currently works with sqlite and postgresql database backends (probably redshift too) as this method uses limit and offset for the queries

Alternatively, you might want to subclass this class. For example, if your backend query is against an API such as and ATLAS instance or ATHENA

If subclassing use inheritance and treat this class as an interface to implement - implementing the methods:

get

**Public fields**

`baseQuery` query string sql

`countQuery` count query string (should match query). Can be auto generated with sub query (default) but this will likely result in slow results

`connectionHandler` ResultModelManager connection handler to execute query inside initialize

**Methods****Public methods:**

- [LargeDataTable\\$new\(\)](#)
- [LargeDataTable\\$getCount\(\)](#)
- [LargeDataTable\\$getPage\(\)](#)
- [LargeDataTable\\$getAllResults\(\)](#)
- [LargeDataTable\\$clone\(\)](#)

**Method new():***Usage:*

```
LargeDataTable$new(connectionHandler, baseQuery, countQuery = NULL)
```

*Arguments:*

`connectionHandler` ResultModelManager connectionHandler instance

`baseQuery` base sql query

`countQuery` count query string (should match query). Can be auto generated with sub query (default) but this will likely result in slow results

*Returns:* self get count

**Method getCount():** execute count query with specified parameters*Usage:*

```
LargeDataTable$getCount(...)
```

*Arguments:*

...

*Returns:* count Get Page

**Method getPage():***Usage:*

```
LargeDataTable$getPage(pageNum, pageSize = self$pageSize, ...)
```

*Arguments:*

`pageNum` page number

`pageSize` page size

...

*Returns:* data.frame of query result get all results

**Method getAllResults():***Usage:*

```
LargeDataTable$getAllResults(...)
```

*Arguments:*

...

*Returns:* data.frame of all results. Used for large file downloads

**Method clone():** The objects of this class are cloneable with this method.

*Usage:*

```
LargeDataTable$clone(deep = FALSE)
```

*Arguments:*

deep Whether to make a deep clone.

---

largeTableServer

*Large Table Component Server*

---

## Description

Display large data tables in a consistent way - server side pagination for reactable objects

## Usage

```
largeTableServer(
  id,
  ldt,
  inputParams,
  modifyData = NULL,
  columns = shiny::reactive(list()),
  ...
)
```

## Arguments

id	Shiny module id. Must match Large Table Viewer
ldt	LargeDataTable instance
inputParams	reactive that returns list of parameters to be passed to ldt
modifyData	optional callback function that takes the data page, page number, page size as parameters must return data.frame compatible instance
columns	List or reactable returning list of reactable::columnDef objects
...	Additional reactable options (searchable, sortable

---

largeTableView	<i>Large Table Component Viewer</i>
----------------	-------------------------------------

---

**Description**

Component for results sets with many thousands of rows More limited than other table components in terms of automatic handling of search and filtering but will allow responsive apps

**Usage**

```
largeTableView(
  id,
  pageSizeChoices = c(10, 25, 50, 100),
  selectedPageSize = 10,
  fullDownloads = TRUE
)
```

**Arguments**

id	Shiny module id. Must match largeTableServer
pageSizeChoices	numeric selection options for pages
selectedPageSize	numeric selection options for pages
fullDownloads	allow download button of full dataset from query

---

makeButtonLabel	<i>Make a label for an html button</i>
-----------------	----------------------------------------

---

**Description**

Make a label for an html button

**Usage**

```
makeButtonLabel(label)
```

**Arguments**

label	The desired label for hte button
-------	----------------------------------

**Value**

html code to make a button label

---

OhdsiShinyModules	<i>OhdsiShinyModules</i>
-------------------	--------------------------

---

**Description**

A selection of shiny modules for exploring standardized OHDSI results

---

orpahanConceptsView	<i>Orphan Concepts View</i>
---------------------	-----------------------------

---

**Description**

Use for customizing UI

**Usage**

```
orpahanConceptsView(id)
```

**Arguments**

id	Namespace Id - use namespaced id ns("orphanConcepts") inside diagnosticsExplorer module
----	-----------------------------------------------------------------------------------------

---

patientLevelPredictionCalibrationServer	<i>The module server for exploring prediction validation results</i>
-----------------------------------------	----------------------------------------------------------------------

---

**Description**

The module server for exploring prediction validation results

**Usage**

```
patientLevelPredictionCalibrationServer(
  id,
  performanceId,
  connectionHandler,
  inputSingleView,
  resultDatabaseSettings
)
```

**Arguments**

id	the unique reference id for the module
performanceId	the performance id in the database
connectionHandler	the connection to the prediction result database
inputSingleView	the current tab
resultDatabaseSettings	a list containing the result schema and prefixes

**Details**

The user specifies the id for the module

**Value**

The server to the prediction calibration module

---

patientLevelPredictionCalibrationViewer

*The module viewer for exploring prediction model calibration results*

---

**Description**

The module viewer for exploring prediction model calibration results

**Usage**

```
patientLevelPredictionCalibrationViewer(id)
```

**Arguments**

id                      the unique reference id for the module

**Details**

The user specifies the id for the module

**Value**

The user interface to the prediction model calibration module

---

patientLevelPredictionCovariateSummaryServer

*The module server for exploring prediction covariate summary results*

---

**Description**

The module server for exploring prediction covariate summary results

**Usage**

```
patientLevelPredictionCovariateSummaryServer(  
  id,  
  modelDesignId,  
  developmentDatabaseId,  
  performanceId,  
  connectionHandler,  
  inputSingleView,  
  resultDatabaseSettings  
)
```

**Arguments**

**id** the unique reference id for the module  
**modelDesignId** unique id for the model design  
**developmentDatabaseId** unique id for the development database  
**performanceId** unique id for the performance results  
**connectionHandler** the connection to the prediction result database  
**inputSingleView** the current tab  
**resultDatabaseSettings** a list containing the result schema and prefixes

**Details**

The user specifies the id for the module

**Value**

The server to the covariate summary module

---

patientLevelPredictionCovariateSummaryViewer

*The module viewer for exploring prediction covariate summary results*

---

**Description**

The module viewer for exploring prediction covariate summary results

**Usage**

```
patientLevelPredictionCovariateSummaryViewer(id)
```

**Arguments**

**id** the unique reference id for the module

**Details**

The user specifies the id for the module

**Value**

The user interface to the covariate summary module



---

**patientLevelPredictionCutoffServer***The module server for exploring prediction cut-off results*

---

**Description**

The module server for exploring prediction cut-off results

**Usage**

```
patientLevelPredictionCutoffServer(  
    id,  
    performanceId,  
    connectionHandler,  
    inputSingleView,  
    resultDatabaseSettings  
)
```

**Arguments**

id	the unique reference id for the module
performanceId	the performance id in the database
connectionHandler	the connection to the prediction result database
inputSingleView	the current tab
resultDatabaseSettings	a list containing the result schema and prefixes

**Details**

The user specifies the id for the module

**Value**

The server to the prediction cut-off module

---

**patientLevelPredictionCutoffViewer***The module viewer for exploring prediction cut-off results*

---

**Description**

The module viewer for exploring prediction cut-off results

**Usage**

```
patientLevelPredictionCutoffViewer(id)
```

**Arguments**

id                      the unique reference id for the module

**Details**

The user specifies the id for the module

**Value**

The user interface to the prediction cut-off module

---

patientLevelPredictionDesignSummaryServer

*The module server for exploring prediction designs in the results*

---

**Description**

The module server for exploring prediction designs in the results

**Usage**

```
patientLevelPredictionDesignSummaryServer(  
  id,  
  connectionHandler,  
  resultDatabaseSettings  
)
```

**Arguments**

id                      the unique reference id for the module

connectionHandler       the connection to the prediction result database

resultDatabaseSettings   a list containing the result schema and prefixes

**Details**

The user specifies the id for the module

**Value**

The server to the prediction design module

---

patientLevelPredictionDesignSummaryViewer

*The module viewer for exploring prediction designs that have been run*

---

### Description

The module viewer for exploring prediction designs that have been run

### Usage

```
patientLevelPredictionDesignSummaryViewer(id)
```

### Arguments

id                      the unique reference id for the module

### Details

The user specifies the id for the module

### Value

The user interface to the prediction design module

---

patientLevelPredictionDiagnosticsServer

*The module server for exploring prediction diagnostic results*

---

### Description

The module server for exploring prediction diagnostic results

### Usage

```
patientLevelPredictionDiagnosticsServer(
  id,
  modelDesignId,
  connectionHandler,
  resultDatabaseSettings
)
```

### Arguments

id                      the unique reference id for the module

modelDesignId    the unique id for the model design

connectionHandler                      the connection to the prediction result database

resultDatabaseSettings                      a list containing the result schema and prefixes

**Details**

The user specifies the id for the module

**Value**

The server to the prediction diagnostic module

---

patientLevelPredictionDiagnosticsViewer

*The module viewer for exploring prediction diagnostic results*

---

**Description**

The module viewer for exploring prediction diagnostic results

**Usage**

```
patientLevelPredictionDiagnosticsViewer(id)
```

**Arguments**

id                      the unique reference id for the module

**Details**

The user specifies the id for the module

**Value**

The user interface to the prediction diagnostic module

---

patientLevelPredictionDiscriminationServer

*The module server for exploring prediction model discrimination results*

---

**Description**

The module server for exploring prediction model discrimination results

**Usage**

```
patientLevelPredictionDiscriminationServer(  
  id,  
  performanceId,  
  connectionHandler,  
  inputSingleView,  
  resultDatabaseSettings  
)
```

**Arguments**

id	the unique reference id for the module
performanceId	the performance id in the database
connectionHandler	the connection to the prediction result database
inputSingleView	the current tab
resultDatabaseSettings	a list containing the result schema and prefixes

**Details**

The user specifies the id for the module

**Value**

The server to the model discrimination module

---

patientLevelPredictionDiscriminationViewer

*The module viewer for exploring prediction model discrimination results*

---

**Description**

The module viewer for exploring prediction model discrimination results

**Usage**

```
patientLevelPredictionDiscriminationViewer(id)
```

**Arguments**

id	the unique reference id for the module
----	----------------------------------------

**Details**

The user specifies the id for the module

**Value**

The user interface to the model discrimination results module

---

`patientLevelPredictionHelperFile`*The location of the prediction module helper file*

---

**Description**

The location of the prediction module helper file

**Usage**

```
patientLevelPredictionHelperFile()
```

**Details**

Returns the location of the prediction helper file

**Value**

string location of the prediction helper file

---

`patientLevelPredictionModelSummaryServer`*The module server for exploring prediction summary results*

---

**Description**

The module server for exploring prediction summary results

**Usage**

```
patientLevelPredictionModelSummaryServer(  
  id,  
  connectionHandler,  
  resultDatabaseSettings,  
  modelDesignId  
)
```

**Arguments**

<code>id</code>	the unique reference id for the module
<code>connectionHandler</code>	the connection to the prediction result database
<code>resultDatabaseSettings</code>	a list containing the result schema and prefixes
<code>modelDesignId</code>	a reactable id specifying the prediction model design identifier

**Details**

The user specifies the id for the module

**Value**

The server to the summary module

---

`patientLevelPredictionModelSummaryViewer`

*The module viewer for exploring prediction summary results*

---

**Description**

The module viewer for exploring prediction summary results

**Usage**

```
patientLevelPredictionModelSummaryViewer(id)
```

**Arguments**

<code>id</code>	the unique reference id for the module
-----------------	----------------------------------------

**Details**

The user specifies the id for the module

**Value**

The user interface to the summary module

---

`patientLevelPredictionNbServer`

*The module server for exploring prediction net-benefit results*

---

**Description**

The module server for exploring prediction net-benefit results

**Usage**

```
patientLevelPredictionNbServer(  
  id,  
  performanceId,  
  connectionHandler,  
  inputSingleView,  
  resultDatabaseSettings  
)
```

**Arguments**

`id` the unique reference id for the module  
`performanceId` the performance id in the database  
`connectionHandler` the connection to the prediction result database  
`inputSingleView` the current tab  
`resultDatabaseSettings` a list containing the result schema and prefixes

**Details**

The user specifies the id for the module

**Value**

The server to the net-benefit module

---

`patientLevelPredictionNbViewer`

*The module viewer for exploring prediction net-benefit results*

---

**Description**

The module viewer for exploring prediction net-benefit results

**Usage**

```
patientLevelPredictionNbViewer(id)
```

**Arguments**

`id` the unique reference id for the module

**Details**

The user specifies the id for the module

**Value**

The user interface to the net-benefit module



---

**patientLevelPredictionServer***The module server for exploring PatientLevelPrediction*

---

**Description**

The module server for exploring PatientLevelPrediction

**Usage**

```
patientLevelPredictionServer(  
    id,  
    connectionHandler,  
    resultDatabaseSettings = list(port = 1)  
)
```

**Arguments**

**id** the unique reference id for the module  
**connectionHandler** a connection to the database with the results  
**resultDatabaseSettings** a list containing the prediction result schema and connection details

**Details**

The user specifies the id for the module

**Value**

The server for the PatientLevelPrediction module

---

**patientLevelPredictionSettingsServer***The module server for exploring prediction settings*

---

**Description**

The module server for exploring prediction settings

**Usage**

```
patientLevelPredictionSettingsServer(  
    id,  
    modelDesignId,  
    developmentDatabaseId,  
    performanceId,  
    connectionHandler,  
    inputSingleView,  
    resultDatabaseSettings  
)
```

**Arguments**

id	the unique reference id for the module
modelDesignId	unique id for the model design
developmentDatabaseId	unique id for the development database
performanceId	unique id for the performance results
connectionHandler	the connection to the prediction result database
inputSingleView	the current tab
resultDatabaseSettings	a list containing the result schema and prefixes

**Details**

The user specifies the id for the module

**Value**

The server to the settings module

---

patientLevelPredictionSettingsViewer

*The module viewer for exploring prediction settings*

---

**Description**

The module viewer for exploring prediction settings

**Usage**

```
patientLevelPredictionSettingsViewer(id)
```

**Arguments**

id	the unique reference id for the module
----	----------------------------------------

**Details**

The user specifies the id for the module

**Value**

The user interface to the settings module

---

`patientLevelPredictionValidationServer`*The module server for exploring prediction validation results*

---

## Description

The module server for exploring prediction validation results

## Usage

```
patientLevelPredictionValidationServer(  
  id,  
  modelDesignId,  
  developmentDatabaseId,  
  performanceId,  
  connectionHandler,  
  inputSingleView,  
  resultDatabaseSettings  
)
```

## Arguments

<code>id</code>	the unique reference id for the module
<code>modelDesignId</code>	identifier for the model design
<code>developmentDatabaseId</code>	identifier for the development database
<code>performanceId</code>	identifier for the performance
<code>connectionHandler</code>	the connection to the prediction result database
<code>inputSingleView</code>	the current tab
<code>resultDatabaseSettings</code>	a list containing the result schema and prefixes

## Details

The user specifies the id for the module

## Value

The server to the validation module

---

**patientLevelPredictionValidationViewer***The module viewer for exploring prediction validation results*

---

**Description**

The module viewer for exploring prediction validation results

**Usage**

```
patientLevelPredictionValidationViewer(id)
```

**Arguments**

<code>id</code>	the unique reference id for the module
-----------------	----------------------------------------

**Details**

The user specifies the id for the module

**Value**

The user interface to the validation module

---

**patientLevelPredictionViewer***The module viewer for exploring PatientLevelPrediction*

---

**Description**

The module viewer for exploring PatientLevelPrediction

**Usage**

```
patientLevelPredictionViewer(id = 1)
```

**Arguments**

<code>id</code>	the unique reference id for the module
-----------------	----------------------------------------

**Details**

The user specifies the id for the module

**Value**

The user interface to the PatientLevelPrediction viewer module

---

phevaluatorHelperFile	<i>The location of the phevaluator module helper file</i>
-----------------------	-----------------------------------------------------------

---

**Description**

The location of the phevaluator module helper file

**Usage**

```
phevaluatorHelperFile()
```

**Details**

Returns the location of the cohort-generator helper file

**Value**

String location of the phevaluator helper file

---

phevaluatorServer	<i>The module server for the main phevaluator module</i>
-------------------	----------------------------------------------------------

---

**Description**

The module server for the main phevaluator module

**Usage**

```
phevaluatorServer(id, connectionHandler, resultDatabaseSettings)
```

**Arguments**

id	The unique reference id for the module
connectionHandler	A connection to the database with the results
resultDatabaseSettings	A named list containing the cohort generator results database details (schema, table prefix)

**Value**

The phevaluator main module server

---

phevaluatorViewer	<i>The viewer of the phevaluator module</i>
-------------------	---------------------------------------------

---

**Description**

The viewer of the phevaluator module

**Usage**

```
phevaluatorViewer(id)
```

**Arguments**

id	The unique reference id for the module
----	----------------------------------------

**Value**

The user interface to the phevaluator results viewer

---

resultTableServer	<i>Result Table Server</i>
-------------------	----------------------------

---

**Description**

Result Table Server

**Usage**

```
resultTableServer(
  id,
  df,
  colDefsInput,
  selectedCols = NULL,
  sortedCols = NULL,
  elementId = NULL,
  addActions = NULL,
  downloadedFileName = NULL,
  groupBy = NULL
)
```

**Arguments**

id	string, table id must match resultsTableViewer function
df	reactive that returns a data frame
colDefsInput	named list of reactable::colDefs
selectedCols	string vector of columns the reactable should display to start by default. Defaults to ALL if not specified.
sortedCols	string vector of columns the reactable should sort by by default. Defaults to no sort if not specified.

elementId	optional string vector of element Id name for custom dropdown filtering if present in the customColDef list. Defaults to NULL.
addActions	add a button row selector column to the table to a column called 'actions'. actions must be a column in df
downloadedFileName	string, desired name of downloaded data file. can use the name from the module that is being used
groupBy	The columns to group by

**Value**

shiny module server

---

resultTableViewer	<i>Result Table Viewer</i>
-------------------	----------------------------

---

**Description**

Result Table Viewer

**Usage**

```
resultTableViewer(id = "result-table", downloadedFileName = NULL)
```

**Arguments**

id	string
downloadedFileName	string, desired name of downloaded data file. can use the name from the module that is being used

**Value**

shiny module UI

---

sccsHelperFile	<i>The location of the description module helper file</i>
----------------	-----------------------------------------------------------

---

**Description**

The location of the description module helper file

**Usage**

```
sccsHelperFile()
```

**Details**

Returns the location of the description helper file

**Value**

string location of the description helper file

---

sccsServer	<i>The module server for exploring SCCS</i>
------------	---------------------------------------------

---

**Description**

The module server for exploring SCCS

**Usage**

```
sccsServer(id, connectionHandler, resultDatabaseSettings = list(port = 1))
```

**Arguments**

id	the unique reference id for the module
connectionHandler	a connection to the database with the results
resultDatabaseSettings	a list containing the prediction result schema and connection details

**Details**

The user specifies the id for the module

**Value**

The server for the PatientLevelPrediction module

---

sccsView	<i>SCCS shiny module UI code</i>
----------	----------------------------------

---

**Description**

Load the ui for the sccs module

**Usage**

```
sccsView(id = "sccs-module")
```

**Arguments**

id	id for module
----	---------------



---

timeDistributionsView	<i>timeDistributions view</i>
-----------------------	-------------------------------

---

**Description**

Use for customizing UI

**Usage**

```
timeDistributionsView(id)
```

**Arguments**

id	Namespace Id - use namespaced id ns("imeDistributions") inside diagnosticsExplorer module
----	-------------------------------------------------------------------------------------------

---

visitContextView	<i>Visit context module view</i>
------------------	----------------------------------

---

**Description**

Use for customizing UI

**Usage**

```
visitContextView(id)
```

**Arguments**

id	Namespace Id - use namespaced id ns("vistConext") inside diagnosticsExplorer module
----	-------------------------------------------------------------------------------------