

Package ‘libsoc’

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Title Read, Create and Write 'PharmML' Standard Output (so) XML Files

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Depends R (>= 2.14.1)

Imports methods

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

SystemRequirements libxml2: libxml2-dev (deb), libxml2-devel (rpm)

NeedsCompilation yes

Description

Handle 'PharmML' (Pharmacometrics Markup Language) standard output (SO) XML files. SO files can be created, read, manipulated and written through a data binding from the XML structure to a tree structure of R objects.

URL <https://github.com/rikardn/libsoc>

BugReports <https://github.com/rikardn/libsoc/issues>

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dv_column *Get the index of the dv column*

Description

Get the index of the dv column of a data.framed imported from an SO

dv_column_name *Get the name of the dv column*

Description

Get the name of the dv column of a data.framed imported from an SO

idv_column *Get the index of the idv column*

Description

Get the index of the idv column of a data.framed imported from an SO

idv_column_name *Get the name of the idv column*

Description

Get the name of the idv column of a data.framed imported from an SO

id_column	<i>Get the index of the id column</i>
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Description

Get the index of the id column of a data.frame imported from an SO

id_column_name	<i>Get the name of the id column</i>
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Description

Get the name of the id column of a data.frame imported from an SO

libsoc	<i>A package to handle PharmML standardized output (SO) XML files</i>
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Description

A package to handle PharmML standardized output (SO) XML files. SO files can be created, read, manipulated and written through a data binding from the XML structure to a tree structure of R objects.

Details

```
Package:  libsoc
Type:    Package
Version:  0.6.2
Date:    2018-01-12
License:  LGPL-3
```

Depends on libxml2, libiconv and zlib. More information and source code for these libraries can be found on the sites linked below.

```
libxml2  http://xmlsoft.org
libiconv https://www.gnu.org/software/libiconv
zlib     http://www.zlib.net
```

You can view the license for libsoc itself and libiconv with `file.show(system.file("licenses", "COPYING-LIB", package="libsoc"))` and libxml2 with `file.show(system.file("licenses", "COPYING-LIBXML2", package="libsoc"))`

Author(s)

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Examples

```
# Read in parameter estimates
file <- system.file("extdata", "pheno.SO.xml", package="libsoc")
so <- so_SO_read(file)
estimates <- so$SOBlock[[1]]$Estimation$PopulationEstimates$MLE

# For more examples see the examples directory
```

so_Bayesian

so_Bayesian reference class

Description

Reference Class for the SO/SOBlock/Estimation/PopulationEstimates/Bayesian element of a PharmML-SO data structure

Methods

so_Bayesian\$new() - Create a new empty so_Bayesian object

Fields

\$PosteriorMean - A data.frame
 \$PosteriorMedian - A data.frame
 \$PosteriorMode - A data.frame

so_Bayesian_PPE

so_Bayesian_PPE reference class

Description

Reference Class for the SO/SOBlock/Estimation/PrecisionPopulationEstimates/Bayesian element of a PharmML-SO data structure

Methods

so_Bayesian_PPE\$new() - Create a new empty so_Bayesian_PPE object

Fields

\$StandardDeviationPosterior - A data.frame
 \$PercentilesCI - A data.frame

so_Bootstrap *so_Bootstrap reference class*

Description

Reference Class for the SO/SOBlock/Estimation/PopulationEstimates/Bootstrap element of a PharmML-SO data structure

Methods

so_Bootstrap\$new() - Create a new empty so_Bootstrap object

Fields

\$Mean - A data.frame
 \$Median - A data.frame

so_ConditionNumber *so_ConditionNumber reference class*

Description

Reference Class for the SO/SOBlock/Estimation/PrecisionPopulationEstimates/ConditionNumber element of a PharmML-SO data structure

Methods

so_ConditionNumber\$new() - Create a new empty so_ConditionNumber object

Fields

\$Real - A numeric

so_Content	<i>so_Content reference class</i>
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Description

Reference Class for the SO/SOBlock/TaskInformation/Message/Content element of a PharmML-SO data structure

Methods

so_Content\$new() - Create a new empty so_Content object

Fields

\$String - A character string

so_DataFile	<i>so_DataFile reference class</i>
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Description

Reference Class for the SO/SOBlock/RawResults/DataFile element of a PharmML-SO data structure

Methods

so_DataFile\$new() - Create a new empty so_DataFile object

Fields

\$Description - A character string

\$path - A character string

\$oid - A character string attribute

so_Design

so_Design reference class

Description

Reference Class for the SO/SOBlock/OptimalDesign/OptimalDesignBlock/Design element of a PharmML-SO data structure

Methods

so_Design\$new() - Create a new empty so_Design object

Fields

\$path - A character string

\$oid - A character string attribute

so_DiagnosticIndividualParams*so_DiagnosticIndividualParams reference class*

Description

Reference Class for the SO/SOBlock/ModelDiagnostic/DiagnosticIndividualParams element of a PharmML-SO data structure

Methods

so_DiagnosticIndividualParams\$new() - Create a new empty so_DiagnosticIndividualParams object

Fields

\$RandomEffects - A data.frame

\$IndivParamsCovariates - A data.frame

\$DistributionIndivParams - A data.frame

`so_DiagnosticPlotsStructuralModel`*so_DiagnosticPlotsStructuralModel reference class*

Description

Reference Class for the SO/SOBlock/ModelDiagnostic/DiagnosticPlotsStructuralModel element of a PharmML-SO data structure

Methods

`so_DiagnosticPlotsStructuralModel$new()` - Create a new empty `so_DiagnosticPlotsStructuralModel` object

Fields

`$IndivFits` - A [so_IndivFits](#) object
`$IndivPredictionVsObserv` - A data.frame
`$VPC` - A data.frame

`so_DiagnosticStructuralModel`*so_DiagnosticStructuralModel reference class*

Description

Reference Class for the SO/SOBlock/ModelDiagnostic/DiagnosticStructuralModel element of a PharmML-SO data structure

Methods

`so_DiagnosticStructuralModel$new()` - Create a new empty `so_DiagnosticStructuralModel` object

Fields

`$IndivObservationPrediction` - A data.frame
`$VPC` - A data.frame

so_Estimates	<i>so_Estimates reference class</i>
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Description

Reference Class for the SO/SOBlock/Estimation/IndividualEstimates/Estimates element of a PharmML-SO data structure

Methods

so_Estimates\$new() - Create a new empty so_Estimates object

Fields

\$Mean - A data.frame
 \$Median - A data.frame
 \$Mode - A data.frame
 \$Samples - A data.frame

so_Estimation	<i>so_Estimation reference class</i>
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Description

Reference Class for the SO/SOBlock/Estimation element of a PharmML-SO data structure

Methods

so_Estimation\$new() - Create a new empty so_Estimation object

Fields

\$PopulationEstimates - A [so_PopulationEstimates](#) object
 \$PrecisionPopulationEstimates - A [so_PrecisionPopulationEstimates](#) object
 \$IndividualEstimates - A [so_IndividualEstimates](#) object
 \$PrecisionIndividualEstimates - A [so_PrecisionIndividualEstimates](#) object
 \$Residuals - A [so_Residuals](#) object
 \$Predictions - A data.frame
 \$OFMeasures - A [so_OFMeasures](#) object
 \$TargetToolMessages - A [so_TargetToolMessages](#) object

so_ExternalFile	<i>so_ExternalFile reference class</i>
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Description

Reference Class for the ExternalFile element of a PharmML-SO data structure

Methods

so_ExternalFile\$new() - Create a new empty so_ExternalFile object

so_ExternalFile\$add_MissingData(object) - Add a MissingData

so_ExternalFile\$remove_MissingData(object, i) - Remove the MissingData having index i

Fields

\$Description - A character string

\$path - A character string

\$format - A character string

\$delimiter - A character string

\$MissingData - A list of [so_MissingData](#) objects

\$oid - A character string attribute

so_File	<i>so_File reference class</i>
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Description

Reference Class for the SO/SOBlock/ToolSettings/File element of a PharmML-SO data structure

Methods

so_File\$new() - Create a new empty so_File object

Fields

\$Description - A character string

\$path - A character string

\$oid - A character string attribute

so_GraphicsFile *so_GraphicsFile reference class*

Description

Reference Class for the SO/SOBlock/RawResults/GraphicsFile element of a PharmML-SO data structure

Methods

so_GraphicsFile\$new() - Create a new empty so_GraphicsFile object

Fields

\$Description - A character string
\$path - A character string
\$oid - A character string attribute

so_IndependentVariable
so_IndependentVariable reference class

Description

Reference Class for the PharmML/IndependentVariable element of a PharmML-SO data structure

Methods

so_IndependentVariable\$new() - Create a new empty so_IndependentVariable object

Fields

\$Description - A character string
\$id - A character string attribute
\$symbol - A character string attribute

so_IndivFits	<i>so_IndivFits reference class</i>
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Description

Reference Class for the SO/SOBlock/ModelDiagnostic/DiagnosticPlotsStructuralModel/IndivFits element of a PharmML-SO data structure

Methods

so_IndivFits\$new() - Create a new empty so_IndivFits object

Fields

\$ObservationTable - A data.frame

\$PredictionTable - A data.frame

so_IndividualEstimates	<i>so_IndividualEstimates reference class</i>
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Description

Reference Class for the SO/SOBlock/Estimation/IndividualEstimates element of a PharmML-SO data structure

Methods

so_IndividualEstimates\$new() - Create a new empty so_IndividualEstimates object

Fields

\$Estimates - A [so_Estimates](#) object

\$RandomEffects - A [so_RandomEffects_IE](#) object

\$EtaShrinkage - A data.frame

so_InformationCriteria

so_InformationCriteria reference class

Description

Reference Class for the SO/SOBlock/Estimation/OFMeasures/InformationCriteria element of a PharmML-SO data structure

Methods

so_InformationCriteria\$new() - Create a new empty so_InformationCriteria object

Fields

\$AIC - A numeric

\$BIC - A numeric

\$DIC - A numeric

so_Level

so_Level reference class

Description

Reference Class for the PharmML/ModelDefinition/VariabilityModel/Level element of a PharmML-SO data structure

Methods

so_Level\$new() - Create a new empty so_Level object

Fields

\$Description - A character string

\$Name - A character string

\$ParentLevel - A [so_ParentLevel](#) object

\$id - A character string attribute

\$referenceLevel - A character string attribute

\$symbId - A character string attribute

so_Likelihood	<i>so_Likelihood reference class</i>
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Description

Reference Class for the SO/SOBlock/Estimation/Likelihood element of a PharmML-SO data structure

Methods

so_Likelihood\$new() - Create a new empty so_Likelihood object

Fields

\$LogLikelihood - A numeric
\$Deviance - A numeric
\$IndividualContribtoLL - A data.frame

so_Message	<i>so_Message reference class</i>
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Description

Reference Class for the SO/SOBlock/TaskInformation/Message element of a PharmML-SO data structure

Methods

so_Message\$new() - Create a new empty so_Message object

Fields

\$Toolname - A character string
\$Name - A character string
\$Content - A character string
\$Severity - An integer
\$type - A character string attribute

so_MissingData	<i>so_MissingData reference class</i>
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Description

Reference Class for the MissingData element of a PharmML-SO data structure

Methods

so_MissingData\$new() - Create a new empty so_MissingData object

Fields

\$dataCode - A character string attribute

\$missingDataType - A character string attribute

so_MLE	<i>so_MLE reference class</i>
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Description

Reference Class for the SO/SOBlock/Estimation/PrecisionPopulationEstimates/MLE element of a PharmML-SO data structure

Methods

so_MLE\$new() - Create a new empty so_MLE object

Fields

\$FIM - A matrix

\$CovarianceMatrix - A matrix

\$CorrelationMatrix - A matrix

\$StandardError - A data.frame

\$RelativeStandardError - A data.frame

\$AsymptoticCI - A data.frame

\$ConditionNumber - A numeric

so_ModelDefinition *so_ModelDefinition reference class*

Description

Reference Class for the PharmML/ModelDefinition element of a PharmML-SO data structure

Methods

so_ModelDefinition\$new() - Create a new empty so_ModelDefinition object

Fields

\$VariabilityModel - A [so_VariabilityModel](#) object

so_ModelDiagnostic *so_ModelDiagnostic reference class*

Description

Reference Class for the SO/SOBlock/ModelDiagnostic element of a PharmML-SO data structure

Methods

so_ModelDiagnostic\$new() - Create a new empty so_ModelDiagnostic object

Fields

\$DiagnosticStructuralModel - A [so_DiagnosticStructuralModel](#) object

\$DiagnosticIndividualParams - A [so_DiagnosticIndividualParams](#) object

so_Name	<i>so_Name reference class</i>
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Description

Reference Class for the SO/SOBlock/TaskInformation/Message/Name element of a PharmML-SO data structure

Methods

so_Name\$new() - Create a new empty so_Name object

Fields

\$String - A character string

so_NumberChains	<i>so_NumberChains reference class</i>
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Description

Reference Class for the SO/SOBlock/TaskInformation/NumberChains element of a PharmML-SO data structure

Methods

so_NumberChains\$new() - Create a new empty so_NumberChains object

Fields

\$Description - A character string

\$Real - A numeric

so_NumberIterations *so_NumberIterations reference class*

Description

Reference Class for the SO/SOBlock/TaskInformation/NumberIterations element of a PharmML-SO data structure

Methods

so_NumberIterations\$new() - Create a new empty so_NumberIterations object

Fields

\$Real - A numeric

so_OFMeasures *so_OFMeasures reference class*

Description

Reference Class for the SO/SOBlock/Estimation/OFMeasures element of a PharmML-SO data structure

Methods

so_OFMeasures\$new() - Create a new empty so_OFMeasures object

Fields

\$Likelihood - A numeric
\$LogLikelihood - A numeric
\$Deviance - A numeric
\$ToolObjFunction - A numeric
\$IndividualContribToLL - A data.frame
\$InformationCriteria - A [so_InformationCriteria](#) object

so_OptimalDesign *so_OptimalDesign reference class*

Description

Reference Class for the SO/SOBlock/OptimalDesign element of a PharmML-SO data structure

Methods

so_OptimalDesign\$new() - Create a new empty so_OptimalDesign object
 so_OptimalDesign\$add_OptimalDesignBlock(object) - Add a OptimalDesignBlock
 so_OptimalDesign\$remove_OptimalDesignBlock(object, i) - Remove the OptimalDesignBlock having index i

Fields

\$OptimalDesignBlock - A list of [so_OptimalDesignBlock](#) objects
 \$type - A character string attribute

so_OptimalDesignBlock *so_OptimalDesignBlock reference class*

Description

Reference Class for the SO/SOBlock/OptimalDesign/OptimalDesignBlock element of a PharmML-SO data structure

Methods

so_OptimalDesignBlock\$new() - Create a new empty so_OptimalDesignBlock object

Fields

\$FIM - A matrix
 \$CovarianceMatrix - A matrix
 \$ParameterPrecision - A data.frame
 \$Criteria - A data.frame
 \$Tests - A data.frame
 \$SimulatedData - A [so_ExternalFile](#) object
 \$Design - A [so_ExternalFile](#) object
 \$blockNumber - An integer attribute

so_OtherMethod	<i>so_OtherMethod reference class</i>
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Description

Reference Class for the SO/SOBlock/Estimation/PopulationEstimates/OtherMethod element of a PharmML-SO data structure

Methods

so_OtherMethod\$new() - Create a new empty so_OtherMethod object

Fields

\$Mean - A data.frame
\$Median - A data.frame
\$method - A character string attribute

so_OtherMethod_PPE	<i>so_OtherMethod_PPE reference class</i>
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Description

Reference Class for the SO/SOBlock/Estimation/PrecisionPopulationEstimates/OtherMethod element of a PharmML-SO data structure

Methods

so_OtherMethod_PPE\$new() - Create a new empty so_OtherMethod_PPE object

Fields

\$CovarianceMatrix - A matrix
\$CorrelationMatrix - A matrix
\$StandardDeviation - A data.frame
\$StandardError - A data.frame
\$AsymptoticCI - A data.frame
\$PercentilesCI - A data.frame

so_OutputFilePath *so_OutputFilePath reference class*

Description

Reference Class for the SO/SOBlock/TaskInformation/OutputFilePath element of a PharmML-SO data structure

Methods

so_OutputFilePath\$new() - Create a new empty so_OutputFilePath object

Fields

\$path - A character string
\$oid - A character string attribute

so_ParentLevel *so_ParentLevel reference class*

Description

Reference Class for the PharmML/ModelDefinition/VariabilityModel/Level/ParentLevel element of a PharmML-SO data structure

Methods

so_ParentLevel\$new() - Create a new empty so_ParentLevel object

Fields

\$Description - A character string
\$SymbRef - A [so_SymbRef](#) object
\$id - A character string attribute

so_PharmML	<i>so_PharmML reference class</i>
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Description

Reference Class for the PharmML element of a PharmML-SO data structure

Methods

so_PharmML\$new() - Create a new empty so_PharmML object

Fields

\$Name - A character string

\$IndependentVariable - A [so_IndependentVariable](#) object

\$ModelDefinition - A [so_ModelDefinition](#) object

so_PharmMLRef	<i>so_PharmMLRef reference class</i>
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Description

Reference Class for the SO/PharmMLRef element of a PharmML-SO data structure

Methods

so_PharmMLRef\$new() - Create a new empty so_PharmMLRef object

Fields

\$Description - A character string

\$name - A character string attribute

\$id - A character string attribute

so_PopulationEstimates

so_PopulationEstimates reference class

Description

Reference Class for the SO/SOBlock/Estimation/PopulationEstimates element of a PharmML-SO data structure

Methods

so_PopulationEstimates\$new() - Create a new empty so_PopulationEstimates object

Fields

\$MLE - A data.frame

\$Bayesian - A [so_Bayesian](#) object

\$OtherMethod - A [so_OtherMethod](#) object

so_PrecisionIndividualEstimates

so_PrecisionIndividualEstimates reference class

Description

Reference Class for the SO/SOBlock/Estimation/PrecisionIndividualEstimates element of a PharmML-SO data structure

Methods

so_PrecisionIndividualEstimates\$new() - Create a new empty so_PrecisionIndividualEstimates object

Fields

\$StandardDeviation - A data.frame

\$PercentilesCI - A data.frame

so_PrecisionPopulationEstimates
so_PrecisionPopulationEstimates reference class

Description

Reference Class for the SO/SOBlock/Estimation/PrecisionPopulationEstimates element of a PharmML-SO data structure

Methods

so_PrecisionPopulationEstimates\$new() - Create a new empty so_PrecisionPopulationEstimates object

Fields

\$MLE - A [so_MLE](#) object
\$Bayesian - A [so_Bayesian_PPE](#) object
\$OtherMethod - A [so_OtherMethod_PPE](#) object

so_RandomEffects_IE *so_RandomEffects_IE reference class*

Description

Reference Class for the SO/SOBlock/Estimation/IndividualEstimates/RandomEffects element of a PharmML-SO data structure

Methods

so_RandomEffects_IE\$new() - Create a new empty so_RandomEffects_IE object

Fields

\$EffectMean - A data.frame
\$EffectMedian - A data.frame
\$EffectMode - A data.frame
\$Samples - A data.frame

so_RawResults *so_RawResults reference class*

Description

Reference Class for the SO/SOBlock/RawResults element of a PharmML-SO data structure

Methods

so_RawResults\$new() - Create a new empty so_RawResults object

so_RawResults\$add_DataFile(object) - Add a DataFile

so_RawResults\$remove_DataFile(object, i) - Remove the DataFile having index i

so_RawResults\$add_GraphicsFile(object) - Add a GraphicsFile

so_RawResults\$remove_GraphicsFile(object, i) - Remove the GraphicsFile having index i

Fields

\$DataFile - A list of data.frames

\$GraphicsFile - A list of [so_ExternalFile](#) objects

so_Residuals *so_Residuals reference class*

Description

Reference Class for the SO/SOBlock/Estimation/Residuals element of a PharmML-SO data structure

Methods

so_Residuals\$new() - Create a new empty so_Residuals object

Fields

\$ResidualTable - A data.frame

\$EpsShrinkage - A data.frame

so_RunTime	<i>so_RunTime reference class</i>
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Description

Reference Class for the SO/SOBlock/TaskInformation/RunTime element of a PharmML-SO data structure

Methods

so_RunTime\$new() - Create a new empty so_RunTime object

Fields

\$Description - A character string
\$Real - A numeric

so_Severity	<i>so_Severity reference class</i>
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Description

Reference Class for the SO/SOBlock/TaskInformation/Message/Severity element of a PharmML-SO data structure

Methods

so_Severity\$new() - Create a new empty so_Severity object

Fields

\$Int - An integer

so_SimulatedData *so_SimulatedData reference class*

Description

Reference Class for the SO/SOBlock/OptimalDesign/OptimalDesignBlock/SimulatedData element of a PharmML-SO data structure

Methods

so_SimulatedData\$new() - Create a new empty so_SimulatedData object

Fields

\$path - A character string
\$oid - A character string attribute

so_Simulation *so_Simulation reference class*

Description

Reference Class for the SO/SOBlock/Simulation element of a PharmML-SO data structure

Methods

so_Simulation\$new() - Create a new empty so_Simulation object
so_Simulation\$add_SimulationBlock(object) - Add a SimulationBlock
so_Simulation\$remove_SimulationBlock(object, i) - Remove the SimulationBlock having index i

Fields

\$SimulationBlock - A list of [so_SimulationBlock](#) objects

so_SimulationBlock *so_SimulationBlock reference class*

Description

Reference Class for the SO/SOBlock/Simulation/SimulationBlock element of a PharmML-SO data structure

Methods

so_SimulationBlock\$new() - Create a new empty so_SimulationBlock object
 so_SimulationBlock\$add_SimulatedProfiles(object) - Add a SimulatedProfiles
 so_SimulationBlock\$remove_SimulatedProfiles(object, i) - Remove the SimulatedProfiles having index i
 so_SimulationBlock\$add_IndivParameters(object) - Add a IndivParameters
 so_SimulationBlock\$remove_IndivParameters(object, i) - Remove the IndivParameters having index i
 so_SimulationBlock\$add_RandomEffects(object) - Add a RandomEffects
 so_SimulationBlock\$remove_RandomEffects(object, i) - Remove the RandomEffects having index i
 so_SimulationBlock\$add_Covariates(object) - Add a Covariates
 so_SimulationBlock\$remove_Covariates(object, i) - Remove the Covariates having index i
 so_SimulationBlock\$add_Regressors(object) - Add a Regressors
 so_SimulationBlock\$remove_Regressors(object, i) - Remove the Regressors having index i
 so_SimulationBlock\$add_PopulationParameters(object) - Add a PopulationParameters
 so_SimulationBlock\$remove_PopulationParameters(object, i) - Remove the PopulationParameters having index i
 so_SimulationBlock\$add_Dosing(object) - Add a Dosing
 so_SimulationBlock\$remove_Dosing(object, i) - Remove the Dosing having index i

Fields

\$SimulatedProfiles - A list of [so_SimulationSubType](#) objects
 \$IndivParameters - A list of [so_SimulationSubType](#) objects
 \$RandomEffects - A list of [so_SimulationSubType](#) objects
 \$Covariates - A list of [so_SimulationSubType](#) objects
 \$Regressors - A list of [so_SimulationSubType](#) objects
 \$PopulationParameters - A list of [so_SimulationSubType](#) objects
 \$Dosing - A list of [so_SimulationSubType](#) objects
 \$RawResultsFile - A [so_ExternalFile](#) object
 \$replicate - An integer attribute

so_SimulationSubType *so_SimulationSubType reference class*

Description

Reference Class for the SimulationSubType element of a PharmML-SO data structure

Methods

so_SimulationSubType\$new() - Create a new empty so_SimulationSubType object

Fields

\$name - A character string attribute
 \$extFileNo - An integer attribute

so_SO *so_SO reference class*

Description

Reference Class for the SO element of a PharmML-SO data structure

Methods

so_SO\$new() - Create a new empty so_SO object
 so_SO\$write(filename, pretty=TRUE) - Write an SO to file. Set pretty to FALSE to not get pretty printed xml
 so_SO\$add_SOBlock(object) - Add a SOBlock
 so_SO\$remove_SOBlock(object, i) - Remove the SOBlock having index i
 so_SO\$all_population_estimates() - Get a data.frame with the population estimates from all SOBlocks
 so_SO\$all_standard_errors() - Get a data.frame with the standard errors from all SOBlocks
 so_SO\$variability_type(parameter_names) - Given an array of parameter names return an array with the variability type of the parameters
 Types are: structParameter, parameterVariability and residualError
 so_SO\$correlation_parameters(parameter_names) - Given an array of parameter names return an array of whether each parameter is a correlation or not
 so_SO\$random_variable_from_variability_parameter(parameter_names) - Given an array of parameter names return an array of names of the corresponding random variable

Fields

\$Description - A character string
 \$PharmMLRef - A [so_PharmMLRef](#) object
 \$SOBlock - A list of [so_SOBlock](#) objects
 \$id - A character string attribute
 \$metadataFile - A character string attribute

so_SOBlock	<i>so_SOBlock reference class</i>
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Description

Reference Class for the SO/SOBlock element of a PharmML-SO data structure

Methods

so_SOBlock\$new() - Create a new empty so_SOBlock object

Fields

\$ToolSettings - A [so_ToolSettings](#) object
 \$RawResults - A [so_RawResults](#) object
 \$TaskInformation - A [so_TaskInformation](#) object
 \$Estimation - A [so_Estimation](#) object
 \$Simulation - A [so_Simulation](#) object
 \$ModelDiagnostic - A [so_ModelDiagnostic](#) object
 \$OptimalDesign - A [so_OptimalDesign](#) object
 \$blkId - A character string attribute

so_S0_read	<i>Read an SO file</i>
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Description

Function to read an SO file from disk into a Reference Class tree structure

so_SymbRef *so_SymbRef reference class*

Description

Reference Class for the SymbRef element of a PharmML-SO data structure

Methods

so_SymbRef\$new() - Create a new empty so_SymbRef object

Fields

\$Description - A character string
\$id - A character string attribute
\$blkIdRef - A character string attribute
\$symbIdRef - A character string attribute

so_TargetToolMessages *so_TargetToolMessages reference class*

Description

Reference Class for the SO/SOBlock/Estimation/TargetToolMessages element of a PharmML-SO data structure

Methods

so_TargetToolMessages\$new() - Create a new empty so_TargetToolMessages object

Fields

\$Termination - A character string
\$Warnings - A character string
\$Errors - A character string
\$ElapsedTime - A numeric
\$OutputFilePath - A [so_ExternalFile](#) object
\$ChainsNumber - A numeric
\$IterationNumber - A numeric

so_TaskInformation *so_TaskInformation reference class*

Description

Reference Class for the SO/SOBlock/TaskInformation element of a PharmML-SO data structure

Methods

so_TaskInformation\$new() - Create a new empty so_TaskInformation object
so_TaskInformation\$add_Message(object) - Add a Message
so_TaskInformation\$remove_Message(object, i) - Remove the Message having index i
so_TaskInformation\$add_OutputFilePath(object) - Add a OutputFilePath
so_TaskInformation\$remove_OutputFilePath(object, i) - Remove the OutputFilePath having index i

Fields

\$Message - A list of [so_Message](#) objects
\$OutputFilePath - A list of [so_ExternalFile](#) objects
\$RunTime - A numeric
\$NumberChains - An integer
\$NumberIterations - An integer

so_Toolname *so_Toolname reference class*

Description

Reference Class for the SO/SOBlock/TaskInformation/Message/Toolname element of a PharmML-SO data structure

Methods

so_Toolname\$new() - Create a new empty so_Toolname object

Fields

\$String - A character string

so_ToolSettings *so_ToolSettings reference class*

Description

Reference Class for the SO/SOBlock/ToolSettings element of a PharmML-SO data structure

Methods

so_ToolSettings\$new() - Create a new empty so_ToolSettings object

so_ToolSettings\$add_File(object) - Add a File

so_ToolSettings\$remove_File(object, i) - Remove the File having index i

Fields

\$File - A list of [so_ExternalFile](#) objects

so_VariabilityModel *so_VariabilityModel reference class*

Description

Reference Class for the PharmML/ModelDefinition/VariabilityModel element of a PharmML-SO data structure

Methods

so_VariabilityModel\$new() - Create a new empty so_VariabilityModel object

Fields

\$Description - A character string

\$Name - A character string

\$Level - A [so_Level](#) object

\$id - A character string attribute

\$blkId - A character string attribute

\$type - A character string attribute

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