

# Package ‘DynTxRegime’

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**Type** Package

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**Description** Methods to estimate dynamic treatment regimes using Interactive Q-Learning, Q-Learning, weighted learning, and value-search methods based on Augmented Inverse Probability Weighted Estimators and Inverse Probability Weighted Estimators. Dynamic Treatment Regimes: Statistical Methods for Precision Medicine, Tsiatis, A. A., Davidian, M. D., Holloway, S. T., and Laber, E. B., Chapman & Hall/CRC Press, 2020, ISBN:978-1-4987-6977-8.

**License** GPL-2

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**Collate** 'A\_generics.R' 'A\_List.R' 'A\_DecisionPointList.R'  
'A\_OptimalInfo.R' 'A\_OptimalObj.R' 'A\_DynTxRegime.R'  
'A\_ModelObjSubset.R' 'A\_SubsetList.R' 'A\_ModelObj\_SubsetList.R'  
'A\_ModelObj\_DecisionPointList.R' 'A\_newModelObjSubset.R'  
'B\_TxInfoBasic.R' 'B\_TxInfoFactor.R' 'B\_TxInfoInteger.R'  
'B\_TxObj.R' 'B\_TxInfoNoSubsets.R' 'B\_TxSubset.R'

'B\_TxSubsetInteger.R' 'B\_TxSubsetFactor.R'  
 'B\_TxInfoWithSubsets.R' 'B\_TxInfoList.R' 'C\_TypedFit.R'  
 'C\_TypedFit\_SubsetList.R' 'C\_TypedFit\_fSet.R' 'C\_TypedFitObj.R'  
 'D\_OutcomeNoFit.R' 'D\_newModel.R' 'D\_OutcomeSimpleFit.R'  
 'D\_OutcomeSimpleFit\_fSet.R' 'D\_OutcomeIterateFit.R'  
 'D\_OutcomeSimpleFit\_SubsetList.R' 'D\_OutcomeObj.R'  
 'E\_class\_QLearn.R' 'E\_class\_IQLearnSS.R' 'E\_class\_IQLearnFS.R'  
 'E\_class\_IQLearnFS\_C.R' 'E\_class\_IQLearnFS\_ME.R'  
 'E\_class\_IQLearnFS\_VHet.R' 'E\_iqLearnFSC.R' 'E\_iqLearnFSM.R'  
 'E\_iqLearnFSV.R' 'E\_iqLearnSS.R' 'E\_qLearn.R'  
 'F\_PropensityFit.R' 'F\_PropensityFit\_fSet.R'  
 'F\_PropensityFit\_SubsetList.R' 'F\_PropensityObj.R' 'G\_Regime.R'  
 'G\_RegimeObj.R' 'H\_class\_OptimalSeq.R'  
 'H\_class\_OptimalSeqCoarsened.R' 'H\_class\_OptimalSeqMissing.R'  
 'H\_optimalSeq.R' 'I\_ClassificationFit.R'  
 'I\_ClassificationFit\_SubsetList.R' 'I\_ClassificationFit\_fSet.R'  
 'I\_ClassificationObj.R' 'J\_class\_OptimalClass.R'  
 'J\_optimalClass.R' 'K\_Kernel.R' 'K\_MultiRadialKernel.R'  
 'K\_RadialKernel.R' 'K\_PolyKernel.R' 'K\_LinearKernel.R'  
 'K\_KernelObj.R' 'L\_Surrogate.R' 'L\_ExpSurrogate.R'  
 'L\_HingeSurrogate.R' 'L\_HuberHingeSurrogate.R'  
 'L\_LogitSurrogate.R' 'L\_SmoothRampSurrogate.R'  
 'L\_SqHingeSurrogate.R' 'M\_MethodObject.R' 'M\_OptimBasic.R'  
 'M\_OptimKernel.R' 'M\_OptimObj.R' 'N\_CVBasic.R' 'N\_CVInfo.R'  
 'N\_CVInfoLambda.R' 'N\_CVInfoParam.R' 'N\_CVInfo2Par.R'  
 'N\_CVInfoObj.R' 'N\_OptimStep.R' 'O\_LearningObject.R'  
 'O\_Learning.R' 'O\_LearningMulti.R' 'P\_class\_owl.R'  
 'P\_class\_OWL.R' 'P\_owl.R' 'Q\_class\_rwl.R' 'Q\_class\_RWL.R'  
 'Q\_rwl.R' 'R\_class\_BOWLBasic.R' 'R\_class\_BOWL.R' 'R\_bowl.R'  
 'S\_class\_earl.R' 'S\_class\_EARL.R' 'S\_earl.R'  
 'checkFSetAndOutcomeModels.R' 'checkFSetAndPropensityModels.R'  
 'checkInputs.R' 'internalTest.R' 'titleIt.R'

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**Description**

A dataset generated to mimic data from a two-stage randomized clinical trial that studied the effect of meal replacement shakes on adolescent obesity. The dataset contains the following covariates collected at the start of the first stage: "gender," "race," "parentBMI," and "baselineBMI." At the second-stage, "month4BMI" was collected. Variables "A1" and "A2" are the randomized treatments at stages one and two, and "month12BMI" is the primary outcome collected at the end of stage two.

**Format**

A matrix with rows corresponding to patients.

**Source**

Generated by Kristin A. Linn in R

---

bowl	<i>Backwards Outcome Weighted Learning.</i>
------	---------------------------------------------

---

**Description**

Function performs a single step of the bowl method. Multiple decision points can be analyzed by repeated calls, as is done for qLearn() and optimalClass().

**Usage**

```
bowl(  
  ...,  
  moPropen,  
  data,  
  reward,  
  txName,  
  regime,  
  response,  
  BOWLObj = NULL,  
  lambdas = 2,  
  cvFolds = 0L,  
  kernel = "linear",  
  kparam = NULL,  
  fSet = NULL,  
  surrogate = "hinge",  
  verbose = 2L  
)
```

**Arguments**

...	Used primarily to require named input. However, inputs for the optimization methods can be sent through the ellipsis. If surrogate is hinge, the optimization method is <code>dfoptim::hjk()</code> . For all other surrogates, <code>stats::optim()</code> is used.
moPropen	An object of class <code>modelObj</code> or <code>modelObjSubset</code> , which defines the model and R methods to be used to obtain parameter estimates and predictions for the propensity for tx. See <code>?moPropen</code> for details.
data	A data frame of the covariates and tx histories.
reward	The response vector.
txName	A character object. The column header of <code>data</code> that corresponds to the tx covariate
regime	A formula object or a list of formula objects. The covariates to be included in the decision function/kernel. If a list is provided, this specifies that there is an underlying subset structure – <code>fSet</code> must then be defined. For subsets, the name of each element of the list must correspond to the name of a subset. If a regime is to be estimated using multiple subsets combined, each subset must be included in the name and separated by a comma (no spaces).
response	A numeric vector. The same as reward above. Allows for naming convention followed in most <code>DynTxRegime</code> methods.
BOWLobj	NULL or <code>BOWL-class</code> object returned from previous call to <code>bowl()</code> . If NULL, indicates that the function call is for the first STEP of the BOWL algorithm (i.e., the final decision point). If a <code>BOWL-class</code> object, assumed that the object was returned by the preceding step of the BOWL algorithm.
lambdas	A numeric object or a numeric vector object giving the penalty tuning parameter(s). If more than 1 is provided, the set of tuning parameter values to be considered in the cross-validation algorithm (note that <code>cvFolds</code> must be positive in this case).
cvFolds	If cross-validation is to be used to select the tuning parameters and/or kernel parameters, the number of folds.
kernel	A character object. Must be one of <code>{'linear', 'poly', 'radial'}</code>
kparam	A numeric object. If kernel = linear, kparam is ignored. If kernel = poly, kparam is the degree of the polynomial. If kernel = radial, kparam is the inverse bandwidth of the kernel. If a vector of bandwidth parameters is given, cross-validation will be used to select the parameter (note that <code>cvFolds</code> must be positive in this case).
fSet	A function or NULL defining subset structure. See <code>?fSet</code> for details.
surrogate	The surrogate 0-1 loss function. Must be one of <code>{'logit', 'exp', 'hinge', 'sqhinge', 'huber'}</code> .
verbose	An integer or logical. If 0, no screen prints are generated. If 1, screen prints are generated with the exception of optimization results obtained in iterative algorithm. If 2, all screen prints are generated.

**Value**

a **BOWL-class** object

**References**

Yingqi Zhao, Donglin Zeng, Eric B. Laber, Michael R. Kosorok (2015) New statistical learning methods for estimating optimal dynamic treatment regimes. *Journal of the American Statistical Association*, 110:510, 583–598.

**See Also**

Other statistical methods: [earl\(\)](#), [iqLearn](#), [optimalClass\(\)](#), [optimalSeq\(\)](#), [owl\(\)](#), [qLearn\(\)](#), [rwl\(\)](#)

Other weighted learning methods: [earl\(\)](#), [owl\(\)](#), [rwl\(\)](#)

Other multiple decision point methods: [iqLearn](#), [optimalClass\(\)](#), [optimalSeq\(\)](#), [qLearn\(\)](#)

**Examples**

```
# Load and process data set
data(bmiData)

# define the negative 12 month change in BMI from baseline
y12 <- -100*(bmiData[,6L] - bmiData[,4L])/bmiData[,4L]

# define the negative 4 month change in BMI from baseline
y4 <- -100*(bmiData[,5L] - bmiData[,4L])/bmiData[,4L]

# reward for second stage
rewardSS <- y12 - y4

#### Second-stage regression

# Constant propensity model
moPropen <- buildModelObj(model = ~1,
                          solver.method = 'glm',
                          solver.args = list('family'='binomial'),
                          predict.method = 'predict.glm',
                          predict.args = list(type='response'))

fitSS <- bowl(moPropen = moPropen,
             data = bmiData, reward = rewardSS, txName = 'A2',
             regime = ~ parentBMI + month4BMI)

##Available methods

# Coefficients of the propensity score regression
coef(fitSS)

# Description of method used to obtain object
DTRstep(fitSS)
```

```
# Estimated value of the optimal treatment regime for training set
estimator(fitSS)

# Value object returned by propensity score regression method
fitObject(fitSS)

# Summary of optimization routine
optimObj(fitSS)

# Estimated optimal treatment for training data
optTx(fitSS)

# Estimated optimal treatment for new data
optTx(fitSS, bmiData)

# Plots if defined by propensity regression method
dev.new()
par(mfrow = c(2,4))

plot(fitSS)
plot(fitSS, suppress = TRUE)

# Value object returned by propensity score regression method
propen(fitSS)

# Parameter estimates for decision function
regimeCoef(fitSS)

# Show main results of method
show(fitSS)

# Show summary results of method
summary(fitSS)

#### First-stage regression

# Constant propensity model
fitFS <- bowl(moPropen = moPropen,
             data = bmiData, reward = y4, txName = 'A1',
             regime = ~ gender + parentBMI,
             BOWLobj = fitSS, lambdas = c(0.5, 1.0), cvFolds = 4L)

##Available methods for fitFS are as shown above for fitSS

# Results of the cross-validation
cvInfo(fitFS)
```

**Description**

Extends the `buildModelObj()` function of package **modelObj**. Here, the returned model object includes a specification of the decision point and subset of the data to which the model is to be applied.

**Usage**

```
buildModelObjSubset(
  ...,
  model,
  solver.method,
  solver.args = NULL,
  predict.method = NULL,
  predict.args = NULL,
  dp = 1L,
  subset = NA
)
```

**Arguments**

<code>...</code>	ignored. Included to require named input.
<code>model</code>	An object of class <code>formula</code> . The symbolic description of the model to be fitted. If the regression method specified in <code>solver.method</code> accepts as input a formula object, <code>model</code> is passed to the <code>solver.method</code> function. If the regression method instead accepts a matrix of covariates as the model to fit, <code>model</code> is used to obtain the model matrix that is passed to the <code>solver.method</code> function.
<code>solver.method</code>	An object of class <code>character</code> . The name of the R function to be used to obtain parameter estimates, e.g., <code>'lm'</code> , <code>'glm'</code> , or <code>'rpart'</code> . The specified function <b>MUST</b> have a corresponding <code>predict</code> method, which can be the generic <code>predict()</code> function.
<code>solver.args</code>	An object of class <code>list</code> . Additional arguments to be sent to the function specified in <code>solver.method</code> . This argument must be provided as a named list, where the name of each element matches a formal argument of the function specified in <code>solver.method</code> . For example, if a logistic regression using <code>'glm'</code> is desired, <pre>solver.method = "glm" solver.args = list("family"=binomial)</pre> See <code>Details</code> section for further information.
<code>predict.method</code>	An object of class <code>character</code> . The name of the R function to be used to obtain predictions, e.g., <code>'predict.lm'</code> , <code>'predict'</code> , or <code>'predict.glm'</code> . If no function is explicitly given, the generic <code>predict()</code> is assumed. For many regression methods, the generic <code>predict()</code> method is appropriate.
<code>predict.args</code>	An object of class <code>list</code> . Additional arguments to be sent to the function specified in <code>predict.method</code> . This argument must be provided as a named list, where the name of each element matches a formal argument of the function specified in <code>predict.method</code> . For example, if a logistic regression using <code>'glm'</code> was used to fit the model and predictions on the scale of the response are desired,

	<pre>predict.method = "predict.glm" predict.args = list("type"="response").</pre> <p>See Details section for further information.</p>
dp	An object of class integer. The decision point for which this model and subset are defined.
subset	An object of class character. A nickname for the subset for which model and methods are to be used. This argument will be used by the methods of <b>DynTxRegime</b> to "link" input arguments. In the event that a model is to be fit using more than 1 subset, collapse the subset names into a single character string separating each with a comma. For example, if the model is to be fit using patients in both subsets "a" and "b," the subset nickname should be "a,b" (no space).

### Details

In some settings, an analyst may want to use different models for unique subsets of the data. `buildModelObjSubset()` provides a mechanism for users to define models for such subset. Specifically, models are specified in connection with the decision point and subset to which they are to be applied.

See `?modelObj` for further details

### Value

An object of class `ModelObjSubset`, which contains a complete description of the conditions under which a model is to be used and the R methods to be used to obtain parameter estimates and predictions.

### Examples

```
# Consider a 2 decision point trial. At the 1st decision point, the subset of
# treatment options available to each patient is always set "set1."
# At the 2nd decision point, some patients are eligible to receive
# treatment from set "set2a" and others from set "set2b." The outcome
# for these subsets will be modeled as ~ x1 + x2 and ~ x2 + x3, respectively.
#
# All parameter estimates are to be obtained used lm and predictions obtained using predict.
#
# The following illustrates how to build these model objects.

model <- list()

model[[1]] <- buildModelObjSubset(dp = 1, subset = "set1",
                                model = ~ x1 + x2 + x3, solver.method = 'lm')

model[[2]] <- buildModelObjSubset(dp = 2, subset = "set2a",
                                model = ~ ~ x1 + x2, solver.method = 'lm')

model[[3]] <- buildModelObjSubset(dp = 2, subset = "set2b",
                                model = ~ x2 + x3, solver.method = 'lm')
```

---

Call	<i>Retrieve Unevaluated Original Call</i>
------	-------------------------------------------

---

**Description**

Returns the unevaluated original call to a DynTxRegime statistical method.

**Usage**

```
Call(name, ...)
```

**Arguments**

name	Object for which call is desired
...	Optional additional input required by R's base call().

**Details**

Methods are defined for all statistical methods implemented in DynTxRegime.

---

classif	<i>Retrieve Classification Regression Analysis</i>
---------	----------------------------------------------------

---

**Description**

Method retrieves the value object returned by the user specified classification regression modeling object(s). Exact structure of the returned object will vary.

**Usage**

```
classif(object, ...)

## S4 method for signature 'OptimalClass'
classif(object, ...)
```

**Arguments**

object	Value object returned from a method that uses classification regression
...	Ignored.

---

coef	<i>Extract Model Coefficients From Objects Returned by Modeling Functions</i>
------	-------------------------------------------------------------------------------

---

**Description**

A list is returned, one element for each regression step required by the statistical method.

**Usage**

```
coef(object, ...)
```

**Arguments**

object	Value object returned by any statistical method implemented in DynTxRegime.
...	Optional additional inputs defined by coefficient methods of selected regression functions.

**Details**

Methods are defined for all statistical methods implemented in DynTxRegime.

The exact structure of the returned list will vary depending on the statistical method. For methods that include a propensity regression, the returned list will include an element named 'propen'. For methods that include an outcome regression, the returned list will include an element named 'outcome'.

---

cvInfo	<i>Extract Cross-Validation Results</i>
--------	-----------------------------------------

---

**Description**

Extract cross-validation results from the value object returned by a weighted learning statistical method of DynTxRegime.

**Usage**

```
cvInfo(object, ...)
```

**Arguments**

object	A value object returned by a weighted learning statistical method of DynTxRegime
...	Ignored.

**Details**

Methods are developed for all weighted learning methods implemented in DynTxRegime. Specifically, OWL, RWL, BOWL, and EARL.

---

DTRstep

*Identify Statistical Method Used to Obtain Result*


---

**Description**

Prints and displays a brief description of the statistical method used to obtain the input object.

**Usage**

```
DTRstep(object)
```

**Arguments**

object            Value object returned by any statistical method of DynTxRegime

**Details**

Methods are defined for all statistical methods implemented in DynTxRegime.

---

earl

*Efficient Augmentation and Relaxation Learning*


---

**Description**

Efficient Augmentation and Relaxation Learning

**Usage**

```
earl(
  ...,
  moPropen,
  moMain,
  moCont,
  data,
  response,
  txName,
  regime,
  iter = 0L,
  fSet = NULL,
  lambdas = 0.5,
  cvFolds = 0L,
  surrogate = "hinge",
  kernel = "linear",
  kparam = NULL,
  verbose = 2L
)
```

**Arguments**

...	Used primarily to require named input. However, inputs for the optimization methods can be sent through the ellipsis. If surrogate is hinge, the optimization method is <code>dfoptim::hjk()</code> . For all other surrogates, <code>stats::optim()</code> is used.
moPropen	An object of class <code>modelObj</code> or <code>modelObjSubset</code> , which defines the model and R methods to be used to obtain parameter estimates and predictions for the propensity for treatment. See <code>?moPropen</code> for details.
moMain	An object of class <code>modelObj</code> or <code>modelObjSubset</code> , which defines the model and R methods to be used to obtain parameter estimates and predictions for the main effects of the outcome. See <code>?modelObj</code> for details.
moCont	An object of class <code>modelObj</code> or <code>modelObjSubset</code> , which defines the model and R methods to be used to obtain parameter estimates and predictions for the contrasts of the outcome. See <code>?modelObj</code> for details.
data	A data frame of the covariates and tx histories
response	The response variable.
txName	A character object. The column header of <code>data</code> that corresponds to the tx covariate
regime	A formula object or a list of formula objects. The covariates to be included in classification. If a list is provided, this specifies that there is an underlying subset structure – <code>fSet</code> must then be defined.
iter	Maximum number of iterations for outcome regression
fSet	A function or NULL defining subset structure
lambdas	A numeric object or a numeric vector object giving the penalty tuning parameter. If more than 1 is provided, the finite set of values to be considered in the cross-validation algorithm
cvFolds	If cross-validation is to be used to select the tuning parameters, the number of folds.
surrogate	The surrogate 0-1 loss function must be one of <code>logit</code> , <code>exp</code> , <code>hinge</code> , <code>sqhinge</code> , <code>huber</code>
kernel	A character object. must be one of <code>{"linear", "poly", "radial"}</code>
kparam	A numeric object of NULL. If <code>kernel = linear</code> , <code>kparam</code> is ignored. If <code>kernel = poly</code> , <code>kparam</code> is the degree of the polynomial. If <code>kernel = radial</code> , <code>kparam</code> is the inverse bandwidth of the kernel. If a vector of bandwidth parameters is given, cross-validation will be used to select the parameter
verbose	An integer or logical. If 0, no screen prints are generated. If 1, screen prints are generated with the exception of optimization results obtained in iterative algorithm. If 2, all screen prints are generated.

**Value**

an EARL object

**References**

Ying-Qi Zhao, Eric Laber, Sumona Saha and Bruce E. Sands (2016+) Efficient augmentation and relaxation learning for treatment regimes using observational data

**See Also**

Other statistical methods: `bowl()`, `iqLearn`, `optimalClass()`, `optimalSeq()`, `owl()`, `qLearn()`, `rwl()`

Other single decision point methods: `optimalClass()`, `optimalSeq()`, `owl()`, `qLearn()`, `rwl()`

Other weighted learning methods: `bowl()`, `owl()`, `rwl()`

**Examples**

```
# Load and process data set
data(bmiData)

# define the negative 12 month change in BMI from baseline
y12 <- -100*(bmiData[,6L] - bmiData[,4L])/bmiData[,4L]

# propensity model
moPropen <- buildModelObj(model = ~parentBMI+month4BMI,
                          solver.method = 'glm',
                          solver.args = list('family'='binomial'),
                          predict.method = 'predict.glm',
                          predict.args = list(type='response'))

# outcome model
moMain <- buildModelObj(model = ~parentBMI+month4BMI,
                        solver.method = 'lm')

moCont <- buildModelObj(model = ~parentBMI+month4BMI,
                        solver.method = 'lm')

fitEARL <- earl(moPropen = moPropen, moMain = moMain, moCont = moCont,
               data = bmiData, response = y12, txName = 'A2',
               regime = ~ parentBMI + month4BMI,
               surrogate = 'logit', kernel = 'poly', kparam = 2)

##Available methods

# Coefficients of the regression objects
coef(fitEARL)

# Description of method used to obtain object
DTRstep(fitEARL)

# Estimated value of the optimal treatment regime for training set
estimator(fitEARL)

# Value object returned by regression methods
fitObject(fitEARL)

# Summary of optimization routine
optimObj(fitEARL)

# Estimated optimal treatment for training data
```

```

optTx(fitEARL)

# Estimated optimal treatment for new data
optTx(fitEARL, bmiData)

# Value object returned by outcome regression method
outcome(fitEARL)

# Plots if defined by regression methods
dev.new()
par(mfrow = c(2,4))

plot(fitEARL)
plot(fitEARL, suppress = TRUE)

# Value object returned by propensity score regression method
propen(fitEARL)

# Parameter estimates for decision function
regimeCoef(fitEARL)

# Show main results of method
show(fitEARL)

# Show summary results of method
summary(fitEARL)

```

---

EARL-class

*Class* EARL

---

## Description

Class EARL contains results for an EARL analysis.

## Slots

analysis Contains a Learning or LearningMulti object.

analysis@txInfo Feasible tx information.

analysis@propen Propensity regression analysis.

analysis@outcome Outcome regression analysis.

analysis@cvInfo Cross-validation analysis if single regime.

analysis@optim Optimization analysis if single regime.

analysis@optimResult list of cross-validation and optimization results if multiple regimes. optimResult[[i]]@cvInfo and optimResult[[i]]@optim.

analysis@optimal Estimated optimal Tx and value.

analysis@call Unevaluated call to statistical method.

**Methods For Post-Processing of Regression Analysis**

**outcome** : Retrieve value object returned by outcome regression methods.

**propen** : Retrieve value object returned by propensity regression methods.

**coef** : Retrieve parameter estimates for all regression steps.

**fitObject** : Retrieve value object returned by regression methods.

**plot** : Generate plots for regression analyses.

**Methods For Post-Processing of Optimization Analysis**

**cvInfo** : Retrieve cross-validation results.

**optimObj** : Retrieve value object returned by optimization method(s).

**regimeCoef** : Retrieve estimated parameters for optimal tx regime.

**Methods For Accessing Main Results**

**DTRstep** : Retrieve description of method used to create object.

**estimator** : Retrieve the estimated value of the estimated optimal regime for the training data set.

**optTx** : Retrieve/predict the estimated decision functions and/or optimal tx.

**print** : Print main results of analysis.

**show** : Show main results of analysis.

**summary** : Retrieve summary information.

---

 estimator

---

*Retrieve the Estimated Value*


---

**Description**

Retrieve the value as estimated by the statistical method.

**Usage**

```
estimator(x, ...)
```

```
## S4 method for signature 'IQLearnFS'
estimator(x, w = NULL, y = NULL, z = NULL, dens = NULL)
```

```
## S4 method for signature 'IQLearnSS'
estimator(x, w = NULL, y = NULL, z = NULL, dens = NULL)
```

**Arguments**

x	a DynTxRegime Object.
...	Optional additional input. Ignored.
w	If IQ-Learning, object of class IQLearnSS, IQLearnFS_C, IQLearnFS_ME, or IQLearnFS_VHet
y	If IQ-Learning, object of class IQLearnSS, IQLearnFS_C, IQLearnFS_ME, or IQLearnFS_VHet
z	If IQ-Learning, object of class IQLearnSS, IQLearnFS_C, IQLearnFS_ME, or IQLearnFS_VHet
dens	If IQ-Learning, one of {"norm", "nonpar"}

---

fitObject

*Objects Returned by Modeling Functions*


---

**Description**

Returns a list of the objects returned by all modeling functions

**Usage**

```
fitObject(object, ...)
```

**Arguments**

object	Value object returned by a statistical method of DynTxRegime
...	Optional additional inputs

**Details**

Methods are defined for all statistical methods implemented in DynTxRegime.

The exact structure of the returned list will vary depending on the statistical method. For methods that include a propensity regression, the returned list will include an element named 'propen'. For methods that include an outcome regression, the returned list will include an element named 'outcome'.

---

fittedCont	<i>Retrieve the Fitted Contrast Component from Second Stage IQ-Learning</i>
------------	-----------------------------------------------------------------------------

---

**Description**

Extracts the contrasts component of the fitted outcome regression the second-stage analysis of the interactive Q-Learning algorithm.

**Usage**

```
fittedCont(object, ...)
```

```
## S4 method for signature 'IQLearnSS'
fittedCont(object, ...)
```

**Arguments**

object	An object of class IQLearnSS
...	Ignored.

---

fittedMain	<i>Retrieve the Fitted Main Effects Component from Second Stage IQ-Learning</i>
------------	---------------------------------------------------------------------------------

---

**Description**

Extracts the main effects component of the fitted outcome regression for the second-stage analysis of the interactive Q-Learning algorithm.

**Usage**

```
fittedMain(object, ...)
```

```
## S4 method for signature 'IQLearnSS'
fittedMain(object, ...)
```

**Arguments**

object	An object of class IQLearnSS
...	Ignored.

**Description**

Several of the statistical methods implemented in package **DynTxRegime** allow for subset modeling or limiting of feasible treatment options. This section details how this input is to be defined.

**Details**

In general, input `fSet` is used to define subsets of patients within an analysis. These subsets can be specified to (1) limit available treatments, (2) use different models for the propensity score and/or outcome regressions, and/or (3) use different decision function models for each subset of patients. The combination of inputs `moPropen`, `moMain`, `moCont`, `fSet`, and/or `regimes` determines which of these scenarios is being considered. We cover some common situations below.

Regardless of the purpose for specifying `fSet`, it must be a function that returns a list. There are two options for defining the function. Version 1 is that of the original **DynTxRegime** package. In this version, `fSet` defines the rules for determining the subset of treatment options for an INDIVIDUAL. The first element of the returned list is a character, which we term the subset 'nickname.' This nickname is for bookkeeping purposes and is used to link models to subsets. The second element of the returned list is a vector of available treatment options for the subset. The formal arguments of the function must include (i) 'data' or (ii) individual covariate names as given by the column headers of data. An example using the covariate name input form is

```
fSet <- function(a1) {
  if (a1 > 1) {
    subset <- list('subA',c(1,2))
  } else {
    subset <- list('subB',c(3,4) )
  }
  return(subset)
}
```

This function indicates that if an individual has covariate  $a1 > 1$ , they are a member of subset 'subA' and their feasible treatment options are {1,2}. If  $a1 \leq 1$ , they are a member of subset 'subB' and their feasible treatment options are {3,4}.

A more efficient implementation for `fSet` is now accepted. In the second form, `fSet` defines the subset of treatment options for the full DATASET. It is again a function with formal arguments (i) 'data' or (ii) individual covariate names as given by the column headers of data. The function returns a list containing two elements: 'subsets' and 'txOpts.' Element 'subsets' is a list comprising all treatment subsets; each element of the list contains the nickname and treatment options for a single subset. Element 'txOpts' is a character vector indicating the subset of which each individual is a member. In this new format, the equivalent definition of `fSet` as that given above is:

```
fSet <- function(a1) {
  subsets <- list(list('subA', c(1,2)),
```

```

        list('subB', c(3,4)))
txOpts <- rep('subB', length(x = a1))
txOpts[a1 > 1] <- 'subA'

return(list("subsets" = subsets,
           "txOpts" = txOpts))
}

```

Though a bit more complicated, this version is much more efficient as it processes the entire dataset at once rather than each individual separately.

The simplest scenario involving fSet is to define feasible treatment options and the rules that dictate how those treatment options are determined. For example, responder/non-responder scenarios are often encountered in multiple-decision-point settings. An example of this scenario is: patients that respond to the first stage treatment remain on the original treatment; those that do not respond to the first stage treatment have all treatment options available to them at the second stage. In this case, the propensity score models for the second stage are fit using only 'non-responders' for whom more than 1 treatment option is available.

An example of an appropriate fSet function for the second-stage is

```

fSet <- function(data) {
  if (data$responder == 0L) {
    subset <- list('subA',c(1L,2L))
  } else if (data$tx1 == 1L) {
    subset <- list('subB',c(1L) )
  } else if (data$tx1 == 2L) {
    subset <- list('subC',c(2L) )
  }
  return(subset)
}

```

for version 1 or for version 2

```

fSet <- function(data) {
  subsets <- list(list('subA', c(1L,2L)),
                 list('subB', c(1L)),
                 list('subC', c(2L)))
  txOpts <- character(nrow(x = data))
  txOpts[data$tx1 == 1L] <- 'subB'
  txOpts[data$tx1 == 2L] <- 'subC'
  txOpts[data$responder == 0L] <- 'subA'

  return(list("subsets" = subsets,
             "txOpts" = txOpts))
}

```

The functions above specify that patients with covariate responder = 0 receive treatments from subset 'subA,' which comprises treatments A = (1,2). Patients with covariate responder = 1 receive treatment from subset 'subB' or 'subC' depending on the first stage treatment received. If fSet is

specified in this way, the form of the model object depends on the training data. Specifically, if the training data obeys the feasible treatment rule (here, all individuals with responder = 1 received tx in accordance with fSet), moPropen would be a "modelObj"; the propensity model will be fit using only those patients with responder = 0; those with responder = 1 always receive the appropriate second stage treatment with probability 1.0. However, if the data are from an observation study and the training data do not obey the feasible treatment rules (here, some individuals with responder = 1 received tx = 0; others tx = 1), the responder = 1 data must be modeled and moPropen must be provided as one or more ModelObjSubset() objects.

If outcome regression is used by the method, moMain and moCont can be either objects of class "modelObj" if only responder = 0 patients are to be used to obtain parameter estimates or as lists of objects of class "ModelObjSubset" if subsets are to be analyzed individually or combined for a single fit of all data.

For a scenario where all patients have the same set of treatment options available, but subsets of patients are to be analyzed using different models. We can define fSet as

```
fSet <- function(data) {
  if (data$a1 == 1) {
    subset <- list('subA',c(1L,2L))
  } else {
    subset <- list('subB',c(1L,2L) )
  }
  return(subset)
}
```

for version 1 or in the format of version 2

```
fSet <- function(data)
{
  subsets <- list(list('subA', c(1L,2L)),
                 list('subB', c(1L,2L)))
  txOpts <- rep('subB', nrow(x = data))
  txOpts[data$a1 == 1L] <- 'subA'

  return(list("subsets" = subsets,
            "txOpts" = txOpts))
}
```

where all patients have the same treatment options available, A = (1,2), but different regression models will be fit for each subset (case 2 above) and/or different decision function models (case 3 above) for each subset. If different propensity score models are used, moPropen must be a list of objects of class "modelObjSubset." Perhaps,

```
propenA <- buildModelObjSubset(model = ~1,
                              solver.method = 'glm',
                              solver.args = list('family'='binomial'),
                              predict.method = 'predict.glm',
                              predict.args = list(type='response'),
                              subset = 'subA')
```

```
propenB <- buildModelObjSubset(model = ~1,
                              solver.method = 'glm',
                              solver.args = list('family'='binomial'),
                              predict.method = 'predict.glm',
                              predict.args = list(type='response'),
                              subset = 'subB')

moPropen <- list(propenA, propenB)
```

If different decision function models are to be fit, regimes would take a form similar to

```
regimes <- list( 'subA' = ~x1 + x2,
                 'subB' = ~x2 )
```

Notice that the names of the elements of `regimes` and the subsets passed to `buildModelObjSubset()` correspond to the names defined by `fSet`, i.e., 'subA' or 'subB.' These nicknames are used for bookkeeping and link subsets to the appropriate models.

For a single-decision-point analysis, `fSet` is a single function. For multiple-decision-point analyses, `fSet` is a list of functions where each element of the list corresponds to the decision point (1st element <- 1st decision point, etc.)

---

genetic

*Retrieve the Genetic Algorithm Results*

---

### Description

Retrieve the value object returned by `rgenoud()` in `optimalSeq()`.

### Usage

```
genetic(object, ...)

## S4 method for signature 'OptimalSeq'
genetic(object, ...)
```

### Arguments

<code>object</code>	Value object returned by <code>optimalSeq()</code>
<code>...</code>	Optional inputs. Ignored.

**Description**

The complete interactive Q-Learning algorithm.

**Usage**

```
## Second-Stage Analysis
iqLearnSS(..., moMain, moCont, data, response, txName, iter = 0L,
          verbose = TRUE)

## First-Stage Analysis for Fitted Main Effects
iqLearnFSM(..., moMain, moCont, data, response, txName, iter = 0L,
           verbose = TRUE)

## First-Stage Analysis for Fitted Contrasts
iqLearnFSC(..., moMain, moCont, data, response, txName, iter = 0L,
           verbose = TRUE)

## First-Stage Analysis of Contrast Variance Log-Linear Model
iqLearnFSV(..., object, moMain, moCont, data, iter = 0L, verbose = TRUE)
```

**Arguments**

...	ignored. Provided to require named inputs.
moMain	An object of class <code>modelObj</code> or a list of objects of class <code>modelObjSubset</code> , which define the models and R methods to be used to obtain parameter estimates and predictions for the main effects component of the outcome regression. See <code>?modelObj</code> and/or <code>?modelObjSubset</code> for details. <code>NULL</code> is an acceptable value if <code>moCont</code> is defined.
moCont	An object of class <code>modelObj</code> or a list of objects of class <code>modelObjSubset</code> , which define the models and R methods to be used to obtain parameter estimates and predictions for the contrasts component of the outcome regression. See <code>?modelObj</code> and/or <code>?modelObjSubset</code> for details. <code>NULL</code> is an acceptable value if <code>moMain</code> is defined.
data	A data frame of covariates and treatment history.
response	For the second stage analysis, the response vector. For first stage analyses, the value <code>object</code> returned by <code>iqLearnSS()</code> .
object	The value <code>object</code> returned by <code>iqLearnFSC()</code>
txName	A character string giving column header of treatment variable in <code>data</code>
iter	An integer. See <code>?iter</code> for details
verbose	A logical. If <code>TRUE</code> , screen prints are generated.

## References

Laber, EB, Linn, KA, and Stefanski, LA (2014). Interactive model building for Q-Learning. *Biometrika*, 101, 831–847. PMID: PMC4274394.

## See Also

Other statistical methods: [bowl\(\)](#), [earl\(\)](#), [optimalClass\(\)](#), [optimalSeq\(\)](#), [owl\(\)](#), [qLearn\(\)](#), [rwl\(\)](#)

Other multiple decision point methods: [bowl\(\)](#), [optimalClass\(\)](#), [optimalSeq\(\)](#), [qLearn\(\)](#)

## Examples

```
# Load and process data set
data(bmiData)

# define the negative 12 month change in BMI from baseline
y12 <- -100*(bmiData[,6L] - bmiData[,4L])/bmiData[,4L]

#### Full Interactive Q-Learning Algorithm

### Second-Stage Analysis

# outcome model
moMain <- buildModelObj(model = ~parentBMI+month4BMI,
                        solver.method = 'lm')

moCont <- buildModelObj(model = ~race + parentBMI+month4BMI,
                        solver.method = 'lm')

fitSS <- iqLearnSS(moMain = moMain, moCont = moCont,
                  data = bmiData, response = y12, txName = 'A2')

### First-Stage Analysis Main Effects Term

# main effects model
moMain <- buildModelObj(model = ~parentBMI+baselineBMI,
                        solver.method = 'lm')

moCont <- buildModelObj(model = ~race + parentBMI+baselineBMI,
                        solver.method = 'lm')

fitFSM <- iqLearnFSM(moMain = moMain, moCont = moCont,
                    data = bmiData, response = fitSS, txName = 'A1')

### First-Stage Analysis Contrasts Term

# contrasts model
moMain <- buildModelObj(model = ~parentBMI+baselineBMI,
                        solver.method = 'lm')

moCont <- buildModelObj(model = ~race + parentBMI+baselineBMI,
```

```

        solver.method = 'lm')

fitFSC <- iqLearnFSC(moMain = moMain, moCont = moCont,
                   data = bmiData, response = fitSS, txName = 'A1')

### First-Stage Analysis Contrasts Variance - Log-linear

# contrasts variance model
moMain <- buildModelObj(model = ~baselineBMI,
                       solver.method = 'lm')

moCont <- buildModelObj(model = ~baselineBMI,
                       solver.method = 'lm')

fitFSV <- iqLearnFSV(object = fitFSC, moMain = moMain, moCont = moCont,
                   data = bmiData)

#### Available methods

### Estimated value
estimator(x = fitFSC, y = fitFSM, z = fitFSV, w = fitSS, dens = 'nonpar')

## Estimated optimal treatment and decision functions for training data
## Second stage optimal treatments
optTx(x = fitSS)

## First stage optimal treatments when contrast variance is modeled.
optTx(x = fitFSM, y = fitFSC, z = fitFSV, dens = 'nonpar')

## First stage optimal treatments when contrast variance is constant.
optTx(x = fitFSM, y = fitFSC, dens = 'nonpar')

## Estimated optimal treatment and decision functions for new data
## Second stage optimal treatments
optTx(x = fitSS, bmiData)

## First stage optimal treatments when contrast variance is modeled.
optTx(x = fitFSM, y = fitFSC, z = fitFSV, dens = 'nonpar', bmiData)

## First stage optimal treatments when contrast variance is constant.
optTx(x = fitFSM, y = fitFSC, dens = 'nonpar', bmiData)

### The following methods are available for all objects: fitSS, fitFSM,
### fitFSC and fitFSV. We include only one here for illustration.

# Coefficients of the outcome regression objects
coef(object = fitSS)

# Description of method used to obtain object
DTRstep(object = fitFSM)

# Value object returned by outcome regression method
fitObject(object = fitFSC)

```

```

# Value object returned by outcome regression method
outcome(object = fitFSV)

# Plots if defined by outcome regression method
dev.new()
par(mfrow = c(2,4))

plot(x = fitSS)
plot(x = fitSS, suppress = TRUE)

# Show main results of method
show(object = fitFSM)

# Show summary results of method
summary(object = fitFSV)

```

---

IQLearnFS_C-class	<i>Class</i> IQLearnFS_C
-------------------	--------------------------

---

### Description

Class IQLearnFS\_C contains the results for the first stage contrasts component of the interactive Q-Learning algorithm. Objects of this class are returned by iqLearnFSC().

### Slots

**txVec** : A numeric. treatment vector from training data  
**residuals** : A numeric. residuals of the fit  
**step** : Not used in this context.  
**outcome** : The outcome regression analysis  
**txInfo** : The feasible tx information  
**optimal** : The estimated optimal tx, decision function, and value

### Methods For Post-Processing of Regression Analysis

**outcome** : Retrieve value object returned by outcome regression methods.  
**coef** : Retrieve parameter estimates for all regression steps.  
**fitObject** : Retrieve value object returned by regression methods.  
**plot** : Generate plots for regression analyses.

**Methods For Accessing Main Results**

- DTRstep** : Retrieve description of method used to create object.
- estimator** : Retrieve the estimated value of the estimated optimal regime for the training data set.
- optTx** : Retrieve/predict the estimated decision functions and/or optimal tx.
- print** : Print main results of analysis.
- show** : Show main results of analysis.
- summary** : Retrieve summary information.
- residuals** :Retrieve the residuals of the regression.
- sd** :Retrieve the standard deviation of the residuals.

---

IQLearnFS_ME-class	<i>Class</i> IQLearnFS_ME
--------------------	---------------------------

---

**Description**

Class IQLearnFS\_ME contains the results for the first stage main effects component of the interactive Q-Learning algorithm. Objects of this class are returned by iqLearnFSM().

**Slots**

- step** : Not used in this context.
- outcome** : The outcome regression analysis
- txInfo** : The feasible tx information
- optimal** : The estimated optimal tx, decision function, and value

**Methods For Post-Processing of Regression Analysis**

- outcome** : Retrieve value object returned by outcome regression methods.
- coef** : Retrieve parameter estimates for all regression steps.
- fitObject** : Retrieve value object returned by regression methods.
- plot** : Generate plots for regression analyses.

**Methods For Accessing Main Results**

- DTRstep** : Retrieve description of method used to create object.
- estimator** : Retrieve the estimated value of the estimated optimal regime for the training data set.
- optTx** : Retrieve/predict the estimated decision functions and/or optimal tx.
- print** : Print main results of analysis.
- show** : Show main results of analysis.
- summary** : Retrieve summary information.

---

IQLearnFS\_VHet-class    *Class* IQLearnFS\_VHet

---

### Description

Class IQLearnFS\_VHet contains the results for the first stage residuals component of the interactive Q-Learning algorithm. Objects of this class are returned by iqLearnFSV().

### Slots

**residuals** : Standardized residuals of contrast after modeling  
**scale** : Scaling factor for stdization  
**step** : Not used in this context.  
**outcome** : The outcome regression analysis  
**txInfo** : The feasible tx information  
**optimal** : The estimated optimal tx, decision function, and value

### Methods For Post-Processing of Regression Analysis

**outcome** : Retrieve value object returned by outcome regression methods.  
**coef** : Retrieve parameter estimates for all regression steps.  
**fitObject** : Retrieve value object returned by regression methods.  
**plot** : Generate plots for regression analyses.

### Methods For Accessing Main Results

**DTRstep** : Retrieve description of method used to create object.  
**estimator** : Retrieve the estimated value of the estimated optimal regime for the training data set.  
**optTx** : Retrieve/predict the estimated decision functions and/or optimal tx.  
**print** : Print main results of analysis.  
**show** : Show main results of analysis.  
**summary** : Retrieve summary information.  
**residuals** : Retrieve the residuals of the regression.  
**qqplot** : QQ plot of the residuals for the interactive Q-Learning algorithm.

---

IQLearnSS-class	Class IQLearnSS
-----------------	-----------------

---

### Description

Class IQLearnSS contains the results for the second stage of the interactive Q-Learning algorithm. Objects of this class are returned by iqLearnSS().

### Slots

**yContHat** : A numeric. Estimated contrast component  
**yMainHat** : A numeric. Estimated main effects component  
**delta** : A numeric. Indicator of compliance \* response used for value calc  
**step** : Not used in this context.  
**outcome** : The outcome regression analysis  
**txInfo** : The feasible tx information  
**optimal** : The estimated optimal tx, decision function, and value

### Methods For Post-Processing of Regression Analysis

**outcome** : Retrieve value object returned by outcome regression methods.  
**coef** : Retrieve parameter estimates for all regression steps.  
**fitObject** : Retrieve value object returned by regression methods.  
**plot** : Generate plots for regression analyses.  
**fittCont** :Retrieve the contrasts component of the regression.  
**fittMain** :Retrieve the main effects component of the regression.

### Methods For Accessing Main Results

**DTRstep** : Retrieve description of method used to create object.  
**estimator** : Retrieve the estimated value of the estimated optimal regime for the training data set.  
**optTx** : Retrieve/predict the estimated decision functions and/or optimal tx.  
**print** : Print main results of analysis.  
**show** : Show main results of analysis.  
**summary** : Retrieve summary information.

---

 iter

*Defining the iter Input Variable*


---

### Description

Several of the statistical methods implemented in package **DynTxRegime** allow for an iterative algorithm when completing an outcome regression. This section details how this input is to be defined.

### Details

Outcome regression models are specified by the main effects components (moMain) and the contrasts component (moCont). Assuming that the treatment is denoted as binary A, the full regression model is: moMain + A\*moCont. There are two ways to fit this model: (i) in the full model formulation (moMain + A\*moCont) or (ii) each component, moMain and moCont, is fit separately. iter specifies if (i) or (ii) should be used.

iter >= 1 indicates that moMain and moCont are to be fit separately using an iterative algorithm. iter is the maximum number of iterations. Assume  $Y = Y_{\text{main}} + Y_{\text{cont}}$ ; the iterative algorithm is as follows:

- (1)  $\hat{Y}_{\text{cont}} = 0$ ;
- (2)  $Y_{\text{main}} = Y - \hat{Y}_{\text{cont}}$ ;
- (3) fit  $Y_{\text{main}} \sim \text{moMain}$ ;
- (4) set  $Y_{\text{cont}} = Y - \hat{Y}_{\text{main}}$
- (5) fit  $Y_{\text{cont}} \sim A * \text{moCont}$ ;
- (6) Repeat steps (2) - (5) until convergence or a maximum of iter iterations.

This choice allows the user to specify, for example, a linear main effects component and a non-linear contrasts component.

iter <= 0 indicates that the full model formulation is to be used. The components moMain and moCont will be combined in the package and fit as a single object. Note that if iter <= 0, all non-model components of moMain and moCont must be identical. Specifically, the regression method and any non-default arguments should be identical. By default, the specifications in moMain are used.

---

 moPropen

*Defining the moPropen Input Variable*


---

### Description

Several of the statistical methods implemented in package **DynTxRegime** use propensity score modeling. This section details how this input is to be defined.

## Details

For input `moPropen`, the method specified to obtain predictions **MUST** return the prediction on the scale of the probability, i.e., predictions must be in the range (0,1). In addition, `moPropen` differs from standard "modelObj" objects in that an additional element may be required in `predict.args`. Recall, `predict.args` is the list of control parameters passed to the prediction method. An additional control parameter, `propen.missing` can be included. `propen.missing` takes value "smallest" or "largest". It will be required if the prediction method returns predictions for only a subset of the treatment data; e.g., `predict.glm()`. `propen.missing` indicates if it is the smallest or the largest treatment value that is missing from the returned predictions.

For example, fitting a binary treatment (A in {0,1}) using

```
moPropen <- buildModelObj(model = ~1,
                          solver.method = 'glm',
                          solver.args = list('family'='binomial'),
                          predict.method = 'predict.glm',
                          predict.args = list(type='response'))
```

returns only P(A=1). P(A=0) is "missing," and thus

```
moPropen <- buildModelObj(model = ~1,
                          solver.method = 'glm',
                          solver.args = list('family'='binomial'),
                          predict.method = 'predict.glm',
                          predict.args = list(type='response',
                                              propen.missing = 'smallest'))
```

If the dimension of the value returned by the prediction method is less than the number of treatment options and no value is provided in `propen.missing`, it is assumed that the smallest valued treatment option is missing. Here, 'smallest' indicates the lowest value integer if treatment is an integer, or the 'base' level if treatment is a factor.

---

optimalClass

*Classification Perspective*

---

## Description

Classification Perspective

## Usage

```
optimalClass(
  ...,
  moPropen,
  moMain,
  moCont,
  moClass,
```

```

    data,
    response,
    txName,
    iter = 0L,
    fSet = NULL,
    verbose = TRUE
  )

```

### Arguments

...	Included to require named inputs
moPropen	An object of class <code>modelObj</code> , which defines the models and R methods to be used to obtain parameter estimates and predictions for the propensity for treatment. See <code>?moPropen</code> for details.
moMain	An object of class <code>modelObj</code> , which defines the models and R methods to be used to obtain parameter estimates and predictions for for the main effects component of the outcome regression. See <code>?modelObj</code> for details. <code>NULL</code> is an appropriate value.
moCont	An object of class <code>modelObj</code> , which defines the models and R methods to be used to obtain parameter estimates and predictions for for the contrasts component of the outcome regression. See <code>?modelObj</code> for details. <code>NULL</code> is an appropriate value.
moClass	An object of class <code>modelObj</code> , which defines the models and R methods to be used to obtain parameter estimates and predictions for the classification. See <code>?modelObj</code> for details.
data	A data frame of the covariates and tx histories
response	The response vector
txName	An character giving the column header of the column in data that contains the tx covariate.
iter	An integer See <code>?iter</code> for details
fSet	A function or <code>NULL</code> . This argument allows the user to specify the subset of tx options available to a patient. See <code>?fSet</code> for details of allowed structure
verbose	A logical If <code>FALSE</code> , screen prints are suppressed.

### Value

an object of class `OptimalClass`

### References

Baqun Zhang, Anastasios A. Tsiatis, Marie Davidian, Min Zhang and Eric B. Laber. "Estimating optimal tx regimes from a classification perspective." *Stat* 2012; 1: 103-114.

Note that this method is a single decision point, binary treatment method. For multiple decision points, can be called repeatedly.

**See Also**

Other statistical methods: `bowl()`, `earl()`, `iqLearn`, `optimalSeq()`, `owl()`, `qLearn()`, `rwl()`

Other single decision point methods: `earl()`, `optimalSeq()`, `owl()`, `qLearn()`, `rwl()`

Other multiple decision point methods: `bowl()`, `iqLearn`, `optimalSeq()`, `qLearn()`

**Examples**

```
# Load and process data set
data(bmiData)

# define the negative 12 month change in BMI from baseline
y12 <- -100*(bmiData[,6L] - bmiData[,4L])/bmiData[,4L]

# Define the propensity for treatment model and methods.
moPropen <- buildModelObj(model = ~ 1,
                          solver.method = 'glm',
                          solver.args = list('family'='binomial'),
                          predict.method = 'predict.glm',
                          predict.args = list(type='response'))

# classification model
library(rpart)
moClass <- buildModelObj(model = ~parentBMI+month4BMI+race+gender,
                          solver.method = 'rpart',
                          solver.args = list(method="class"),
                          predict.args = list(type='class'))

#### Second-Stage Analysis using IPW
fitSS_IPW <- optimalClass(moPropen = moPropen,
                          moClass = moClass,
                          data = bmiData, response = y12, txName = 'A2')

# outcome model
moMain <- buildModelObj(model = ~parentBMI+month4BMI,
                          solver.method = 'lm')

moCont <- buildModelObj(model = ~race + parentBMI+month4BMI,
                          solver.method = 'lm')

#### Second-Stage Analysis using AIPW
fitSS_AIPW <- optimalClass(moPropen = moPropen,
                          moMain = moMain, moCont = moCont,
                          moClass = moClass,
                          data = bmiData, response = y12, txName = 'A2')

##Available methods

# Retrieve the classification regression object
classif(object = fitSS_AIPW)

# Coefficients of the outcome regression objects
```

```

coef(object = fitSS_AIPW)

# Description of method used to obtain object
DTRstep(object = fitSS_AIPW)

# Estimated value of the optimal treatment regime for training set
estimator(x = fitSS_AIPW)

# Value object returned by outcome regression method
fitObject(object = fitSS_AIPW)

# Estimated optimal treatment and decision functions for training data
optTx(x = fitSS_AIPW)

# Estimated optimal treatment and decision functions for new data
optTx(x = fitSS_AIPW, newdata = bmiData)

# Value object returned by outcome regression method
outcome(object = fitSS_AIPW)
outcome(object = fitSS_IPW)

# Plots if defined by outcome regression method
dev.new()
par(mfrow = c(2,4))

plot(x = fitSS_AIPW)
plot(x = fitSS_AIPW, suppress = TRUE)

# Retrieve the value object returned by propensity regression method
propen(object = fitSS_AIPW)

# Show main results of method
show(object = fitSS_AIPW)

# Show summary results of method
summary(object = fitSS_AIPW)

#### First-stage Analysis using AIPW

# Define the propensity for treatment model and methods.
moPropen <- buildModelObj(model = ~ 1,
                          solver.method = 'glm',
                          solver.args = list('family'='binomial'),
                          predict.method = 'predict.glm',
                          predict.args = list(type='response'))

# classification model
moClass <- buildModelObj(model = ~parentBMI+baselineBMI+race+gender,
                         solver.method = 'rpart',
                         solver.args = list(method="class"),
                         predict.args = list(type='class'))

# outcome model

```

```

moMain <- buildModelObj(model = ~parentBMI+baselineBMI,
                        solver.method = 'lm')

moCont <- buildModelObj(model = ~race + parentBMI+baselineBMI,
                        solver.method = 'lm')

fitFS_AIPW <- optimalClass(moPropen = moPropen,
                          moMain = moMain, moCont = moCont,
                          moClass = moClass,
                          data = bmiData, response = fitSS_AIPW,
                          txName = 'A1')

##Available methods for fitFS_AIPW are as shown above for fitSS_AIPW

```

---

OptimalClass-class      *Class* OptimalClass

---

### Description

Class *OptimalClass* contains results for a single decision point when estimates are obtained from the classification perspective. Objects of this class are returned by `optimalClass()`.

### Slots

`step` Step in the algorithm.  
`analysis` Analysis results.

### Methods For Post-Processing of Regression Analysis

**outcome** : Retrieve value object returned by outcome regression methods.  
**propen** : Retrieve value object returned by propensity regression methods.  
**classif** : Retrieve value object returned by classification regression methods.  
**coef** : Retrieve parameter estimates for all regression steps.  
**fitObject** : Retrieve value object returned by regression methods.  
**plot** : Generate plots for regression analyses.

### Methods For Accessing Main Results

**DTRstep** : Retrieve description of method used to create object.  
**estimator** : Retrieve the estimated value of the estimated optimal regime for the training data set.  
**optTx** : Retrieve/predict the estimated decision functions and/or optimal tx.  
**print** : Print main results of analysis.  
**show** : Show main results of analysis.  
**summary** : Retrieve summary information.

---

OptimalClassObj-class *Class* OptimalClassObj

---

### Description

Class OptimalClassObj contains results for a single decision point when estimates are obtained from the classification perspective. Objects of this class are returned by optimalClass().

### Slots

class Results of the classification step.  
 outcome Results of the outcome regression step.  
 propen Results of the propensity step.  
 optimal Estimated optimal tx and value  
 Call Unevaluated call.

### Methods For Post-Processing of Regression Analysis

**outcome** : Retrieve value object returned by outcome regression methods.  
**propen** : Retrieve value object returned by propensity regression methods.  
**classif** : Retrieve value object returned by classification regression methods.  
**coef** : Retrieve parameter estimates for all regression steps.  
**fitObject** : Retrieve value object returned by regression methods.  
**plot** : Generate plots for regression analyses.

### Methods For Accessing Main Results

**DTRstep** : Retrieve description of method used to create object.  
**estimator** : Retrieve the estimated value of the estimated optimal regime for the training data set.  
**optTx** : Retrieve/predict the estimated decision functions and/or optimal tx.  
**print** : Print main results of analysis.  
**show** : Show main results of analysis.  
**summary** : Retrieve summary information.

---

OptimalInfo-class	<i>Class</i> OptimalInfo
-------------------	--------------------------

---

**Description**

Class OptimalInfo stores the estimated optimal tx, decision functions, and estimated value.

**Slots**

optimalTx a vector of the estimated optimal tx

estimatedValue a vector of the estimated value

decisionFunc a vector or matrix containing the values used to determine @optimalTx (if applicable)

---

optimalSeq	<i>Missing or Coarsened Data Perspective - Genetic Algorithm</i>
------------	------------------------------------------------------------------

---

**Description**

Missing or Coarsened Data Perspective - Genetic Algorithm

**Usage**

```
optimalSeq(
  ...,
  moPropen,
  moMain,
  moCont,
  data,
  response,
  txName,
  regimes,
  fSet = NULL,
  refit = FALSE,
  iter = 0L,
  verbose = TRUE
)
```

**Arguments**

... Additional arguments required by rgenoud. At a minimum this should include Domains, pop.size and starting.values. See ?rgenoud for more information.

moPropen	An object of class modelObj, a list of objects of class modelObj, or a list of object of class modelObjSubset, which define the models and R methods to be used to obtain parameter estimates and predictions for the propensity for treatment. See ?moPropen for details.
moMain	An object of class modelObj, a list of objects of class modelObj, or a list of object of class modelObjSubset, which define the models and R methods to be used to obtain parameter estimates and predictions for the main effects component of the outcome regression. See ?modelObj and/or ?modelObjSubset for details. NULL is an acceptable input if IPWE is desired or there is no main effects component of the outcome regression model.
moCont	An object of class modelObj, a list of objects of class modelObj, or a list of object of class modelObjSubset, which define the models and R methods to be used to obtain parameter estimates and predictions for the contrasts component of the outcome regression. See ?modelObj and/or ?modelObjSubset for details. NULL is an acceptable input if IPWE is desired or there is no contrast component of the outcome regression model.
data	A data frame of the covariates and tx history
response	The response vector
txName	A vector of characters. The column headers of <i>data</i> that correspond to the tx covariate for each decision point. The ordering should be sequential, i.e., the 1st element gives column name for the 1st decision point tx, the 2nd gives column name for the 2nd decision point tx, etc.
regimes	A function or a list of functions. For each decision point, a function defining the tx rule. For example, if the tx rule is : $I(\eta_1 < x_1)$ , regimes is defined as <code>regimes &lt;- function(a,data) {as.numeric(a &lt; data\$x1)}</code> THE LAST ARGUMENT IS ALWAYS TAKEN TO BE THE DATA.FRAME
fSet	A function or a list of functions. This argument allows the user to specify the subset of tx options available to a patient or the subset of patients that will be modeled uniquely. see ?fSet for details
refit	No longer used
iter	An integer. See ?iter for details
verbose	A logical. If FALSE, screen prints are suppressed.

### Value

An object inheriting from class OptimalSeq

### References

Baqun Zhang, Anastasios A. Tsiatis, Eric B. Laber & Marie Davidian, "A Robust Method for Estimating Optimal Treatment Regimes", *Biometrics*, 68, 1010-1018.

Baqun Zhang, Anastasios A. Tsiatis, Eric B. Laber & Marie Davidian, "Robust estimation of optimal treatment regimes for sequential treatment decisions", *Biometrika* (2013) pp.1-14.

**See Also**

Other statistical methods: `bowl()`, `earl()`, `iqLearn`, `optimalClass()`, `owl()`, `qLearn()`, `rwl()`

Other single decision point methods: `earl()`, `optimalClass()`, `owl()`, `qLearn()`, `rwl()`

Other multiple decision point methods: `bowl()`, `iqLearn`, `optimalClass()`, `qLearn()`

**Examples**

```
# Load and process data set
data(bmiData)

# define the negative 12 month change in BMI from baseline
y12 <- -100*(bmiData[,6L] - bmiData[,4L])/bmiData[,4L]

# Define the propensity for treatment model and methods.
# Will use constant model for both decision points
moPropen <- buildModelObj(model = ~ 1,
                          solver.method = 'glm',
                          solver.args = list('family'='binomial'),
                          predict.method = 'predict.glm',
                          predict.args = list(type='response'))
moPropen <- list(moPropen, moPropen)

# outcome model second stage
moMain2 <- buildModelObj(model = ~parentBMI+month4BMI,
                        solver.method = 'lm')

moCont2 <- buildModelObj(model = ~race + parentBMI+month4BMI,
                        solver.method = 'lm')

# outcome model first stage
moMain1 <- buildModelObj(model = ~parentBMI+baselineBMI,
                        solver.method = 'lm')

moCont1 <- buildModelObj(model = ~race + parentBMI+baselineBMI,
                        solver.method = 'lm')

moMain <- list(moMain1, moMain2)
moCont <- list(moCont1, moCont2)

# regime function second stage
regime2 <- function(eta1, eta2, data) {
  tst <- {data$parentBMI > eta1} & {data$month4BMI > eta2}
  rec <- rep('MR', nrow(x = data))
  rec[!tst] <- 'CD'
  return( rec )
}

# regime function first stage
regime1 <- function(eta1, eta2, data) {
  tst <- {data$parentBMI > eta1} & {data$baselineBMI > eta2}
  rec <- rep('MR', nrow(x = data))
}
```

```

        rec[!tst] <- 'CD'
        return( rec )
    }

regimes <- list(regime1, regime2)

#### Analysis using AIPW
## Not run:
fit_AIPW <- optimalSeq(moPropen = moPropen,
                      moMain = moMain, moCont = moCont,
                      regimes = regimes,
                      data = bmiData, response = y12, txName = c('A1','A2'),
                      Domains = cbind(rep(0,4),rep(100,4)),
                      pop.size = 100, starting.values = rep(25,4))

##Available methods

# Coefficients of the regression objects
coef(object = fit_AIPW)

# Description of method used to obtain object
DTRstep(object = fit_AIPW)

# Estimated value of the optimal treatment regime for training set
estimator(x = fit_AIPW)

# Value object returned by regression methods
fitObject(object = fit_AIPW)

# Retrieve the results of genetic algorithm
genetic(object = fit_AIPW)

# Estimated optimal treatment and decision functions for training data
optTx(x = fit_AIPW)

# Estimated optimal treatment and decision functions for new data
optTx(x = fit_AIPW, newdata = bmiData)

# Value object returned by outcome regression method
outcome(object = fit_AIPW)

# Plots if defined by regression methods
dev.new()
par(mfrow = c(2,4))

plot(x = fit_AIPW)
plot(x = fit_AIPW, suppress = TRUE)

# Retrieve the value object returned by propensity regression method
propen(object = fit_AIPW)

# Show main results of method
show(object = fit_AIPW)

```

```

# Show summary results of method
summary(object = fit_AIPW)

## End(Not run)
#### Single Decision Point Analysis using IPW

# Define the propensity for treatment model and methods.
moPropen <- buildModelObj(model = ~ 1,
                          solver.method = 'glm',
                          solver.args = list('family'='binomial'),
                          predict.method = 'predict.glm',
                          predict.args = list(type='response'))

# regime function second stage
regime <- function(eta1, eta2, data) {
  tst <- {data$parentBMI > eta1} & {data$month4BMI > eta2}
  rec <- rep('MR', nrow(x = data))
  rec[!tst] <- 'CD'
  return( rec )
}

## Not run:
fit_IPW <- optimalSeq(moPropen = moPropen,
                     regimes = regime,
                     data = bmiData, response = y12, txName = 'A2',
                     Domains = cbind(rep(0,2),rep(100,2)),
                     pop.size = 100, starting.values = rep(25,2))

##Available methods

# Coefficients of the regression objects
coef(object = fit_IPW)

# Description of method used to obtain object
DTRstep(object = fit_IPW)

# Estimated value of the optimal treatment regime for training set
estimator(x = fit_IPW)

# Value object returned by regression method
fitObject(object = fit_IPW)

# Retrieve the results of genetic algorithm
genetic(object = fit_IPW)

# Estimated optimal treatment and decision functions for training data
optTx(x = fit_IPW)

# Estimated optimal treatment and decision functions for new data
optTx(x = fit_IPW, newdata = bmiData)

# Value object returned by outcome regression method
outcome(object = fit_IPW)

```

```

# Plots if defined by outcome regression method
dev.new()
par(mfrow = c(2,4))

plot(x = fit_IPW)
plot(x = fit_IPW, suppress = TRUE)

# Retrieve the value object returned by propensity regression method
propen(object = fit_IPW)

# Show main results of method
show(object = fit_IPW)

# Show summary results of method
summary(object = fit_IPW)

## End(Not run)

```

---

OptimalSeq-class	Class OptimalSeq
------------------	------------------

---

## Description

Class `OptimalSeq` contains the results for the estimated optimal tx and value when estimated from a coarsened or missing data perspective.

## Slots

`genetic` A list containing the results from the genetic algorithm

`propen` Results of the propensity regression step

`outcome` Results of the outcome regression step

`regime` Results for the regime.

`optimal` Results for the estimated optimal tx and value

`Call` The unevaluated call.

## Methods For Post-Processing of Regression Analysis

**outcome** : Retrieve value object returned by outcome regression methods.

**propen** : Retrieve value object returned by propensity regression methods.

**coef** : Retrieve parameter estimates for all regression steps.

**fitObject** : Retrieve value object returned by regression methods.

**plot** : Generate plots for regression analyses.

**Methods For Accessing Main Results**

**regimeCoef** : Retrieve the estimated regime parameters.

**DTRstep** : Retrieve description of method used to create object.

**estimator** : Retrieve the estimated value of the estimated optimal regime for the training data set.

**optTx** : Retrieve/predict the estimated decision functions and/or optimal tx.

**print** : Print main results of analysis.

**show** : Show main results of analysis.

**summary** : Retrieve summary information.

---

OptimalSeqCoarsened-class

*Class Contains Results for the Coarsened Data IPW/AIPW Method*

---

**Description**

Methods for multiple decision point analyses. Class inherits directly from OptimalSeq and all methods defined for objects of class OptimaSeq are defined for this class.

---

OptimalSeqMissing-class

*Class Contains Results for the Missing Data IPW/AIPW Method*

---

**Description**

Methods for single decision point analyses. Class inherits directly from OptimalSeq and all methods defined for objects of class OptimaSeq are defined for this class.

---

optimObj

*Extract Optimization Results*

---

**Description**

Retrieves the value object returned by the optimization method for weighted learning methods.

**Usage**

```

optimObj(object, ...)

## S4 method for signature 'OWL'
optimObj(object, ...)

## S4 method for signature 'RWL'
optimObj(object, ...)

## S4 method for signature 'BOWL'
optimObj(object, ...)

## S4 method for signature 'EARL'
optimObj(object, ...)

```

**Arguments**

object	A value object returned by a statistical method of DynTxRegime that uses optimization to estimate regime parameters.
...	Ignored.

---

 optTx

---

*Extract or Estimate the Optimal Tx and Decision Functions*


---

**Description**

If newdata is provided, the results of the statistical method are used to estimate the decision functions and/or optimal tx. If newdata is missing, the estimated decision functions and/or optimal tx obtained for the original training data are returned.

**Usage**

```

optTx(x, newdata, ...)

## S4 method for signature 'IQLearnFS,data.frame'
optTx(x, newdata, ..., y = NULL, z = NULL, dens = NULL)

## S4 method for signature 'IQLearnFS,missing'
optTx(x, newdata, ..., y = NULL, z = NULL, dens = NULL)

```

**Arguments**

x	a DynTxRegime Object.
newdata	Optional data.frame if estimates for new patients are desired.
...	Optional additional input.
y	Object of class IQLearnFS

z	Object of class IQLearnFS
dens	one of {norm, nonpar}

**Details**

Methods are defined for all statistical methods implemented in DynTxRegime.

---

outcome	<i>Retrieve Outcome Regression Analysis</i>
---------	---------------------------------------------

---

**Description**

For statistical methods that require an outcome regression analysis, the value object returned by the modeling function(s) is retrieved.

**Usage**

```
outcome(object, ...)
```

**Arguments**

object	A value object returned by a statistical method of DynTxRegime.
...	Ignored.

**Details**

Methods are defined for all statistical methods implemented in DynTxRegime that use outcome regression.

---

owl	<i>Outcome Weighted Learning</i>
-----	----------------------------------

---

**Description**

Outcome Weighted Learning

**Usage**

```
owl(
  ...,
  moPropen,
  data,
  reward,
  txName,
  regime,
  response,
  lambdas = 2,
  cvFolds = 0L,
  kernel = "linear",
  kparam = NULL,
  surrogate = "hinge",
  verbose = 2L
)
```

**Arguments**

...	Used primarily to require named input. However, inputs for the optimization methods can be sent through the ellipsis. If surrogate is hinge, the optimization method is kernlab::ipop(). For all other surrogates, stats::optim() is used.
moPropen	An object of class modelObj, which defines the model and R methods to be used to obtain parameter estimates and predictions for the propensity for treatment. See ?moPropen for details.
data	A data frame of the covariates and tx histories
reward	The response vector
txName	A character object. The column header of <i>data</i> that corresponds to the tx covariate
regime	A formula object or a character vector. The covariates to be included in classification
response	A numeric vector. The reward. Allows for naming convention followed in most DynTxRegime methods.
lambdas	A numeric object or a numeric vector object giving the penalty tuning parameter. If more than 1 is provided, the finite set of values to be considered in the cross-validation algorithm
cvFolds	If cross-validation is to be used to select the tuning parameters, the number of folds.
kernel	A character object. must be one of {"linear", "poly", "radial"}
kparam	A numeric object of NULL. If kernel = linear, kparam is ignored. If kernel = poly, kparam is the degree of the polynomial. If kernel = radial, kparam is the inverse bandwidth of the kernel. If a vector of bandwidth parameters is given, cross-validation will be used to select the parameter
surrogate	The surrogate 0-1 loss function must be one of logit, exp, hinge, sqhinge, huber

`verbose` An integer or logical. If 0, no screen prints are generated. If 1, screen prints are generated with the exception of optimization results obtained in iterative algorithm. If 2, all screen prints are generated.

### Value

an OWL object

### References

Yingqi Zhao, Donglin Zeng, A. John Rush, Michael R. Kosorok (2012) Estimated individualized treatment rules using outcome weighted learning. *Journal of the American Statistical Association*, 107(409): 1106-1118. PMID: 3636816

### See Also

Other statistical methods: [bowl\(\)](#), [earl\(\)](#), [iqLearn](#), [optimalClass\(\)](#), [optimalSeq\(\)](#), [qLearn\(\)](#), [rwl\(\)](#)

Other weighted learning methods: [bowl\(\)](#), [earl\(\)](#), [rwl\(\)](#)

Other single decision point methods: [earl\(\)](#), [optimalClass\(\)](#), [optimalSeq\(\)](#), [qLearn\(\)](#), [rwl\(\)](#)

### Examples

```
# Load and process data set
data(bmiData)

# define the negative 12 month change in BMI from baseline
y12 <- -100*(bmiData[,6L] - bmiData[,4L])/bmiData[,4L]

# propensity model
moPropen <- buildModelObj(model = ~parentBMI+month4BMI,
                          solver.method = 'glm',
                          solver.args = list('family'='binomial'),
                          predict.method = 'predict.glm',
                          predict.args = list(type='response'))

fitOWL <- owl(moPropen = moPropen,
               data = bmiData, reward = y12, txName = 'A2',
               regime = ~ parentBMI + month4BMI,
               surrogate = 'hinge', kernel = 'linear', kparam = NULL)

##Available methods

# Coefficients of the propensity score regression
coef(fitOWL)

# Description of method used to obtain object
DTRstep(fitOWL)

# Estimated value of the optimal treatment regime for training set
estimator(fitOWL)
```

```

# Value object returned by propensity score regression method
fitObject(fitOWL)

# Summary of optimization routine
optimObj(fitOWL)

# Estimated optimal treatment for training data
optTx(fitOWL)

# Estimated optimal treatment for new data
optTx(fitOWL, bmiData)

# Plots if defined by propensity regression method
dev.new()
par(mfrow = c(2,4))

plot(fitOWL)
plot(fitOWL, suppress = TRUE)

# Value object returned by propensity score regression method
propen(fitOWL)

# Parameter estimates for decision function
regimeCoef(fitOWL)

# Show main results of method
show(fitOWL)

# Show summary results of method
summary(fitOWL)

```

---

OWL-class

*Class OWL*


---

## Description

Class OWL contains results for an OWL analysis.

## Slots

analysis Contains a Learning or LearningMulti object.

analysis@txInfo Feasible tx information.

analysis@propen Propensity regression analysis.

analysis@outcome Outcome regression analysis.

analysis@cvInfo Cross-validation analysis if single regime.

analysis@optim Optimization analysis if single regime.

`analysis@optimResult` list of cross-validation and optimization results if multiple regimes. `optimResult[[i]]@cvInfo` and `optimResult[[i]]@optim`.  
`analysis@optimal` Estimated optimal Tx and value.  
`analysis@call` Unevaluated call to statistical method.

### Methods For Post-Processing of Regression Analysis

**propen** : Retrieve value object returned by propensity regression methods.  
**coef** : Retrieve parameter estimates for all regression steps.  
**fitObject** : Retrieve value object returned by regression methods.  
**plot** : Generate plots for regression analyses.

### Methods For Post-Processing of Optimization Analysis

**cvInfo** : Retrieve cross-validation results.  
**optimObj** : Retrieve value object returned by optimization method(s).  
**regimeCoef** : Retrieve estimated parameters for optimal tx regime.

### Methods For Accessing Main Results

**DTRstep** : Retrieve description of method used to create object.  
**estimator** : Retrieve the estimated value of the estimated optimal regime for the training data set.  
**optTx** : Retrieve/predict the estimated decision functions and/or optimal tx.  
**print** : Print main results of analysis.  
**show** : Show main results of analysis.  
**summary** : Retrieve summary information.

---

plot

*Generates Plots as Defined by Modeling Functions*

---

### Description

Calls `plot()` method for all regression steps of a statistical method

### Arguments

<code>x</code>	Value object returned by a statistical method
<code>y</code>	Ignored
<code>suppress</code>	T/F indicating if titles should be concatenated with information indicating the specific regression step
<code>...</code>	Optional additional inputs

### Details

Methods are defined for all statistical methods implemented in `DynTxRegime`.

---

propen	<i>Retrieve Propensity Regression Analysis</i>
--------	------------------------------------------------

---

**Description**

For statistical methods that require a propensity regression analysis, the value object returned by the modeling function(s) is retrieved.

**Usage**

```
propen(object, ...)
```

**Arguments**

object	A value object returned by a statistical method of DynTxRegime.
...	Ignored.

**Details**

Methods are defined for all statistical methods implemented in DynTxRegime that use propensity regression.

---

qLearn	<i>A Step of the Q-Learning Algorithm</i>
--------	-------------------------------------------

---

**Description**

Performs a single step of the Q-Learning algorithm. If an object of class QLearn is passed through input response, it is assumed that the QLearn object is the value object returned from the preceding step of the Q-Learning algorithm, and the value fit by the regression is taken from the QLearn object. If a vector is passed through input response, it is assumed that the call is for the first step in the Q-Learning algorithm, and models are fit using the provided response.

**Usage**

```
qLearn(
  ...,
  moMain,
  moCont,
  data,
  response,
  txName,
  fSet = NULL,
  iter = 0L,
  verbose = TRUE
)
```

**Arguments**

...	ignored. Provided to require named inputs.
moMain	An object of class <code>modelObj</code> or a list of objects of class <code>modelObjSubset</code> , which define the models and R methods to be used to obtain parameter estimates and predictions for the main effects component of the outcome regression. See <code>?modelObj</code> and/or <code>?modelObjSubset</code> for details. NULL is an acceptable value if <code>moCont</code> is defined.
moCont	An object of class <code>modelObj</code> or a list of objects of class <code>modelObjSubset</code> , which define the models and R methods to be used to obtain parameter estimates and predictions for the contrasts component of the outcome regression. See <code>?modelObj</code> and/or <code>?modelObjSubset</code> for details. NULL is an acceptable value if <code>moMain</code> is defined.
data	A data frame of covariates and treatment history.
response	A response vector or object of class <code>QLearn</code> from a previous Q-Learning step.
txName	A character string giving column header of treatment variable in data
fSet	NULL or a function. This argument allows the user to specify the subset of treatment options available to a patient. See <code>?fSet</code> for details of allowed structure
iter	An integer. See <code>?iter</code> for details
verbose	A logical. If TRUE, screen prints are generated.

**Value**

An object of class [QLearn-class](#)

**See Also**

Other statistical methods: [bowl\(\)](#), [earl\(\)](#), [iqLearn](#), [optimalClass\(\)](#), [optimalSeq\(\)](#), [owl\(\)](#), [rwl\(\)](#)

Other multiple decision point methods: [bowl\(\)](#), [iqLearn](#), [optimalClass\(\)](#), [optimalSeq\(\)](#)

Other single decision point methods: [earl\(\)](#), [optimalClass\(\)](#), [optimalSeq\(\)](#), [owl\(\)](#), [rwl\(\)](#)

**Examples**

```
# Load and process data set
data(bmiData)

# define the negative 12 month change in BMI from baseline
y12 <- -100*(bmiData[,6L] - bmiData[,4L])/bmiData[,4L]

# outcome model
moMain <- buildModelObj(model = ~parentBMI+month4BMI,
                        solver.method = 'lm')

moCont <- buildModelObj(model = ~race + parentBMI+month4BMI,
                        solver.method = 'lm')

#### Second-Stage Analysis
```

```

fitSS <- qLearn(moMain = moMain, moCont = moCont,
               data = bmiData, response = y12, txName = 'A2')

##Available methods

# Coefficients of the outcome regression objects
coef(fitSS)

# Description of method used to obtain object
DTRstep(fitSS)

# Estimated value of the optimal treatment regime for training set
estimator(fitSS)

# Value object returned by outcome regression method
fitObject(fitSS)

# Estimated optimal treatment and decision functions for training data
optTx(fitSS)

# Estimated optimal treatment and decision functions for new data
optTx(fitSS, bmiData)

# Value object returned by outcome regression method
outcome(fitSS)

# Plots if defined by outcome regression method
dev.new()
par(mfrow = c(2,4))

plot(fitSS)
plot(fitSS, suppress = TRUE)

# Show main results of method
show(fitSS)

# Show summary results of method
summary(fitSS)

#### First-stage Analysis

# outcome model
moMain <- buildModelObj(model = ~parentBMI+baselineBMI,
                       solver.method = 'lm')

moCont <- buildModelObj(model = ~race + parentBMI+baselineBMI,
                       solver.method = 'lm')

fitFS <- qLearn(moMain = moMain, moCont = moCont,
               data = bmiData, response = fitSS, txName = 'A1')

##Available methods for fitFS are as shown above for fitSS

```

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QLearn-class	Class QLearn
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**Description**

Class QLearn contains the results for a Q-Learning step

**Slots**

**step** An integer indicating the step of the Q-Learning algorithm.

**outcome** The outcome regression analysis

**txInfo** The feasible tx information

**optimal** The estimated optimal tx, decision function, and value

**Methods For Post-Processing of Regression Analysis**

**outcome** : Retrieve value object returned by outcome regression methods.

**coef** : Retrieve parameter estimates for all regression steps.

**fitObject** : Retrieve value object returned by regression methods.

**plot** : Generate plots for regression analyses.

**Methods For Accessing Main Results**

**DTRstep** : Retrieve description of method used to create object.

**estimator** : Retrieve the estimated value of the estimated optimal regime for the training data set.

**optTx** : Retrieve/predict the estimated decision functions and/or optimal tx.

**print** : Print main results of analysis.

**show** : Show main results of analysis.

**summary** : Retrieve summary information.

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QLearnObj-class	Class QLearnObj
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**Description**

Class QLearnObj contains the results for a Q-Learning step

**Slots**

**outcome** The outcome regression analysis

**txInfo** The feasible tx information

**optimal** The estimated optimal tx, decision function, and value

**Methods For Post-Processing of Regression Analysis**

**outcome** : Retrieve value object returned by outcome regression methods.

**coef** : Retrieve parameter estimates for all regression steps.

**fitObject** : Retrieve value object returned by regression methods.

**plot** : Generate plots for regression analyses.

**Methods For Accessing Main Results**

**DTRstep** : Retrieve description of method used to create object.

**estimator** : Retrieve the estimated value of the estimated optimal regime for the training data set.

**optTx** : Retrieve/predict the estimated decision functions and/or optimal tx.

**print** : Print main results of analysis.

**show** : Show main results of analysis.

**summary** : Retrieve summary information.

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 regimeCoef

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*Extract Regime Parameters*


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**Description**

Extract the estimated regime parameters.

**Usage**

```
regimeCoef(object, ...)
```

**Arguments**

object	A value object returned by a statistical method of DynTxRegime.
...	Ignored.

**Details**

Methods are defined for all statistical methods implemented in DynTxRegime that use a non-regression based regime. Specifically, OptimalSeq, OWL, BOWL, RWL, and EARL.

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residuals	<i>Extract Model Residuals</i>
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**Description**

Retrieve residuals from an interactive Q-Learning step.

**Usage**

```
residuals(object, ...)

## S4 method for signature 'IQLearnFS_C'
residuals(object, ...)

## S4 method for signature 'IQLearnFS_VHet'
residuals(object, ...)
```

**Arguments**

object	A value object returned by iqLearnC() or iqLearnVar()
...	Ignored.

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rwl	<i>Residual Weighted Learning</i>
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**Description**

Residual Weighted Learning

**Usage**

```
rwl(
  ...,
  moPropen,
  moMain,
  data,
  reward,
  txName,
  regime,
  response,
  fSet = NULL,
  lambdas = 2,
  cvFolds = 0L,
  kernel = "linear",
  kparam = NULL,
```

```

  responseType = "continuous",
  verbose = 2L
)

```

## Arguments

...	Used primarily to require named input. However, inputs for the optimization methods can be sent through the ellipsis. The optimization method is <code>stats::optim()</code> .
moPropen	An object of class <code>modelObj</code> or <code>modelObjSubset</code> , which defines the model and R methods to be used to obtain parameter estimates and predictions for the propensity for treatment. See <code>?moPropen</code> for details.
moMain	An object of class <code>modelObj</code> or <code>modelObjSubset</code> , which defines the model and R methods to be used to obtain parameter estimates and predictions for the main effects of the outcome. See <code>?modelObj</code> for details.
data	A data frame of the covariates and tx histories
reward	The response vector
txName	A character object. The column header of <code>data</code> that corresponds to the tx covariate
regime	A formula object or a list of formula objects. The covariates to be included in classification. If a list is provided, this specifies that there is an underlying subset structure – <code>fSet</code> must then be defined.
response	A numeric vector. The reward. Allows for naming convention followed in most <code>DynTxRegime</code> methods.
fSet	A function or NULL defining subset structure
lambdas	A numeric object or a numeric vector object giving the penalty tuning parameter. If more than 1 is provided, the finite set of values to be considered in the cross-validation algorithm
cvFolds	If cross-validation is to be used to select the tuning parameters, the number of folds.
kernel	A character object. must be one of {"linear", "poly", "radial"}
kparam	A numeric object of NULL. If <code>kernel = linear</code> , <code>kparam</code> is ignored. If <code>kernel = poly</code> , <code>kparam</code> is the degree of the polynomial. If <code>kernel = radial</code> , <code>kparam</code> is the inverse bandwidth of the kernel. If a vector of bandwidth parameters is given, cross-validation will be used to select the parameter
responseType	A character indicating if response is continuous, binary or count data.
verbose	An integer or logical. If 0, no screen prints are generated. If 1, screen prints are generated with the exception of optimization results obtained in iterative algorithm. If 2, all screen prints are generated.

## Value

an RWL object

## References

Xin Zhou, Nicole Mayer-Hamblett, Umer Khan, and Michael R Kosorok (2017) Residual weighted learning for estimating individualized treatment rules. *Journal of the American Statistical Association*, 112, 169–187.

## See Also

Other statistical methods: [bowl\(\)](#), [earl\(\)](#), [iqLearn](#), [optimalClass\(\)](#), [optimalSeq\(\)](#), [owl\(\)](#), [qLearn\(\)](#)

Other weighted learning methods: [bowl\(\)](#), [earl\(\)](#), [owl\(\)](#)

Other single decision point methods: [earl\(\)](#), [optimalClass\(\)](#), [optimalSeq\(\)](#), [owl\(\)](#), [qLearn\(\)](#)

## Examples

```
## Not run:
# Load and process data set
data(bmiData)

# define the negative 12 month change in BMI from baseline
y12 <- -100*(bmiData[,6L] - bmiData[,4L])/bmiData[,4L]

# propensity model
moPropen <- buildModelObj(model = ~parentBMI+month4BMI,
                          solver.method = 'glm',
                          solver.args = list('family'='binomial'),
                          predict.method = 'predict.glm',
                          predict.args = list(type='response'))

# outcome model
moMain <- buildModelObj(model = ~parentBMI+month4BMI,
                       solver.method = 'lm')

fitRWL <- rwl(moPropen = moPropen, moMain = moMain,
             data = bmiData, reward = y12, txName = 'A2',
             regime = ~ parentBMI + month4BMI,
             kernel = 'radial', kparam = 1.5)

##Available methods

# Coefficients of the regression objects
coef(fitRWL)

# Description of method used to obtain object
DTRstep(fitRWL)

# Estimated value of the optimal treatment regime for training set
estimator(fitRWL)

# Value object returned by regression methods
fitObject(fitRWL)
```

```

# Summary of optimization routine
optimObj(fitRWL)

# Estimated optimal treatment for training data
optTx(fitRWL)

# Estimated optimal treatment for new data
optTx(fitRWL, bmiData)

# Value object returned by outcome regression method
outcome(fitRWL)

# Plots if defined by regression methods
dev.new()
par(mfrow = c(2,4))

plot(fitRWL)
plot(fitRWL, suppress = TRUE)

# Value object returned by propensity score regression method
propen(fitRWL)

# Parameter estimates for decision function
regimeCoef(fitRWL)

# Show main results of method
show(fitRWL)

# Show summary results of method
summary(fitRWL)

## End(Not run)

```

---

RWL-class

*Class* RWL

---

## Description

Class RWL contains results for an RWL analysis.

## Slots

responseType character indicating type of response  
residuals vector of outcome residuals  
beta vector of regime parameters  
analysis Contains a Learning or LearningMulti object  
analysis@txInfo Feasible tx information  
analysis@propen Propensity regression analysis

**analysis@outcome** Outcome regression analysis  
**analysis@cvInfo** Cross-validation analysis if single regime  
**analysis@optim** Optimization analysis if single regime  
**analysis@optimResult** list of cross-validation and optimization results if multiple regimes. `optimResult[[i]]@cvInfo` and `optimResult[[i]]@optim`  
**analysis@optimal** Estimated optimal Tx and value  
**analysis@Call** Unevaluated Call

### Methods For Post-Processing of Regression Analysis

**outcome** : Retrieve value object returned by outcome regression methods.  
**propen** : Retrieve value object returned by propensity regression methods.  
**coef** : Retrieve parameter estimates for all regression steps.  
**fitObject** : Retrieve value object returned by regression methods.  
**plot** : Generate plots for regression analyses.

### Methods For Post-Processing of Optimization Analysis

**cvInfo** : Retrieve cross-validation results.  
**optimObj** : Retrieve value object returned by optimization method(s).  
**regimeCoef** : Retrieve estimated parameters for optimal tx regime.

### Methods For Accessing Main Results

**DTRstep** : Retrieve description of method used to create object.  
**estimator** : Retrieve the estimated value of the estimated optimal regime for the training data set.  
**optTx** : Retrieve/predict the estimated decision functions and/or optimal tx.  
**print** : Print main results of analysis.  
**show** : Show main results of analysis.  
**summary** : Retrieve summary information.

### Description

Retrieve the standard deviation of the residuals for the first-stage contrasts regression in the interactive Q-Learning algorithm.

**Usage**

```
sd(x, na.rm=FALSE)

## S4 method for IQLearnFS_C
sd(x, na.rm=FALSE)
```

**Arguments**

x	An object of class IQLearnFS_C
na.rm	logical. Should missing values be removed?

---

summary

*Result Summaries*


---

**Description**

Returns a list of the primary results, including regression results, optimization results, estimated tx and value, etc.

**Usage**

```
summary(object, ...)
```

**Arguments**

object	Value object returned by a statistical method
...	Optional additional inputs

**Details**

Methods are defined for all statistical methods implemented in DynTxRegime.

The exact structure of the returned list will vary depending on the statistical method.

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