

# Package ‘commandr’

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**Title** Command pattern in R

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**Depends** methods

**Imports** utils

**Description** An S4 representation of the Command design pattern. The Operation class is a simple implementation using closures and supports forward and reverse (undo) evaluation. The more complicated Protocol framework represents each type of command (or analytical protocol) by a formal S4 class. Commands may be grouped and consecutively executed using the Pipeline class. Example use cases include logging, do/undo, analysis pipelines, GUI actions, parallel processing, etc.

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Command-class

*Virtual Command Class*


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### Description

Command represents any generic operation and is often combined with other such objects in a sequence. This is the foundation for implementations of pipelines, logging, undo stacks, etc, according to the Command design pattern. Since Command is virtual, it cannot be constructed directly. Rather, one should construct an instance of a concrete derivative, like [Operation](#) or [Protocol](#).

### Details

Developers are encouraged to extend Command for new implementations of the Command design pattern.

There are a number of generics for which a Command derivative should provide methods:

`displayName(object)`: Gets the display name of the command, i.e., the name displayed in a user interface. The default implementation returns the class name. A Command may provide other visual attributes; the display name is considered fundamental for integration with user interfaces.

`widget(object, ...)`: Creates a widget for viewing and controlling this object. No default implementation.

`rev(object)`: Returns a Command that performs the opposite action, i.e., to undo an operation. This will not always be possible, so it is acceptable for a subclass to leave this unimplemented.

`active(object)`: Gets whether the command is considered active. This is meant for temporarily disabling or enabling a command without removing it completely from, e.g., a pipeline or GUI menu. No default implementation.

Of course, a Command implementation also needs a method that executes the command. The signature for such a function highly depends on the nature of the command, so the generic depends on the class.

### Author(s)

Michael Lawrence

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Operation-class

*Operation: A Simple Command Implementation*


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### Description

An Operation object implements a Command with an R closure. This may be useful as a base for customized Command derivatives. Otherwise, consider it a skeletal proof-of-concept.

**Constructors**

`Operation(do, undo = NULL)`: Constructs an `Operation` that invokes the closure `do`. If `undo` is specified, it is the closure invoked for the reverse operation.

`OperationQ(do, undo)`: Constructs an `Operation` that invokes a function with the body taken from the quoted argument `do`. The function is enclosed in the calling environment. If `undo` is specified, it is treated equivalently to `do`, except it should implement the reverse operation.

**Methods**

`eval(expr)`: Executes the operation by evaluating the closure.

`rev(x)`: Returns a new `Operation` that performs the reverse operation, as long as `undo` was provided.

**Author(s)**

Michael Lawrence

**Examples**

```
op <- OperationQ(message("hello world"))
eval(op)

x <- 2
op <- OperationQ(x^2, sqrt(x))
x <- eval(op)
rop <- rev(op)
identical(2, eval(rop))
```

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Pipeline-class

*Pipeline: A Sequence of Protocols*


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**Description**

A `Pipeline` represents a sequence of [Protocols](#). When executed, it executes each of the protocols in turn, where each protocol is passed the output of the previous protocol. `Pipeline` extends `list`, so, in general, it can be treated as one when it comes to subsetting, etc.

**Constructor**

`Pipeline(..., displayName = NULL)`: Constructs a `Pipeline` object with the protocols named in `...`. The arguments in `...` should be named and be either a `Protocol` object or a role name for which a default `Protocol` is constructed. Optionally, a user-readable display name can be specified as `displayName`.

## Execution

`perform(object, data, ...)`: Executes the protocols in order, with the output of each pipeline passed as input to the next. Takes data as input to the first protocol and returns the output of the last protocol.

## Accessors

`inType(object)`: Get the input type of the first protocol in the pipeline, or NULL if there are no protocols.

`outType(object)`: Get the output type of the first protocol in the pipeline, or NULL if there are no protocols.

`parameters(object)`: Obtains a list, each element of which is a list of the parameters for the corresponding protocol.

`protocol(object, role, method = character())`: Gets the first protocol with the matching role and method.

`protocol(object, role) <- value`: Replace the first protocol with the role given by role with value.

## Subsetting

`pipeline(object, intype = "ANY", outtype = "ANY")`: Gets the sub-pipeline that spans from the first protocol with the input type derived from intype and the last protocol with the output type derived from outtype.

`head(x, n = 6L, role, method = character(), outtype)`: Like ordinary `head`, takes a prefix of the pipeline. If outtype is provided, this returns the pipeline through the first protocol with outtype as its output type. Otherwise, if role is specified, the result is the pipeline through the first protocol performing that role. This can optionally be qualified by method. If neither role nor outtype are specified, the first n elements are returned, as usual.

`tail(x, n = 6L, role, method = character(), intype)`: Like ordinary `tail`, takes a suffix of the pipeline. If intype is provided, this returns the pipeline starting at the last protocol with intype as its input type. Otherwise, if role is specified, the result is the pipeline starting at the last protocol performing that role. This can optionally be qualified by method. If neither role nor outtype are specified, the last n elements are returned, as usual.

Pipeline extends list, so, in general, it can be treated as one when it comes to subsetting, etc. For example, `[` method works for subsetting of Pipeline object.

## Utilities

`findProtocols(object, role, method = character())`: Get the indices of the protocols in the pipeline with the specified role and method.

## Author(s)

Michael Lawrence

**Examples**

```

setStage("average", intype = "numeric")
setProtocol("mean", fun = mean, parent = "average")
setProtocol("quantile", representation = list(probs = "numeric"),
            fun = quantile, parent = "average")
setProtocol("range", representation = list(low = "numeric", high = "numeric"),
            fun = function(x, low = 0, high = Inf) x[x >= low & x <= high],
            parent = setStage("trim", intype = "numeric"))

d <- c(1, 2, 4)
p <- Pipeline("trim", "average")
perform(p, d)

p <- Pipeline(Protocol("trim", low = 2), "average")
perform(p, d)

p <- Pipeline(Protocol("trim", low = 2),
              Protocol("average", "quantile", probs = 0.75),
              displayName = "Filter and Average")
perform(p, d)

## accessor
inType(p)
outType(p)
parameters(p)
protocol(p, "average")
protocol(p, "average", "quantile")
displayName(p)

## utils
findProtocols(p, "average")

## subsetting
# make a new example
setStage("DemoCastN2C", intype = "numeric", outtype = "character")
setProtocol("cast", fun = function(x){
  message("Convert from numeric to character")
  as.character(x)
},
parent = "DemoCastN2C")

setStage("DemoCastC2F", intype = "character", outtype = "factor")
setProtocol("cast", fun = function(x){
  message("Convert from character to factor")
  as.factor(x)
},
parent = "DemoCastC2F")

setStage("DemoCastF2L", intype = "factor", outtype = "list")
setProtocol("cast", fun = function(x){
  message("Convert from factor to list")
  as.list(x)
})

```

```

    },
    parent = "DemoCastF2L")

d <- 1:3
p <- Pipeline(Protocol("DemoCastN2C"),
              Protocol("DemoCastC2F"),
              Protocol("DemoCastF2L"))

p
perform(p, d)
# subsetting
# convert to a factor
p12 <- p[1:2]
p12
perform(p12, d)

#
p23 <- pipeline(p, intype = "character")
p23
perform(p23, as.character(d))

#
p12 <- head(p, 2)
p12
#or
head(p, outtype = "factor")
head(p, role = "DemoCastC2F")

tail(p, 2)
tail(p, intype = "character")
tail(p, intype = "factor")
tail(p, role = "DemoCastC2F")

#combination
p1 <- Pipeline(Protocol("DemoCastN2C"))
p2 <- Pipeline(Protocol("DemoCastC2F"))
p3 <- Pipeline(Protocol("DemoCastF2L"))
c(p1 ,p2)
p[2] <- p2

setClass("ExChar", contains = "character")

setStage("DemoCastC2FV2", intype = "ExChar", outtype = "factor")
setProtocol("cast", fun = function(x){
  as.factor(x)
},
parent = "DemoCastC2FV2")

p4 <- Pipeline(Protocol("DemoCastC2FV2"))

## Not run:
## doesn't work, input 'charcter' is super class of output 'ExChar'.
p[2] <- p4

```

```
## End(Not run)
p

## as a subclass, works.
setStage("DemoCastN2CV2", intype = "numeric", outtype = "ExChar")
setProtocol("cast", fun = function(x){
  new("ExChar", as.character(x))
},
  parent = "DemoCastN2CV2")
p5 <- Pipeline(Protocol("DemoCastN2CV2"))
p[1] <- p5
p

## Not run:
## won't work, because the outtype doesn't match the intype.
c(p1, p3, p2)
p[c(1, 3)]
p[2] <- p3

## End(Not run)
```

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PipelineData-class	<i>PipelineData: Data with history</i>
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## Description

PipelineData is a virtual class representing a dataset with an attached pipeline that describes the series of steps that produced the object. The storage of the data is up to the implementation. The methods described here apply equally to PipelineData and any other object that has pipeline as a slot/attribute.

## Methods

`pipeline(object, ancestry = TRUE, local = TRUE)`: Gets the pipeline that produced the object. If ancestry is TRUE, the returned pipeline includes the protocols that produced predecessors of a different type. If local is TRUE, the pipeline includes protocols after the last protocol that output an object of a different type, i.e., all local protocols have this type as both their input and output.

`explore(object)`: Produces an interactive, exploratory visualization of this data, in the context of the last applied protocol.

## Author(s)

Michael Lawrence

## Examples

```
## A non-PipelineData data example
setStage("average", intype = "numeric")
setProtocol("mean", fun = mean, parent = "average")
setProtocol("quantile", representation = list(probs = "numeric"),
            fun = quantile, parent = "average")
setProtocol("range", representation = list(low = "numeric", high = "numeric"),
            fun = function(x, low = 0, high = Inf) x[x >= low & x <= high],
            parent = setStage("trim", intype = "numeric"))

d <- c(1, 2, 4)
p <- Pipeline("trim", "average")
d2 <- perform(p, d)
attr(d2, 'pipeline')
pipeline(d2)
## Not run:
## this will give an error, no slot called pipelinem, just numeric value.
d2@pipeline

## End(Not run)

setClass("ProcessNumeric", contains = c("numeric", "PipelineData"))
d <- new("ProcessNumeric", c(1, 2, 4))
d@pipeline
setStage("average", intype = "ProcessNumeric")
setProtocol("mean", fun = function(x) new("ProcessNumeric", mean(x)), parent = "average")
setProtocol("quantile", representation = list(probs = "numeric"),
            fun = function(x) new("ProcessNumeric", quantile(x)), parent = "average")
setProtocol("range", representation = list(low = "numeric", high = "numeric"),
            fun = function(x, low = 0, high = Inf) new("ProcessNumeric",
                                                    x[x >= low & x <= high]),
            parent = setStage("trim", intype = "ProcessNumeric"))

p <- Pipeline("trim", "average")
d2 <- perform(p, d)
attr(d2, 'pipeline')
pipeline(d2)
class(d2)
d2@pipeline
```

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Protocol-class

*Protocol: Concrete Step in a Pipeline*


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## Description

A Protocol object performs a [Stage](#) in a particular way, as part of a [Pipeline](#). Most users will simply construct a Protocol and add it to a pipeline. To define a new type of Protocol, see [setProtocol](#).



## Constructors

`Protocol(role, method = defaultMethod(role), ...)`: Creates a protocol of the stage identified by `role` and method given by `method`. The `role` argument may be either a `Stage` object or a string naming the role. Parameters in `...` are passed to the initializer, i.e., they specify parameters of the protocol by name.

## Accessors

`stage(object, where = topenv(parent.frame()))`: Return a [Stage](#) object that represents the role this protocol plays in a pipeline. Searches for the class definition of the stage in `where`.

`method(object, where = topenv(parent.frame()))`: Returns the method name of this protocol. This is derived from the class name of the protocol by removing the stage name. The environment `where` should contain the definition of the stage class.

`displayName(object)`: Gets the name for displaying this protocol in a user interface.

`inType(object)`: Gets the class of data that this protocol accepts as input.

`outType(object)`: Gets the class of data that this protocol yields as output.

`parameters(object)`: Gets the list of parameters, i.e., the slots of the object, that control the execution of the protocol.

`pipeline(object)`: Some protocols delegate to a secondary pipeline, i.e., they have a slot named "pipeline". This function retrieves that, or returns `NULL` if the protocol does not delegate to a pipeline.

## Author(s)

Michael Lawrence

## See Also

[setProtocol](#) for defining new types of protocols

## Examples

```
setStage("average", intype = "numeric")
setProtocol("mean", fun = mean, parent = "average")
setProtocol("quantile", representation = list(probs = "numeric"),
           fun = quantile, parent = "average")

proto_avg_mean <- Protocol("average")
proto_avg_mean <- Protocol("average", "mean")
proto_avg_quantile <- Protocol("average", "quantile")
proto_avg_quantile_075 <- Protocol("average", "quantile", probs = 0.75)

proto <- proto_avg_quantile_075
proto
stage(proto)
inType(proto)
parameters(proto)
```

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setProtocol	<i>Define a Protocol Type</i>
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---

**Description**

This function defines new derivatives of the Protocol class. It is a wrapper around [setClass](#) and thus has a very similar interface.

**Usage**

```
setProtocol(method, dispname = method, representation = list(), fun,
            parent, prototype = list(), validity = NULL,
            where = toenv(parent.frame()))
```

**Arguments**

method	The name of the method performed by protocols of this type
dispname	The display name for protocols of this type
representation	A list declaring the names and types of the parameters, implemented as slots in the S4 class
fun	The function implementing the protocol. If omitted, this protocol type will be virtual. This function will be passed the input data, any parameters named in its formals, and any arguments passed to perform. Default values for its arguments override values in prototype. Use <a href="#">callNextProtocol</a> to chain up to the implementation of a parent protocol.
parent	The single parent/super class for this protocol class. Usually, this is the role, i.e., the name of the <a href="#">Stage</a> for this protocol type. Also could be the name of a class inheriting from Protocol, or the concatenation of the role and method names.
prototype	As in <a href="#">setClass</a> , the list indicating initial values for the parameters/slots. Usually not necessary, because it is derived from the formals of fun.
validity	The function for checking the validity of an object, see <a href="#">setClass</a> .
where	The environment in which this protocol class is defined.

**Details**

Every type of protocol in a pipeline is implemented as an S4 class, ultimately derived from Protocol. The parameters controlling the execution of the protocol are represented by slots in that S4 class.

Through S4 inheritance, each protocol is associated with a Stage, which represents the role a protocol plays in the pipeline. For example, a protocol might have an “average” stage, with two protocols: “mean” and “median”. Here, “average” would be the role name and would have an associated Stage derivative. Meanwhile, “mean” and “median” are method names and would each have a corresponding Protocol derivative. Protocols that have the same stage all derive from a common, virtual Protocol derivative corresponding to that stage. In our example, we would have two protocol classes: ProtoAverageMean and ProtoAverageMedian. Both would inherit from ProtoAverage, which in turn inherits from Protocol.

Another side effect of this function is that a generic is defined, named of the form `role.Method`, that performs this protocol, given the data and additional arguments. There is a method for the `inType` of the stage. Thus, in our example, we would have generics `average.mean` and `average.median`.

### Value

The name of the class

### Author(s)

Michael Lawrence

### See Also

[Protocol](#) for constructing protocol objects, [setStage](#) for defining Stage classes.

### Examples

```
setStage("average")
setProtocol("mean", fun = mean, parent = "average")
setProtocol("median", fun = median, parent = "average")
d <- c(1, 2, 4)
average(d)
average(d, "median")
average.median(d)
```

---

setStage

*Define a Stage Class*

---

### Description

This function defines new derivatives of the Stage class. It is a wrapper around [setClass](#) and thus has a similar interface.

### Usage

```
setStage(name, dispname = name, intype = "ANY", outtype = intype,
         where = topenv(parent.frame()))
```

### Arguments

name	The name of the stage, i.e., the role string
dispname	The name for display in a user interface
intype	The class of the data that protocols of this stage accept as input
outtype	The class of the data that protocols of this stage accept as output
where	The environment in which to define the stage class

## Details

Calling `setStage` defines two classes:

- A derivative of `Stage` that represents this stage
- A derivative of `Protocol` from which all protocols that implement this stage derive

For example, if we had a stage named “average”, calling `setStage` would create the classes `StageAverage` and `ProtoAverage`.

The function also defines a generic, named by the name argument, that performs a protocol of this stage. There is a method that takes an object of type `intype` as first argument and a method name as its second. Additional arguments are passed to the `perform` method of the protocol. In our prior example, there would be a generic called `average` and method `average,numeric` if `intype` was given as “numeric”.

It also defines a generic of the form `nameProto` that serves as an accessor for protocols of this stage. A method is defined for `Pipeline` and `outtype`, so that one could retrieve our “average” protocol with `averageProto(pipeline)` or `averageProto(result)`. Similarly, a replacement generic and methods are defined.

## Value

The name of the role

## Author(s)

Michael Lawrence

## See Also

The `Stage` class; `setProtocol` for defining a new type of protocol

## Examples

```
## simplest definition
setStage("average")
## add a display name and specialize to numeric input
setStage("average", "Average Vector", intype = "numeric")
setProtocol("mean", fun = mean, parent = "average")
setProtocol("quantile", representation = list(probs = "numeric"),
            fun = quantile, parent = "average")
setProtocol("range", representation = list(low = "numeric", high = "numeric"),
            fun = function(x, low = 0, high = Inf) x[x >= low & x <= high],
            parent = setStage("trim", intype = "numeric"))

## Class Stage derivative
showClass("StageAverage")
## Class Protocol derivative
showClass("ProtoAverage")

## generic defined
showMethods("average")
```

```
# try this generic method
d <- c(1, 2, 4)
average(d, "mean")

## create a pipeline
p <- Pipeline("trim", "average")
res <- perform(p, d)
res
## generic *Proto
averageProto(p)
averageProto(res)
```

---

Stage-class

*Stage: Abstract Step in a Pipeline*


---

## Description

A Stage object represents a role to be played by protocols in a pipeline. In other words, a stage is an abstract step that transforms one data type into another. The transformation may be implemented in a number of ways, each corresponding to a protocol. Users normally do not have to interact with this object. Developers can define new types of stages with [setStage](#).

## Constructors

`Stage(role)`: Creates a stage object given the role name.

## Accessors

`role(object)`: Gets the name of the role represented by this stage.

`displayName(object)`: Gets the name for displaying this stage in a user interface.

`inType(object)`: Gets the class of data that protocols of this stage accept as input.

`outType(object)`: Gets the class of data that protocols of this stage yield as output.

`defaultMethod(object)`: Gets the name of the default method associated with the role of this stage. If not explicitly set, this becomes the first protocol registered for the stage.

`defaultMethod(object) <- value`: Sets the name of the default method associated with the role of this stage.

`methodNames(object, where = topenv(parent.frame()))`: Gets the names of the methods for this stage, looking in `where` for the protocol classes.

## Author(s)

Michael Lawrence

## See Also

[setStage](#) for defining new types of stages

**Examples**

```
setStage("average", "Average Numbers", intype = "numeric")
setProtocol("mean", fun = mean, parent = "average")
setProtocol("median", fun = median, parent = "average")

stage <- Stage("average")
stage

defaultMethod(stage)
defaultMethod(stage) <- "median"
defaultMethod(stage)
```

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