

Package ‘RadOnc’

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Description This package is designed for the import, analysis, and visualization of dosimetric and volumetric data in Radiation Oncology. The tools herein enable import of DVH information from Varian's Aria/Eclipse platform and 3D structural representations and dosimetric information from DICOM-RT files. These tools also enable subsequent visualization and statistical analysis of these data.

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RadOnc-package

*Analytical Tools for Radiation Oncology***Description**

This package is designed for the import, analysis, and visualization of dosimetric and volumetric data in Radiation Oncology. The tools herein enable import of DVH information from Varian's Aria/Eclipse platform and 3D structural representations from DICOM-RT files. These tools also enable subsequent visualization and statistical analysis of this data.

Details

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Author(s)

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See Also

[DVH](#), [DVH.list](#), [structure3D](#), [structure.list](#), [RTdata](#)

calculate.DVH	<i>Calculate DVH data for one or more structure(s) using a dose grid</i>
---------------	--

Description

Function to calculate DVH data for one or more structure(s) using a dose grid.

Usage

```
## S4 method for signature 'RTdata,missing'
calculate.DVH(x, dose, resolution.xyz=c(0.2,0.2,NA),
resolution.dose=0.01, method=NULL, dose.units=NULL)

## S4 method for signature 'RTdata,array'
calculate.DVH(x, dose, resolution.xyz=c(0.2,0.2,NA),
resolution.dose=0.01, method=NULL, dose.units=NULL)

## S4 method for signature 'structure3D,array'
calculate.DVH(x, dose, resolution.xyz=c(0.2,0.2,NA),
resolution.dose=0.01, method=NULL, dose.units=NULL)

## S4 method for signature 'structure.list,array'
calculate.DVH(x, dose, resolution.xyz=c(0.2,0.2,NA),
resolution.dose=0.01, method=NULL, dose.units=NULL)
```

Arguments

x	One of either a "structure3D" object, a "structure.list", or a "RTdata" object containing one or more structure(s).
dose	Object of class "array" containing dose grid data. This parameter is not required if x contains a "RTdata" object including dose grid information.
resolution.xyz	A numeric list containing three positive values representing x, y, and z resolution to be used for DVH calculation (specified in units of mm). The smaller each value, the longer the overall calculation time (default is c(0.2, 0.2, NA)). z resolution defaults to axial slice thickness when method="ATC".
resolution.dose	A positive numeric value specifying the dose calculation interval (bin width) for DVH calculation (values interpreted in Gy).
method	Character value specifying the DVH calculation algorithm to employ. Must be one of "ATC", "surface", or "axial". See below for further details about the dose calculation algorithms.
dose.units	Value specifying units of dose. Must be one of "cGy" (default) or "Gy".

Value

Returns a single calculated "DVH" object or a "DVH.list" object consisting of multiple DVHs where relevant, or otherwise a "zDVH" or "DVH.list" containing multiple zDVHs when method="axial".

Author(s)

Reid F. Thompson (<reid.thompson@gmail.com>)

References

Straube, W., Matthews, J., Bosch, W., and Purdy, J.A. (2005) DVH Analysis: Consequences for Quality Assurance of Multi-Institutional Clinical Trials. *Med Phys* **32**(6):2021.

See Also

[DVH](#), [DVH.list](#), [new](#)

Examples

```
data("Rad0nc")
# zDVHs <- calculate.DVH(janedoe.RTdata, method="axial")
```

compareStructures

Compare Axially-Defined Three-Dimensional Structures

Description

Three-dimensional structural comparison of a `structure.list` composed of two or more `structure3D` objects.

Usage

```
compareStructures(structures, method = NULL,
  hausdorff.method = NULL, verbose = TRUE, plot = TRUE, pixels = 100)
```

Arguments

structures	An object of class <code>structure.list</code> containing two or more <code>structure3D</code> objects.
method	One of "axial", "surface", "hausdorff", or "DSC" specifying the comparison between structures. For the "axial" method (default), the volumetric region of comparison is divided into discrete evenly-spaced voxels and the degree of overlap is measured across each voxel in axial cross-sections. For the "surface" method, overlap is calculated for each point on each structure's surface. For the "hausdorff" method, Hausdorff distances are calculated for each pairwise combination of structures as the distance between two point clouds.

hausdorff.method	One of "mean", "median", or "absolute", specifying the method to use for Hausdorff distance measurement when method = "hausdorff". The "absolute" Hausdorff distance yields the maximum distance required to connect any point from one point cloud to its closest neighbor in the other. This metric is highly subject to outliers, thus an aggregate metric is implemented by selecting the average ("mean") or median ("median") distance required to connect all points in one point cloud to their closest neighboring points in the other. Note that the Hausdorff distance between two completely superimposable point clouds is zero. This parameter is ignored for other values of method.
verbose	Logical value (default is TRUE) indicating whether or not to print status updates to the active command line interface or workspace.
plot	Logical value (default is TRUE) indicating whether or not to display graphical comparison of structures. This parameter is only relevant when method = "axial", as it is otherwise ignored.
pixels	Integer value (default is 100) specifying the number of pixels in the x- and y-directions used for comparative calculations when method = "axial".

Value

When method = "hausdorff", the function returns a $N \times N$ matrix of pairwise Hausdorff distances, where N is the number of structures in structures. When method = "axial" or method = "surface", the function returns a $M \times (N+3)$ dimensional matrix representing a list of M points in three-dimensional space and a table of values denoting whether each point is internal or external to each structure (note that the first three columns in the matrix represent the xyz coordinates for each point and values of 1 and 0 represent internal and external points, respectively).

Author(s)

Reid F. Thompson (<reid.thompson@gmail.com>)

See Also

[structure.list](#), [structure3D](#)

Examples

```
data("Rad0nc")
compareStructures(teeth, method="DSC")
# teeth.compare <- compareStructures(teeth, method="axial", plot=TRUE)
# compareStructures(teeth, method="hausdorff", hausdorff.method="mean")
```

 DVH-class

 Class "DVH"

Description

A data structure containing Dose-Volume Histogram (DVH) data and associated parameters for a single structure

Objects from the Class

Objects can be created by calls of the form `new("DVH", patient, structure.name, structure.volume, type, dose.max)`

Slots

`patient`: Name of the patient (e.g. "Jane Doe")

`ID`: Additional patient identifier or medical record number (e.g. "123456789")

`structure.name`: Name of the structure (e.g. "Stomach")

`structure.volume`: Volume of the structure (in cubic centimeters)

`type`: A character string specifying the DVH type (must be one of "cumulative" or "differential")

`dose.max`: Maximum (point) dose contained within the structure

`dose.min`: Minimum dose contained within the structure

`dose.mean`: Mean dose to the structure

`dose.median`: Median dose to the structure

`dose.mode`: Modal dose to the structure

`dose.STD`: Standard deviation of dose to the structure

`conf.index`: Conformality index

`equiv.sphere`: Equivalent sphere (diameter in centimeters)

`gradient`: Dose gradient (in centimeters)

`dose.rx`: Prescription dose (in units specified by `dose.units`)

`dose.fx`: Fractional dose (in units specified by `dose.units`)

`rx.isodose`: Isodose line (%) receiving prescription dose (default is 100%)

`doses`: List of doses corresponding to "volumes"

`dose.type`: A character string specifying the dose type (must be one of "relative" or "absolute")

`dose.units`: A character string specifying the dose units (must be one of "cGy" or "Gy")

`volumes`: List of volumes corresponding to "doses"

`volume.type`: A character string specifying the volume type (must be one of "relative" or "absolute")

Methods

[Extract dose or volume parameter(s) from DVH object. Only one parameter may be specified at a time. Parameter specification should be of the form ["<A><C>"]: <A> is equivalent to "V" or "D", representing a volume or dose, respectively; usually denotes a numerical value specifying the dose or volume; and <C> represents the dose or volume units ("cGy", "Gy", "%", or "cc"). An example would be ["V20Gy"] which represents the volume of the structure receiving at least 20Gy dose. Specialized dosimetric keywords may also be used: "Dmax" (maximum dose), "Dmin" (minimum dose), "Dmean" (mean dose), "Dintegral" (estimated integral dose), "DRx" (prescription dose), and "volume" (total structure volume). If an improper parameter is specified however, NA results will be returned. See package documentation (vignette) for more details.

\$ Extract a given parameter from a DVH object

\$<- Assign a value to a given parameter within a DVH object

c Combine multiple DVH objects into a single list

lines Plot DVH object (see [link{lines}](#))

max Extract maximum dose from DVH object

mean Extract mean dose from DVH object

min Extract minimum dose from DVH object

names Extract structure name from DVH object

names<- Assign structure name to DVH object

plot Plot DVH object

points Plot DVH object (see [link{points}](#))

print signature(x = "DVH"): Display summary of DVH object

range signature(x = "DVH"): Extract dose range from DVH object

show signature(x = "DVH"): Display summary of DVH object

sum signature(x = "DVH"): Compute the total (summed) DVH from two or more DVH objects. *Note that structures are assumed to be non-overlapping; any overlaps in structure volumes may generate inaccurate dose summation.*

Author(s)

Reid F. Thompson (<reid.thompson@gmail.com>)

See Also

[DVH.list](#), [read.DVH](#), [plot](#)

Examples

```
# Description of structure/slots in class
showClass("DVH")
```

DVH.list-class	Class "DVH.list"
----------------	------------------

Description

A data structure containing one or more Dose-Volume Histogram ([DVH](#)) objects

Objects from the Class

Objects can be created by calls of the form `new("DVH.list", structures, ...)`.

Slots

`structures`: List of DVH objects

Methods

[Extract subset of DVH list (regular expressions may be specified if desired, see [regex](#) for more details)

[[Extract single DVH object from DVH list

[[<- Replace single DVH object in DVH list

[<- Replace multiple elements of DVH list

\$ Extract dose or volume parameter(s) from DVH objects within DVH list. Note that multiple parameters may be specified by use of the comma (e.g. `"V20Gy, D5%"`). See [DVH](#) documentation (`[]` usage) for additional details. Note that this functionality can also be used to extract patient name(s) and/or identifier(s) (e.g. `$patients` or `$ID`).

as.list Convert a `DVH.list` object to a list containing individual DVH objects. Note that the reverse conversion can be performed using the `as` command and specifying `class="DVH.list"`.

c Combine two or more DVH lists and/or [DVH](#) objects

lapply Apply function to a list of [DVH](#) objects

length Extract number of [DVH](#) objects in DVH list

mad Compute the median absolute deviation (i.e. the median of the absolute deviations from the median) for all doses extracted from DVH object list

max Compute the maximum dose contained within the DVH list

mean Compute the mean DVH from all DVH objects within the list

median Compute the median DVH from all DVH objects within the list

min Compute the minimum dose contained within the DVH list

names Extract structure names for DVH objects in DVH list

names<- Assign structure name(s) to one or more DVH objects in DVH list

print Display summary of DVH list

range Compute the range (minimum and maximum doses) contained within the DVH list

rev Return a DVH list whose DVH objects are in reverse order

- sd** Compute the standard deviation for all doses extracted from DVH object list
- show** Display summary of DVH list
- sum** Compute the total (summed) DVH from all DVH objects within the list. *Note that structures are assumed to be non-overlapping; any overlaps in structure volumes may generate inaccurate dose summation.*
- t.test** Apply Student's t-Test to compare two DVH lists (see also [t.test](#))
- var** Compute the variance for all doses extracted from DVH object list
- wilcox.test** Apply Wilcoxon Rank Sum and Signed Rank Tests to compare two DVH lists (see also [wilcox.test](#))

Author(s)

Reid F. Thompson (<reid.thompson@gmail.com>)

See Also

[DVH](#), [plot](#)

Examples

```
# Description of structure/slots in class
showClass("DVH.list")
data(list="Rad0nc", package="Rad0nc")
print(johndoe)
plot(johndoe[c("LIVER", "PTV")], plot.type="i", col=c("red", "blue"), lty=1:2, lwd=1:2)
```

<code>getStructureList</code>	<i>Extract a DVH list of one or more structure(s)</i>
-------------------------------	---

Description

This function is designed to isolate one or more structure(s) from a list of DVH lists (generated by applying the `read.DVH()` command to multiple input files)

Usage

```
## S4 method for signature 'DVH'
getStructureList(x, structures)

## S4 method for signature 'DVH.list'
getStructureList(x, structures)

## S4 method for signature 'list'
getStructureList(x, structures)
```

Arguments

x	Can represent either a list of DVH lists (generated by <code>read.DVH()</code> applied to multiple input files) or a single object of class DVH or DVH.list.
structures	Vector used to sub-select structures from x; may be a character vector containing structure names (regular expressions may be specified if desired, see regex for more details). This parameter is ignored when x is of class DVH.

Value

Returns a single DVH list

Author(s)

Reid F. Thompson (<reid.thompson@gmail.com>)

See Also

[DVH.list](#)

Examples

```
patients <- list(janedoe, johndoe)
getStructureList(patients, "(?i)Liver")
```

gEUD

Generalized Equivalent Uniform Dose (gEUD) Calculation

Description

This function and its associated methods calculate gEUD value(s) for a given DVH or DVH.list object.

Usage

```
## S4 method for signature 'DVH,numeric'
gEUD(x, a, dose.units = c("cGy", "Gy"))
```

```
## S4 method for signature 'DVH.list,numeric'
gEUD(x, a, dose.units = c("cGy", "Gy"))
```

Arguments

x	Can represent either an object of class DVH or DVH.list for which to calculate gEUD value(s).
a	Numeric value specifying tissue-specific parameter, should be negative for target structures (e.g. tumor) and positive for organs at risk. For a=1, the EUD is equivalent to mean dose, while for a=Inf and a=-Inf, the EUD is equivalent to maximum and minimum doses, respectively.
dose.units	Value specifying dose units (must be one of "cGy" or "Gy").

Value

Returns a numeric vector containing the gEUD values (in units of `dose.units`) for all input objects.

Author(s)

Reid F. Thompson (<reid.thompson@gmail.com>)

References

Thieke, C., Bortfeld, T., Niemierko, A., and Nill, S. (2003) From physical dose constraints to equivalent uniform dose constraints in inverse radiotherapy planning. *Med Phys* **30**(9), 2332-2339.

See Also

[DVH](#), [DVH.list](#)

Examples

```
data("RadOnc")
gEUD(janedoe, 1) == unlist(janedoe$"Dmean")
gEUD(janedoe, Inf) == unlist(janedoe$"Dmax")
gEUD(janedoe, -Inf) == unlist(janedoe$"Dmin")
```

LQE

Linear Quadratic Extrapolated (LQE) Dose Conversion

Description

This function and its associated methods calculate LQE-weighted dose(s) for a given DVH or DVH.list object, allowing iso-effect conversion between one or more DVH(s) employing different dose fractionation.

Usage

```
## S4 method for signature 'DVH,numeric'
LQE(x, aB, fractions = NULL, N = NULL, dose.units = c("cGy", "Gy"))

## S4 method for signature 'DVH.list,numeric'
LQE(x, aB, fractions = NULL, N = NULL, dose.units = NULL)

## S4 method for signature 'numeric,numeric'
LQE(x, aB, fractions = NULL, N = NULL, dose.units = c("cGy", "Gy"))
```

Arguments

x	Can represent either numeric value(s) or otherwise an object of class DVH or DVH.list for which to calculate isoeffective dose(s) based on LQE. Note that input doses should be specified in units of dose.units (default is "cGy").
aB	Numeric value specifying tissue-specific parameter "alpha/beta ratio". Multiple values may be specified for LQE conversion of x, where x is a DVH.list object containing multiple DVH objects.
fractions	Numeric value specifying the fraction sizes in which doses are deposited. Multiple values may be specified for LQE conversion of x, where x is a DVH.list object containing multiple DVH objects. Two values should be specified when x contains numeric value(s), with the first element representing the fractionation for the input dose and the second element used to compute iso-effective output dose. Only a single value should be used to calculate iso-effective doses for a single DVH input.
N	Numeric value specifying the number of fractions in which doses are deposited. Multiple values may be specified for LQE conversion of x, where x is a DVH.list object containing multiple DVH objects. Two values should be specified when x contains numeric value(s), with the first element representing the fractionation for the input dose and the second element used to compute iso-effective output dose. Only a single value should be used to calculate iso-effective doses for a single DVH input. Note that parameter N is ignored unless fractions=NULL.
dose.units	Value specifying output dose units (must be one of "cGy" or "Gy"). Note that this value also determines input dose units when x is numeric. Multiple values may be specified for LQE conversion of x, where x is a DVH.list object containing multiple DVH objects.

Value

Returns a DVH or DVH.list object, corresponding to original input type for parameter x.

Author(s)

Reid F. Thompson (<reid.thompson@gmail.com>)

References

Barendsen, G.W. (1982) Dose fractionation, dose-rate and iso-effect relationships for normal-tissue response. *Int J Radiat Oncol Biol Phys* **8**(11):1981-1997.

See Also

[DVH, DVH.list](#)

Examples

```
# 5x 300cGy == 9x 200cGy (1800cGy isoeffective dose)
LQE(1500, aB=3, fractions=c(300, 200), dose.units="cGy")
LQE(15, aB=3, N=c(5, 9), dose.units="Gy")
```

```
LQE(18, aB=3, fractions=c(2, 3), dose.units="Gy")

# Multiple simultaneous numerical queries
LQE(c(4500, 5400), aB=3, fractions=c(300, 200), dose.units="cGy")

# DVH processing
LQE(janedoe[["LIVER"]], aB=3, fractions=200, dose.units="cGy")

# DVH list processing (default dose.units is "cGy")
plot(janedoe)
plot(LQE(janedoe, aB=3, fractions=200), col="red", new=FALSE)
```

plot-methods

*Additional Methods for Function plot in Package **graphics***

Description

These additional methods extend function plot in package **graphics**, enabling DVH visualization in package **RadOnc**

Usage

```
## S3 method for class 'DVH'
plot(x, ..., plot.type = c("individual", "grouped", "ttest", "wilcox", "bars"))

## S3 method for class 'DVH.list'
plot(x, ..., plot.type = c("individual", "grouped", "ttest", "wilcox", "bars"))
```

Arguments

x	Can represent either an object of class DVH, zDVH, or DVH.list
...	May contain any number of objects of class DVH or DVH.list. Note that at least one object of either class is required if plot.type = "ttest" or "wilcox". Specification of more than one zDVH will reduce all input zDVH objects to DVH objects for standard plotting.
plot.type	A character string specifying the type of plot to generate, must be one of "individual" (default), "grouped", "ttest", "wilcox" or "bars". plot.type parameter will be ignored if x is a zDVH object.

Details

See package vignette and examples (below) for more details about each plotting subtype.

Graphical Parameters

- angle** The slope of shading lines, given as an angle in counter-clockwise degrees (default is 45). This parameter is ignored if `density=NULL` or `NA` or wherever `fill=FALSE` or is ignored (e.g. when `plot.type="individual"` or `"bars"`). Also note that this parameter can represent a list of different angles, with length of the list corresponding to the number of DVH or DVH.list objects.
- back** A character value specifying the back-facing surface fill method when `x` is a zDVH object (the parameter is otherwise ignored). Value must be one of `"filled"`, `"lines"`, `"points"`, or `"culled"`. Default value is assigned from input parameter `front`.
- center** A character value specifying where to plot the center of a group when `plot.type="grouped"` (the parameter is otherwise ignored). Value must be one of `"mean"` or `"median"`. *Note: As of package v.1.0.3, this parameter is considered defunct and will be disregarded accordingly.*
- col** The color to be used for drawing lines. This parameter can also represent a list of different colors, with length corresponding to the number of DVH, zDVH, or DVH.list objects (if `plot.type="individual"`, number of colors should correspond to number of individual DVH objects).
When `plot.type="bars"`, `col` instead represents a list of colors used to define the shading scheme applied to the entire dose range. Default color scheme is a standard rainbow, with colors ranging from `"blue"` to `"red"`. Actual default is specified as `rev(rainbow(n=10, start=0, end=2/3))`. See [colors](#) for more options and information.
- density** The density of shading lines, in lines per inch. The default value of `NULL` means that no shading lines are drawn. A zero value of `density` means no shading nor filling, whereas negative values and `NA` suppress shading lines but allow solid color filling. Note that this parameter can also represent a list of different densities, with length of the list corresponding to the number of DVH or DVH.list objects.
- fill** Logical, defaulting to `TRUE`. Determines whether or not to draw shading around groups of DVH lines. Note that this parameter is relevant when `plot.type="grouped"`, `"ttest"` or `"wilcox"` (it is ignored when `plot.type="individual"` or `"bars"`).
- fill.lty** The line type used for shading (per `density` and `angle` parameters). See `lty` above for further specifications of line types. Note that this parameter can represent a list of different line types, with length corresponding to the number of DVH or DVH.list objects.
- fill.transparency** Factor modifying the transparency of filling/shading (value must be between `[0, 1]`), with `fill.transparency=0` specifying complete transparency and `1` specifying complete opacity. Note that this parameter can represent a list of different transparency factors, with length corresponding to the number of DVH or DVH.list objects. Default value is `line.transparency/2`.
- front** A character value specifying the front-facing surface fill method when `x` is a zDVH object (the parameter is otherwise ignored). Value must be one of `"filled"` (default), `"lines"`, `"points"`, or `"culled"`.
- legend** Value specifying the location to draw a figure legend, must be one of `"topright"`, `"bottomright"`, `"bottom"`, `"bottomleft"`, `"left"`, `"topleft"`, `"top"`, `"right"`, or `"center"`. These keywords place the legend on the inside of the plot frame at the location specified. Partial argument matching is used. If `legend=NA` (default), the legend is not drawn.
When `plot.type="bars"`, `legend` is interpreted instead as a logical value and must be either `TRUE` (default) or `FALSE`. If `TRUE`, labels are drawn at the bottom of the plot, outside of the actual plotting frame.

- legend.labels** A character or [expression](#) vector specifying the text to appear in the legend, when relevant. Length of `legend.labels` must match the number of DVH and DVH.list objects, otherwise legend text will default to the form: "Group 1", "Group 2", ...
- line.transparency** Factor modifying the transparency of line drawings (value must be between $[0, 1]$), with `fill.transparency=0` specifying complete transparency and 1 (default) specifying complete opacity. Note that this parameter can represent a list of different transparency factors, with length corresponding to the number of DVH or DVH.list objects (if `plot.type="individual"`, number of transparency factors should correspond to number of individual DVH objects).
- lty** The line type. Line types can either be specified as an integer (0=blank, 1=solid (default), 2=dashed, 3=dotted, 4=dotdash, 5=longdash, 6=twodash) or as one of the character strings "blank", "solid", "dashed", "dotted", "dotdash", "longdash", or "twodash", where "blank" uses 'invisible lines' (i.e., does not draw them).
Alternatively, a string of up to 8 characters (from `c(1:9, "A":"F")`) may be given, giving the length of line segments which are alternatively drawn and skipped (see [par](#) for more details). Note that this parameter can also represent a list of different line types, with length corresponding to the number of DVH or DVH.list objects (if `plot.type="individual"`, number of line types should correspond to number of individual DVH objects).
- lwd** The line width, a emphpositive number, defaulting to 1. The interpretation is device-specific, and some devices do not implement line widths less than one (see the help on the device for details of the interpretation). Note that this parameter can also represent a list of different line widths, with length of the list corresponding to the number of DVH or DVH.list objects (if `plot.type="individual"`, number of line widths should correspond to number of individual DVH objects).
- main** An overall title for the plot (see [title](#), default is "").
- multiplier** A single numerical value (default is 1) specifying the degree to which group display width should be shrunken or magnified. This parameter is only processed when `plot.type="grouped"` or `"ttest"` and `width="mad", "sd", or "var"`.
- new** Logical, defaulting to TRUE. If set to FALSE, the next high-level plotting command (actually [plot.new](#)) should *not clean* the frame before drawing *as if it were on a new device*. It is an error (ignored with a warning) to try to use `new=FALSE` on a device that does not currently contain a high-level plot.
- quantile** A numeric vector containing two values in $[0, 1]$ (default is the interquartile range: $(0.25, 0.75)$), specifying the lower and upper probabilities (respectively) to be used when `width="quantile"` and `plot.type="grouped"` or `"ttest"`. See [quantile](#) for more details.
- width** A character vector specifying the width of shading to use, when relevant (for a group of DVHs). Value must be one of "range" (default), "mad", "IQR", "quantile", "var", or "sd", specifying the absolute range, the mean-absolute-deviation, the interquartile (25-75%) range, the arbitrary inter-quantile range (see `quantile` parameter), the group variance, or standard deviation, respectively. This parameter is ignored unless `plot.type="grouped"`. If `plot.type="ttest"`, the parameter can be optionally specified (if `width=NULL` (default), shading will default to the confidence interval).

Additional Parameters

- dose** Value specifying dose scale (must be one of "relative" or "absolute").

dose.units Value specifying dose units (must be one of "cGy" or "Gy").

type Value specifying type of dose-volume histogram to plot (must be one of "cumulative" or "default").

volume Value specifying volume scale (must be one of "relative" or "absolute").

See Also

[plot](#)

Examples

```
# plot(x, ..., plot.type="individual")
OARs <- c("LIVER", "STOMACH", "DUODENUM")
cols <- c("red", "darkgreen", "blue")
plot(johndoe[OARs], col=cols, lty=1:3, legend="topright", legend.labels=OARs, main="OARs")

# plot(x, ..., plot.type="bars")
plot(janedoe[2:9], plot.type="bars", volume="absolute", dose="relative")

# plot(x, ..., plot.type="grouped")
plot(c(johndoe["STOMACH"], janedoe["STOMACH"]), #group 1
     c(johndoe[c("CTV", "PTV")], janedoe[c("CTV", "PTV")]), #group 2
     c(janedoe["LIVER"], johndoe["LIVER"]), #group 3
     c(johndoe["DUODENUM"], janedoe["DUODENUM"]), #group 4
     plot.type="grouped", col=c("orange", "green", "blue", "red"), lwd=2, dose="relative")

# plot(x, ..., plot.type="ttest")
# OARs <- c("LIVER", "STOMACH", "SMALL_BOWEL")
# plot(c(johndoe[c("CTV", "PTV")], janedoe[c("CTV", "PTV")]), #group 1
#      c(janedoe[OARs], johndoe[OARs]), #group 2
#      # plot.type="t", col=c("red", "blue"), lty=2, fill.lty=1, main="Target v. OAR t-Test")

# plot(x, ..., plot.type="wilcox")
# plot(c(johndoe[c("CTV", "PTV")], janedoe[c("CTV", "PTV")]), #group 1
#      c(janedoe[OARs], johndoe[OARs]), #group 2
#      # plot.type="w", col=c("red", "blue"), lty=2, fill.lty=1, main="Target v. OAR")
```

RadOnc

DVH data for 'John Doe' and 'Jane Doe'; 3D structural data for 'cord', 'mandible', and 'teeth'; RT data for 'Jane Doe'; and a zDVH object for 'stomach'

Description

List of 10 DVH objects corresponding to structures (e.g. liver) for patients 'John Doe' and 'Jane Doe'; Two structure3D objects ('cord' and 'mandible') and one structure list ('teeth') containing 3 structures; an RTdata object for 'Jane Doe' containing dose grid information and a structure list with 3 structures; and one zDVH object ('stomach').

Usage

```
data(package="RadOnc")
```

Format

The format for johndoe is:

```
Formal class 'DVH.list' [package "RadOnc"] with 1 slots
..@ structures:List of 10
.. ..$ LIVER      :Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. . . . . .@ patient      : chr "John Doe"
.. .. . . . . .@ ID         : chr "5555555555"
.. .. . . . . .@ structure.name : chr "LIVER"
.. .. . . . . .@ structure.volume: num 1367
.. .. . . . . .@ type          : chr "cumulative"
.. .. . . . . .@ dose.max      : num 92.9
.. .. . . . . .@ dose.min      : num 0
.. .. . . . . .@ dose.mean     : num 4.9
.. .. . . . . .@ dose.median   : num 0
.. .. . . . . .@ dose.mode     : num 0
.. .. . . . . .@ dose.STD     : num 10.8
.. .. . . . . .@ conf.index    : num 0
.. .. . . . . .@ equiv.sphere  : num 0
.. .. . . . . .@ gradient      : num 0
.. .. . . . . .@ dose.rx       : num 5500
.. .. . . . . .@ dose.fx       : num 25
.. .. . . . . .@ rx.isodose    : num 100
.. .. . . . . .@ doses        : num [1:1026] 0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 ...
.. .. . . . . .@ dose.type     : chr "relative"
.. .. . . . . .@ dose.units    : chr "cGy"
.. .. . . . . .@ volumes      : num [1:1026] 1367 414 392 378 368 ...
.. .. . . . . .@ volume.type   : chr "absolute"
.. .. $ SMALL_BOWEL :Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. . . . . .@ patient      : chr "John Doe"
.. .. . . . . .@ ID         : chr "5555555555"
.. .. . . . . .@ structure.name : chr "SMALL_BOWEL"
.. .. . . . . .@ structure.volume: num 206
.. .. . . . . .@ type          : chr "cumulative"
.. .. . . . . .@ dose.max      : num 99.8
.. .. . . . . .@ dose.min      : num 0
.. .. . . . . .@ dose.mean     : num 4.3
.. .. . . . . .@ dose.median   : num 0
.. .. . . . . .@ dose.mode     : num 0
.. .. . . . . .@ dose.STD     : num 15.3
.. .. . . . . .@ conf.index    : num 0
.. .. . . . . .@ equiv.sphere  : num 0
.. .. . . . . .@ gradient      : num 0
.. .. . . . . .@ dose.rx       : num 5500
```

```

.. .. .. ..@ dose.fx          : num 25
.. .. .. ..@ rx.isodose       : num 100
.. .. .. ..@ doses           : num [1:1026] 0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 ...
.. .. .. ..@ dose.type       : chr "relative"
.. .. .. ..@ dose.units      : chr "cGy"
.. .. .. ..@ volumes         : num [1:1026] 206.2 43.1 39.5 37.4 35.8 ...
.. .. .. ..@ volume.type     : chr "absolute"
.. .. $ DUODENUM             : Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. .. ..@ patient         : chr "John Doe"
.. .. .. ..@ ID             : chr "5555555555"
.. .. .. ..@ structure.name  : chr "DUODENUM"
.. .. .. ..@ structure.volume: num 93.1
.. .. .. ..@ type           : chr "cumulative"
.. .. .. ..@ dose.max       : num 102
.. .. .. ..@ dose.min       : num 0
.. .. .. ..@ dose.mean      : num 70.7
.. .. .. ..@ dose.median    : num 81.3
.. .. .. ..@ dose.mode      : num 100
.. .. .. ..@ dose.STD       : num 30.3
.. .. .. ..@ conf.index     : num 0
.. .. .. ..@ equiv.sphere   : num 0
.. .. .. ..@ gradient       : num 0
.. .. .. ..@ dose.rx        : num 5500
.. .. .. ..@ dose.fx        : num 25
.. .. .. ..@ rx.isodose     : num 100
.. .. .. ..@ doses         : num [1:1026] 0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 ...
.. .. .. ..@ dose.type     : chr "relative"
.. .. .. ..@ dose.units    : chr "cGy"
.. .. .. ..@ volumes       : num [1:1026] 93.1 93.1 93 93 92.9 ...
.. .. .. ..@ volume.type   : chr "absolute"
.. .. $ STOMACH             : Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. .. ..@ patient         : chr "John Doe"
.. .. .. ..@ ID             : chr "5555555555"
.. .. .. ..@ structure.name  : chr "STOMACH"
.. .. .. ..@ structure.volume: num 304
.. .. .. ..@ type           : chr "cumulative"
.. .. .. ..@ dose.max       : num 101
.. .. .. ..@ dose.min       : num 0
.. .. .. ..@ dose.mean      : num 7.9
.. .. .. ..@ dose.median    : num 0
.. .. .. ..@ dose.mode      : num 0
.. .. .. ..@ dose.STD       : num 22.8
.. .. .. ..@ conf.index     : num 0
.. .. .. ..@ equiv.sphere   : num 0
.. .. .. ..@ gradient       : num 0
.. .. .. ..@ dose.rx        : num 5500
.. .. .. ..@ dose.fx        : num 25
.. .. .. ..@ rx.isodose     : num 100

```

```

.. .. . .@ doses          : num [1:1026] 0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 ...
.. .. . .@ dose.type      : chr "relative"
.. .. . .@ dose.units     : chr "cGy"
.. .. . .@ volumes        : num [1:1026] 303.6 78 71.5 67.8 65.1 ...
.. .. . .@ volume.type    : chr "absolute"
.. .. $ CTV               : Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. . .@ patient        : chr "John Doe"
.. .. . .@ ID             : chr "5555555555"
.. .. . .@ structure.name  : chr "CTV"
.. .. . .@ structure.volume: num 88.4
.. .. . .@ type           : chr "cumulative"
.. .. . .@ dose.max       : num 103
.. .. . .@ dose.min       : num 96.8
.. .. . .@ dose.mean      : num 100
.. .. . .@ dose.median    : num 100
.. .. . .@ dose.mode      : num 100
.. .. . .@ dose.STD       : num 0.7
.. .. . .@ conf.index     : num 0
.. .. . .@ equiv.sphere   : num 0
.. .. . .@ gradient       : num 0
.. .. . .@ dose.rx        : num 5500
.. .. . .@ dose.fx        : num 25
.. .. . .@ rx.isodose     : num 100
.. .. . .@ doses          : num [1:1026] 0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 ...
.. .. . .@ dose.type      : chr "relative"
.. .. . .@ dose.units     : chr "cGy"
.. .. . .@ volumes        : num [1:1026] 88.4 88.4 88.4 88.4 88.4 ...
.. .. . .@ volume.type    : chr "absolute"
.. .. $ PTV               : Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. . .@ patient        : chr "John Doe"
.. .. . .@ ID             : chr "5555555555"
.. .. . .@ structure.name  : chr "PTV"
.. .. . .@ structure.volume: num 156
.. .. . .@ type           : chr "cumulative"
.. .. . .@ dose.max       : num 103
.. .. . .@ dose.min       : num 84.1
.. .. . .@ dose.mean      : num 99.6
.. .. . .@ dose.median    : num 99.8
.. .. . .@ dose.mode      : num 99.9
.. .. . .@ dose.STD       : num 1.2
.. .. . .@ conf.index     : num 0
.. .. . .@ equiv.sphere   : num 0
.. .. . .@ gradient       : num 0
.. .. . .@ dose.rx        : num 5500
.. .. . .@ dose.fx        : num 25
.. .. . .@ rx.isodose     : num 100
.. .. . .@ doses          : num [1:1026] 0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 ...
.. .. . .@ dose.type      : chr "relative"

```

```

.. .. .. ..@ dose.units      : chr "cGy"
.. .. .. ..@ volumes        : num [1:1026] 156 156 156 156 156 ...
.. .. .. ..@ volume.type    : chr "absolute"
.. .. $ BODY                :Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. .. ..@ patient       : chr "John Doe"
.. .. .. ..@ ID           : chr "5555555555"
.. .. .. ..@ structure.name : chr "BODY"
.. .. .. ..@ structure.volume: num 17666
.. .. .. ..@ type          : chr "cumulative"
.. .. .. ..@ dose.max      : num 103
.. .. .. ..@ dose.min      : num 0
.. .. .. ..@ dose.mean     : num 5.6
.. .. .. ..@ dose.median   : num 0
.. .. .. ..@ dose.mode     : num 0
.. .. .. ..@ dose.STD     : num 17.1
.. .. .. ..@ conf.index    : num 0
.. .. .. ..@ equiv.sphere  : num 0
.. .. .. ..@ gradient     : num 0
.. .. .. ..@ dose.rx       : num 5500
.. .. .. ..@ dose.fx       : num 25
.. .. .. ..@ rx.isodose    : num 100
.. .. .. ..@ doses        : num [1:1026] 0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 ...
.. .. .. ..@ dose.type     : chr "relative"
.. .. .. ..@ dose.units    : chr "cGy"
.. .. .. ..@ volumes      : num [1:1026] 17666 3424 3290 3206 3143 ...
.. .. .. ..@ volume.type   : chr "absolute"
.. .. $ LEFT_KIDNEY        :Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. .. ..@ patient       : chr "John Doe"
.. .. .. ..@ ID           : chr "5555555555"
.. .. .. ..@ structure.name : chr "LEFT_KIDNEY"
.. .. .. ..@ structure.volume: num 154
.. .. .. ..@ type          : chr "cumulative"
.. .. .. ..@ dose.max      : num 44.4
.. .. .. ..@ dose.min      : num 0
.. .. .. ..@ dose.mean     : num 4.7
.. .. .. ..@ dose.median   : num 0
.. .. .. ..@ dose.mode     : num 0
.. .. .. ..@ dose.STD     : num 9.5
.. .. .. ..@ conf.index    : num 0
.. .. .. ..@ equiv.sphere  : num 0
.. .. .. ..@ gradient     : num 0
.. .. .. ..@ dose.rx       : num 5500
.. .. .. ..@ dose.fx       : num 25
.. .. .. ..@ rx.isodose    : num 100
.. .. .. ..@ doses        : num [1:1026] 0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 ...
.. .. .. ..@ dose.type     : chr "relative"
.. .. .. ..@ dose.units    : chr "cGy"
.. .. .. ..@ volumes      : num [1:1026] 154.2 48.3 46.4 45.3 44.4 ...

```

```

.. .. .. ..@ volume.type      : chr "absolute"
.. .. $ RIGHT_KIDNEY:Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. .. ..@ patient         : chr "John Doe"
.. .. .. ..@ ID              : chr "5555555555"
.. .. .. ..@ structure.name   : chr "RIGHT_KIDNEY"
.. .. .. ..@ structure.volume: num 155
.. .. .. ..@ type             : chr "cumulative"
.. .. .. ..@ dose.max         : num 98.5
.. .. .. ..@ dose.min         : num 0
.. .. .. ..@ dose.mean        : num 24.2
.. .. .. ..@ dose.median      : num 24.3
.. .. .. ..@ dose.mode        : num 0
.. .. .. ..@ dose.STD         : num 22.8
.. .. .. ..@ conf.index       : num 0
.. .. .. ..@ equiv.sphere     : num 0
.. .. .. ..@ gradient         : num 0
.. .. .. ..@ dose.rx          : num 5500
.. .. .. ..@ dose.fx          : num 25
.. .. .. ..@ rx.isodose       : num 100
.. .. .. ..@ doses            : num [1:1026] 0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 ...
.. .. .. ..@ dose.type        : chr "relative"
.. .. .. ..@ dose.units       : chr "cGy"
.. .. .. ..@ volumes          : num [1:1026] 155 134 132 130 129 ...
.. .. .. ..@ volume.type     : chr "absolute"
.. .. $ CORD                  :Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. .. ..@ patient         : chr "John Doe"
.. .. .. ..@ ID              : chr "5555555555"
.. .. .. ..@ structure.name   : chr "CORD"
.. .. .. ..@ structure.volume: num 40.7
.. .. .. ..@ type             : chr "cumulative"
.. .. .. ..@ dose.max         : num 55.5
.. .. .. ..@ dose.min         : num 0
.. .. .. ..@ dose.mean        : num 20.7
.. .. .. ..@ dose.median      : num 4.1
.. .. .. ..@ dose.mode        : num 0
.. .. .. ..@ dose.STD         : num 23.2
.. .. .. ..@ conf.index       : num 0
.. .. .. ..@ equiv.sphere     : num 0
.. .. .. ..@ gradient         : num 0
.. .. .. ..@ dose.rx          : num 5500
.. .. .. ..@ dose.fx          : num 25
.. .. .. ..@ rx.isodose       : num 100
.. .. .. ..@ doses            : num [1:1026] 0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 ...
.. .. .. ..@ dose.type        : chr "relative"
.. .. .. ..@ dose.units       : chr "cGy"
.. .. .. ..@ volumes          : num [1:1026] 40.7 23 22.7 22.4 22.2 ...
.. .. .. ..@ volume.type     : chr "absolute"

```

The format for janedoe is:

```

Formal class 'DVH.list' [package "RadOnc"] with 1 slots
..@ structures:List of 10
.. ..$ LIVER      :Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. . . . . .@ patient      : chr "Jane Doe"
.. .. . . . . .@ ID         : chr "1111111111"
.. .. . . . . .@ structure.name : chr "LIVER"
.. .. . . . . .@ structure.volume: num 1636
.. .. . . . . .@ type          : chr "cumulative"
.. .. . . . . .@ dose.max      : num 5634
.. .. . . . . .@ dose.min      : num 42.7
.. .. . . . . .@ dose.mean     : num 707
.. .. . . . . .@ dose.median   : num 276
.. .. . . . . .@ dose.mode     : num 99.5
.. .. . . . . .@ dose.STD      : num 917
.. .. . . . . .@ conf.index    : num 0
.. .. . . . . .@ equiv.sphere  : num 0
.. .. . . . . .@ gradient      : num 0
.. .. . . . . .@ dose.rx       : num 5500
.. .. . . . . .@ dose.fx       : num 25
.. .. . . . . .@ rx.isodose    : num 100
.. .. . . . . .@ doses        : num [1:1133] 0 5 10 15 20 25 30 35 40 45 ...
.. .. . . . . .@ dose.type     : chr "absolute"
.. .. . . . . .@ dose.units    : chr "cGy"
.. .. . . . . .@ volumes      : num [1:1133] 100 100 100 100 100 ...
.. .. . . . . .@ volume.type   : chr "relative"
.. ..$ LEFT_KIDNEY :Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. . . . . .@ patient      : chr "Jane Doe"
.. .. . . . . .@ ID         : chr "1111111111"
.. .. . . . . .@ structure.name : chr "LEFT_KIDNEY"
.. .. . . . . .@ structure.volume: num 196
.. .. . . . . .@ type          : chr "cumulative"
.. .. . . . . .@ dose.max      : num 3847
.. .. . . . . .@ dose.min      : num 75.8
.. .. . . . . .@ dose.mean     : num 1021
.. .. . . . . .@ dose.median   : num 703
.. .. . . . . .@ dose.mode     : num 119
.. .. . . . . .@ dose.STD      : num 802
.. .. . . . . .@ conf.index    : num 0
.. .. . . . . .@ equiv.sphere  : num 0
.. .. . . . . .@ gradient      : num 0
.. .. . . . . .@ dose.rx       : num 5500
.. .. . . . . .@ dose.fx       : num 25
.. .. . . . . .@ rx.isodose    : num 100
.. .. . . . . .@ doses        : num [1:1133] 0 5 10 15 20 25 30 35 40 45 ...
.. .. . . . . .@ dose.type     : chr "absolute"
.. .. . . . . .@ dose.units    : chr "cGy"
.. .. . . . . .@ volumes      : num [1:1133] 100 100 100 100 100 100 100 100 100 100 ...
.. .. . . . . .@ volume.type   : chr "relative"

```

```

.. ..$ STOMACH      :Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. . . . .@ patient      : chr "Jane Doe"
.. .. . . . .@ ID         : chr "1111111111"
.. .. . . . .@ structure.name : chr "STOMACH"
.. .. . . . .@ structure.volume: num 695
.. .. . . . .@ type          : chr "cumulative"
.. .. . . . .@ dose.max      : num 5353
.. .. . . . .@ dose.min      : num 59
.. .. . . . .@ dose.mean     : num 1280
.. .. . . . .@ dose.median   : num 1302
.. .. . . . .@ dose.mode     : num 111
.. .. . . . .@ dose.STD      : num 1062
.. .. . . . .@ conf.index    : num 0
.. .. . . . .@ equiv.sphere  : num 0
.. .. . . . .@ gradient      : num 0
.. .. . . . .@ dose.rx       : num 5500
.. .. . . . .@ dose.fx       : num 25
.. .. . . . .@ rx.isodose    : num 100
.. .. . . . .@ doses        : num [1:1133] 0 5 10 15 20 25 30 35 40 45 ...
.. .. . . . .@ dose.type     : chr "absolute"
.. .. . . . .@ dose.units    : chr "cGy"
.. .. . . . .@ volumes      : num [1:1133] 100 100 100 100 100 100 100 100 100 100 ...
.. .. . . . .@ volume.type   : chr "relative"
.. ..$ DUODENUM    :Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. . . . .@ patient      : chr "Jane Doe"
.. .. . . . .@ ID         : chr "1111111111"
.. .. . . . .@ structure.name : chr "DUODENUM"
.. .. . . . .@ structure.volume: num 34.2
.. .. . . . .@ type          : chr "cumulative"
.. .. . . . .@ dose.max      : num 5620
.. .. . . . .@ dose.min      : num 2708
.. .. . . . .@ dose.mean     : num 4755
.. .. . . . .@ dose.median   : num 4943
.. .. . . . .@ dose.mode     : num 5365
.. .. . . . .@ dose.STD      : num 635
.. .. . . . .@ conf.index    : num 0
.. .. . . . .@ equiv.sphere  : num 0
.. .. . . . .@ gradient      : num 0
.. .. . . . .@ dose.rx       : num 5500
.. .. . . . .@ dose.fx       : num 25
.. .. . . . .@ rx.isodose    : num 100
.. .. . . . .@ doses        : num [1:1133] 0 5 10 15 20 25 30 35 40 45 ...
.. .. . . . .@ dose.type     : chr "absolute"
.. .. . . . .@ dose.units    : chr "cGy"
.. .. . . . .@ volumes      : num [1:1133] 100 100 100 100 100 100 100 100 100 100 ...
.. .. . . . .@ volume.type   : chr "relative"
.. ..$ RIGHT_KIDNEY:Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. . . . .@ patient      : chr "Jane Doe"

```

```

.. .. . .@ ID      : chr "1111111111"
.. .. . .@ structure.name : chr "RIGHT_KIDNEY"
.. .. . .@ structure.volume: num 224
.. .. . .@ type       : chr "cumulative"
.. .. . .@ dose.max    : num 4202
.. .. . .@ dose.min    : num 102
.. .. . .@ dose.mean   : num 1511
.. .. . .@ dose.median : num 1624
.. .. . .@ dose.mode   : num 1638
.. .. . .@ dose.STD    : num 714
.. .. . .@ conf.index  : num 0
.. .. . .@ equiv.sphere : num 0
.. .. . .@ gradient    : num 0
.. .. . .@ dose.rx     : num 5500
.. .. . .@ dose.fx     : num 25
.. .. . .@ rx.isodose  : num 100
.. .. . .@ doses      : num [1:1133] 0 5 10 15 20 25 30 35 40 45 ...
.. .. . .@ dose.type   : chr "absolute"
.. .. . .@ dose.units  : chr "cGy"
.. .. . .@ volumes    : num [1:1133] 100 100 100 100 100 100 100 100 100 100 ...
.. .. . .@ volume.type : chr "relative"
.. .. $ CTV          :Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. . .@ patient    : chr "Jane Doe"
.. .. . .@ ID      : chr "1111111111"
.. .. . .@ structure.name : chr "CTV"
.. .. . .@ structure.volume: num 147
.. .. . .@ type       : chr "cumulative"
.. .. . .@ dose.max    : num 5647
.. .. . .@ dose.min    : num 5169
.. .. . .@ dose.mean   : num 5500
.. .. . .@ dose.median : num 5505
.. .. . .@ dose.mode   : num 5500
.. .. . .@ dose.STD    : num 59.8
.. .. . .@ conf.index  : num 0
.. .. . .@ equiv.sphere : num 0
.. .. . .@ gradient    : num 0
.. .. . .@ dose.rx     : num 5500
.. .. . .@ dose.fx     : num 25
.. .. . .@ rx.isodose  : num 100
.. .. . .@ doses      : num [1:1133] 0 5 10 15 20 25 30 35 40 45 ...
.. .. . .@ dose.type   : chr "absolute"
.. .. . .@ dose.units  : chr "cGy"
.. .. . .@ volumes    : num [1:1133] 100 100 100 100 100 100 100 100 100 100 ...
.. .. . .@ volume.type : chr "relative"
.. .. $ PTV          :Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. . .@ patient    : chr "Jane Doe"
.. .. . .@ ID      : chr "1111111111"
.. .. . .@ structure.name : chr "PTV"

```



```

.. .. . .@ structure.volume: num 239
.. .. . .@ type           : chr "cumulative"
.. .. . .@ dose.max       : num 5665
.. .. . .@ dose.min       : num 4750
.. .. . .@ dose.mean      : num 5471
.. .. . .@ dose.median    : num 5493
.. .. . .@ dose.mode      : num 5500
.. .. . .@ dose.STD       : num 98.6
.. .. . .@ conf.index     : num 0
.. .. . .@ equiv.sphere   : num 0
.. .. . .@ gradient       : num 0
.. .. . .@ dose.rx        : num 5500
.. .. . .@ dose.fx        : num 25
.. .. . .@ rx.isodose     : num 100
.. .. . .@ doses          : num [1:1133] 0 5 10 15 20 25 30 35 40 45 ...
.. .. . .@ dose.type      : chr "absolute"
.. .. . .@ dose.units     : chr "cGy"
.. .. . .@ volumes       : num [1:1133] 100 100 100 100 100 100 100 100 100 100 ...
.. .. . .@ volume.type    : chr "relative"
.. .. $ SMALL_BOWEL :Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. . .@ patient       : chr "Jane Doe"
.. .. . .@ ID           : chr "1111111111"
.. .. . .@ structure.name : chr "SMALL_BOWEL"
.. .. . .@ structure.volume: num 232
.. .. . .@ type           : chr "cumulative"
.. .. . .@ dose.max       : num 4934
.. .. . .@ dose.min       : num 59.6
.. .. . .@ dose.mean      : num 294
.. .. . .@ dose.median    : num 171
.. .. . .@ dose.mode      : num 127
.. .. . .@ dose.STD       : num 391
.. .. . .@ conf.index     : num 0
.. .. . .@ equiv.sphere   : num 0
.. .. . .@ gradient       : num 0
.. .. . .@ dose.rx        : num 5500
.. .. . .@ dose.fx        : num 25
.. .. . .@ rx.isodose     : num 100
.. .. . .@ doses          : num [1:1133] 0 5 10 15 20 25 30 35 40 45 ...
.. .. . .@ dose.type      : chr "absolute"
.. .. . .@ dose.units     : chr "cGy"
.. .. . .@ volumes       : num [1:1133] 100 100 100 100 100 100 100 100 100 100 ...
.. .. . .@ volume.type    : chr "relative"
.. .. $ CORD         :Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. . .@ patient       : chr "Jane Doe"
.. .. . .@ ID           : chr "1111111111"
.. .. . .@ structure.name : chr "CORD"
.. .. . .@ structure.volume: num 64.9
.. .. . .@ type           : chr "cumulative"

```

```

.. .. .. ..@ dose.max      : num 3443
.. .. .. ..@ dose.min      : num 0
.. .. .. ..@ dose.mean     : num 732
.. .. .. ..@ dose.median   : num 136
.. .. .. ..@ dose.mode     : num 6.9
.. .. .. ..@ dose.STD      : num 953
.. .. .. ..@ conf.index    : num 0
.. .. .. ..@ equiv.sphere  : num 0
.. .. .. ..@ gradient      : num 0
.. .. .. ..@ dose.rx       : num 5500
.. .. .. ..@ dose.fx       : num 25
.. .. .. ..@ rx.isodose    : num 100
.. .. .. ..@ doses        : num [1:1133] 0 5 10 15 20 25 30 35 40 45 ...
.. .. .. ..@ dose.type     : chr "absolute"
.. .. .. ..@ dose.units    : chr "cGy"
.. .. .. ..@ volumes      : num [1:1133] 100 98.5 95.9 93.8 90.8 ...
.. .. .. ..@ volume.type   : chr "relative"
.. .. $ BODY              : Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. .. ..@ patient      : chr "Jane Doe"
.. .. .. ..@ ID          : chr "1111111111"
.. .. .. ..@ structure.name : chr "BODY"
.. .. .. ..@ structure.volume: num 25508
.. .. .. ..@ type        : chr "cumulative"
.. .. .. ..@ dose.max     : num 5665
.. .. .. ..@ dose.min     : num 0
.. .. .. ..@ dose.mean    : num 478
.. .. .. ..@ dose.median  : num 66.4
.. .. .. ..@ dose.mode    : num 0.4
.. .. .. ..@ dose.STD     : num 946
.. .. .. ..@ conf.index   : num 0
.. .. .. ..@ equiv.sphere : num 0
.. .. .. ..@ gradient     : num 0
.. .. .. ..@ dose.rx      : num 5500
.. .. .. ..@ dose.fx      : num 25
.. .. .. ..@ rx.isodose   : num 100
.. .. .. ..@ doses       : num [1:1133] 0 5 10 15 20 25 30 35 40 45 ...
.. .. .. ..@ dose.type    : chr "absolute"
.. .. .. ..@ dose.units   : chr "cGy"
.. .. .. ..@ volumes     : num [1:1133] 100 77.7 75.1 73 71.3 ...
.. .. .. ..@ volume.type  : chr "relative"

```

The format for janedoe.RTdata is:

```

Formal class 'RTdata' [package "RadOnc"] with 4 slots
..@ name      : chr "Jane Doe"
..@ CT        : logi[0 , 0 , 0 ]
..@ dose      : num [1:74, 1:72, 1:51] 2.79 2.87 2.96 3.08 3.32 ...
.. ..- attr(*, "dimnames")=List of 3
.. .. ..$ : chr [1:74] "-57.5120192" "-55.0120192" "-52.5120192" "-50.0120192" ...

```

```
.. . . . $ : chr [1:72] "-309.3547858" "-306.8547858" "-304.3547858" "-301.8547858" ...
.. . . . $ : chr [1:51] "-102" "-99" "-96" "-93" ...
..@ structures:Formal class 'structure.list' [package "RadOnc"] with 1 slots
.. . . . @ structures:List of 3
.. . . . . $ STOMACH:Formal class 'structure3D' [package "RadOnc"] with 9 slots
.. . . . . . @ name : chr "STOMACH"
.. . . . . . @ volume : num 0
.. . . . . . @ volume.units : chr "cc"
.. . . . . . @ coordinate.units: chr "cm"
.. . . . . . @ vertices : num [1:9222, 1:3] -23.4 -21.5 -19.5 -17.6 -15.6 ...
.. . . . . . @ origin : num [1:3] 42.5 -202.6 -26.8
.. . . . . . @ triangles : logi[1:3, 0 ]
.. . . . . . @ closed.polys :List of 52
.. . . . . . . $ : num [1:192, 1:3] -23.4 -21.5 -19.5 -17.6 -15.6 ...
.. . . . . . . $ : num [1:188, 1:3] -9.77 -7.81 -5.86 -3.91 -1.95 0 1.95 3.91 5.86 7.81 ...
.. . . . . . . $ : num [1:4, 1:3] 70.3 70.1 70.3 70.5 -191.9 ...
.. . . . . . . $ : num [1:192, 1:3] -5.86 -3.91 -1.95 0 1.95 ...
.. . . . . . . $ : num [1:182, 1:3] -29.3 -27.3 -25.4 -23.4 -21.5 ...
.. . . . . . . $ : num [1:180, 1:3] -35.2 -33.2 -31.2 -29.3 -27.3 ...
.. . . . . . . $ : num [1:174, 1:3] -35.2 -33.2 -31.2 -29.3 -27.3 ...
.. . . . . . . $ : num [1:180, 1:3] -33.2 -31.2 -29.3 -27.3 -25.4 ...
.. . . . . . . $ : num [1:170, 1:3] -29.3 -27.3 -25.4 -23.4 -21.5 ...
.. . . . . . . $ : num [1:168, 1:3] -3.91 -1.95 0 1.95 3.91 ...
.. . . . . . . $ : num [1:160, 1:3] -17.58 -15.63 -13.67 -11.72 -9.77 ...
.. . . . . . . $ : num [1:152, 1:3] -15.63 -13.67 -11.72 -9.77 -7.81 ...
.. . . . . . . $ : num [1:174, 1:3] -9.77 -7.81 -5.86 -3.91 -1.95 0 1.95 3.91 5.86 6.48 ...
.. . . . . . . $ : num [1:176, 1:3] -7.81 -5.86 -3.91 -1.95 0 1.95 3.91 5.86 7.81 9.77 ...
.. . . . . . . $ : num [1:176, 1:3] -19.5 -17.6 -15.6 -13.7 -11.7 ...
.. . . . . . . $ : num [1:4, 1:3] 7.81 6.99 7.81 8.11 -158.68 ...
.. . . . . . . $ : num [1:194, 1:3] -17.58 -15.63 -13.67 -11.72 -9.77 ...
.. . . . . . . $ : num [1:4, 1:3] -29.3 -29.3 -29.3 -29.3 -160.8 ...
.. . . . . . . $ : num [1:194, 1:3] -9.77 -7.81 -5.86 -3.91 -1.95 0 1.95 3.91 5.86 7.81 ...
.. . . . . . . $ : num [1:192, 1:3] -13.67 -11.72 -9.77 -7.81 -5.86 ...
.. . . . . . . $ : num [1:214, 1:3] -11.72 -9.77 -7.81 -5.86 -3.91 ...
.. . . . . . . $ : num [1:216, 1:3] -9.77 -7.81 -5.86 -3.91 -1.95 0 1.95 3.91 4.51 5.86 ...
.. . . . . . . $ : num [1:214, 1:3] -11.72 -9.77 -7.81 -5.86 -3.91 ...
.. . . . . . . $ : num [1:204, 1:3] -19.5 -17.6 -15.6 -13.7 -11.7 ...
.. . . . . . . $ : num [1:208, 1:3] -5.86 -3.91 -1.95 0 1.95 3.81 3.91 5.86 7.81 9.77 ...
.. . . . . . . $ : num [1:210, 1:3] 7.81 9.77 11.72 13.67 15.63 ...
.. . . . . . . $ : num [1:4, 1:3] 7.81 7.71 7.81 7.91 -164.59 ...
.. . . . . . . $ : num [1:208, 1:3] -7.81 -5.86 -3.91 -1.95 0 1.95 3.91 5.86 7.81 9.77 ...
.. . . . . . . $ : num [1:198, 1:3] -9.77 -7.81 -5.86 -3.91 -1.95 0 1.95 3.91 5.86 7.81 ...
.. . . . . . . $ : num [1:198, 1:3] -1.95 0 1.95 3.91 5.57 ...
.. . . . . . . $ : num [1:232, 1:3] 1.95 3.91 5.86 6.47 7.81 ...
.. . . . . . . $ : num [1:236, 1:3] 7.81 9.77 11.72 13.67 15.63 ...
.. . . . . . . $ : num [1:290, 1:3] 1.95 3.91 5.86 7.81 9.77 ...
.. . . . . . . $ : num [1:278, 1:3] 21.5 23.4 25.4 27.3 28.5 ...
.. . . . . . . $ : num [1:246, 1:3] 44.9 46.9 48.8 50.8 52.7 ...
```

```

.. .. .$. : num [1:248, 1:3] 44.9 46.9 48.8 50.8 52.7 ...
.. .. .$. : num [1:234, 1:3] 56.6 58.6 60.5 62.5 64.5 ...
.. .. .$. : num [1:234, 1:3] 62.5 64.5 66.4 68.4 70.3 ...
.. .. .$. : num [1:232, 1:3] 70.3 72.3 74.2 76.2 78.1 ...
.. .. .$. : num [1:216, 1:3] 78.1 80.1 82 84 85.9 ...
.. .. .$. : num [1:212, 1:3] 80.1 82 84 85.9 87.9 ...
.. .. .$. : num [1:202, 1:3] 80.1 82 84 85.9 86.4 ...
.. .. .$. : num [1:198, 1:3] 80.1 82 84 85.9 87.9 ...
.. .. .$. : num [1:180, 1:3] 87.9 89.5 89.8 91.8 93.8 ...
.. .. .$. : num [1:176, 1:3] 91.8 93.8 95.7 97.7 99.6 ...
.. .. .$. : num [1:158, 1:3] 84 85.9 87.9 89.8 90 ...
.. .. .$. : num [1:158, 1:3] 84 85.9 87.9 88.1 89.8 ...
.. .. .$. : num [1:142, 1:3] 80.1 82 84 85.9 87.9 ...
.. .. .$. : num [1:146, 1:3] 78.1 80.1 82 84 85.9 ...
.. .. .$. : num [1:130, 1:3] 76.2 78.1 80.1 82 84 ...
.. .. .$. : num [1:74, 1:3] 80.1 82 84 85.9 86.1 ...
.. .. .$. : num [1:70, 1:3] 82 84 85.9 87.3 87.9 ...
.. .. .- attr(*, "dim")= int [1:2] 52 1
.. .. .@ DVH :Formal class 'DVH' [package "RadOnc"] with 22 slots
.. .. .@ patient : chr ""
.. .. .@ ID : chr ""
.. .. .@ structure.name : chr "STOMACH"
.. .. .@ structure.volume: num 699
.. .. .@ type : chr "differential"
.. .. .@ dose.max : num 53.6
.. .. .@ dose.min : num 0.594
.. .. .@ dose.mean : num 12.8
.. .. .@ dose.median : num 0
.. .. .@ dose.mode : num 0
.. .. .@ dose.STD : num 0
.. .. .@ conf.index : num 0
.. .. .@ equiv.sphere : num 0
.. .. .@ gradient : num 0
.. .. .@ dose.rx : num 55
.. .. .@ dose.fx : num 25
.. .. .@ rx.isodose : num 100
.. .. .@ doses : num [1:5665] 0 0.01 0.02 0.03 0.04 0.05 0.06 0.07 0.08 0.09 ...
.. .. .@ dose.type : chr "absolute"
.. .. .@ dose.units : chr "Gy"
.. .. .@ volumes : num [1:5665] 0 0 0 0 0 0 0 0 0 ...
.. .. .@ volume.type : chr "absolute"
.. .. .$. CTV :Formal class 'structure3D' [package "RadOnc"] with 9 slots
.. .. .@ name : chr "CTV"
.. .. .@ volume : num 0
.. .. .@ volume.units : chr "cc"
.. .. .@ coordinate.units: chr "cm"
.. .. .@ vertices : num [1:2440, 1:3] -29.3 -27.3 -25.4 -23.4 -21.5 ...
.. .. .@ origin : num [1:3] -11.9 -237.5 -52.7

```

```

.. .. .@ triangles      : logi[1:3, 0 ]
.. .. .@ closed.polys   :List of 23
.. .. .$. : num [1:56, 1:3] -29.3 -27.3 -25.4 -23.4 -21.5 ...
.. .. .$. : num [1:74, 1:3] -31.2 -29.3 -27.3 -25.4 -23.4 ...
.. .. .$. : num [1:92, 1:3] -27.3 -25.4 -23.4 -21.5 -19.5 ...
.. .. .$. : num [1:96, 1:3] -29.3 -27.3 -25.4 -23.4 -21.5 ...
.. .. .$. : num [1:102, 1:3] -27.3 -25.4 -23.4 -21.5 -19.5 ...
.. .. .$. : num [1:112, 1:3] -23.4 -22.5 -21.5 -19.5 -17.6 ...
.. .. .$. : num [1:116, 1:3] -39.1 -37.1 -35.2 -33.2 -31.2 ...
.. .. .$. : num [1:112, 1:3] -35.2 -33.2 -31.2 -29.3 -27.3 ...
.. .. .$. : num [1:114, 1:3] -21.5 -19.5 -17.6 -15.6 -13.7 ...
.. .. .$. : num [1:110, 1:3] -21.5 -19.5 -17.6 -15.6 -13.7 ...
.. .. .$. : num [1:112, 1:3] -15.63 -13.67 -11.72 -9.77 -7.81 ...
.. .. .$. : num [1:108, 1:3] -17.58 -15.63 -13.67 -11.72 -9.77 ...
.. .. .$. : num [1:116, 1:3] -15.63 -13.67 -11.72 -9.77 -7.81 ...
.. .. .$. : num [1:120, 1:3] -11.72 -9.77 -8.79 -7.81 -5.86 ...
.. .. .$. : num [1:126, 1:3] -17.58 -15.63 -13.67 -11.72 -9.77 ...
.. .. .$. : num [1:124, 1:3] -19.5 -17.6 -15.6 -13.7 -11.7 ...
.. .. .$. : num [1:124, 1:3] -15.63 -13.67 -11.72 -9.77 -7.81 ...
.. .. .$. : num [1:120, 1:3] -17.58 -15.63 -13.67 -11.72 -9.77 ...
.. .. .$. : num [1:110, 1:3] -15.63 -13.67 -11.72 -9.77 -7.81 ...
.. .. .$. : num [1:106, 1:3] -13.67 -11.72 -9.77 -7.81 -5.86 ...
.. .. .$. : num [1:102, 1:3] -13.67 -11.72 -9.77 -7.81 -5.86 ...
.. .. .$. : num [1:100, 1:3] -11.72 -9.77 -7.81 -5.86 -3.91 ...
.. .. .$. : num [1:88, 1:3] -11.72 -9.77 -7.81 -5.86 -3.91 ...
.. .. .- attr(*, "dim")= int [1:2] 23 1
.. .. .@ DVH            :Formal class 'DVH' [package "RadOnc"] with 22 slots
.. .. .@ patient        : chr ""
.. .. .@ ID              : chr ""
.. .. .@ structure.name  : chr "CTV"
.. .. .@ structure.volume: num 148
.. .. .@ type            : chr "differential"
.. .. .@ dose.max        : num 56.5
.. .. .@ dose.min        : num 51.7
.. .. .@ dose.mean       : num 55
.. .. .@ dose.median     : num 0
.. .. .@ dose.mode       : num 0
.. .. .@ dose.STD        : num 0
.. .. .@ conf.index      : num 0
.. .. .@ equiv.sphere    : num 0
.. .. .@ gradient        : num 0
.. .. .@ dose.rx         : num 55
.. .. .@ dose.fx         : num 25
.. .. .@ rx.isodose      : num 100
.. .. .@ doses           : num [1:5665] 0 0.01 0.02 0.03 0.04 0.05 0.06 0.07 0.08 0.09 ...
.. .. .@ dose.type       : chr "absolute"
.. .. .@ dose.units      : chr "Gy"
.. .. .@ volumes         : num [1:5665] 0 0 0 0 0 0 0 0 0 ...

```

```

.. .. .@ volume.type      : chr "absolute"
.. .. .$. PTV      :Formal class 'structure3D' [package "RadOnc"] with 9 slots
.. .. .@ name          : chr "PTV"
.. .. .@ volume        : num 0
.. .. .@ volume.units   : chr "cc"
.. .. .@ coordinate.units: chr "cm"
.. .. .@ vertices      : num [1:3314, 1:3] -29.3 -27.3 -25.4 -23.4 -21.5 ...
.. .. .@ origin        : num [1:3] -11.8 -237.1 -52.7
.. .. .@ triangles     : logi[1:3, 0 ]
.. .. .@ closed.polys  :List of 27
.. .. .$. : num [1:64, 1:3] -29.3 -27.3 -25.4 -23.4 -21.5 ...
.. .. .$. : num [1:78, 1:3] -31.2 -29.3 -27.3 -25.4 -23.4 ...
.. .. .$. : num [1:94, 1:3] -33.2 -31.2 -29.3 -27.3 -25.4 ...
.. .. .$. : num [1:106, 1:3] -29.3 -27.3 -25.4 -23.4 -21.5 ...
.. .. .$. : num [1:112, 1:3] -31.2 -29.3 -27.3 -25.4 -23.4 ...
.. .. .$. : num [1:126, 1:3] -33.2 -31.2 -29.3 -27.3 -25.4 ...
.. .. .$. : num [1:130, 1:3] -31.2 -29.3 -27.3 -25.4 -23.4 ...
.. .. .$. : num [1:136, 1:3] -29.3 -27.3 -25.4 -23.4 -21.5 ...
.. .. .$. : num [1:134, 1:3] -27.3 -25.4 -23.4 -21.5 -20.4 ...
.. .. .$. : num [1:136, 1:3] -41 -39.1 -37.1 -35.2 -33.2 ...
.. .. .$. : num [1:134, 1:3] -37.1 -35.2 -33.2 -31.2 -29.3 ...
.. .. .$. : num [1:132, 1:3] -23.4 -21.5 -19.5 -17.6 -15.6 ...
.. .. .$. : num [1:128, 1:3] -19.5 -17.6 -15.6 -13.7 -11.7 ...
.. .. .$. : num [1:134, 1:3] -21.5 -19.5 -17.6 -15.6 -13.7 ...
.. .. .$. : num [1:138, 1:3] -13.67 -11.72 -9.77 -7.81 -6.71 ...
.. .. .$. : num [1:144, 1:3] -19.5 -17.6 -15.6 -13.7 -11.7 ...
.. .. .$. : num [1:142, 1:3] -21.5 -19.5 -17.6 -15.6 -13.7 ...
.. .. .$. : num [1:144, 1:3] -17.58 -15.63 -13.67 -11.72 -9.77 ...
.. .. .$. : num [1:142, 1:3] -19.5 -17.6 -15.6 -13.7 -11.7 ...
.. .. .$. : num [1:140, 1:3] -21.5 -19.5 -17.6 -15.6 -13.7 ...
.. .. .$. : num [1:136, 1:3] -19.5 -17.6 -15.6 -13.7 -11.7 ...
.. .. .$. : num [1:130, 1:3] -17.58 -15.63 -13.67 -11.72 -9.77 ...
.. .. .$. : num [1:122, 1:3] -17.58 -15.63 -13.67 -11.72 -9.77 ...
.. .. .$. : num [1:118, 1:3] -15.63 -13.67 -11.72 -9.77 -7.81 ...
.. .. .$. : num [1:116, 1:3] -13.67 -11.72 -9.77 -7.81 -5.86 ...
.. .. .$. : num [1:104, 1:3] -13.67 -11.72 -9.77 -7.81 -5.86 ...
.. .. .$. : num [1:94, 1:3] -9.77 -7.81 -5.86 -3.91 -1.95 -0.6 0 1.95 3.91 5.14 ...
.. .. .- attr(*, "dim")= int [1:2] 27 1
.. .. .@ DVH          :Formal class 'DVH' [package "RadOnc"] with 22 slots
.. .. .@ patient      : chr ""
.. .. .@ ID           : chr ""
.. .. .@ structure.name : chr "PTV"
.. .. .@ structure.volume: num 241
.. .. .@ type         : chr "differential"
.. .. .@ dose.max     : num 56.6
.. .. .@ dose.min     : num 47.1
.. .. .@ dose.mean    : num 54.7
.. .. .@ dose.median  : num 0

```

```

.. .. .. .. .. .. .. .. ..@ dose.mode           : num 0
.. .. .. .. .. .. .. .. ..@ dose.STD           : num 0
.. .. .. .. .. .. .. .. ..@ conf.index         : num 0
.. .. .. .. .. .. .. .. ..@ equiv.sphere       : num 0
.. .. .. .. .. .. .. .. ..@ gradient           : num 0
.. .. .. .. .. .. .. .. ..@ dose.rx            : num 55
.. .. .. .. .. .. .. .. ..@ dose.fx            : num 25
.. .. .. .. .. .. .. .. ..@ rx.isodose         : num 100
.. .. .. .. .. .. .. .. ..@ doses              : num [1:5665] 0 0.01 0.02 0.03 0.04 0.05 0.06 0.07 0.08 0.09 .
.. .. .. .. .. .. .. .. ..@ dose.type          : chr "absolute"
.. .. .. .. .. .. .. .. ..@ dose.units         : chr "Gy"
.. .. .. .. .. .. .. .. ..@ volumes            : num [1:5665] 0 0 0 0 0 0 0 0 0 ...
.. .. .. .. .. .. .. .. ..@ volume.type        : chr "absolute"

```

The format for cord is:

Formal class 'structure3D' [package "RadOnc"] with 9 slots

```

..@ name           : chr "Spinal Cord"
..@ volume         : num 0
..@ volume.units   : chr "cc"
..@ coordinate.units: chr "cm"
..@ vertices       : num [1:2682, 1:3] -10.74 -8.79 -6.84 -4.88 -3.13 ...
.. ..- attr(*, "dimnames")=List of 2
.. .. ..$ : chr [1:2682] "" "" "" "" ...
.. .. ..$ : NULL
..@ origin         : num [1:3] -3.43 -235.27 -173.95
..@ triangles      : num [1:3, 1:5360] 20 1 21 1 2 22 2 3 23 3 ...
..@ closed.polys   :List of 130
.. ..$ : num [1:20, 1:3] -10.74 -8.79 -6.84 -4.88 -3.13 ...
.. ..$ : num [1:18, 1:3] -10.74 -8.79 -6.84 -4.88 -3.15 ...
.. ..$ : num [1:20, 1:3] -6.84 -6.1 -4.88 -2.93 -2.62 -1.68 -1.77 -2.53 -2.93 -4.88 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.95 -4.88 -2.93 -2.16 -1.36 -1.41 -2.33 -2.93 -4.88 ...
.. ..$ : num [1:20, 1:3] -8.79 -6.84 -4.88 -3.34 -2.93 -2.07 -1.72 -2.38 -2.93 -4.26 ...
.. ..$ : num [1:20, 1:3] -8.79 -6.84 -4.88 -4.67 -2.93 -2.67 -2.12 -2.31 -2.93 -3.45 ...
.. ..$ : num [1:20, 1:3] -8.79 -6.84 -4.88 -3.99 -2.93 -2.14 -1.77 -2.01 -2.93 -3.61 ...
.. ..$ : num [1:20, 1:3] -8.79 -6.84 -4.88 -2.93 -2.91 -1.75 -1.55 -2.01 -2.93 -3.65 ...
.. ..$ : num [1:20, 1:3] -8.79 -6.84 -4.88 -2.93 -2.62 -1.53 -1.4 -1.95 -2.93 -4.08 ...
.. ..$ : num [1:20, 1:3] -8.79 -6.84 -4.88 -2.93 -2.51 -1.4 -1.37 -2.18 -2.93 -4.88 ...
.. ..$ : num [1:18, 1:3] -8.79 -6.84 -4.88 -2.93 -1.77 -1.28 -1.89 -2.93 -3.54 -4.88 ...
.. ..$ : num [1:16, 1:3] -6.84 -4.88 -2.99 -2.93 -1.06 -1.34 -2.51 -2.93 -4.88 -6.84 ...
.. ..$ : num [1:18, 1:3] -6.84 -4.88 -2.93 -2.21 -0.98 -0.67 -0.8 -0.98 -2.01 -2.93 ...
.. ..$ : num [1:18, 1:3] -8.79 -6.84 -4.88 -2.93 -1.37 -0.98 -0.54 -0.56 -0.98 -1.49 ...
.. ..$ : num [1:20, 1:3] -8.79 -6.84 -4.88 -2.93 -1.43 -0.98 -0.34 -0.38 -0.98 -1.61 ...
.. ..$ : num [1:18, 1:3] -8.79 -6.84 -4.88 -2.93 -1.36 -0.98 -0.55 -0.56 -0.98 -1.49 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -2.87 -1.03 -0.98 -0.23 -0.46 -0.98 -1.89 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -2.26 -0.98 -0.64 -0.23 -0.55 -0.98 -2.03 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -2.34 -0.98 -0.57 -0.18 -0.57 -0.98 -2.44 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -2.26 -0.98 -0.67 -0.27 -0.92 -0.98 -2.93 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -2.18 -0.98 -0.79 -0.49 -0.98 -1.12 -2.93 ...

```

```
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -3.66 -2.93 -1.04 -0.98 -0.18 -0.16 -0.98 -1.46 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -1.51 -0.98 -0.06 0.28 -0.14 -0.98 -1.75 ...
.. ..$ : num [1:18, 1:3] -6.84 -4.88 -2.93 -0.98 -0.92 0.31 0.18 -0.92 -0.98 -2.93 ...
.. ..$ : num [1:18, 1:3] -6.84 -4.88 -2.93 -0.98 -0.46 0.44 -0.09 -0.98 -2.93 -4.83 ...
.. ..$ : num [1:18, 1:3] -6.84 -4.88 -2.93 -0.98 -0.92 0.34 0.31 -0.98 -1.95 -2.93 ...
.. ..$ : num [1:18, 1:3] -6.84 -4.88 -2.93 -1.64 -0.98 0.07 0.56 -0.69 -0.98 -2.93 ...
.. ..$ : num [1:20, 1:3] -4.88 -2.93 -2.83 -0.98 -0.46 0.43 0.34 -0.98 -1.07 -2.93 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -1.03 -0.98 0.26 0.55 -0.02 -0.98 -1.5 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -2.25 -0.98 -0.31 0.46 0.23 -0.92 -0.98 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -0.98 -0.62 0.4 0.51 -0.2 -0.98 -2.61 ...
.. ..$ : num [1:22, 1:3] -4.88 -2.93 -2.83 -0.98 -0.23 0.55 0.55 -0.18 -0.98 -2.83 ...
.. ..$ : num [1:22, 1:3] -4.88 -2.93 -2.2 -0.98 -0.08 0.53 0.49 -0.33 -0.98 -2.93 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -1.65 -0.98 0.11 0.43 0.23 -0.98 -1.07 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -1.21 -0.98 0.02 0.27 -0.27 -0.98 -2.15 ...
.. ..$ : num [1:20, 1:3] -4.88 -2.93 -2.81 -0.98 -0.06 0.92 0.67 -0.34 -0.98 -2.93 ...
.. ..$ : num [1:20, 1:3] -4.88 -2.93 -0.98 -0.58 0.95 0.98 1.37 0.98 0.98 -0.54 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -0.98 -0.79 0.49 0.8 0.18 -0.98 -2.05 ...
.. ..$ : num [1:20, 1:3] -8.79 -6.84 -4.88 -2.93 -1.09 -0.98 -0.11 -0.03 -0.76 -0.98 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -2.25 -0.98 -0.18 0.46 -0.06 -0.98 -1.86 ...
.. ..$ : num [1:18, 1:3] -6.84 -4.88 -2.93 -0.98 -0.6 0.58 0.8 -0.3 -0.98 -2.93 ...
.. ..$ : num [1:18, 1:3] -6.84 -4.88 -2.93 -0.98 -0.16 0.92 0.92 -0.13 -0.98 -2.93 ...
.. ..$ : num [1:22, 1:3] -4.88 -2.93 -2.29 -0.98 0.32 0.98 1.07 0.98 0.94 -0.05 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -1.07 -0.98 0.34 0.92 0.34 -0.98 -1.56 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -0.98 -0.5 0.43 0.49 -0.3 -0.98 -2.93 ...
.. ..$ : num [1:18, 1:3] -6.84 -4.88 -2.93 -0.98 -0.18 0.79 0.8 -0.34 -0.98 -2.93 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -0.98 0.03 0.97 0.98 1.06 0.98 -0.4 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -1.34 -0.98 0.31 0.79 0.43 -0.98 -2.34 ...
.. ..$ : num [1:18, 1:3] -6.84 -4.88 -2.93 -0.98 -0.57 0.41 0.5 -0.29 -0.98 -2.93 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -2.1 -0.98 -0.46 0 -0.55 -0.98 -2.49 ...
.. ..$ : num [1:22, 1:3] -6.84 -4.88 -3.95 -2.93 -1.28 -0.98 -0.54 -0.59 -0.98 -1.59 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -3.09 -2.93 -1.03 -0.98 -0.23 -0.46 -0.98 -1.89 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -2.47 -0.98 -0.72 -0.24 -0.51 -0.98 -1.92 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -2.08 -0.98 -0.23 0.06 -0.16 -0.98 -1.88 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -1.59 -0.98 -0.08 0.31 -0.11 -0.98 -1.68 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -2.7 -0.98 -0.69 0.06 -0.06 -0.98 -1.17 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -1.33 -0.98 -0.2 0 -0.57 -0.98 -2.64 ...
.. ..$ : num [1:20, 1:3] -4.88 -2.93 -2.85 -0.98 -0.55 0.34 0.23 -0.79 -0.98 -2.93 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -1.59 -0.98 0.09 0.56 0.23 -0.98 -1.14 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -0.98 -0.67 0.43 0.55 -0.11 -0.98 -2.31 ...
.. ..$ : num [1:20, 1:3] -4.88 -2.93 -2.3 -0.98 -0.1 0.52 0.34 -0.77 -0.98 -2.93 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -1.24 -0.98 0.18 0.43 -0.11 -0.98 -2.05 ...
.. ..$ : num [1:20, 1:3] -4.88 -3.48 -2.93 -0.98 -0.56 0.23 0.18 -0.73 -0.98 -2.93 ...
.. ..$ : num [1:20, 1:3] -4.88 -2.93 -2.66 -0.98 -0.11 0.55 0.46 -0.55 -0.98 -2.93 ...
.. ..$ : num [1:20, 1:3] -4.88 -2.93 -2.24 -0.98 0.11 0.78 0.63 -0.43 -0.98 -2.93 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -1.38 -0.98 0.34 0.67 0.18 -0.98 -1.3 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -1.3 -0.98 0.18 0.67 0.34 -0.98 -1.38 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -0.98 -0.41 0.64 0.78 0.1 -0.98 -2.27 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -1.27 -0.98 0.06 0.55 0.06 -0.98 -1.27 ...
```



```

.. ..$ : num [1:20, 1:3] -4.88 -2.93 -2.49 -0.98 -0.17 0.52 0.38 -0.68 -0.98 -2.93 ...
.. ..$ : num [1:22, 1:3] -6.84 -4.88 -2.93 -0.98 -0.92 0.67 0.98 1.04 0.98 0.55 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -0.98 0.22 0.98 1.27 1.33 0.98 0.63 ...
.. ..$ : num [1:22, 1:3] -4.88 -2.93 -2.12 -0.98 0.34 0.98 1.38 1.26 0.98 0.11 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -0.98 -0.23 0.98 1.15 1.49 0.98 0.69 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -0.98 0.37 0.98 1.31 1.32 0.98 0.51 ...
.. ..$ : num [1:20, 1:3] -6.84 -4.88 -2.93 -0.98 -0.34 0.92 0.98 1.26 0.98 0.46 ...
.. ..$ : num [1:20, 1:3] -4.88 -2.93 -0.98 -0.69 0.92 0.98 1.36 1.03 0.98 -0.43 ...
.. ..$ : num [1:20, 1:3] -4.88 -2.93 -0.98 -0.35 0.98 1.4 1.9 1.53 0.98 -0.13 ...
.. ..$ : num [1:20, 1:3] -4.88 -2.93 -0.98 0.08 0.98 1.7 2.16 1.82 0.98 0.39 ...
.. ..$ : num [1:20, 1:3] -4.88 -2.93 -0.98 0 0.98 1.53 2.3 2.01 0.98 0.9 ...
.. ..$ : num [1:20, 1:3] -2.93 -0.98 0 0.98 2.26 2.91 2.75 1.66 0.98 -0.98 ...
.. ..$ : num [1:18, 1:3] -4.88 -2.93 -0.98 0.98 1.16 2.38 2.62 1.89 0.98 -0.12 ...
.. ..$ : num [1:18, 1:3] -4.88 -2.93 -0.98 -0.17 0.98 1.82 2.39 2.16 1 0.98 ...
.. ..$ : num [1:20, 1:3] -4.88 -2.93 -0.98 0.57 0.98 2.07 2.38 1.77 0.98 0.1 ...
.. ..$ : num [1:20, 1:3] -2.93 -0.98 0.08 0.98 1.9 2.38 2.07 0.98 0.57 -0.98 ...
.. ..$ : num [1:20, 1:3] -4.88 -2.93 -0.98 0.91 0.98 2.14 2.4 1.86 0.98 -0.11 ...
.. ..$ : num [1:20, 1:3] -4.88 -2.93 -0.98 0.98 1.16 2.3 2.38 1.61 0.98 -0.71 ...
.. ..$ : num [1:20, 1:3] -4.88 -2.93 -0.98 0 0.98 1.79 2.26 1.95 0.98 0.45 ...
.. ..$ : num [1:20, 1:3] -4.88 -2.93 -0.98 0.52 0.98 1.85 2.15 1.66 0.98 -0.07 ...
.. ..$ : num [1:22, 1:3] -2.93 -2.44 -0.98 0.98 1.28 2.33 2.26 1.4 0.98 -0.73 ...
.. ..$ : num [1:20, 1:3] -4.88 -2.93 -0.98 0.98 1.88 2.93 2.99 3.22 2.93 2.26 ...
.. ..$ : num [1:22, 1:3] -2.93 -0.98 -0.02 0.98 2.7 2.93 3.43 3.38 2.93 2.4 ...
.. ..$ : num [1:20, 1:3] -2.93 -0.98 0.84 0.98 2.87 2.93 3.63 3.33 2.93 1.89 ...
.. ..$ : num [1:20, 1:3] -2.93 -0.98 0.98 1.88 2.93 3.45 3.56 2.93 2.62 0.98 ...
.. ..$ : num [1:18, 1:3] -4.88 -2.93 -0.98 0.98 2.41 2.93 3.44 3.4 2.93 2.47 ...
.. ..$ : num [1:20, 1:3] -4.88 -2.93 -0.98 0.98 2.34 2.93 3.63 3.56 2.93 2.38 ...
.. ..$ : num [1:22, 1:3] -0.98 -0.37 0.98 2.5 2.93 3.63 3.56 2.93 2.38 0.98 ...
.. ..$ : num [1:20, 1:3] -0.98 -0.37 0.98 2.64 2.93 3.43 3.4 2.93 2.47 0.98 ...
.. ..$ : num [1:20, 1:3] -2.93 -0.98 0.37 0.98 2.75 2.93 3.56 3.33 2.93 2.01 ...
.. .. [list output truncated]
.. ..- attr(*, "dim")= int [1:2] 130 1
..@ DVH :Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. ..@ patient : chr ""
.. .. ..@ ID : chr ""
.. .. ..@ structure.name : chr ""
.. .. ..@ structure.volume: num 0
.. .. ..@ type : chr "cumulative"
.. .. ..@ dose.max : num 0
.. .. ..@ dose.min : num 0
.. .. ..@ dose.mean : num 0
.. .. ..@ dose.median : num 0
.. .. ..@ dose.mode : num 0
.. .. ..@ dose.STD : num 0
.. .. ..@ conf.index : num 0
.. .. ..@ equiv.sphere : num 0
.. .. ..@ gradient : num 0
.. .. ..@ dose.rx : num 0

```

```

.. .. ..@ dose.fx      : num 0
.. .. ..@ rx.isodose   : num 100
.. .. ..@ doses        : num(0)
.. .. ..@ dose.type    : chr "absolute"
.. .. ..@ dose.units   : chr "cGy"
.. .. ..@ volumes      : num(0)
.. .. ..@ volume.type  : chr "relative"

```

The format for mandible is:

Formal class 'structure3D' [package "RadOnc"] with 9 slots

```

..@ name      : chr "Mandible"
..@ volume    : num 0
..@ volume.units : chr "cc"
..@ coordinate.units: chr "cm"
..@ vertices  : num [1:6994, 1:3] -12.7 -10.74 -8.79 -6.84 -4.88 ...
.. ..- attr(*, "dimnames")=List of 2
.. .. ..$ : chr [1:6994] "" "" "" "" ...
.. .. ..$ : NULL
..@ origin    : num [1:3] -1.93 -151.83 -122.85
..@ triangles : num [1:3, 1:13984] 46 47 49 48 1 50 1 2 51 2 ...
..@ closed.polys :List of 104
.. ..$ : num [1:48, 1:3] -12.7 -10.74 -8.79 -6.84 -4.88 ...
.. ..$ : num [1:52, 1:3] -14.65 -12.7 -10.74 -8.79 -6.84 ...
.. ..$ : num [1:68, 1:3] -14.65 -12.7 -10.74 -8.79 -6.84 ...
.. ..$ : num [1:74, 1:3] -14.65 -12.7 -10.74 -8.79 -6.84 ...
.. ..$ : num [1:80, 1:3] -6.84 -6.51 -4.88 -2.93 -0.98 0.98 1.17 2.93 4.88 6.08 ...
.. ..$ : num [1:90, 1:3] -10.74 -8.79 -6.84 -4.88 -2.93 ...
.. ..$ : num [1:94, 1:3] -10.74 -8.79 -6.84 -4.88 -2.93 ...
.. ..$ : num [1:98, 1:3] -10.74 -8.79 -6.84 -4.88 -2.93 ...
.. ..$ : num [1:110, 1:3] -8.79 -6.84 -5.62 -4.88 -2.93 -0.98 0.98 1.27 2.93 4.77 ...
.. ..$ : num [1:118, 1:3] -8.79 -6.84 -5.09 -4.88 -2.93 -0.98 0.98 1.52 2.93 4.88 ...
.. ..$ : num [1:124, 1:3] -8.79 -6.84 -4.88 -2.93 -0.98 -0.61 0.98 2.93 3.35 4.88 ...
.. ..$ : num [1:136, 1:3] -8.79 -6.84 -4.88 -2.93 -0.98 0.94 0.98 2.93 4.88 5.94 ...
.. ..$ : num [1:140, 1:3] -12.7 -10.74 -8.79 -6.84 -4.88 ...
.. ..$ : num [1:150, 1:3] -8.79 -6.84 -4.88 -2.93 -2.66 -0.98 0.98 2.93 4.88 5.28 ...
.. ..$ : num [1:154, 1:3] -12.7 -10.74 -8.79 -6.84 -4.88 ...
.. ..$ : num [1:172, 1:3] -10.74 -8.79 -6.84 -4.88 -2.93 ...
.. ..$ : num [1:178, 1:3] -14.65 -12.7 -10.74 -8.79 -6.84 ...
.. ..$ : num [1:184, 1:3] -8.79 -6.84 -4.88 -2.93 -1.95 -0.98 0.98 2.93 4.88 6.84 ...
.. ..$ : num [1:202, 1:3] -8.79 -6.84 -4.88 -2.93 -1.46 -0.98 0.98 2.93 4.88 6.84 ...
.. ..$ : num [1:210, 1:3] -8.79 -6.84 -4.88 -2.93 -0.98 0.9 0.98 2.93 4.88 6.84 ...
.. ..$ : num [1:108, 1:3] -0.98 0.98 1.95 2.93 3.91 4.88 6.84 6.98 8.79 9.94 ...
.. ..$ : num [1:94, 1:3] -20.5 -18.6 -16.6 -14.7 -12.7 ...
.. ..$ : num [1:94, 1:3] 12.7 14.7 15.5 16.6 17.3 ...
.. ..$ : num [1:84, 1:3] -26.4 -24.4 -22.5 -20.9 -20.5 ...
.. ..$ : num [1:94, 1:3] 14.7 15.3 16.6 17.4 18.6 ...
.. ..$ : num [1:86, 1:3] -26.4 -24.4 -22.7 -22.5 -20.5 ...
.. ..$ : num [1:90, 1:3] 12.7 14.7 16.6 18.3 18.6 ...

```

```
.. ..$ : num [1:82, 1:3] -26.4 -24.4 -22.5 -22 -20.5 ...
.. ..$ : num [1:80, 1:3] 22.5 24.4 24.8 26.4 26.9 ...
.. ..$ : num [1:76, 1:3] -30.3 -28.3 -26.4 -24.4 -22.5 ...
.. ..$ : num [1:78, 1:3] 20.5 22.5 24.4 26.1 26.4 ...
.. ..$ : num [1:74, 1:3] -32.2 -30.3 -28.3 -26.4 -24.4 ...
.. ..$ : num [1:74, 1:3] -32.2 -30.3 -28.3 -26.4 -24.4 ...
.. ..$ : num [1:76, 1:3] 20.5 22.5 24.4 26.4 27.2 ...
.. ..$ : num [1:72, 1:3] -32.2 -30.3 -28.3 -26.4 -24.6 ...
.. ..$ : num [1:72, 1:3] 22.5 24.4 26.4 28.3 30.3 ...
.. ..$ : num [1:72, 1:3] -32.2 -30.3 -28.3 -26.4 -25.6 ...
.. ..$ : num [1:70, 1:3] 22.5 24.4 26.4 28.3 30.3 ...
.. ..$ : num [1:68, 1:3] -36.1 -34.2 -32.2 -30.3 -28.3 ...
.. ..$ : num [1:70, 1:3] 24.4 26.4 28.3 30.3 32.2 ...
.. ..$ : num [1:70, 1:3] 30.3 32.2 34.2 36.1 38.1 ...
.. ..$ : num [1:68, 1:3] -38.1 -36.1 -34.2 -32.8 -32.2 ...
.. ..$ : num [1:66, 1:3] 34.2 36.1 37.7 38.1 39.3 ...
.. ..$ : num [1:64, 1:3] -42 -40 -38.1 -36.1 -34.2 ...
.. ..$ : num [1:66, 1:3] 36.1 36.8 38.1 38.7 39.8 ...
.. ..$ : num [1:62, 1:3] -44 -42 -40 -38.1 -36.1 ...
.. ..$ : num [1:64, 1:3] 36.1 36.8 38.1 39.2 40 ...
.. ..$ : num [1:60, 1:3] -40 -38.1 -36.1 -34.7 -34.2 ...
.. ..$ : num [1:62, 1:3] 36.1 36.6 38.1 39.5 40 ...
.. ..$ : num [1:56, 1:3] -42 -40 -38.1 -36.1 -34.2 ...
.. ..$ : num [1:62, 1:3] 36.1 36.3 38.1 39.3 40 ...
.. ..$ : num [1:56, 1:3] -42 -40 -38.1 -36.1 -34.2 ...
.. ..$ : num [1:60, 1:3] 34.2 36.1 38.1 39 40 ...
.. ..$ : num [1:58, 1:3] -44 -42 -40 -38.7 -38.1 ...
.. ..$ : num [1:58, 1:3] 34.2 36.1 38.1 38.8 40 ...
.. ..$ : num [1:58, 1:3] -44 -42 -40 -39.4 -38.1 ...
.. ..$ : num [1:58, 1:3] 34.2 36.1 38.1 39.2 40 ...
.. ..$ : num [1:58, 1:3] -44 -42 -40 -39.4 -38.1 ...
.. ..$ : num [1:56, 1:3] 36.1 38.1 38.9 40 40.3 ...
.. ..$ : num [1:54, 1:3] -42 -41.9 -40 -39.6 -38.1 ...
.. ..$ : num [1:56, 1:3] 36.1 38.1 39.6 40 40.6 ...
.. ..$ : num [1:58, 1:3] -44 -42 -41.8 -40 -39.7 ...
.. ..$ : num [1:56, 1:3] 36.1 38.1 39.7 40 40.9 ...
.. ..$ : num [1:54, 1:3] -44 -42 -41.4 -40 -39.5 ...
.. ..$ : num [1:58, 1:3] 36.1 38.1 38.9 40 40.3 ...
.. ..$ : num [1:54, 1:3] -44 -42 -40.9 -40 -39.3 ...
.. ..$ : num [1:58, 1:3] 36.1 38.1 39.3 40 40.4 ...
.. ..$ : num [1:50, 1:3] -44 -42 -40.6 -40 -39.5 ...
.. ..$ : num [1:54, 1:3] 36.1 38.1 39.5 40 41 ...
.. ..$ : num [1:52, 1:3] -45.9 -44 -42 -40.1 -40 ...
.. ..$ : num [1:52, 1:3] 38.1 39.9 40 41.4 41.9 ...
.. ..$ : num [1:52, 1:3] -45.9 -44.8 -44 -42 -40 ...
.. ..$ : num [1:54, 1:3] 38.1 38.4 40 40.6 41.7 ...
.. ..$ : num [1:52, 1:3] -45.9 -44 -42 -41.9 -40.1 ...
.. ..$ : num [1:54, 1:3] 38.1 39.9 40 41 41.8 ...
```

```

.. ..$ : num [1:48, 1:3] -45.9 -44 -42.2 -42 -40.8 ...
.. ..$ : num [1:52, 1:3] 38.1 40 40.7 41.6 42 ...
.. ..$ : num [1:48, 1:3] -45.9 -44 -42.4 -42 -41.5 ...
.. ..$ : num [1:54, 1:3] 38.1 39.1 40 41.3 42 ...
.. ..$ : num [1:48, 1:3] -45.9 -44.1 -44 -42.6 -42.6 ...
.. ..$ : num [1:54, 1:3] 38.1 40 40.5 41.8 42 ...
.. ..$ : num [1:48, 1:3] -45.9 -44 -43.4 -42.7 -42.6 ...
.. ..$ : num [1:54, 1:3] 38.1 40 41.3 42 42.1 ...
.. ..$ : num [1:52, 1:3] -45.9 -44.2 -44 -43.1 -43.1 ...
.. ..$ : num [1:22, 1:3] 40 40.2 41.9 42 43 ...
.. ..$ : num [1:22, 1:3] -45.9 -44 -43.6 -43 -43.1 ...
.. ..$ : num [1:24, 1:3] 45.9 47.5 47.8 47.9 49.2 ...
.. ..$ : num [1:24, 1:3] -49.8 -47.9 -47.4 -46.8 -46.7 ...
.. ..$ : num [1:16, 1:3] 40 40.8 42 42.4 43.2 ...
.. ..$ : num [1:22, 1:3] -45.9 -45.5 -44 -43.8 -43.5 ...
.. ..$ : num [1:26, 1:3] 45.9 46.4 47.9 48.1 49.3 ...
.. ..$ : num [1:22, 1:3] -49.8 -47.9 -47.8 -46.8 -46.2 ...
.. ..$ : num [1:12, 1:3] 40 41.7 42 42.6 43.2 ...
.. ..$ : num [1:18, 1:3] -47.9 -45.9 -44.5 -44 -44.1 ...
.. ..$ : num [1:24, 1:3] 45.9 47.9 48.2 49.4 49.8 ...
.. ..$ : num [1:22, 1:3] -49.8 -49.5 -47.9 -47.1 -46.2 ...
.. ..$ : num [1:12, 1:3] 40 41.3 42 43 43.4 ...
.. ..$ : num [1:18, 1:3] -47.9 -45.9 -44.9 -44.5 -44.5 ...
.. ..$ : num [1:24, 1:3] 47.9 48.5 49.6 49.8 50.8 ...
.. .. [list output truncated]
.. ..- attr(*, "dim")= int [1:2] 104 1
..@ DVH :Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. ..@ patient : chr ""
.. .. ..@ ID : chr ""
.. .. ..@ structure.name : chr ""
.. .. ..@ structure.volume: num 0
.. .. ..@ type : chr "cumulative"
.. .. ..@ dose.max : num 0
.. .. ..@ dose.min : num 0
.. .. ..@ dose.mean : num 0
.. .. ..@ dose.median : num 0
.. .. ..@ dose.mode : num 0
.. .. ..@ dose.STD : num 0
.. .. ..@ conf.index : num 0
.. .. ..@ equiv.sphere : num 0
.. .. ..@ gradient : num 0
.. .. ..@ dose.rx : num 0
.. .. ..@ dose.fx : num 0
.. .. ..@ rx.isodose : num 100
.. .. ..@ doses : num(0)
.. .. ..@ dose.type : chr "absolute"
.. .. ..@ dose.units : chr "cGy"
.. .. ..@ volumes : num(0)

```

```
.. .. ..@ volume.type      : chr "relative"
```

The format for teeth is:

Formal class 'structure.list' [package "RadOnc"] with 1 slots

```
..@ structures:List of 3
.. ..$ Tooth #1:Formal class 'structure3D' [package "RadOnc"] with 9 slots
.. .. ..@ name           : chr "Tooth #1"
.. .. ..@ volume         : num 0
.. .. ..@ volume.units   : chr "cc"
.. .. ..@ coordinate.units: chr "cm"
.. .. ..@ vertices       : num [1:324, 1:3] -28.3 -26.4 -24.4 -23.4 -22.5 ...
.. .. ..@ origin         : num [1:3] -25.2 -129.3 -100.7
.. .. ..@ triangles      : logi[1:3, 0 ]
.. .. ..@ closed.polys   :List of 23
.. .. .. ..$ : num [1:14, 1:3] -28.3 -26.4 -24.4 -23.4 -22.5 ...
.. .. .. ..$ : num [1:20, 1:3] -28.3 -26.4 -25.8 -24.4 -22.5 ...
.. .. .. ..$ : num [1:22, 1:3] -30.3 -28.3 -26.4 -24.4 -24.1 ...
.. .. .. ..$ : num [1:24, 1:3] -30.3 -28.3 -26.4 -24.4 -24.4 ...
.. .. .. ..$ : num [1:22, 1:3] -30.3 -28.3 -26.4 -24.4 -23.4 ...
.. .. .. ..$ : num [1:24, 1:3] -28.3 -27.5 -26.4 -24.4 -23.1 ...
.. .. .. ..$ : num [1:22, 1:3] -28.3 -26.4 -26.2 -24.4 -22.8 ...
.. .. .. ..$ : num [1:20, 1:3] -28.3 -26.4 -25.3 -24.4 -22.5 ...
.. .. .. ..$ : num [1:30, 1:3] -28.3 -27.9 -26.4 -24.4 -24.1 ...
.. .. .. ..$ : num [1:12, 1:3] -28.3 -26.6 -26.4 -24.4 -24 ...
.. .. .. ..$ : num [1:10, 1:3] -30.3 -28.3 -26.9 -26.4 -25 ...
.. .. .. ..$ : num [1:10, 1:3] -22.5 -20.5 -18.6 -17.9 -18.1 ...
.. .. .. ..$ : num [1:10, 1:3] -28.3 -28.2 -26.4 -24.4 -23.9 ...
.. .. .. ..$ : num [1:10, 1:3] -30.3 -28.3 -26.4 -25.6 -25.3 ...
.. .. .. ..$ : num [1:8, 1:3] -20.5 -18.6 -17 -17.6 -18.6 ...
.. .. .. ..$ : num [1:16, 1:3] -28.3 -26.4 -25 -24.5 -26.3 ...
.. .. .. ..$ : num [1:8, 1:3] -20.5 -18.6 -17.4 -18.1 -18.6 ...
.. .. .. ..$ : num [1:14, 1:3] -28.3 -26.4 -25.1 -26.3 -26.4 ...
.. .. .. ..$ : num [1:6, 1:3] -18.6 -17.3 -18.3 -18.6 -20.4 ...
.. .. .. ..$ : num [1:6, 1:3] -30.3 -28.3 -27.4 -28.3 -30.3 ...
.. .. .. ..$ : num [1:4, 1:3] -18.6 -17.3 -18.6 -19.7 -128.7 ...
.. .. .. ..$ : num [1:6, 1:3] -30.3 -28.3 -27.5 -28.3 -30.3 ...
.. .. .. ..$ : num [1:6, 1:3] -18.6 -17.4 -16.8 -18.6 -20.4 ...
.. .. .. ..- attr(*, "dim")= int [1:2] 23 1
.. .. ..@ DVH           :Formal class 'DVH' [package "RadOnc"] with 18 slots
.. .. .. ..@ patient     : chr ""
.. .. .. ..@ ID          : chr ""
.. .. .. ..@ structure.name : chr ""
.. .. .. ..@ structure.volume: num(0)
.. .. .. ..@ type        : chr "cumulative"
.. .. .. ..@ dose.max     : num 0
.. .. .. ..@ dose.min     : num 0
.. .. .. ..@ dose.mean    : num 0
.. .. .. ..@ dose.median  : num 0
```

```

.. .. .. .. .. .. ..@ dose.mode      : num 0
.. .. .. .. .. .. ..@ dose.STD      : num 0
.. .. .. .. .. .. ..@ conf.index     : num 0
.. .. .. .. .. .. ..@ equiv.sphere   : num 0
.. .. .. .. .. .. ..@ gradient       : num 0
.. .. .. .. .. .. ..@ dose.rx        : num 0
.. .. .. .. .. .. ..@ dose.fx        : num 0
.. .. .. .. .. .. ..@ rx.isodose     : num 100
.. .. .. .. .. .. ..@ doses          : num(0)
.. .. .. .. .. .. ..@ dose.type      : chr "absolute"
.. .. .. .. .. .. ..@ dose.units     : chr "cGy"
.. .. .. .. .. .. ..@ volumes        : num(0)
.. .. .. .. .. .. ..@ volume.type    : chr "relative"
.. .. $ Tooth #2:Formal class 'structure3D' [package "RadOnc"] with 9 slots
.. .. .. .. .. .. ..@ name           : chr "Tooth #2"
.. .. .. .. .. .. ..@ volume         : num 0
.. .. .. .. .. .. ..@ volume.units   : chr "cc"
.. .. .. .. .. .. ..@ coordinate.units: chr "cm"
.. .. .. .. .. .. ..@ vertices       : num [1:338, 1:3] -26.4 -26.2 -24.4 -23.5 -22.5 ...
.. .. .. .. .. .. ..@ origin         : num [1:3] -25.1 -129.4 -100.9
.. .. .. .. .. .. ..@ triangles      : logi[1:3, 0 ]
.. .. .. .. .. .. ..@ closed.polys   :List of 24
.. .. .. .. .. .. ..$ : num [1:16, 1:3] -26.4 -26.2 -24.4 -23.5 -22.5 ...
.. .. .. .. .. .. ..$ : num [1:22, 1:3] -28.3 -26.4 -25.8 -24.4 -22.5 ...
.. .. .. .. .. .. ..$ : num [1:24, 1:3] -30.3 -28.3 -26.4 -24.5 -24.4 ...
.. .. .. .. .. .. ..$ : num [1:22, 1:3] -28.3 -26.4 -24.4 -23.9 -22.5 ...
.. .. .. .. .. .. ..$ : num [1:24, 1:3] -30.3 -28.3 -26.4 -24.4 -22.8 ...
.. .. .. .. .. .. ..$ : num [1:24, 1:3] -28.3 -27.1 -26.4 -24.4 -23.2 ...
.. .. .. .. .. .. ..$ : num [1:24, 1:3] -28.3 -26.4 -25.9 -24.4 -22.5 ...
.. .. .. .. .. .. ..$ : num [1:24, 1:3] -30.3 -28.3 -26.4 -25 -24.4 ...
.. .. .. .. .. .. ..$ : num [1:18, 1:3] -28.3 -26.4 -24.7 -24.4 -22.8 ...
.. .. .. .. .. .. ..$ : num [1:10, 1:3] -22.5 -20.5 -18.6 -17.8 -18.6 ...
.. .. .. .. .. .. ..$ : num [1:14, 1:3] -28.3 -26.4 -26.3 -24.6 -24.4 ...
.. .. .. .. .. .. ..$ : num [1:10, 1:3] -30.3 -28.3 -26.6 -26.4 -25.7 ...
.. .. .. .. .. .. ..$ : num [1:10, 1:3] -22.5 -20.5 -18.6 -17.9 -18.3 ...
.. .. .. .. .. .. ..$ : num [1:24, 1:3] -28.3 -27.5 -26.4 -24.6 -24.4 ...
.. .. .. .. .. .. ..$ : num [1:8, 1:3] -20.5 -18.6 -16.9 -16.8 -18.6 ...
.. .. .. .. .. .. ..$ : num [1:10, 1:3] -28.3 -26.4 -24.4 -24.2 -24.3 ...
.. .. .. .. .. .. ..$ : num [1:8, 1:3] -30.3 -28.3 -27 -26.4 -28.3 ...
.. .. .. .. .. .. ..$ : num [1:10, 1:3] -20.5 -18.6 -16.6 -16.3 -16.4 ...
.. .. .. .. .. .. ..$ : num [1:6, 1:3] -28.3 -26.4 -25.3 -26.4 -28.3 ...
.. .. .. .. .. .. ..$ : num [1:6, 1:3] -30.3 -28.3 -27.1 -28.3 -30.3 ...
.. .. .. .. .. .. ..$ : num [1:6, 1:3] -18.6 -17.1 -17.6 -18.6 -18.6 ...
.. .. .. .. .. .. ..$ : num [1:6, 1:3] -30.3 -28.3 -26.9 -28.3 -30.3 ...
.. .. .. .. .. .. ..$ : num [1:8, 1:3] -18.6 -18.5 -16.6 -16.4 -16.6 ...
.. .. .. .. .. .. ..$ : num [1:4, 1:3] -18.6 -16.8 -18.6 -19.1 -129.4 ...
.. .. .. .. .. .. ..- attr(*, "dim")= int [1:2] 24 1
.. .. .. .. .. .. ..@ DVH           :Formal class 'DVH' [package "RadOnc"] with 18 slots

```



```

.. . . . . .$ : num [1:10, 1:3] -20.5 -18.6 -16.6 -16.5 -16.6 ...
.. . . . . .$ : num [1:16, 1:3] -28.3 -27.3 -26.4 -25.4 -26.4 ...
.. . . . . .$ : num [1:8, 1:3] -20.5 -18.6 -16.7 -17.7 -18.6 ...
.. . . . . .$ : num [1:6, 1:3] -30.3 -28.3 -27.2 -28.3 -30.3 ...
.. . . . . .$ : num [1:6, 1:3] -18.6 -18 -17.6 -18.6 -20.1 ...
.. . . . . .$ : num [1:6, 1:3] -30.3 -29.7 -28.7 -30.3 -30.6 ...
.. . . . . .$ : num [1:6, 1:3] -18.6 -16.7 -16.7 -18.6 -18.7 ...
.. . . . . .- attr(*, "dim")= int [1:2] 24 1
.. . . . .@ DVH      :Formal class 'DVH' [package "RadOnc"] with 18 slots
.. . . . . . .@ patient      : chr ""
.. . . . . . .@ ID         : chr ""
.. . . . . . .@ structure.name : chr ""
.. . . . . . .@ structure.volume: num(0)
.. . . . . . .@ type         : chr "cumulative"
.. . . . . . .@ dose.max      : num 0
.. . . . . . .@ dose.min      : num 0
.. . . . . . .@ dose.mean     : num 0
.. . . . . . .@ dose.median   : num 0
.. . . . . . .@ dose.mode     : num 0
.. . . . . . .@ dose.STD     : num 0
.. . . . . . .@ conf.index    : num 0
.. . . . . . .@ equiv.sphere  : num 0
.. . . . . . .@ gradient      : num 0
.. . . . . . .@ dose.rx       : num 0
.. . . . . . .@ dose.fx       : num 0
.. . . . . . .@ rx.isodose    : num 100
.. . . . . . .@ doses        : num(0)
.. . . . . . .@ dose.type     : chr "absolute"
.. . . . . . .@ dose.units    : chr "cGy"
.. . . . . . .@ volumes      : num(0)
.. . . . . . .@ volume.type   : chr "relative"

```

The format for stomach is:

Formal class 'zDVH' [package "RadOnc"] with 22 slots

```

..@ patient      : chr ""
..@ ID          : chr ""
..@ structure.name : chr "STOMACH"
..@ structure.volume: num 699
..@ type         : chr "differential"
..@ dose.max     : num 53.6
..@ dose.min     : num 0.594
..@ dose.mean    : num 12.5
..@ dose.median  : num 0
..@ dose.mode    : num 0
..@ dose.STD    : num 0
..@ conf.index   : num 0
..@ equiv.sphere : num 0
..@ gradient     : num 0

```



```

..@ dose.rx          : num 55
..@ dose.fx          : num 25
..@ rx.isodose       : num 100
..@ doses            : num [1:114] 0.125 0.5 1 1.5 2 2.5 3 3.5 4 4.5 ...
..@ dose.type        : chr "absolute"
..@ dose.units       : chr "Gy"
..@ volumes          : numeric [1:114, 1:48] 0 0 0 0 0 ...
.. ..- attr(*, "dimnames")=List of 2
.. .. ..$ : NULL
.. .. ..$ : chr [1:48] "-96" "-93" "-90" "-87" ...
.. ..- attr(*, "class")= chr [1:2] "numeric" "matrix"
..@ volume.type      : chr "absolute"

```

Examples

```
data(list="Rad0nc",package="Rad0nc")
```

read.DICOM.RT	<i>Read DICOM-RT data from an input directory</i>
---------------	---

Description

Function to extract three-dimensional structural and dosimetric data from input file(s) in DICOM-RT format

Usage

```
read.DICOM.RT(path, exclude=NULL, recursive=TRUE, verbose=TRUE, limit=NULL,
DVH=TRUE, zDVH=FALSE, ...)
```

Arguments

path	Location of directory containing relevant DICOM-RT information
exclude	Character string specifying exclusion criteria used to skip processing of specific file(s) within the DICOM-RT directory.
recursive	Logical (default is TRUE) specifying whether to recursively extract nested files located within a parent directory
verbose	Logical value (default is TRUE) indicating whether or not to output verbose information and status in text
limit	Numerical value specifying size threshold over which to skip processing of specific structures (number corresponds to the number of points used to define each structure surface)
DVH	Logical value (default is TRUE) indicating whether or not to calculate DVH data from DICOM-RT files (involves trilinear dose grid interpolation)
zDVH	Logical value (default is FALSE) indicating whether or not to extract axially-segmented (zDVH) data from DICOM-RT files (this parameter is ignored unless DVH=TRUE)
...	Additional parameters passed to readDICOM function

Value

Returns a single `structure.list` object containing all structures from input DICOM-RT file(s)

Author(s)

Reid F. Thompson (<reid.thompson@gmail.com>)

See Also

[readDICOM](#), [structure.list](#), [structure3D](#)

read.DVH	<i>Read DVH data from input file</i>
----------	--------------------------------------

Description

Function to extract DVH data from input file(s). Supported file formats include Aria (v8-11), DICOM-RT, CadPlan, and TomoTherapy.

Usage

```
read.DVH(file, type=NA, verbose=TRUE)
```

Arguments

file	Location of file containing relevant DVH information. One or more files may be specified. If multiple files are specified, all will be imported simultaneously.
type	Character vector specifying the DVH file format corresponding to each element in file. Value(s) must be one of "aria8", "aria10", "aria11", "dicom", "cadplan", or "tomo" (default is NA). Note that multiple different types can be processed so long as the length of type corresponds to the number of files specified.
verbose	Single logical value indicating whether or not to output verbose information and status in text

Value

Returns a single `DVH.list` object containing all DVH information from a single input file. If multiple files are specified, a list of `DVH.list` objects will be returned.

Author(s)

Reid F. Thompson (<reid.thompson@gmail.com>)

See Also

[DVH](#), [DVH.list](#), [new](#)

Examples

```
# Read two DVH example files
file1 <- system.file("extdata/John_Doe.dvh", package="Rad0nc")
johndoe <- read.DVH(file=file1, type="aria10", verbose=TRUE)
file2 <- system.file("extdata/Jane_Doe.dvh", package="Rad0nc")
janedoe <- read.DVH(file=file2, type="aria10", verbose=TRUE)
```

RTdata-class	<i>Class "RTdata"</i>
--------------	-----------------------

Description

A data structure containing a corresponding CT image, dose grid, and structure set

Objects from the Class

Objects can be created by calls of the form `new("RTdata", name, CT, dose, structures, ...)`.

Slots

name: Name of the dataset (e.g. "Patient XX")
CT: Object of class "array" containing computed tomography (CT) image data in Hounsfield units
dose: Object of class "array" containing dose grid data (pre-calculated using a separate treatment planning system) with a "dose.units" attribute specifying the units of dose.
structures: Object of class "structure.list" containing the corresponding structure set, indexed to the CT and dose grid coordinate systems

Methods

\$ Extract a given parameter from a RTdata object
\$<- Assign a value to a given parameter within a RTdata object
names Extract dataset name from an RTdata object
names<- Assign a name to an RTdata object
print Display summary of RTdata object
show Display summary of RTdata object

Author(s)

Reid F. Thompson (<reid.thompson@gmail.com>)

See Also

[structure.list](#)

Examples

```
showClass("RTdata")
```

structure.list-class *Class "structure.list"*

Description

A data structure containing one or more 3D structure ([structure3D](#)) objects

Objects from the Class

Objects can be created by calls of the form `new("structure.list", structures, ...)`.

Slots

structures: List of [structure3D](#) objects

Methods

[Extract subset of structure list (regular expressions may be specified if desired, see [regex](#) for more details)

[[Extract single [structure3D](#) object from structure list

[[<- Replace single [structure3D](#) object in structure list

\$ Extract parameter(s) from structure3D objects within structure list

as.list Convert a structure.list object to a list containing individual structure3D objects. Note that the reverse conversion can be performed using the [as](#) command and specifying `class="structure.list"`.

c Combine two or more structure lists and/or [structure3D](#) objects

lapply Apply function to a list of [structure3D](#) objects

length Extract number of [structure3D](#) objects in structure list

names Extract structure names for structure3D objects in structure list

names<- Assign structure name(s) to one or more structure3D objects in structure list

plot Plot all structures within a structure.list

print Display summary of structure list

range Compute the range (minimum and maximum coordinates) containing all structure3D objects in structure list

rev Return a structure list whose structure3D objects are in reverse order

show Display summary of structure list

Author(s)

Reid F. Thompson (<reid.thompson@gmail.com>)

See Also

[structure3D](#)

Examples

```
# Description of structure/slots in class
showClass("structure.list")
```

```
structure3D-class      Class "structure3D"
```

Description

A data structure containing 3D volumetric (structure3D) data and associated parameters for a single structure object

Objects from the Class

Objects can be created by calls of the form `new("structure3D", name, volume, volume.units, coordinate.units, vertices, origin, triangles, closed.polys, DVH)`

Slots

name: Name of the structure (e.g. "Stomach")

volume: Volume of the structure (in `volume.units`)

volume.units: A character string specifying the units of volume (must be "cc")

coordinate.units: A character string specifying the units of the coordinate system (must be one of "cm" or "mm")

vertices: Specifies all points defining the given structure, with data contained in a $N \times 3$ matrix where each column represents x , y , and z coordinates, respectively, for each of N points

origin: A numeric vector containing the x , y , and z coordinates corresponding to the center of the structure

triangles: Specifies a complete combination of points which define the triangular mesh surface of the structure; data is contained in a $3 \times N$ matrix where each row represents one of the three vertices of a each triangle within the mesh, with N columns corresponding to the number of triangles; note that the value of each element in `triangles` references a point in `vertices`, such that all values in `triangles` must be between 1 and `dim(vertices)[1]`

closed.polys: Specifies a complete set of axially-defined closed polygons which, together, comprise the surface of the structure; data is contained in a list of $N \times 3$ matrices where each row represents the x , y , and z coordinates of a point in a single polygon

DVH: Object of class [DVH](#)

Methods

\$ Extract a given parameter from a structure3D object

\$<- Assign a value to a given parameter within a structure3D object

c Combine multiple structure3D objects into a single `structure.list`

dim Extract dimensions (number of vertices and axial slices) from structure3D object

names Extract structure name from structure3D object
names<- Assign structure name to a structure3D object
plot Plot structure3D object
print Display summary of structure3D object
range Extract coordinate range from structure3D object
show Display summary of structure3D object

Author(s)

Reid F. Thompson (<reid.thompson@gmail.com>)

See Also

[DVH](#)

Examples

```
# Description of structure/slots in class
showClass("structure3D")
data(list="Rad0nc", package="Rad0nc")
plot(mandible)
points3d(range(mandible), col="red")
```

zDVH-class

Class "zDVH"

Description

A data structure containing axially-segmented Dose-Volume Histogram (zDVH) data and associated parameters for a single structure

Objects from the Class

Objects can be created by calls of the form `new("zDVH", patient, structure.name, structure.volume, type, dose.m`

Slots

patient: Name of the patient (e.g. "Jane Doe")
ID: Additional patient identifier or medical record number (e.g. "123456789")
structure.name: Name of the structure (e.g. "Stomach")
structure.volume: Volume of the structure (in cubic centimeters)
type: A character string specifying the DVH type (must be one of "cumulative" or "differential")
dose.max: Maximum (point) dose contained within the structure
dose.min: Minimum dose contained within the structure
dose.mean: Mean dose to the structure

dose.median: Median dose to the structure
dose.mode: Modal dose to the structure
dose.STD: Standard deviation of dose to the structure
conf.index: Conformality index
equiv.sphere: Equivalent sphere (diameter in centimeters)
gradient: Dose gradient (in centimeters)
dose.rx: Prescription dose (in units specified by `dose.units`)
dose.fx: Fractional dose (in units specified by `dose.units`)
rx.isodose: Isodose line (%) receiving prescription dose (default is 100%)
doses: List of doses corresponding to "volumes"
dose.type: A character string specifying the dose type (must be one of "relative" or "absolute")
dose.units: A character string specifying the dose units (must be one of "cGy" or "Gy")
volumes: Matrix containing $N \times M$ dimensions, with $N = \text{length}(\text{doses})$ and M representing the number of axial segments for which of each a DVH was obtained
volume.type: A character string specifying the volume type (must be one of "relative" or "absolute")

Methods

[Extract dose or volume parameter(s) from zDVH object. Only one parameter may be specified at a time. Parameter specification should be of the form [`"<A><C>"`]: `<A>` is equivalent to "V" or "D", representing a volume or dose, respectively; `` usually denotes a numerical value specifying the dose or volume; and `<C>` represents the dose or volume units ("cGy", "Gy", "%", or "cc"). An example would be [`"V20Gy"`] which represents the volume of the structure receiving at least 20Gy dose. Specialized dosimetric keywords may also be used: "Dmax" (maximum dose), "Dmin" (minimum dose), "Dmean" (mean dose), "Dintegral" (estimated integral dose), "DRx" (prescription dose), and "volume" (total structure volume). If an improper parameter is specified however, NA results will be returned. See package documentation (vignette) for more details.

\$ Extract a given parameter from a zDVH object

\$<- Assign a value to a given parameter within a zDVH object

c Combine multiple zDVH objects into a single list

max Extract maximum dose from zDVH object

mean Extract mean dose from zDVH object

min Extract minimum dose from zDVH object

names Extract structure name from zDVH object

names<- Assign structure name to zDVH object

plot Plot zDVH object

print Display summary of zDVH object

range Extract dose range from zDVH object

show Display summary of zDVH object

sum Compute the total (summed) DVH from two or more zDVH and/or DVH objects. *Note that structures are assumed to be non-overlapping; any overlaps in structure volumes may generate inaccurate dose summation.*

Author(s)

Reid F. Thompson (<reid.thompson@gmail.com>)

See Also

[DVH](#), [DVH.list](#), [read.DVH](#), [plot](#)

Examples

```
# Description of structure/slots in class  
showClass("zDVH")
```


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