Package 'RadOnc'

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Type Package

Title Analytical Tools for Radiation Oncology

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Imports stats, utils

Depends R (>= 3.0.0), graphics, grDevices, methods, rgl, geometry, oro.dicom (>= 0.5.0), ptinpoly

Description Designed for the import, analysis, and visualization of dosimetric and volumetric data in Radiation Oncology, the tools herein enable import of dose-volume histogram information from multiple treatment planning system platforms and 3D structural representations and dosimetric information from 'DICOM-RT' files. These tools also enable subsequent visualization and statistical analysis of these data.

License GPL (>= 2)

LazyData yes

LazyLoad yes

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`RadOnc-package` *Analytical Tools for Radiation Oncology*

Description

Designed for the import, analysis, and visualization of dosimetric and volumetric data in Radiation Oncology, the tools herein enable import of dose-volume histogram information from multiple treatment planning system platforms and 3D structural representations and dosimetric information from 'DICOM-RT' files. These tools also enable subsequent visualization and statistical analysis of these data.

Details

The DESCRIPTION file:

Package:	RadOnc
Type:	Package
Title:	Analytical Tools for Radiation Oncology
Version:	1.1.5
Date:	2019-03-18
Author:	Reid F. Thompson <reid.thompson@gmail.com>
Maintainer:	Reid F. Thompson <reid.thompson@gmail.com>
Imports:	stats, utils
Depends:	R (>= 3.0.0), graphics, grDevices, methods, rgl, geometry, oro.dicom (>= 0.5.0), ptinpoly
Description:	Designed for the import, analysis, and visualization of dosimetric and volumetric data in Radiation Oncology, t
License:	GPL (>=2)
LazyData:	yes
LazyLoad:	yes

Index of help topics:

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DVH.list-class          Class '"DVH.list"'
LQE                     Linear Quadratic Extrapolated (LQE) Dose
                        Conversion
```

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RadOnc-package	Analytical Tools for Radiation Oncology
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compareStructures	Compare Axially-Defined Three-Dimensional Structures
gEUD	Generalized Equivalent Uniform Dose (gEUD) Calculation
get.HU	Extract Hounsfield Unit (HU) data for one or more structure(s) from a CT image
johndoe	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'
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structure3D-class	Class '"structure3D"'
subset.DVH.list	Extract a subset of a larger DVH list
zDVH-class	Class '"zDVH"'

Further information is available in the following vignettes:

RadOnc Documentation (source, pdf)

Author(s)

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References

Thompson, R.F. (2014) RadOnc: An R Package for Analysis of Dose-Volume Histogram and Three-Dimensional Structural Data. *J Radiat Oncol Inform* **6**(1):98-110.

See Also

DVH, DVH.list, structure3D, structure.list, RTdata

Examples

```
## See sub-documentation for detailed examples of important package functions ##
```

`calculate.DVH` *Calculate DVH data for one or more structure(s) using a dose grid*

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("RadOnc")
# 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 structure.list containing two or more structure3D objects.
method	One of "axial", "surface", "hausdorff", "DSC", or "EMD" 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. The "EMD" method is currently not currently supported (in development), but will return a modified earth mover's distance between two structures, accounting for radiation dose.

`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 NxN matrix of pairwise Hausdorff distances, where N is the number of structures in `structures`. When `method = "axial"` or `method = "surface"`, the function returns a Mx(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("RadOnc")
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.ma

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)

plan.sum: Logical specifying whether or not data represents a plan sum (default is FALSE)

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><B><C>"]: <A> is equivalent to "V" or "D", representing a volume or dose, respectively; <B> 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. Dose ranges may also be specified, for instance ["V10-20Gy"] or ["V<20Gy"]. Specialized dosimetric keywords may also be used: "Dmax" (maximum dose), "Dmin" (minimum dose), "Dmean" (mean dose), "Dmedian" (median 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 based on pattern matching with structure names (regular expressions may be specified if desired, see `regex` for more details). Note that case-insensitive matching is supported using the `"(?i)"` prefix, such that `DVHs["(?i)LIVER"]` will match any combination of upper and lowercase letters spelling "liver".

[[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="RadOnc", package="RadOnc")
print(johndoe)
plot(johndoe[c("LIVER", "PTV")], plot.type="i", col=c("red","blue"), lty=1:2, lwd=1:2)
```

---

get.HU *Extract Hounsfield Unit (HU) data for one or more structure(s) from a CT image*

Description

Function to extract Hounsfield Unit (HU) data for one or more structure(s) from a CT image.

Usage

```
## S4 method for signature 'RTdata,missing'
get.HU(x, CT, resolution.xyz=NA,resolution.HU=1, method=NULL)

## S4 method for signature 'structure3D,array'
get.HU(x, CT, resolution.xyz=NA, resolution.HU=1, method=NULL)

## S4 method for signature 'structure.list,array'
get.HU(x, CT, resolution.xyz=NA, resolution.HU=1, method=NULL)
```

Arguments

x	One of either a "structure3D" object, a "structure.list", or a "RTdata" object containing one or more structure(s).
CT	Object of class "array" containing CT imaging data. This parameter is not required if x contains a "RTdata" object including CT imaging data.
resolution.xyz	A numeric list containing three positive values representing *x*, *y*, and *z* resolution to be used for Hounsfield Unit (HU) interpolation from CT imaging data (specified in units of mm). The smaller each value, the longer the overall calculation time (default is c(NA, NA, NA) which is interpreted as the native CT image resolution). *z* resolution defaults to axial slice thickness when method="axial".
resolution.HU	A positive numeric value specifying the HU calculation interval (bin width) for histogram calculation.
method	Character value specifying the Hounsfield Unit (HU) calculation algorithm to employ. Must be NULL or "axial".

Value

Returns a single calculated "histogram" object or a "list" of "histogram" objects consisting of Hounsfield Unit values contained within the input "structure3D" or "structure.list", respectively.

Author(s)

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

See Also

RTdata, hist

---

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 = NULL)

## S3 method for class 'DVH.list'
plot(x, ..., plot.type = NULL)
```

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"`, `"bars"`, or `"correlation"`. Parameter `plot.type` 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

`alpha` When `plot.type="ttest"`, `"wilcox"`, or `"correlation"`, this specifies the numerical value (threshold) used to display significant p-values.

`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 paramater 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 paramater 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 paramater 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".

grid Logical, defaulting to FALSE. Determines whether or not to draw gridlines on 2D plot. Note that this parameter is relevant when plot.type="individual", "grouped", "ttest", or "wilcox" (it is ignored when plot.type="bars" or when plotting zDVH objects).

highlight The color to be used for shading p-value data when plot.type="ttest" or "wilcox". See colors for more options and information.

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.

Note that legend parameter is ignored when plot.type="wilcox" and panel.lower="difference".

legend.labels A character or expression vector specifying the text to appear in the legend, when relevant. Length of legend.labels must match the numer 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 paramater 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 paramater 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.

panel.lower Value specifying the lower panel plot content when plot.type="wilcox" (panel.lower must be one of "grouped" or "wilcox" [default]). Partial argument matching is used. When panel.lower="wilcox", the median groupwise differences will be displayed with associated confidence intervals obtained from wilcox.test(). When panel.lower="grouped", the individual groups are displayed with surrounding user-specified intervals (see width, quantile, and multiplier parameters).

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).

xlim A numeric vector of length 2 specifying the minimum and maximum x coordinates for plotting (note that this parameter is ignored when plot.type="bars", new=FALSE, or plotting object(s) of class zDVH).

ylim A numeric vector of length 2 specifying the minimum and maximum y coordinates for plotting (note that this parameter is ignored when plot.type="bars", new=FALSE, or plotting object(s) of class zDVH).

Additional Parameters

alternative When plot.type="ttest", "wilcox", or "correlation", alternative indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter. "greater" corresponds to positive association, "less" to negative association. See cor.test for more details.

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").

exact When plot.type="wilcox" or plot.type="correlation" and method="kendall" or "spearman", exact specifies a logical indicating whether an exact p-value should be computed. See cor.test or wilcox.test for more details.

method When plot.type="correlation", method specifies a character string indicating which correlation coefficient is to be computed. Value must be one of "pearson" (default), "kendall", or "spearman". See cor.test for more details.

mu When plot.type="ttest" or "wilcox", specifies an optional parameter used to form the null hypothesis. See t.test or wilcox.test for more details.

paired A logical value (default is FALSE) specifying whether or not to perform paired groupwise comparisons when plot.type="ttest" or "wilcox".

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

`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",
  # panel.lower="grouped")

  # plot(x, ..., plot.type="correlation")
# plot(janedoe, sample(1:100, 10), plot.type="correlation", method="kendall")
```

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
  .. .. .. ..@ plan.sum        : log FALSE
  .. .. .. ..@ 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
.. .. .. ..@ plan.sum        : log FALSE
.. .. .. ..@ 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
.. .. .. ..@ plan.sum        : log FALSE
.. .. .. ..@ 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
.. .. .. ..@ plan.sum        : log FALSE
.. .. .. ..@ 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
.. .. .. ..@ plan.sum        : log FALSE
.. .. .. ..@ 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
.. .. .. ..@ plan.sum        : log FALSE
.. .. .. ..@ 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
.. .. .. ..@ plan.sum        : log FALSE
.. .. .. ..@ 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
.. .. .. ..@ plan.sum        : log FALSE
.. .. .. ..@ 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
  .. .. .. ..@ plan.sum        : log FALSE
  .. .. .. ..@ 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
  .. .. .. ..@ plan.sum        : log FALSE
  .. .. .. ..@ 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
.. .. .. ..@ plan.sum        : log FALSE
.. .. .. ..@ 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
.. .. .. ..@ plan.sum        : log FALSE
.. .. .. ..@ 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
.. .. .. ..@ plan.sum        : log FALSE
.. .. .. ..@ 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
.. .. .. ..@ plan.sum        : log FALSE
.. .. .. ..@ 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
.. .. .. ..@ plan.sum        : log FALSE
.. .. .. ..@ 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
.. .. .. ..@ plan.sum        : log FALSE
.. .. .. ..@ 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
.. .. .. ..@ plan.sum        : log FALSE
.. .. .. ..@ 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
.. .. .. ..@ plan.sum        : log FALSE
.. .. .. ..@ 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
  .. .. .. ..@ plan.sum        : log FALSE
  .. .. .. ..@ 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
.. .. .. .. .. .. .. ..@ plan.sum        : log FALSE
.. .. .. .. .. .. .. ..@ 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 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
.. .. .. .. .. .. ..@ plan.sum        : log FALSE
.. .. .. .. .. .. ..@ 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 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
 .. .. .. .. .. .. .. ..@ plan.sum        : log FALSE
 .. .. .. .. .. .. .. ..@ 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 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
  .. .. ..@ plan.sum        : log FALSE
  .. .. ..@ 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
  .. .. ..@ plan.sum        : log FALSE
  .. .. ..@ 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
.. .. .. .. .. ..@ plan.sum        : log FALSE
.. .. .. .. .. ..@ 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
.. .. .. .. .. ..@ 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
.. .. .. .. .. ..@ plan.sum        : log FALSE
```

```
.. .. .. .. .. ..@ 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 #3:Formal class 'structure3D' [package "RadOnc"] with 9 slots
.. .. .. ..@ name            : chr "Tooth #3"
.. .. .. ..@ volume          : num 0
.. .. .. ..@ volume.units    : chr "cc"
.. .. .. ..@ coordinate.units: chr "cm"
.. .. .. ..@ vertices      : num [1:310, 1:3] -28.3 -26.4 -28.3 -29.4 -24.4 ...
.. .. .. ..@ origin          : num [1:3] -24.7 -129.4 -100.3
.. .. .. ..@ triangles       : logi[1:3, 0 ]
.. .. .. ..@ closed.polys    :List of 24
.. .. .. .. ..$ : num [1:4, 1:3] -28.3 -26.4 -28.3 -29.4 -126.7 ...
.. .. .. .. ..$ : num [1:6, 1:3] -24.4 -22.5 -22 -22.5 -24.4 ...
.. .. .. .. ..$ : num [1:16, 1:3] -28.3 -26.4 -24.4 -24 -22.5 ...
.. .. .. .. ..$ : num [1:22, 1:3] -28.3 -26.4 -24.4 -24.1 -22.5 ...
.. .. .. .. ..$ : num [1:22, 1:3] -28.3 -26.4 -24.4 -23.6 -22.5 ...
.. .. .. .. ..$ : num [1:24, 1:3] -28.3 -26.4 -24.4 -23.4 -22.5 ...
.. .. .. .. ..$ : num [1:22, 1:3] -28.3 -26.4 -24.4 -23 -22.5 ...
.. .. .. .. ..$ : num [1:24, 1:3] -28.3 -26.4 -25.2 -24.4 -22.5 ...
.. .. .. .. ..$ : num [1:22, 1:3] -28.3 -26.4 -24.7 -24.4 -22.5 ...
.. .. .. .. ..$ : num [1:22, 1:3] -28.3 -26.4 -24.4 -24.2 -22.9 ...
.. .. .. .. ..$ : num [1:14, 1:3] -28.3 -26.4 -24.4 -23.6 -24 ...
.. .. .. .. ..$ : num [1:10, 1:3] -22.5 -20.5 -18.6 -16.8 -17.6 ...
.. .. .. .. ..$ : num [1:8, 1:3] -28.3 -26.4 -24.4 -23.5 -24.4 ...
.. .. .. .. ..$ : num [1:8, 1:3] -28.3 -26.4 -26 -25.4 -26.4 ...
.. .. .. .. ..$ : num [1:10, 1:3] -20.5 -18.6 -16.6 -16.5 -16.6 ...
.. .. .. .. ..$ : num [1:10, 1:3] -28.3 -27.3 -26.4 -24.4 -24.2 ...
.. .. .. .. ..$ : num [1:8, 1:3] -30.3 -28.3 -26.4 -26.3 -26.4 ...
.. .. .. .. ..$ : 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
  .. .. .. .. .. ..@ plan.sum        : log FALSE
  .. .. .. .. .. ..@ 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
  ..@ plan.sum        : log FALSE
  ..@ 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="RadOnc",package="RadOnc")
```

`read.DICOM.RT` *Read DICOM-RT data from an input directory*

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, modality="CT", ...)
```

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`)
`modality`	Parameter used to specify the scan type expected in importing DICOM-RT data (must be one one of `"CT"` [default] or `"MR"`).
`...`	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 *Read DVH data from input file*

Description

Function to extract DVH data from input file(s). Supported file formats include Aria (v8-13), DICOM-RT, CadPlan, Monaco, RayStation, and TomoTherapy.

Usage

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

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 corresonding to each element in file. Value(s) must be one of "aria8", "aria10", "aria11", "aria13", "dicom", "cadplan", "monaco", "raystation", 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
collapse	Single logical value indicating whether or not to collapse input from multiple files into a single DVH.list with all structures (default) or to output a nested list of individual DVH.list objects with each one corresponding to a single input file
modality	When type="dicom", this parameter is used to specify the scan type expected in importing DICOM-RT data (must be one one of "CT" [default] or "MR").

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="RadOnc")
johndoe <- read.DVH(file=file1, type="aria10", verbose=TRUE)
file2 <- system.file("extdata/Jane_Doe.dvh", package="RadOnc")
janedoe <- read.DVH(file=file2, type="aria10", verbose=TRUE)
combined <- read.DVH(file=c(file1, file2), type="aria10", collapse=TRUE)
```

RTdata-class *Class* "RTdata"

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 Houndsfield 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 ojbects 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, ve

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 *Nx3* 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 *3xN* 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 *Nx3* 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="RadOnc", package="RadOnc")
# plot(mandible)
# points3d(range(mandible), col="red")
```

`subset.DVH.list` *Extract a subset of a larger DVH list*

Description

This function is designed to isolate one or more structure(s) from a list of DVH lists according to user input.

Usage

```
## S3 method for class 'DVH.list'
subset(x, structure, patient, ID, constraint, ignore.case=TRUE, select)
```

Arguments

x	Represents a DVH.list object (e.g. generated by read.DVH()).
structure	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).
patient	Vector used to sub-select specific patient data from x; may be a character vector containing patient names (regular expressions may be specified if desired, see regex for more details).
ID	Vector used to sub-select specific patient data from x using exact matching on patient identifiers.
constraint	Vector of one or more dosimetric constraints to apply to x to assess whether or not each component DVH should be included in the resultant list. More than one parameter may be specified at a time. Parameter specification should be of the form "<A><B><C> <?> <D>(<E>)": <A> is equivalent to "V" or "D", representing a volume or dose, respectively; <B> usually denotes a numerical value specifying the dose or volume; <C> represents the dose or volume units ("cGy", "Gy", "%", or "cc"); <?> represents a logical comparator (e.g. ">=" or "<" or "!="); <D> represents a comparative value; and <E> represents the units of comparison (e.g. "%" or "Gy"). An example would be "V20Gy < 50(%)" which represents a test of whether or not the volume of the structure receiving at least 20Gy dose is less than 50% of the overall structure volume. Dose ranges may also be specified, for instance "V10-20Gy" or "V<20Gy". Specialized dosimetric keywords may also be used: "Dmax" (maximum dose), "Dmin" (minimum dose), "Dmean" (mean dose), "Dmedian" (median 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.
ignore.case	Logical value specifying whether or not to use case-sensitive pattern matching; if TRUE (default), case is ignored during matching, and if FALSE, the pattern matching is *case sensitive*.
select	Must be one of "all" (default), "any", or "none". This value specifies the how to combine multiple selection inputs. When select = "all", a given DVH is only included in the resulting DVH list when it matches with all specififed inputs (for instance, must be a specific structure from a specific patient). When select = "any", a DVH may be included in the result DVH list if it matches any specified inputs. When select = "none", a DVH will only be included int eh resulting DVH list if it does not match with any of the specified criteria. For more details, see examples, below.

Value

Returns a single DVH list

Author(s)

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

See Also

DVH.list

Examples

```
data(list="RadOnc", package="RadOnc")
subset(johndoe, structure="kidney", constraint="Dmean < 500(cGy)", ignore.case=TRUE)
subset(johndoe, constraint="volume > 200(cc)")
```

---

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*x*M* dimensions, with *N*=`length(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><B><C>"]`: `<A>` is equivalent to `"V"` or `"D"`, representing a volume or dose, respectively; `<B>` 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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