

# Package ‘espadon’

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---

add.margin                      *Adding or removing a margin to a volume*

---

### Description

The add.margin function adds or subtracts a margin of the rectangular parallelepiped circumscribed by a volume.

### Usage

```
add.margin(vol, xyz.margin, alias = "", description = NULL)
```

### Arguments

vol	"volume" class object.
xyz.margin	Vector of the 3 positive or negative x, y and z margins in mm, in the frame of reference of volume cut planes.
alias	Character string, \$alias of the created object
description	Character string, describing the created object. If description = NULL (default value), it will be set to vol\$description

### Value

Returns a "volume" class object (see [espadon.class](#) for class definitions), in which 3D volume is restricted or increased by the requested margins. If the created volume exceeds the initial volume, new voxels are set to NA.

### See Also

[nesting.cube](#)

### Examples

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = "ct", roi.name = "",
                             dxyz = rep (step, 3))

CT <- patient$ct[[1]]

# Calculation of new volumes decreased by 10 mm in all directions.
new.CT <- add.margin (CT, xyz.margin = c (-10, -10, 10), alias = "new CT")
# display of the CT before and after, in the middle plane
z.mid <- apply (get.extreme.pt (CT), 1, mean)[3]
display.plane (bottom = CT, view.coord = z.mid, bottom.col = pal.RVV(1000),
               bottom.breaks = seq(-1000, 1000, length.out = 1001),
               bg = "#00ffff", interpolate = FALSE)
display.plane (bottom = new.CT, view.coord = z.mid, bottom.col = pal.RVV(1000),
               bottom.breaks = seq(-1000, 1000, length.out = 1001),
               bg = "#00ffff", interpolate = FALSE)
```

---

bin.closing	<i>Binary volume closing</i>
-------------	------------------------------

---

### Description

The `bin.closing` function performs a morphological operation of closing, using a sphere, on a "volume" class object of "binary" modality. Closing is useful for :

- filling holes that are smaller than the radius,
- merging two shapes close to each other.

### Usage

```
bin.closing(vol, radius = 10, alias = "", description = NULL)
```

### Arguments

<code>vol</code>	"volume" class object, of "binary" modality
<code>radius</code>	Positive number, in millimeters. By default, <code>radius = 10</code> .
<code>alias</code>	Character string, <code>\$object.alias</code> of the created object.
<code>description</code>	Character string, describing the created object. If <code>description = NULL</code> (default value), it will be set to <code>paste (vol\$object.alias, "closing r =", radius)</code> .

### Value

Returns a "volume" class object of "binary" modality (see [espadon.class](#) for class definitions), with the same grid as `vol`, in which `$vol3D.data` has been transformed by the closing operation.

### Note

Closing can be time consuming, try to reduce the binary volume to the strict minimum, before any operations.

### See Also

[bin.dilation](#), [bin.erosion](#), [bin.opening](#), [add.margin](#), [nesting.cube](#).

### Examples

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = "mr", roi.name = "",
                           dxyz = rep (step, 3))
MR <- patient$mr[[1]]

# generation of a binary volume
b <- bin.from.vol(MR, min = 15, max = 30)

b.closing <- bin.closing (b, radius = step)
display.plane (bottom = MR, top = b, main = "Before closing",
              view.coord = -20, interpolate = FALSE)
display.plane (bottom = MR, top = b.closing, main = "After closing",
              view.coord = -20, interpolate = FALSE)
```

---

bin.clustering      *Binary volume clustering*

---

### Description

The `bin.clustering` function groups and labels TRUE voxels that have a 6-connectivity (i.e. sharing a common side).

### Usage

```
bin.clustering(vol, alias = "", description = NULL)
```

### Arguments

<code>vol</code>	"volume" class object, of "binary" modality
<code>alias</code>	Character string, \$alias of the created object.
<code>description</code>	Character string, describing the created object. If <code>description = NULL</code> (default value), it will be set to <code>paste (vol\$object.alias, "clustering")</code>

### Value

Returns "volume" class object (see [espadon.class](#) for class definitions), of "cluster" modality. This object contains the `$cluster.info` field, detailing the label and volumes in  $cm^3$  of the different clusters. Note that the label "0" is used for the background.

### Examples

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = "ct", roi.name = "",
                             dxyz = rep (step, 3))
CT <- patient$ct[[1]]

# generation of a binary volume
b <- bin.from.vol(CT, min = -80, max = 20)

# Display of the n = 3 largest volumes
n <- 3
cluster.b <- bin.clustering (b)

col = c ("#00000000", rainbow (n))
breaks <- seq (0, n, length.out = n+2)
display.plane (CT, top = b, main = "Before clustering",
               view.coord = 50, top.col = col, top.breaks = breaks,
               interpolate = FALSE)
display.plane (CT, top = cluster.b, main = "After clustering",
               view.coord = 50, top.col = col, top.breaks = breaks,
               interpolate = FALSE)
```

---

bin.dilation	<i>Binary volume dilation</i>
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---

### Description

The `bin.dilation` function enlarges a "volume" class object, of "binary" modality, by means of convolution with a sphere. Dilation is useful for :

- filling holes that are smaller than the radius,
- enlarging capes,
- filling narrow channels,
- merging two shapes close to each other.

### Usage

```
bin.dilation(vol, radius = 10, alias = "", description = NULL)
```

### Arguments

<code>vol</code>	"volume" class object, of "binary" modality
<code>radius</code>	Positive number, in millimeters. By default, <code>radius = 10</code> .
<code>alias</code>	Character string, <code>\$object.alias</code> of the created object.
<code>description</code>	Character string, describing the created object. If <code>description = NULL</code> (default value), it will be set to <code>paste(vol\$object.alias, "dilatation r =", radius)</code> .

### Value

Returns a "volume" class object of "binary" modality (see [espadon.class](#) for class definitions), with the same grid as `vol`, in which the selected volume has been enlarged by the radius.

### Note

Dilation can be time consuming, try to reduce the binary volume to the strict minimum, before any operations.

### See Also

[bin.erosion](#), [bin.opening](#), [bin.closing](#), [add.margin](#), [nesting.cube](#).

### Examples

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient(modality = "mr", roi.name = "",
                           dxyz = rep(step, 3))
MR <- patient$mr[[1]]

# generation of a binary volume
b <- bin.from.vol(MR, min = 15,max = 30)
```

```

b.dilation <- bin.dilation (b, radius = step)
display.plane (bottom = MR, top = b, main = "Before dilation",
               view.coord = -20, interpolate = FALSE)
display.plane (bottom = MR, top = b.dilation, main = "After dilation",
               view.coord = -20, interpolate = FALSE)

```

---

bin.erosion

*Binary volume erosion*


---

### Description

The `bin.erosion` function decreases a "volume" class object, of "binary" modality, by means of convolution with a sphere. Erosion is useful for :

- removing volumes that are smaller than the radius,
- eliminating narrow capes,
- enlarging channels,
- turning peninsulas into islands.

### Usage

```
bin.erosion(vol, radius = 10, alias = "", description = NULL)
```

### Arguments

<code>vol</code>	"volume" class object, of "binary" modality
<code>radius</code>	Positive number, in millimeters. By default, <code>radius = 10</code> .
<code>alias</code>	Character string, <code>\$object.alias</code> of the created object.
<code>description</code>	Character string, describing the created object. If <code>description = NULL</code> (default value), it will be set to <code>paste (vol\$object.alias, "erosion r =", radius)</code> .

### Value

Returns a "volume" class object of "binary" modality (see [espadon.class](#) for class definitions), with the same grid as `vol`, in which the selected volume has been reduced by the radius.

### Note

Erosion can be time consuming, try to reduce the binary volume to the strict minimum, before any operations.

### See Also

[bin.dilation](#), [bin.opening](#), [bin.closing](#), [add.margin](#), [nesting.cube](#).



## Examples

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = "mr", roi.name = "",
                             dxyz = rep (step, 3))
MR <- patient$mr[[1]]

# generation of a binary volume
b <- bin.from.vol(MR, min = 15,max = 30)

b.erosion <- bin.erosion (b, radius = step)
display.plane (bottom = MR, top = b, main = "Before erosion",
               view.coord = -20, interpolate = FALSE)
display.plane (bottom = MR, top = b.erosion, main = "After erosion",
               view.coord = -20, interpolate = FALSE)
```

---

bin.from.roi

*Creation of a binary volume according to RoI*


---

## Description

The `bin.from.roi` function creates a "volume" class object, of "binary" modality, in which all the voxels of a RoI are set to TRUE.

## Usage

```
bin.from.roi(
  vol,
  struct,
  roi.name = NULL,
  roi.sname = NULL,
  roi.idx = NULL,
  T.MAT = NULL,
  within = TRUE,
  alias = "",
  description = NULL
)
```

## Arguments

<code>vol</code>	"volume" class object.
<code>struct</code>	"struct" class object.
<code>roi.name</code>	Vector of exact names of the RoI in the struct object. By default <code>roi.name = NULL</code> . See Details.
<code>roi.sname</code>	Vector of names or parts of names of the RoI in the struct object. By default <code>roi.sname = NULL</code> . See Details.
<code>roi.idx</code>	Vector of indices of the RoI that belong to the struct object. By default <code>roi.idx = NULL</code> . See Details.
<code>T.MAT</code>	"t.mat" class object, created by <a href="#">load.patient.from.Rdcm</a> or <a href="#">load.T.MAT</a> . If <code>T.MAT = NULL</code> , <code>struct\$ref.pseudo</code> must be equal to <code>vol\$ref.pseudo</code> or set to <code>NULL</code> .

within	Boolean, defaults to TRUE. If within = TRUE, the contours included in a ROI are managed, depending on their \$level field. If within = FALSE, only the \$level = 0 fields of the ROI are used (i.e. only the external outlines).
alias	Character string, \$alias of the created object.
description	Character string, describing the created object. If description = NULL (default value), it will be set to struct\$roi.info\$roi.pseudo[roi.idx].

### Details

roi.name, roi.sname, and roi.idx must select only one ROI.

### Value

Returns a "volume" class object of "binary" modality (see [espadon.class](#) for class definitions), with the same grid as vol, in which the voxels in the ROI are set to TRUE.

### See Also

[bin.from.vol](#).

### Examples

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 3
patient <- toy.load.patient (modality = c("ct", "rtstruct"),
                           roi.name = c("eye", "optical nerve", "brain"),
                           dxyz = rep (step, 3))

CT <- patient$ct[[1]]
S <- patient$rtstruct[[1]]

# "optical nerve" binary without inclusions management
bin <- bin.from.roi (CT, struct = S, roi.sname = "left optical",
                  alias = "left_optical_nerve")
display.plane (CT, top = bin, struct = S,
              view.coord = S$roi.info[S$roi.info$roi.pseudo == "leftopticalnerve",]$Gz,
              legend.shift = -80, interpolate = FALSE, main = "Left nerve selection")

## Not run:
# with a smaller step
step <- 1
patient <- toy.load.patient (modality = c("ct", "rtstruct"),
                           roi.name = c("eye", "optical nerve", "brain"),
                           dxyz = rep (step, 3))

CT <- patient$ct[[1]]
S <- patient$rtstruct[[1]]

# "optical nerve" binary without inclusions management
bin <- bin.from.roi (CT, struct = S, roi.sname = "left optical",
                  alias = "left_optical_nerve", within = FALSE)
display.plane (CT, top = bin, struct = S,
              view.coord = S$roi.info[S$roi.info$roi.pseudo == "leftopticalnerve",]$Gz,
              legend.shift = -80, interpolate = FALSE, main = "Left nerve selection")

# "optical nerve" binary with inclusions management
bin <- bin.from.roi (CT, struct = S, roi.sname = "left optical",
                  alias = "left_optical_nerve", within = TRUE)
```

```

display.plane (CT, top = bin, struct = S,
              view.coord = S$roi.info[S$roi.info$roi.pseudo == "leftopticalnerve",]$Gz,
              legend.shift = -80, interpolate = FALSE, main = "Left nerve selection")

## End(Not run)

```

---

bin.from.vol

*Creation of a binary volume according to the voxel values of a volume*


---

## Description

The `bin.from.vol` function creates a "volume" class object, of "binary" modality, in which the voxels fulfilling a condition on their value are selected.

## Usage

```

bin.from.vol(
  vol,
  min = -Inf,
  max = Inf,
  in.selection = TRUE,
  alias = "",
  description = NULL
)

```

## Arguments

<code>vol</code>	"volume" class object.
<code>min</code>	Minimum value of the selected voxel. Default to <code>-Inf</code> .
<code>max</code>	Maximum value of the selected voxel. Default to <code>+Inf</code> .
<code>in.selection</code>	Boolean, defaults to <code>TRUE</code> . If <code>in.selection = FALSE</code> , the selected pixels are those whose value is not between <code>min</code> and <code>max</code> .
<code>alias</code>	Character string, <code>\$alias</code> of the created object.
<code>description</code>	Character string, describing the created object. If <code>description = NULL</code> (default value), it will be set to <code>paste(min, vol\$object.alias, max, sep = "&lt;=")</code> or if <code>in.selection = FALSE</code> , <code>paste("!( ", description, " )"</code> .

## Value

Returns a "volume" class object of "binary" modality, with the same grid as `vol`, in which the selected voxels (i.e. set to `TRUE`) are those satisfying the following conditions :

- If `in.selection = TRUE`, then `min <= vol$vol3D.data <= max`.
- If `in.selection = FALSE`, then `vol$vol3D.data < min` or `max < vol$vol3D.data`

**Examples**

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 3
patient <- toy.load.patient (modality = "ct", roi.name = "",
                             dxyz = rep (step, 3))
CT <- patient$ct[[1]]

bin.bone <- bin.from.vol (CT, min = 300, max = 3000, alias = "bone")
display.plane (CT, top = bin.bone, interpolate = FALSE)
```

---

bin.intersection      *Intersection of two binaries*

---

**Description**

The `bin.intersection` function creates a "volume" class object, of "binary" modality, representing the intersection (logical AND) of two binary objects.

**Usage**

```
bin.intersection(vol1, vol2, alias = "", description = NULL)
```

**Arguments**

<code>vol1, vol2</code>	"volume" class objects, of "binary" modality.
<code>alias</code>	Character string, \$alias of the created object.
<code>description</code>	Character string, describing the created object. If <code>description = NULL</code> (default value), it will be set to <code>paste (vol1\$object.alias, "&amp;", vol2\$object.alias)</code> .

**Value**

Returns a "volume" class object of "binary" modality (see [espadon.class](#) for class definitions), with the same grid as `vol1` and `vol2`, intersection of `vol1` and `vol2`.

**Examples**

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 3
patient <- toy.load.patient (modality = c("mr", "rtstruct"),
                             roi.name = c("brain", "labyrinth processing unit"),
                             dxyz = rep (step, 3))
MR <- patient$mr[[1]]
S <- patient$rtstruct[[1]]

z.brain <- S$roi.info$Gz[S$roi.info$roi.pseudo == "brain"]

# Try to discriminate the processing unit with binary selections
bin.brain <- bin.from.roi (MR, struct = S, roi.name = "brain",
                          alias = "brain", T.MAT = patient$T.MAT)
bin.pu.density <- bin.from.vol (MR, min = 160)

display.plane (MR, top = bin.pu.density, display.ref = S$ref.pseudo,
```

```

        view.coord = z.brain, T.MAT = patient$T.MAT,
        interpolate = FALSE, main = "before brain intersection")
bin.pu <- bin.intersection (vol1 = bin.pu.density, vol2 = bin.brain,
                           alias = "processing unit")
display.plane (MR, top = bin.pu, display.ref = S$ref.pseudo,
               view.coord = z.brain, T.MAT = patient$T.MAT,
               interpolate = FALSE, main = "after brain intersection")

```

---

bin.inversion	<i>Inversion of a binary</i>
---------------	------------------------------

---

## Description

The `bin.inversion` function creates a "volume" class object, of "binary" modality, representing the inverse (logical NOT) of another binary object.

## Usage

```
bin.inversion(vol, alias = "", description = NULL)
```

## Arguments

<code>vol</code>	"volume" class object, of "binary" modality
<code>alias</code>	Character string, \$alias of the created object.
<code>description</code>	Character string, describing the created object. If <code>description = NULL</code> (default value), it will be set to <code>paste("!", vol\$object.alias, sep = "")</code> .

## Value

Returns a "volume" class object of "binary" modality (see [espadon.class](#) for class definitions), with the same grid as `vol`, inverse of `vol`.

## Examples

```

# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = c("ct", "rtstruct"), roi.name = "",
                            dxyz = rep (step, 3))

CT <- patient$ct[[1]]
S <- patient$rtstruct[[1]]

bin.patient <- bin.from.roi (CT, struct = S, roi.name = c ("patient"),
                           alias = "patient")
inverse.patient <- bin.inversion (bin.patient, alias = "inv (patient)")

display.plane(CT, top = inverse.patient, interpolate = FALSE)

```

---

bin.opening	<i>Binary volume opening</i>
-------------	------------------------------

---

### Description

The `bin.opening` function performs a morphological operation of opening, using a sphere, on a "volume" class object of "binary" modality. Opening is useful for :

- removing volumes that are smaller than the radius,
- smoothing shapes.

### Usage

```
bin.opening(vol, radius = 10, alias = "", description = NULL)
```

### Arguments

vol	"volume" class object, of "binary" modality.
radius	Positive number, in millimeters. By default, radius = 10.
alias	Character string, <code>\$object.alias</code> of the created object.
description	Character string, describing the created object. If <code>description = NULL</code> (default value), it will be set to <code>paste (vol\$object.alias, "opening r =", radius)</code> .

### Value

Returns a "volume" class object of "binary" modality (see [espadon.class](#) for class definitions), with the same grid as `vol`, in which `$vol3D.data` has been transformed by the opening operation.

### Note

Opening can be time consuming, try to reduce the binary volume to the strict minimum, before any operations.

### See Also

[bin.dilation](#), [bin.erosion](#), [bin.closing](#), [add.margin](#), [nesting.cube](#).

### Examples

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = "mr", roi.name = "",
                           dxyz = rep (step, 3))
MR <- patient$mr[[1]]

# generation of a binary volume
b <- bin.from.vol(MR, min = 15,max = 30)

b.opening <- bin.opening (b, radius = step)
display.plane (bottom = MR, top = b, main = "Before opening",
              view.coord = -20, interpolate = FALSE)
display.plane (bottom = MR, top = b.opening, main = "After opening",
              view.coord = -20, interpolate = FALSE)
```

---

bin.subtraction	<i>Subtraction of two binaries</i>
-----------------	------------------------------------

---

### Description

The `bin.subtraction` function creates a "volume" class object of "binary" modality, representing the subtraction of two binary objects.

### Usage

```
bin.subtraction(vol1, vol2, alias = "", description = NULL)
```

### Arguments

<code>vol1, vol2</code>	"volume" class objects of "binary" modality.
<code>alias</code>	Character string, \$alias of the created object.
<code>description</code>	Character string, describing the created object. If <code>description = NULL</code> (default value), it will be set to <code>paste (vol1\$object.alias, "-", vol2\$object.alias)</code> .

### Value

Returns a "volume" class object of "binary" modality (see [espadon.class](#) for class definitions), with the same grid as `vol1` and `vol2`, in which `vol2` is subtracted from `vol1`.

### Examples

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = c("mr", "rtstruct"), roi.name = "",
                             dxyz = rep (step, 3))

MR <- patient$mr[[1]]
S <- patient$rtstruct[[1]]

z.ptv <- S$roi.info$Gz[S$roi.info$roi.pseudo == "ptv"]

# binaries
bin.patient <- bin.from.roi (MR, struct = S, roi.name = "patient",
                             alias = "patient", T.MAT = patient$T.MAT)
bin.ptv <- bin.from.roi (MR, struct = S, roi.name = "ptv",
                             alias = "ptv", T.MAT = patient$T.MAT)

#' calculation of the 'patient - ptv' binary
bin <- bin.subtraction (bin.patient, bin.ptv, alias = "patient - ptv")
display.plane (MR, top = bin, view.coord = z.ptv,
               display.ref = S$ref.pseudo, T.MAT = patient$T.MAT,
               interpolate = FALSE)
```

---

bin.sum	<i>Sum of two binaries</i>
---------	----------------------------

---

### Description

The `bin.sum` function creates a "volume" class object of "binary" modality, representing the sum (logical OR) of two binary objects.

### Usage

```
bin.sum(vol1, vol2, alias = "", description = NULL)
```

### Arguments

<code>vol1, vol2</code>	"volume" class objects of "binary" modality.
<code>alias</code>	Character string, \$alias of the created object.
<code>description</code>	Character string, describing the created object. If <code>description = NULL</code> (default value), it will be set to <code>paste (vol1\$object.alias, "+", vol2\$object.alias)</code> .

### Value

Returns a "volume" class object of "binary" modality (see [espadon.class](#) for class definitions), with the same grid as `vol1` and `vol2`, sum of `vol1` and `vol2`.

### Examples

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = c("ct", "rtstruct"), roi.name = "eye",
                             dxyz = rep (step, 3))

CT <- patient$ct[[1]]
S <- patient$rtstruct[[1]]

z.leye <- S$roi.info$Gz[S$roi.info$roi.pseudo == "lefteye"]

# 'left eye' et 'right eye' binaries
bin.left.eye <- bin.from.roi (CT, struct = S, roi.sname = "lefteye",
                             alias = "left eye")
bin.right.eye <- bin.from.roi (CT, struct = S, roi.name = "righteye",
                              alias = "right eye")
bin.eyes <- bin.sum (bin.left.eye, bin.right.eye, alias = "eyes")

display.plane (CT, top = bin.eyes, struct = S, roi.sname = "eye",
               view.coord = z.leye, legend.shift = -90 ,
               interpolate = FALSE)
```



---

castlow.str	<i>Cast of a character string</i>
-------------	-----------------------------------

---

**Description**

The `castlow.str` function converts a word to lowercase, without accents and spaces.

**Usage**

```
castlow.str(st)
```

**Arguments**

st	character string
----	------------------

**Value**

Returns the ASCII//TRANSLIT transcription of the word `st`, without accents, spaces and in lowercase letters.

**See Also**

[castup.str](#).

**Examples**

```
castlow.str (st = c("Right eye", "Left_Lung", "Right-Lung"))
```

---

castup.str	<i>Cast of a character string</i>
------------	-----------------------------------

---

**Description**

The `castup.str` function converts a word to upper case, without accents and spaces.

**Usage**

```
castup.str(st)
```

**Arguments**

st	character string
----	------------------

**Value**

Returns the ASCII//TRANSLIT transcription of the word `st`, without accents, spaces and in capitals.

**See Also**

[castlow.str](#).

**Examples**

```
castup.str (st = c("Right eye", "Left_Lung", "Right-Lung"))
```

---

dicom.browser

*DICOM raw data browser*


---

**Description**

the dicom.browser function creates a dataframe describing the tags contained in the raw data of a DICOM file, as well as the information to access them.

**Usage**

```
dicom.browser(
  dicom.raw.data,
  nbTAG = 0,
  stop.tag = "",
  stop.level = 0,
  full.info = FALSE,
  tag.dictionary = dicom.tag.dictionary()
)
```

**Arguments**

dicom.raw.data	Raw vector, representing the binary extraction of the DICOM file.
nbTAG	Integer. If nbTAG = 0 (default), and stop.tag = "", all the DICOM raw data is browsed. Otherwise, the function only browses the first nbTAG tags.
stop.tag	Character string, representing the tag that stops the browse of the dicom.raw.data.
stop.level	Positive integer, specifying the encapsulation level of the stop.tag in dicom.raw.data.
full.info	Boolean. If TRUE, more information about the DICOM data is returned.
tag.dictionary	Dataframe, by default equal to <a href="#">dicom.tag.dictionary</a> , whose structure it must keep. This dataframe is used to parse DICOM files.

**Value**

Returns a dataframe if dicom.raw.data is DICOM raw data, NULL otherwise.

If full.info = FALSE, dataframe columns are

- tag : the tags contained in dicom.raw.data,
- VR : value representation of the content of the tag,
- endian : the endianness of the tag content,
- start : the start address in dicom.raw.data of the tag content.
- stop : the stop address in dicom.raw.data of the tag content.

If full.info = TRUE, the following columns are added :

- encaps.load : If the tag contains nested data, this column gives the number of bytes remaining until the end of the nesting. If there are several levels of nesting, these numbers are collapsed and separated by a space.
- load.start : the start address in dicom.raw.data of the tag load size.
- load.stop : the stop address in dicom.raw.data of the tag load size.
- tag.start : the start address in dicom.raw.data of the tag.

**See Also**

[dicom.raw.data.loader](#), [dicom.tag.parser](#)

**Examples**

```
# DICOM information dataframe of the dummy raw data toy.dicom.raw ()
df <- dicom.browser (toy.dicom.raw (), full.info = TRUE)
str (df)
```

---

dicom.parser	<i>Conversion of DICOM raw data into a dataframe or a list of DICOM TAG information</i>
--------------	---

---

**Description**

The `dicom.parser` function creates a dataframe or a list from DICOM raw data. The created dataframe or list provides information about the content of the DICOM TAGs included in the raw data.

**Usage**

```
dicom.parser(
  dicom.raw.data,
  as.txt = TRUE,
  nested.list = FALSE,
  try.parse = FALSE,
  txt.sep = "\\ ",
  txt.length = 100,
  tag.dictionary = dicom.tag.dictionary()
)
```

**Arguments**

<code>dicom.raw.data</code>	Raw vector, representing the binary extraction of the DICOM file.
<code>as.txt</code>	Boolean. If <code>as.txt = TRUE</code> , the function returns a dataframe, a list otherwise.
<code>nested.list</code>	Boolean. Only used if <code>as.txt = FALSE</code> . If <code>nested.list = FALSE</code> , the returned list consists of nested lists.
<code>try.parse</code>	Boolean. If <code>TRUE</code> , the tag with unknown DICOM VR (value representation) is converted into string if possible.
<code>txt.sep</code>	String. Used if <code>as.txt = TRUE</code> . Separator of the tag value elements.
<code>txt.length</code>	Positive integer. Used if <code>as.txt = TRUE</code> . Maximum number of letters in the representation of the TAG value.
<code>tag.dictionary</code>	Dataframe, by default equal to <a href="#">dicom.tag.dictionary</a> , whose structure it must keep. This dataframe is used to parse DICOM files.

**Value**

Returns a list of elements or a dataframe, depending on `as.list`.

If it returns a dataframe, the columns are names TAG, VR (value representation), VM (value multiplicity), loadsize and Value. The field `$Value` is a string representation of the true value.

If it returns a list, each of its elements, named by a TAG, is either a vector or a string, depending of the TAG included in `dicom.raw.data`.

**See Also**

[dicom.raw.data.loader](#), [dicom.tag.parser](#)

**Examples**

```
# content of the dummy raw data toy.dicom.raw (), as a list.
L <- dicom.parser (toy.dicom.raw (), as.txt = FALSE)
str(L[40:57])

L <- dicom.parser (toy.dicom.raw (), as.txt = FALSE, nested.list = TRUE)
str(L[40:45])

# content of the dummy raw data toy.dicom.raw (), as a dataframe.
L <- dicom.parser (toy.dicom.raw (), as.txt = TRUE)
str (L)
```

---

dicom.raw.data.anonymizer

*DICOM anonymizer*

---

**Description**

the `dicom.raw.data.anonymizer` function anonymizes `dicom.raw.data`.

**Usage**

```
dicom.raw.data.anonymizer(
  dicom.raw.data,
  offset = 0,
  new.PIN = "Anonymous ",
  reset.private.tag = FALSE,
  tag.dictionary = dicom.tag.dictionary()
)
```

**Arguments**

<code>dicom.raw.data</code>	Raw vector, representing the binary extraction of the DICOM file.
<code>offset</code>	Integer, default to 0. Each date of the DICOM will be shifted by this offset expressed in days.
<code>new.PIN</code>	Character string, representing the PIN replacing the old one.
<code>reset.private.tag</code>	Boolean, if TRUE, the value of tags that are not in the <code>tag.dictionary</code> is removed.

tag.dictionary Dataframe, by default equal to [dicom.tag.dictionary](#), whose structure it must keep. This dataframe is used to parse DICOM files.

**Value**

Returns an anonymized raw vector. See Note.

**Note**

The raw data is anonymized as follows:

- Each date of the DICOM file will be shifted by offset expressed in days.
- Each patient's name, and patient'ID are replaced by new.PIN
- All other patient data are deleted, except age, weight, height, gender and shifted birthday.
- All address, phone, physician, operator, author, reviewer, service.
- If reset.private.tag = TRUE, the values of the tags not contained in the tag.dictionary are deleted.

**Examples**

```
# pseudomization of the dummy raw data toy.dicom.raw ()
an.raw.data <- dicom.raw.data.anonymizer (toy.dicom.raw (), offset = -2)
data <- dicom.parser (toy.dicom.raw ())
an.data <- dicom.parser (an.raw.data)
# Checking for differences
flag.dif <- data$Value != an.data$Value
df <- cbind (data[flag.dif, c ("VM", "Value")], an.data[flag.dif, "Value"])
colnames (df) <- c ("VM", "old Value", "new Value")
df
```

---

dicom.raw.data.loader *DICOM file loading in raw data*

---

**Description**

the dicom.raw.data.loader function loads a DICOM file as raw data.

**Usage**

```
dicom.raw.data.loader(dcm.filename)
```

**Arguments**

dcm.filename Character string, representing the full name of a DICOM file.

**Value**

Returns a vector of raw data from dcm.filename.

**See Also**

[dicom.browser](#), [dicom.tag.parser](#)

**Examples**

```

# First, save toy.dicom.raw () raw data to a temporary file for testing.
pat.src.dir <- file.path (tempdir(), "toy_dccm")
dir.create (pat.src.dir, recursive = TRUE)
dcm.filename <- tempfile (pattern = "toyrtplan", tmpdir = pat.src.dir,
                          fileext = ".dcm")
zz <- file (dcm.filename, "wb")
writeBin (toy.dicom.raw (), zz, size = 1)
close (zz)

# loading of file
dicom.raw.data <- dicom.raw.data.loader (dcm.filename)

# checks if it is consistent with the original raw data
all ( dicom.raw.data == toy.dicom.raw () )

# Cleaning temporary directory
unlink (pat.src.dir, recursive = TRUE)

```

---

dicom.set.tag.value     *Change TAG value in DICOM raw data*

---

**Description**

The `dicom.set.tag.value` function changes, in the DICOM raw data, the values of the TAG whose VR is a string of characters.

**Usage**

```

dicom.set.tag.value(
  dicom.raw.data,
  tag,
  tag.value,
  tag.dictionary = dicom.tag.dictionary()
)

```

**Arguments**

`dicom.raw.data` Raw vector, representing the binary extraction of the DICOM file.

`tag` String vector, representing the list of tags whose value is to be changed. See note 1.

`tag.value` String vector, representing the list of new tag values.

`tag.dictionary` Dataframe, by default equal to [dicom.tag.dictionary](#), whose structure it must keep. This dataframe is used to parse DICOM files.

**Value**

Returns a raw vector, with new tag values.

**Note**

1- The list of tags included in the DICOM file are given by the first columns of the dataframe provided by the functions `dicom.browser` and `dicom.parser`.

2- The `dicom.set.tag.value` function may take some processing time. To minimize this time, it is recommended to prepare in advance all the tags to be modified, and use the `dicom.set.tag.value` function only once, as shown in the example.

**Examples**

```
# change the value of tags "(0010,0010)" and "(0010,0020)" in the
# dummy raw data toy.dicom.raw ()
new.raw.data <- dicom.set.tag.value (toy.dicom.raw (),
                                   tag = c ("(0010,0010)", "(0010,0020)"),
                                   tag.value = c ("unknown", "000001"))

# change control
data <- dicom.parser (new.raw.data)
data[data$TAG %in% c ("(0010,0010)", "(0010,0020)"), ]
```

---

dicom.tag.dictionary *DICOM TAG dictionary*

---

**Description**

The `dicom.tag.dictionary` function gives the dictionary of tags used by default in the **espadon** package.

**Usage**

```
dicom.tag.dictionary(add.dict = c("raysearch.tag"))
```

**Arguments**

`add.dict`            Vector of the list of additional dictionaries. Put to NULL, if no additional dictionary is requested.

**Value**

Returns a 3-column dataframe, describing the VR (value representation) and the name of each DICOM TAG.

This dataframe is the fusion of the "nema.tag" dictionary, provided by *nema* [1], with the dictionaries defined in the `add.dict` vector:

- "raysearch.tag" dictionary is provided by *RaySearch laboratories* [2]

**References**

[1] DICOM nema (Online; accessed 2022-02-16). "Current Edition." <https://www.dicomstandard.org/current>.

[2] Raysearch Laboratories (Online; accessed 2022-04-25). "RAYPLAN 11A, DICOM Conformance Statement." <https://www.raysearchlabs.com/4aaf2e/siteassets/raystation-landing-page/dicom-conformance-statements/raystation-pdfs/rs1-d-rs-11a-dcs-en-1.0-2021-05-07-raystation-11a.pdf>.

**Examples**

```
str (dicom.tag.dictionary ())
str (dicom.tag.dictionary (NULL))
```

---

dicom.tag.parser	<i>DICOM TAG parser</i>
------------------	-------------------------

---

**Description**

the dicom.tag.parser function decodes the content between two DICOM raw data addresses.

**Usage**

```
dicom.tag.parser(start, stop, VR, endian, dicom.raw.data, try.parse = FALSE)
```

**Arguments**

start	Positive integer. Index of the first raw data to parse in the dicom.raw.data.
stop	Positive integer. Index of the last raw data to parse in the dicom.raw.data.
VR	Character string, representing the value representation of DICOM data. See DICOM standard.
endian	Character string, equal to "little" or "big".
dicom.raw.data	Raw vector, representing the binary extraction of the DICOM file.
try.parse	Boolean. If TRUE, the value, with an undocumented VR, is considered, as far as possible, as a string.

**Value**

Returns the dicom.raw.data content between the addresses start and stop. Depending on the representation of the value (VR), it can be a character string or a numerical vector.

**Examples**

```
# creation of the toy.dicom.raw () addresses dataframe:
df <- dicom.browse (toy.dicom.raw ())

# search for modality of toy.dicom.raw ()
idx <- grep ("^([0008,0060])$", df$tag)
modality <- dicom.tag.parser (df$start[idx], df$stop[idx], df$VR[idx],
                             df$endian[idx], toy.dicom.raw ())

modality
```



---

 dicom.to.Rdcm.converter

*Conversion of DICOM object into files that can be interpreted by the **espadon** package*

---

## Description

The `dicom.to.Rdcm.converter` function creates, for each DICOM object, a `*.Rdcm` file usefull for using **espadon** package. Each `Rdcm` file created is referenced by the date of acquisition of the object (if it is not available, its creation date), the patient's PIN, a reference number, an object number in this reference system, and the object modality (`mr`, `ct`, `rtstruct`...).

## Usage

```
dicom.to.Rdcm.converter(
  dcm.files,
  pat.dest.dir,
  update = TRUE,
  tag.dictionary = dicom.tag.dictionary(),
  verbose = TRUE
)
```

## Arguments

<code>dcm.files</code>	String vector, representing the list of the full names of the DICOM files of the same patient, or its directory.
<code>pat.dest.dir</code>	Character string, representing the full name of patient directory, which will contain files converted <b>espadon</b> .
<code>update</code>	Boolean. If set to <code>TRUE</code> , and if <code>pat.dest.dir</code> contains previously converted files, these files will keep the same <b>espadon</b> reference frame affectation.
<code>tag.dictionary</code>	Dataframe, by default equal to <code>dicom.tag.dictionary</code> , whose structure it must keep. This dataframe is used to parse DICOM files.
<code>verbose</code>	Boolean. If <code>TRUE</code> , a progress bar indicates the progress of the conversion.

## Value

Returns the list of basenames of the created files.

Returns `NULL` if there are no DICOM files in `dcm.files`

## Note

For each DICOM object, `dicom.to.Rdcm.converter` creates a `*.Rdcm` file whose basename is made up of the date of the acquisition (or creation date if previous not found), the patient's PIN, the pseudonym of the frame of reference (`"ref1"`, `"ref2"`...), the number of the volume object in the directory in this frame of reference (`"do1"`, `"do2"`...), and the object modality (`"mr"`, `"ct"`, `"rtdose"`, `"rtstruct"`...).

For example: `BASE = "20160514_a008e9ac_ref2_do1_mr"`

## Examples

```
# First, save toy.dicom.raw () raw data to a temporary file for testing.
pat.src.dir <- file.path (tempdir(), "PM_dcm")
dir.create (pat.src.dir, recursive = TRUE)
dcm.filename <- tempfile (pattern = "PM_rtplan", tmpdir = pat.src.dir,
                          fileext = ".dcm")
zz <- file (dcm.filename, "wb")
writeBin (toy.dicom.raw (), zz, size = 1)
close (zz)

# Create a temporary destination directory where the *.Rdcm file will be saved
pat.dest.dir <- file.path (tempdir(), "PM_Rdcm")

dicom.to.Rdcm.converter (pat.src.dir, pat.dest.dir, update = TRUE)
# or
dicom.to.Rdcm.converter (dcm.filename, pat.dest.dir, update = TRUE)

list.files (pat.dest.dir)

# Cleaning temporary directories
unlink (pat.src.dir, recursive = TRUE)
unlink (pat.dest.dir, recursive = TRUE)
```

---

dicom.viewer

*DICOM content viewer*

---

## Description

the dicom.viewer function displays the data of a DICOM file.

## Usage

```
dicom.viewer(
  dcm,
  txt.sep = "\\ ",
  txt.length = 100,
  tag.dictionary = dicom.tag.dictionary(),
  height = 600,
  width = 900
)
```

## Arguments

dcm	String Character representing the list of the full names of a DICOM file or raw data vector of this DICOM file.
txt.sep	String. Used if as.txt = TRUE. Separator of the tag value elements.
txt.length	Positive integer. Used if as.txt = TRUE. Maximum number of letters in the representation of the TAG value.
tag.dictionary	Dataframe, by default equal to <a href="#">dicom.tag.dictionary</a> , whose structure it must keep. This dataframe is used to parse DICOM files.
height, width	Height and width in pixel of the DICOM table.

**Value**

Returns the DICOM file description in a browser window.

**See Also**

[xlsx.from.dcm](#), [dicom.parser](#)

**Examples**

```
if (interactive ()) dicom.viewer (toy.dicom.raw ())
```

---

display.2D.histo	<i>Display of a 2D histogram</i>
------------------	----------------------------------

---

**Description**

The `display.2D.histo` function displays the density map of a "histo2D" class object.

**Usage**

```
display.2D.histo(
  histo.2D,
  add = TRUE,
  main = NULL,
  x.lab = NULL,
  y.lab = NULL,
  x.lim = NULL,
  y.lim = NULL,
  bg = "#000000",
  i.rng = NULL,
  display.mode = c("mono.color", "rainbow.color", "line"),
  col = "#ffffff",
  alpha = 1,
  line.pc.levels = c(1, 100),
  line.lwd = 2,
  line.lty = 1
)
```

**Arguments**

<code>histo.2D</code>	"histo2D" class object.
<code>add</code>	Boolean indicating whether to display the background image.
<code>main</code>	Title of the background image. If <code>main = NULL</code> , the title indicates "2D histogram".
<code>x.lab</code>	Label of the x-axis of the background image. If <code>x.lab = NULL</code> , this label is <code>histo.2D\$x.file.src</code>
<code>y.lab</code>	Label of the y-axis of the background image. If <code>y.lab = NULL</code> , this label is <code>histo.2D\$y.file.src</code> .
<code>x.lim</code>	Vector, representing the range of the x-axis.

<code>y.lim</code>	Vector, representing the range of the y-axis.
<code>bg</code>	Background color of the image. By default, this color is black.
<code>i.rng</code>	Vector of 2 elements giving the minimum and the maximum intensity of the image. If <code>i.rng = NULL</code> , then the minimum is 0 and the maximum the maximum density.
<code>display.mode</code>	function display mode. See Details.
<code>col</code>	Color of the color gradient in <code>display.mode = "mono.color"</code> , or of the level lines in <code>display.mode = "line"</code> . By default, this color is white.
<code>alpha</code>	A number from 0 to 1, indicating the opacity of the image in <code>"rainbow.color"</code> mode. Default <code>alpha = 1</code> .
<code>line.pc.levels</code>	Vector of level lines in percent of maximum density in <code>display.mode = "line"</code> . By default lines 1% and 100% are displayed.
<code>line.lwd</code>	Line thickness of the level lines in <code>display.mode = "line"</code> .
<code>line.lty</code>	Type of lines for level lines in <code>display.mode = "line"</code> .

### Details

The `display.mode` argument can be set to three values: `"mono.color"`, `"rainbow.color"`, or `"line"`. The 2D histogram graph is displayed by default in `"mono.color"` mode.

- The `"mono.color"` mode displays a gradient of the color defined by the `col` argument, depending on the intensity of `$density.map` 2-dimensional array.
- The `"rainbow.color"` mode makes a display according to the `"rainbow"` palette, while managing the opacity of the colors.
- The `"line"` mode draws level lines defined in percent by the `line.pc.levels` argument.

### Value

Returns a display of the density map of `histo.2D`. This one must be an object of class `"histo2D"`. See [espadon.class](#) for class definitions.

### See Also

[histo.2D](#).

### Examples

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = c("ct", "mr", "rtstruct"),
                           roi.name = "brain",
                           dxyz = rep (step, 3))

CT <- patient$ct[[1]]
MR <- patient$mr[[1]]
S <- patient$rtstruct[[1]]
T.MAT <- patient$T.MAT

# restriction of the volume around the RoI
CT.on.roi <- nesting.roi (CT, S, roi.name = "brain", vol.restrict = TRUE,
                        xyz.margin = c (1, 1, 1), alias = CT$description)
MR.on.CT <- vol.regrid (vol = MR, back.vol = CT.on.roi, interpolate = TRUE,
                      T.MAT = T.MAT, alias = CT$description,
```

```

                                description = NULL)
# selection of voxels included in the RoI.
roi.bin <- bin.from.roi (vol = CT.on.roi, struct = S, roi.sname = "brain")
MR.select <- vol.from.bin (MR.on.CT, roi.bin, alias = MR$description)
CT.select <- vol.from.bin (CT.on.roi, roi.bin, alias = CT$description)
# 2D histogram
H2D <- histo.2D (MR.select, CT.select, x.breaks = seq (50, 400, 10),
  y.breaks = seq (50, 400, 10), alias = "H2D MR1 MR2")
display.2D.histo (H2D, display.mode = "mono.color", col = "#ffff00",
  main ="mono color mode")
display.2D.histo (H2D, display.mode = "rainbow.color", main ="rainbow mode")
display.2D.histo (H2D, display.mode = "line", main ="level lines mode",
  line.pc.levels = c (0, 25, 50, 75, 100), col = "#ff0000")

```

---

display.3D.contour      *Display the 3D contours of the RoI*

---

## Description

The `display.3D.contour` function performs a 3D display of the selected RoI in the chosen coordinate system.

## Usage

```

display.3D.contour(
  struct,
  roi.name = NULL,
  roi.sname = NULL,
  roi.idx = NULL,
  roi.col = NULL,
  roi.print = FALSE,
  roi.lwd = 1,
  roi.cex = 1,
  display.ref = struct$ref.pseudo,
  T.MAT = NULL,
  FoR.axis = FALSE,
  FoR.col = "black"
)

```

## Arguments

<code>struct</code>	"struct" class object. See <a href="#">espadon.class</a> for class definitions.
<code>roi.name</code>	Vector of exact names of the RoI in the struct object. By default <code>roi.name = NULL</code> . See Details.
<code>roi.sname</code>	Vector of names or parts of names of the RoI in the struct object. By default <code>roi.sname = NULL</code> . See Details.
<code>roi.idx</code>	Vector of indices of the RoI that belong to the struct object. By default <code>roi.idx = NULL</code> . See Details.
<code>roi.col</code>	Color of the RoI. If <code>roi.col = NULL</code> (default), the RoI colors are specified in the <code>struct\$roi.info</code> .
<code>roi.print</code>	Boolean vector indicating whether to display the pseudonym of the RoI.

roi.lwd	Line width of the RoI, by default at 1.
roi.cex	Numeric character expansion factor of RoI name if roi.print = TRUE, defaults to 1.
display.ref	Pseudonym of frame of reference of the display.
T.MAT	"t.mat" class object, created by <a href="#">load.patient.from.Rdcm</a> or <a href="#">load.T.MAT</a> . If T.MAT = NULL, display.ref must be equal to NULL or to struct\$ref.pseudo.
FoR.axis	Boolean or numeric, by default set to FALSE. If FoR.axis = TRUE, the function displays 200 mm length director vectors of the frame of reference. If FoR.axis is numeric, it represent the length in mm of the director vectors.
FoR.col	Color of the frame of reference.

### Details

If roi.name, roi.sname, and roi.idx are all NULL, then all of the RoI are selected.

### Value

If the concerned regions of interest (RoI) struct exist, it displays the 3D contours of these RoI in the current **RGL** window if it exists, in a new window otherwise.

### Examples

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient(modality = "rtstruct", roi.name = "eye",
                           dxyz = rep(step, 3))

library(rgl)
open3d()
bg3d("black")
display.3D.contour(struct = patient$rtstruct[[1]], roi.print = TRUE)
```

---

display.3D.mesh      *3D display of a mesh*

---

### Description

The display.3D.mesh function performs a 3D display of a mesh.

### Usage

```
display.3D.mesh(mesh, display.ref = mesh$ref.pseudo, T.MAT = NULL, ...)
```

### Arguments

mesh	"mesh" class object, created by the <a href="#">mesh.from.bin</a> function. See <a href="#">espardon.class</a> for class definitions.
display.ref	Character string. Pseudonym of the frame of reference used for display.
T.MAT	"t.mat" class object, created by <a href="#">load.patient.from.Rdcm</a> or <a href="#">load.T.MAT</a> . If T.MAT is NULL, mesh must be displayed in display.ref = mesh\$ref.pseudo.
...	Arguments passed to <a href="#">shade3d</a> as color, specular, alpha...

**Value**

Returns a display of mesh in the current **RGL** window if it exists, in a new window otherwise.

**See Also**

[mesh.from.bin.](#)

**Examples**

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = c("ct", "rtstruct"), roi.name = "",
                             dxyz = rep (step, 3))

CT <- patient$ct[[1]]
S <- patient$rtstruct[[1]]

# creation of the patient mesh
bin <- bin.from.roi (CT, struct = S, roi.name = "patient")
mesh.patient <- mesh.from.bin (bin, alias = "patient", verbose = FALSE)

# display of the patient mesh, with transparency
library (rgl)
open3d()
display.3D.mesh (mesh.patient, color = "burlywood2", specular = "#404040")
```

---

display.3D.sections     *Display 3D sections of a patient*

---

**Description**

The `display.3D.sections` function displays transverse, sagittal and frontal views at a point in 3D.

**Usage**

```
display.3D.sections(
  vol,
  cross.pt = c(0, 0, 0),
  display.ref = vol$ref.pseudo,
  T.MAT = NULL,
  col = grey.colors(10, start = 0, end = 1, alpha = c(rep(0, 1), rep(1, 9))),
  breaks = NULL,
  trans = TRUE,
  sagi = TRUE,
  front = TRUE,
  border = TRUE,
  border.col = "#379DA2"
)
```

**Arguments**

vol	"volume" class object to display. See <a href="#">espadon.class</a> for class definitions.
cross.pt	Vector of x, y, z coordinates, representing the cross point of the 3 planes.
display.ref	Character string. Pseudonym of the frame of reference used for display.
T.MAT	"t.mat" class object, created by <a href="#">load.patient.from.Rdcm</a> or <a href="#">load.T.MAT</a> . If T.MAT is NULL, vol must be displayed in display.ref = vol\$ref.pseudo.
col	Vector, representing the color palette of the image. Transparent colors are not represented.
breaks	One of : <ul style="list-style-type: none"> <li>• NULL : the minimum and the maximum value of the vol define the range.</li> <li>• Vector giving the breakpoints of each color.</li> </ul>
trans	Boolean. If TRUE (default), the transverse view is displayed.
sagi	Boolean. If TRUE (default), the sagittal view is displayed.
front	Boolean. If TRUE (default), the frontal view is displayed.
border	Boolean. If TRUE (default), the borders of the planes are displayed
border.col	Color of planes borders

**Value**

Returns a display of transverse, sagittal and frontal views of vol at cross.pt in the current **RGL** window if it exists, in a new window otherwise. Palette colors are managed by col and breaks.

**Examples**

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = "ct", dxyz = rep (step, 3))
CT <- patient$ct[[1]]

library (rgl)
open3d()
display.3D.sections(CT, cross.pt= c(0, 50, 80),
                   col= pal.RVV(200, alpha= c(rep(0,90), rep(1,110))),
                   breaks = seq(-1000, 1000, length.out = 201))
```

---

display.3D.stack

*Display in 3D the selected planes of an **espadon** class volume*


---

**Description**

The display.3D.stack function displays in 3D the requested planes of a "volume" class object.



**Usage**

```
display.3D.stack(
  vol,
  k.idx = unique(vol$k.idx[seq(1, vol$n.ijk[3], length.out = 10)]),
  display.ref = vol$ref.pseudo,
  T.MAT = NULL,
  col = grey.colors(10, start = 0, end = 1, alpha = c(rep(0, 1), rep(1, 9))),
  breaks = NULL,
  cube = TRUE,
  border = TRUE,
  ktext = TRUE,
  line.col = "#379DA2",
  line.lwd = 1,
  cex = 1
)
```

**Arguments**

vol	"volume" class object to display.
k.idx	vector of plane numbers to be displayed, to be chosen in vol\$k.idx. By default k.idx is a vector of 10 uniformly distributed planes in the volume.
display.ref	Character string. Pseudonym of the frame of reference used for display.
T.MAT	"t.mat" class object, created by <a href="#">load.patient.from.Rdcm</a> or <a href="#">load.T.MAT</a> . If T.MAT is NULL, vol must be displayed in display.ref = vol\$ref.pseudo.
col	Vector, representing the color palette of the image. Transparent colors are not represented.
breaks	One of : <ul style="list-style-type: none"> <li>• NULL : The minimum and the maximum value of the vol define the range.</li> <li>• Vector giving the breakpoints of each color.</li> </ul>
cube	Boolean. If TRUE (default), the "volume" edges are displayed.
border	Boolean. If TRUE (default), the borders of the planes defined in k.idx are displayed.
ktext	Boolean. If TRUE (default), the selected plane numbers are displayed.
line.col	Color of cube, planes and texts displayed.
line.lwd	Line width of the border and cube, by default at 1.
cex	Numeric character expansion factor of displayed plan numbers.

**Value**

Returns a display of the k.idx cutting planes of vol, in the current **RGL** window if it exists, in a new window otherwise. The colors of the palettes are managed by col and breaks.

**Examples**

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = "ct", dxyz = rep (step, 3))

# display o 3 planes
```

```

library (rgl)
open3d()
display.3D.stack (patient$ct[[1]],
                  col = pal.RVV (200, alpha = c(rep(0,90), rep (1, 110))),
                  breaks = seq (-1000, 1000, length.out = 201))

```

---

display.DVH

*Display of a DVH*


---

### Description

The `display.DVH` function displays the Dose Volume Histogram of a "dvh" class object. Y-units are  $cm^3$ .

### Usage

```

display.DVH(
  dvh,
  add = FALSE,
  xgrid = TRUE,
  ygrid = TRUE,
  MC.plot = FALSE,
  MC.col = grey.colors(4, rev = TRUE),
  ...
)

```

### Arguments

dvh	"dvh" class object.
add	Boolean indicating whether to display the background image.
xgrid	Boolean indicating the display of the x grid.
ygrid	Boolean indicating the display of the y grid.
MC.plot	Boolean. If <code>MC.plot = TRUE</code> , then <code>display.DVH</code> displays, if they exist, the quantile zones (Prob = 0, .025, .25, .5, .75, .975, 1) of MC DVH variations.
MC.col	Character string, a valid palette with 4 colours corresponding to 100%, 95%, 50% and median of MC data.
...	Arguments <code>xlab</code> , <code>ylab</code> , <code>xlim</code> , <code>ylim</code> , <code>main</code> , <code>type</code> , <code>col</code> , <code>lwd</code> , <code>lty</code> and <code>log</code> managed by the <a href="#">plot</a> function.

### Value

Returns a plot of the cumulative histogram included in `dvh`, with its median, and the quantile areas (0%-100%), (2.5%-97.5%) and (25%-75%) of the `dvh$vol` variations, if they exist.

### See Also

[display.DVH.pc](#)

**Examples**

```

# DVH without MCMC
# loading of toy-patient objects (decrease dxyz and increase beam.nb for
# better result)
step <- 5
patient <- toy.load.patient (modality = c("rtdose", "rtstruct"), roi.name = "",
                           dxyz = rep (step, 3), beam.nb = 3)
H <- histo.from.roi (patient$rtdose[[1]], patient$rtstruct[[1]], roi.name = "ptv",
                   breaks = seq (0, 60, by = 2))
DVH <- histo.DVH (H)
display.DVH (DVH)

## Not run:
# loading of toy-patient objects
patient <- toy.load.patient (modality = c("rtdose", "rtstruct"),
                           roi.name = "gizzard",
                           dxyz = c (2, 2, 2), beam.nb = 3)

# Calculation of the histogram
H <- histo.from.roi (patient$rtdose[[1]], patient$rtstruct[[1]],
                   roi.name = "gizzard",
                   breaks = seq (0, 60, by = 1), MC = 100)

# DVH
DVH <- histo.DVH (H)
display.DVH (DVH, MC.plot = TRUE, ylim = c (0, 40))

## End(Not run)

```

---

display.DVH.pc

*Display of a cumulative DVH in percent of total volume*


---

**Description**

The `display.DVH.pc` function displays the Dose Volume Histogram of "dvh" class object. Y-units are percents of total volume.

**Usage**

```

display.DVH.pc(
  dvh,
  add = FALSE,
  xgrid = TRUE,
  ygrid = TRUE,
  MC.plot = FALSE,
  MC.col = grey.colors(4, rev = TRUE),
  ...
)

```

**Arguments**

`dvh` "dvh" class object. See [espardon.class](#) for class definitions.  
`add` Boolean indicating whether to display the background image.

xgrid	Boolean indicating the display of the x grid.
ygrid	Boolean indicating the display of the y grid.
MC.plot	Boolean. If MC.plot = TRUE, then display.DVH.pc displays, if they exist, the quantile zones (Prob = 0, .025, .25, .5, .75, .975, 1) of MC DVH variations.
MC.col	Character string, a valid palette with 4 colours corresponding to 100%, 95%, 50% and median of MC data.
...	Arguments xlab, ylab, xlim, ylim, main, type, col, lwd, lty and log managed by the <a href="#">plot</a> function.

### Value

Returns a plot in percent of total volume of the cumulative histogram included in dvh, with its median, and the quantile areas (0%-100%), (2.5%-97.5%) and (25%-75%) of the dvh\$pcv variations, if they exist.

### See Also

[display.DVH](#)

### Examples

```
# loading of toy-patient objects (decrease dxyz and increase beam.nb for
# better result)
step <- 5
patient <- toy.load.patient (modality = c("rtdose", "rtstruct"),
                           roi.name = "gizzard", dxyz = rep (step, 3),
                           beam.nb = 3)

# Calculation of the histogram
H <- histo.from.roi (patient$rtdose[[1]], patient$rtstruct[[1]],
                   roi.name = "gizzard",
                   breaks = seq (0, 60, by = 1))

# DVH
DVH <- histo.DVH (H)
display.DVH.pc (DVH)
```

---

display.dV\_dx

*Display of the volume density of a histogram*

---

### Description

The display.dV\_dx function displays the volume density of a "histo" class object. Y-units are  $cm^3.Gy^{-1}$ .

### Usage

```
display.dV_dx(
  histo,
  add = FALSE,
  xgrid = TRUE,
  ygrid = TRUE,
```

```

MC.plot = FALSE,
MC.col = grey.colors(4, rev = TRUE),
...
)

```

### Arguments

histo	"histo" class object. See <a href="#">espadon.class</a> for class definitions.
add	Boolean indicating whether to display the background image.
xgrid	Boolean indicating the display of the x grid.
ygrid	Boolean indicating the display of the y grid.
MC.plot	Boolean. If MC.plot = TRUE, then <code>display.dv_dx</code> displays, if they exist, the quantile zones (Prob = 0, .025, .25, .5, .75, .975, 1) of variations in volume density.
MC.col	Character string, a valid palette with 4 colours corresponding to 100%, 95%, 50% and median of MC data.
...	Arguments xlab, ylab, xlim, ylim, main, type, col, lwd, lty and log managed by the <a href="#">plot</a> function.

### Value

Returns a plot of the differential histogram included in `histo`, with its median, and the quantile areas (0%-100%), (2.5%-97.5%) and (25%-75%) of the `histo$dv_dx` variations, if they exist.

### See Also

[display.histo](#).

### Examples

```

# loading of toy-patient objects (decrease dxyz and increase beam.nb for
# better result)
step <- 5
patient <- toy.load.patient (modality = c("rtdose", "rtstruct"),
                           roi.name = "gizzard", dxyz = rep (step, 3),
                           beam.nb = 3)

# Calculation of the differential histogram
H <- histo.from.roi (patient$rtdose[[1]], patient$rtstruct[[1]],
                   roi.name = "gizzard", breaks = seq (0, 60, by = 2))
display.dv_dx (H, lwd = 2, col = '#00ff00', ylim = c (0,10))

```

---

display.histo

*Display of the counts of a histogram*

---

### Description

The `display.histo` function displays the counts of "histo" class object.

**Usage**

```
display.histo(
  histo,
  add = FALSE,
  xgrid = TRUE,
  ygrid = TRUE,
  MC.plot = FALSE,
  MC.col = grey.colors(4, rev = TRUE),
  ...
)
```

**Arguments**

histo	"histo" class object.
add	Boolean indicating whether to display the background image.
xgrid	Boolean indicating the display of the x grid.
ygrid	Boolean indicating the display of the y grid.
MC.plot	Boolean. If MC.plot = TRUE, then display.histo displays, if they exist, the quantile zones (Prob = 0, .05, .25, .5, .75, .95, 1) of variations in counts.
MC.col	Character string, a valid palette with 4 colours corresponding to 100%, 95%, 50% and median of MC data.
...	Arguments xlab, ylab, xlim, ylim, main, type, col, lwd, lty and log managed by the <a href="#">plot</a> function.

**Value**

Returns a plot of the counts included in histo, with its median, and the quantile areas (0%-100%), (2.5%-97.5%) and (25%-75%) of the histo\$counts variations, if they exist.

**See Also**

[display.dV\\_dx](#).

**Examples**

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 3
patient <- toy.load.patient (modality = "ct", dxyz = rep (step, 3))
CT <- patient$ct[[1]]

# histogram and display
H <- histo.vol (CT, breaks = seq (3, ceiling (CT$max.pixel), 1),
               alias = "CT_hist")
display.histo (H, log = "y", lwd = 2)
```

---

display.kplane	<i>Display of a plane of a volume</i>
----------------	---------------------------------------

---

### Description

The `display.kplane` function displays the requested plane of a "volume" class object. This function is low-level, used for example in the function [display.plane](#) with more intuitive arguments.

### Usage

```
display.kplane(
  vol,
  k = vol$k.idx[ceiling(length(vol$k.idx)/2)],
  pt00 = c(0, 0),
  dxy = c(1, 1),
  col = grey.colors(255, start = 0, end = 1),
  breaks = NULL,
  sat.transp = FALSE,
  add = FALSE,
  main = NULL,
  abs.lab = "i",
  ord.lab = "j",
  abs.flip = FALSE,
  ord.flip = FALSE,
  bg = "#000000",
  abs.rng = NULL,
  ord.rng = NULL,
  interpolate = FALSE
)
```

### Arguments

<code>vol</code>	"volume" class object to display. See <a href="#">espadon.class</a> for class definitions.
<code>k</code>	Number of the plane to display. By default <code>k</code> is located at mid-plane of the volume.
<code>pt00</code>	Origin point of the displayed plane. By default <code>pt00 = c(0, 0)</code> , corresponding to the bottom left of the displayed non-flipped image.
<code>dxy</code>	width and height of a pixel in the plane. If <code>dxy = c(1, 1)</code> (default) abscissa and ordinate correspond to pixel number in the plane.
<code>col</code>	Vector, representing the color palette of the image.
<code>breaks</code>	One of : <ul style="list-style-type: none"> <li>• <code>NULL</code> : the minimum and the maximum value of the <code>vol</code> define the range.</li> <li>• Vector giving the breakpoints of each color. Outside values are transparent, leaving the background visible, depending on <code>sat.transp</code>.</li> </ul>
<code>sat.transp</code>	Boolean. If <code>TRUE</code> , outside values are transparent, else set to <code>breaks</code> limits colors.
<code>add</code>	Boolean indicating whether to display the background image.
<code>main</code>	Title of the background image. If <code>main = NULL</code> , the title just indicates the value of <code>k</code> .

abs.lab	Label of the image abscissa. By default abs.lab = 'i'.
ord.lab	Label of the image ordinate. By default ord.lab = 'j'.
abs.flip	Boolean defaults to FALSE flipping the horizontal axis of the background image.
ord.flip	Boolean defaults to FALSE flipping the vertical axis of the background image.
bg	Background color of the image. By default, this color is black.
abs.rng	Vector of 2 elements indicating the minimum and maximum background image abscissa to display.
ord.rng	Vector of 2 elements indicating the minimum and maximum background image ordinate to display.
interpolate	Boolean, indicating whether to apply linear interpolation to the image.

### Value

Returns a display of the  $k^{th}$  image plane of vol.

### See Also

[display.plane](#).

### Examples

```
# loading of toy-patient objects (decrease dxyz and increase beam.nb for
# better result)
step <- 5
patient <- toy.load.patient (modality = c("ct","mr", "rtdose"),
                           dxyz = rep (step, 3), beam.nb = 3)

MR <- patient$mr[[1]]
CT <- patient$ct[[1]]
D <- patient$rtdose[[1]]

# display

display.kplane (CT)

display.kplane (MR, k = floor (length(MR$k.idx)*5/8),
               col = grey.colors (256, start = 0, end = 1),
               breaks = seq (0, 500, length.out = 257), bg = "darkblue")

display.kplane (D, k = floor (length(D$k.idx)*3/8),
               col = rainbow (256, s = seq (1, 0, length.out = 256),
                             start = 0, end = 4/6,
                             alpha = seq (0.8, 0, length.out=256),
                             rev = TRUE),
               bg = "darkblue", ord.flip = TRUE, sat.transp = FALSE,
               interpolate = FALSE)

display.kplane (CT, k = floor (length(CT$k.idx)/3), col = pal.RVV (1000),
               breaks = seq(-1000, 1000, length.out = 1001),
               bg = "darkblue", ord.flip = TRUE, interpolate = FALSE)
```



---

display.legend	<i>Display of the ROI legend</i>
----------------	----------------------------------

---

### Description

The `display.legend` function displays in an image the list of requested ROI and their associated color.

### Usage

```
display.legend(  
  struct = NULL,  
  roi.name = NULL,  
  roi.sname = NULL,  
  roi.idx = NULL,  
  lwd = 1,  
  cex = 1,  
  displayed.roi.name = NULL,  
  bg = "black",  
  text.col = "white"  
)
```

### Arguments

<code>struct</code>	"struct" class object.
<code>roi.name</code>	Vector of exact names of the ROI in the struct object. By default <code>roi.name = NULL</code> . See Details.
<code>roi.sname</code>	Vector of names or parts of names of the ROI in the struct object. By default <code>roi.sname = NULL</code> . See Details.
<code>roi.idx</code>	Vector of indices of the ROI that belong to the struct object. By default <code>roi.idx = NULL</code> . See Details.
<code>lwd</code>	Line thickness, defaults to 1
<code>cex</code>	Font size, default to 1.
<code>displayed.roi.name</code>	Vector. If different from <code>NULL</code> , it represents the replacement names of selected ROI if needed.
<code>bg</code>	color of the background.
<code>text.col</code>	color of the legend text.

### Details

`roi.name`, `roi.sname`, and `roi.idx` indicates the ROI to display. If all three are set to `NULL`, all ROI are selected.

### Value

Returns display of the ROI names and their associated color in the active graphics window.

**Examples**

```
# loading of toy-patient objects
patient <- toy.load.patient (modality = c("rtstruct"), dxyz = c (5, 5, 5))
S <- patient$rtstruct[[1]]

display.legend (struct = S, roi.idx = 2:10, lwd = 2)
```

---

display.obj.links      *Display patient objects links*

---

**Description**

The `display.obj.links` function displays a graph of connections between objects of a patient. The name of the objects corresponds to their modality (ct, mr, rtdose...) followed by their position in their respective lists in the patient list objects. Connected objects are linked by arrows. Objects sharing the same frame of reference have the same color except for objects with warnings, errors or missing planes which are all in grey. Approved objects are circled in green. By default, objects shapes are circles, except rtdose represented as squares.

**Usage**

```
display.obj.links(
  pat,
  obj.selected = NULL,
  exclusion = NULL,
  square = "rtdose",
  group.by.connected.FoR = TRUE,
  interactive = FALSE
)
```

**Arguments**

pat	"patient" class object, as loaded using <a href="#">load.patient.from.dicom</a> , <a href="#">load.patient.from.Rdcm</a> or <a href="#">toy.load.patient</a> .
obj.selected	Dataframe (default to NULL) containing the objects already selected, created by a previous call of <code>display.obj.links</code> for example.
exclusion	Vector of patient file modalities that should not be displayed, as for instance "mr"...
square	Vector of patient file modalities that should be enclosed by a square, as for instance c ("ct", "mr")... If NULL no object name is squared.
group.by.connected.FoR	Boolean. If TRUE (default), all objects sharing the same frame of reference or connected by a registration matrix have the same color. If <code>group.by.connected.FoR</code> = FALSE, only objects sharing the same FoR have the same color.
interactive	Boolean. If <code>interactive</code> = TRUE, buttons are available on the graph to get information about the objects and select or remove them from the data frame of the selected objects. Then simply click on the name of the object on which to apply the chosen action. If <code>interactive</code> = FALSE no interaction possible with the plot.

**Value**

The function displays all patient objects, linked by an arrow when they are connected, and with a color and a shape depending on square, group.by.connected.FoR.

When interactive = TRUE, it returns a dataframe of the selected objects, or NULL if no object is selected.

**Examples**

```
# loading of toy-patient objects
patient <- toy.load.patient (dxyz = c (5, 5, 5), beam.nb = 1)
display.obj.links (patient, group.by.connected.FoR = FALSE)
display.obj.links (patient, group.by.connected.FoR = TRUE)
```

---

display.palette	<i>Display of the color scale of a color palette</i>
-----------------	--

---

**Description**

The Display.palette function displays the color scale as it is used for representations in espadon functions

**Usage**

```
display.palette(
  col,
  breaks = NULL,
  factors = NULL,
  override.breaks = FALSE,
  bg = "black",
  new.window = TRUE,
  ylab = ""
)
```

**Arguments**

col	Vector of colors like the ones generated by rainbow, heat.colors, etc.
breaks	Vector of breaks for the color palette. It is the usual option for images or dose, for instance. Its length must be one unit more than col length.
factors	Vector containing the labels associated to each col. It should be used for tissue identification or image segment labelling. Its length must be col length.
override.breaks	Boolean. When FALSE (by default) ordinates are set to breaks. when TRUE colors are uniformly displayed, and associated breaks set to the correct ordinates for the given colors.
bg	Color of the background, seen by transparency for palette having alpha channel.
new.window	Boolean. If TRUE, it opens a new window for displaying the palette.
ylab	character string. Label of ordinates.

**Value**

Returns in a new device (if `new.window = TRUE`), or in the active graphics window (if `new.window = FALSE`), the palette color defined by `col` and breaks in priority, or by `col` and factors.

**Note**

the breaks are not necessarily evenly spaced. In this case, the colour palette can be represented as the breaks are defined (default option) or by choosing a constant spacing for each colour and displaying the associated abscissa calculated from the breaks (`override.breaks = TRUE`).

**Examples**

```
## Not run:
# simple example for breaks and factors

display.palette (c ("red", "green", "blue"), breaks = c(0, 1, 3, 7),
                 ylab = "a simple color palette")
display.palette (c ("red", "green", "blue"), breaks = c(0, 1, 3, 7),
                 override.breaks = TRUE)
display.palette (c ("red", "green", "blue"), factors = c ("red", "green", "blue"))
display.palette (c ("gray", "green", "blue"), factors = c (NA, 1, 2))

# for RVV palette, HU range must be [-1000, 1000]
display.palette (pal.RVV (255), breaks = seq (-1000, 1000, length.out=256))

# a palette for dose, for instance
display.palette (rainbow (255, start = 0, end = 4/6, rev = TRUE),
                 breaks = seq (0, 60, length.out = 256))

# black & white palette for CTs or MRs
display.palette (grey.colors (255, start = 0, end = 1),
                 breaks = seq (0, 60, length.out = 256))

# transparency affects colors depending on background (black in first exemple,
# white in the second one)
display.palette (rainbow (255, s = seq (1, 0, length.out = 255),
                           start = 0, end = 4/6,
                           alpha = seq (0.8, 0, length.out = 255), rev = TRUE),
                 breaks = seq (0, 60, length.out=256))
display.palette (rainbow (255, s = seq (1, 0, length.out = 255),
                           start = 0, end = 4/6,
                           alpha = seq (0.8, 0, length.out = 255), rev = TRUE),
                 breaks = seq (0, 60, length.out=256), bg = "white")

## End(Not run)
# colors contracted range using non uniform breaks in the plot window
display.palette (rainbow(255, s = seq(1, 0.8, length.out = 255),
                       start = 0, end = 4/6,
                       alpha = seq(0.8, 0.6, length.out = 255), rev = TRUE),
                 breaks = seq (0, 1, length.out = 256)^0.25 * 60, bg="grey",
                 new.window = FALSE)

# the same using breaks override
display.palette (rainbow(255, s = seq(1, 0.8, length.out = 255),
                       start = 0, end = 4/6,
                       alpha = seq(0.8, 0.6, length.out = 255), rev = TRUE),
```

```
breaks = seq (0, 1, length.out = 256)^0.25 * 60, bg="grey",
override.breaks = TRUE, new.window = FALSE)
```

---

display.plane	<i>Display the transverse frontal or sagittal view in the patient reference system</i>
---------------	--

---

### Description

The `display.plane` function displays an overlay of images and ROI closed planar contours on a plane defined by the equations  $x = \text{constant}$  (sagittal view), or  $y = \text{constant}$  (frontal view) or  $z = \text{constant}$  (transverse view) in a frame of reference chosen by the user.

### Usage

```
display.plane(
  bottom = NULL,
  top = NULL,
  struct = NULL,
  roi.name = NULL,
  roi.sname = NULL,
  roi.idx = NULL,
  struct.dxyz = c(1, 1, 1),
  display.ref = NULL,
  T.MAT = NULL,
  interpolate = TRUE,
  view.type = c("trans", "front", "sagi"),
  view.coord = 0,
  bg = "#000000",
  abs.rng = NULL,
  ord.rng = NULL,
  bottom.col = grey.colors(255, start = 0, end = 1),
  top.col = rainbow(255, s = seq(1, 0, length.out = 255), start = 0, end = 4/6, alpha =
    seq(0.8, 0, length.out = 255), rev = TRUE),
  bottom.breaks = NULL,
  top.breaks = NULL,
  sat.transp = FALSE,
  struct.lwd = 2,
  main = NULL,
  legend.plot = TRUE,
  legend.shift = 0
)
```

### Arguments

bottom	"volume" class object, displayed using <code>bottom.col</code> palette. If <code>bottom = NULL</code> , no bottom image is displayed.
top	"volume" class object, displayed as an overlay, using <code>top.col</code> palette. If <code>top = NULL</code> , no overlay image is displayed.
struct	"struct" class object. If <code>NULL</code> , no ROI is displayed.

roi.name	Vector of exact names of the ROI in the struct object. By default roi.name = NULL. See Details.
roi.sname	Vector of names or parts of names of the ROI in the struct object. By default roi.sname = NULL. See Details.
roi.idx	Vector of indices of the ROI that belong to the struct object. By default roi.idx = NULL. See Details.
struct.dxyz	Vector of 3 numbers. Used in case of bottom and top are set to NULL. It represents the virtual steps of a temporary volume created in the display.ref frame of reference, initialized at 1 mm in the 3 directions x, y and z.
display.ref	Character string. Pseudonym of the frame of reference used for display. If NULL (default), the bottom image FoR, or top image FoR (when no bottom image), or struct FoR (when no volume displayed).
T.MAT	"t.mat" class object, created by <a href="#">load.patient.from.Rdcm</a> or <a href="#">load.T.MAT</a> . If T.MAT is NULL, bottom, top and struct must have the same frame of reference.
interpolate	Boolean, indicating whether to apply trilinear interpolation to the bottom and top volumes. If interpolate = FALSE, the values of the nearest voxels are used. When TRUE (by default), trilinear interpolation is used.
view.type	Character string, defining the view to display. It must be set to <ul style="list-style-type: none"> <li>• "trans" for a transverse view,</li> <li>• "front" for a frontal view or,</li> <li>• "sagi" for a sagittal view.</li> </ul>
view.coord	Numeric vector of the coordinates along the normal vector of the selected view.
bg	Background color of the image. By default, this color is black.
abs.rng	Vector of 2 elements indicating the minimum and maximum abscissa to display on the background image.
ord.rng	Vector of 2 elements indicating the minimum and maximum ordinate to display on the background image.
bottom.col, top.col	Vectors, representing the palette color of bottom and top.
bottom.breaks, top.breaks	One of : <ul style="list-style-type: none"> <li>• NULL : the minimum and the maximum value of bottom or top define the range.</li> <li>• Vector giving the breakpoints of each color. Outside values are transparent, leaving the background visible, depending on sat.transp.</li> </ul> <p>When breaks are specified, the number of breaks must be one unit more than the number of colors.</p>
sat.transp	Boolean. If TRUE, outside values are transparent, else set to bottom.breaks or top.breaks limits.
struct.lwd	Line thickness of the ROI contours.
main	Character string. When main different from NULL, it replaces the title, and removes the subtitle and the maximum dose indication if top is of modality rtdose.
legend.plot	Boolean, that indicates whether the ROI legend should be displayed on the image. It is displayed by default.
legend.shift	Numeric. It shifts (in mm) the display of the ROI legend on x-axis.

**Details**

If `roi.name`, `roi.sname`, and `roi.idx` are all set to `NULL`, all closed planar ROI are selected. If a ROI is not present in the requested plane, the ROI legend won't mention it.

**Value**

Returns a display of the transverse, sagittal or frontal plane. This plane has the coordinate  $z = \text{view.coord}$  (transverse),  $y = \text{view.coord}$  (sagittal) or  $x = \text{view.coord}$  (frontal). The display is an overlay of:

- a background image of uniform color `bg`
- the bottom image if it exists
- the top image if it exists
- the contours of the regions of interest if they exist in the plane considered.

**Note**

- 1- The main title is given by `bottom`, the subtitle by `top`.
- 2- When `top` is in the "rtdose" modality, the maximum dose is written on the image.

**See Also**

[display.kplane](#).

**Examples**

```
# loading of toy-patient objects (decrease dxyz and increase beam.nb for
# better result)
step <- 5
patient <- toy.load.patient (modality = c("ct", "rtstruct", "rtdose"),
                           roi.name = "",
                           dxyz = rep (step, 3), beam.nb = 3)

CT <- patient$ct[[1]]
D <- patient$rtdose[[1]]
S <- patient$rtstruct[[1]]

display.plane (bottom = CT, top = D, struct = S, view.coord = -30,
              interpolate = FALSE, legend.shift = -80)
```

---

espadon.class

*ESPADON class*

---

**Description**

ESPADON class

**Usage**

```
espadon.class()
```

**Value**

Returns a vector of **espadon** class names.

**Note**

Each object of a class has specific features that are used to display or process that object.

- the "patient" class includes :

- \$patient : dataframe providing patient's information as PIN, birth date and gender.
- \$pat.pseudo : patient's pseudonym, initialized to the patient's PIN of \$patient dataframe.
- \$description : dataframe describing the patient's DICOM objects: their modality (rtstruct, ct, mr, rtplan ...), the base name of the relevant source file in the patient's directory, the pseudonym of their frame of reference (ref1, ref2 ...), their number of sub-objects, their description if any, their numbers of slices/ROI for all sub-objects, their maximum voxels (for volume sub-objects), and finally the aliases of the sub-objects.
- \$description.by.reg: list of DICOM objects descriptions that are linked by a transfer matrix.
- \$T.MAT : list of class "t.mat" containing the information of the transfer matrices to move from one frame of reference to another. See [load.T.MAT](#).
- \$ct : list of CT, if any. They are named by their \$object.alias See [load.obj.from.Rdcm](#).
- \$mr : list of MRI, if any. They are formatted like the \$ct.
- \$rtdose : list of dose matrices. They are formatted like the \$ct.
- \$rtstruct: list of struct objects.
- ...any DICOM objects other than the reg files, and those previously mentioned, or any modalities created by **espadon**.
- \$dicom.dvh: if any, list of DVH computed in rt-dose DICOM files.

- the "t.mat" class includes :

- \$ref.info: dataframe giving the correspondence between the frame of reference (column \$ref) of the DICOM object (TAG (0020,0052) ) and its pseudonym (column \$ref\_pseudo).
- \$reg.info: list of dataframes : the first one gives the PID, birthday, and sex of the patient, the second one gives the name of the source file of transfer matrices.
- \$matrix.description: dataframe giving the transfer matrix names (column \$t), its source frame of reference (column \$src), the destination frame of reference (column \$dest), and its type (\$type). Note that only the RIGID type is supported.
- \$matrix.list: list of 4X4 transfer matrices. This list contains at least as many Identity matrices as there are ref.pseudo.

A **espadon** object of class "dvh","histo","histo2D","mesh", "reg", "struct", "t.mat","undef","volume" is a list containing at least:

- \$patient: patient's PIN.
- \$patient.bd: patient's birthday.
- \$patient.sex: patient's sex
- \$file.basename: vector of .Rdcm or .dcm file basenames of the object, if it exists
- \$file.dirname : directory including the .Rdcm or .dcm file, if it exists
- \$object.name: name of the object.



- `$object.alias`: alias of the object.
- `$frame.of.reference`: value of TAG (0020,0052).
- `$ref.pseudo`: pseudonym of the `$frame.of.reference`
- `$modality`: modality of the object (e.g. ct, mr, bin, rtplan..)
- `$description`: description of the object.
- `$creation.date`: creation date of the object.

If the object was generated from a DICOM file, the list also contains:

- `$object.info`: Information of the object. It includes:
  - the SOP ID (value of TAG (0008,0016)),
  - the transfer syntax UID (value of TAG (0002,0010)),
  - the SOP implementation ID (value of TAG (0002,0012)),
  - the SOP type (value of TAG (0008,0008)),
  - the study ID (value of TAG (0020,0010)),
  - the study UID (value of TAG (0020,000D)),
  - the serie UID (value of TAG (0020,000E)),
  - the scanning sequence (value of TAG (0018,0020)),
  - the list of SOP labels (values of TAG (0008,0018)),
  - the dicom source files,
  - the encoding of the content of text tags (values of TAG (0008,0005)) and
  - the number of sub-objects.

if the object is linked to another DICOM object, the list also contains:

- `$ref.object.name`: Name of the reference object. Available only for rtdose.
- `$ref.object.info`: Information of the reference object (not available for mr and ct). It includes:
  - the SOP ID of the reference object,
  - the list of SOP names of the reference object.

- the "dvh" class also includes :

- `$nb.MC`: set to `histo$nb.MC`.
- `$breaks`: vector breakpoints.
- `$mids`: vector of cell centers.
- `$mids.unit`: Character string, representing the unit of the abscissa of the DVH. For instance, "Gy".
- `$vol`: cumulative volume receiving at least the doses defined by `$mids`.
- `$pcv`: percentage of the total volume receiving at least the doses defined by `$mids`.
- if `$nb.MC` is different from 0, the arrays `MC.vol`, `MC.pcv` and `MC.dxyz` are added. See [histo.DVH](#).

- the "histo" class also includes :

- `$nb.MC`: number of Monte-Carlo simulations
- `$breaks`: vector breakpoints
- `$mids`: vector of cell centers.

- `$mids.unit`: Character string, representing the unit of the abscissa of the histogram. For instance, "Gy".
- `counts`: count of voxels whose value is included in the limits defined by `$breaks`.
- `dV_dx`: differential histogram, expressed in  $cm^3$  by voxel units, at each `$mids`.
- if `$nb.MC` is different from 0, the arrays `MC.counts`, `MC.dV_dx` and `MC.dxyz` are added. See [histo.from.roi](#).

- the "histo2D" class also includes :

- `$nb.pixels`: number of elements in the `density.map`.
- `$x.file.src`: x label. See [histo.2D](#).
- `$y.file.src`: y label. See [histo.2D](#).
- `x.breaks`: vector of x-axis breakpoints.
- `y.breaks`: vector of y-axis breakpoints.
- `x.mids`: vector of x-axis cell centers.
- `y.mids`: vector of y-axis cell centers.
- `density.map`: array of densities.
- `total.counts`: number of counted voxels.

- the "mesh" class also includes :

- `$nb.faces`: set to the number of faces of the mesh.
- `$mesh`: list of 3 elements defining the mesh : `$vb`, `$it` and `$normals`. See [mesh.from.bin](#).

- the "reg" class also includes :

- `$nb.of.ref`: number of transfer matrices.
- `$ref.data`: list including the lists of information on transfer matrices, namely: the source frame of reference (`$src`), the matrix type (`$type`, for example 'RIGID') and the transfer matrix (`$matrix`).

- the "rtplan" class also includes :

- `$approval.status`: value of TAG (300E,0002).
- `$number`: sub-object number.
- `$plan.info`: dataframe containing, if they exist,
  - `$label` the label for the treatment plan,
  - `$plan.name` the name for the treatment plan,
  - `$plan.description` description of treatment plan,
  - `$tt.protocol` the treatment protocol,
  - `$plan.intent` the intent of this plan,
  - `$tt.site` describing the anatomical treatment site,
  - `$geometry` describing whether RT Plan is based on patient or treatment device geometry.
- `$presc.dose`: dataframe containing, if they exist,
  - `$ref.roi.nb` value of TAG (3006,0084),
  - `$dose.ref.nb` value of TAG (300A,0012),
  - `$dose.ref.id` value of TAG (300A,0013),

- \$struct.type value of TAG (300A,0014),
- \$description value of TAG (300A,0016),
- \$pt.coord value of TAG (300A,0018),
- \$nominal.prior.dose value of TAG (300A,001A),
- \$dose.type value of TAG (300A,0020),
- \$constraint.weight value of TAG (300A,0021),
- \$deliv.warn.dose value of TAG (300A,0022),
- \$deliv.max.dose value of TAG (300A,0023),
- \$targ.min.dose value of TAG (300A,0025),
- \$targ.presc.dose value of TAG (300A,0026),
- \$targ.max.dose value of TAG (300A,0027),
- \$targ.underdose.vol.frac value of TAG (300A,0028),
- \$org.risk.full.vol.dose value of TAG (300A,002A),
- \$org.risk.lim.dose value of TAG (300A,002B),
- \$org.risk.max.dose value of TAG (300A,002C),
- \$org.risk.overdose.vol.frac value of TAG (300A,002D)

- \$fraction.info: dataframe containing, if they exist,

- \$fraction.id the id of the fraction group,
- \$description its description,
- \$planned.frac.nb the total number of treatments (Fractions) prescribed for current fraction group,
- \$frac.pattern.digit.per.day.nb the number of digits in \$frac.pattern used to represent one day,
- \$repeat.frac.cycle.le the number of weeks needed to describe treatment pattern,
- \$frac.pattern the value of TAG (300A,007B) describing treatment pattern every day,
- \$beam.nb the number of beams in current fraction group,
- \$beam.dose.meaning the value of TAG (300A,008B) indicating the meaning of Beam Dose,
- \$brachy.app.nb the number of brachy application setups in current fraction group.

- \$beam.info (in case of beam treatment): dataframe containing, if they exist,

- \$fraction.id,
- \$planned.frac.nb,
- \$beam.dose the value of TAG (00A,0084),
- \$beam.specif.pt the value of TAG (300A,0082),
- \$beam.meterset the value of TAG (300A,0086),
- \$beam.type the value of TAG (300A,0090),
- \$alt.dose the value of TAG (300A,0091),
- \$alt.type the value of TAG (300A,0092),
- \$duration.lim the value of TAG (300A,00C5),
- \$beam.nb the value of TAG (300C,0006) or (300A,00C0),
- \$beam.name the value of TAG (300A,00C2),
- \$beam.description the value of TAG (300A,00C3),
- \$beam.type the value of TAG (300A,00C4),
- \$radiation.type the value of TAG (300A,00C6),
- \$high.dose.technique.type the value of TAG (300A,00C7),
- \$treatment.machine.name the value of TAG (300A,00B2),
- \$device.serial.nb the value of TAG (0018,1000),
- \$primary.dosimeter.unit the value of TAG (300A,00B3),
- \$referenced.tolerance.table.nb the value of TAG (300C,00A0),
- \$src.axis.dist the value of TAG (300A,00B4),
- \$referenced.patient.setup.nb the value of TAG (300C,006A),
- \$treatment.delivery.type the value of TAG (300A,00CE),

- \$wedges.nb the value of TAG (300A,00D0),
- \$compensators.nb the value of TAG (300A,00E0),
- \$total.compensator.tray.factor the value of TAG (300A,00E2),
- \$boli.nb the value of TAG (300A,00ED),
- \$blocks.nb the value of TAG (300A,00F0),
- \$total.block.tray.factor the value of TAG (300A,00F2),
- \$final.cumul.meterset.weight the value of TAG (300A,010E),
- \$ctl.pts.nb the value of TAG (300A,0110),
- \$radiation.mass.nb the value of TAG (300A,0302),
- \$radiation.atomic.nb the value of TAG (300A,0304),
- \$radiation.charge.state the value of TAG (300A,0306),
- \$scan.mode the value of TAG (300A,0308),
- \$modulated.scan.mode.type the value of TAG (300A,0309),
- \$virtual.src.axis.dist the value of TAG (300A,030A),
- \$total.wedge.tray.water.equ.thickness the value of TAG (300A,00D7),
- \$total.compensator.tray.water.equ.thickness the value of TAG (300A,02E3),
- \$total.block.tray.water.equ.thickness the value of TAG (300A,00F3),
- \$range.shifters.nb the value of TAG (300A,0312),
- \$lateral.spreading.devices.nb the value of TAG (300A,0330),
- \$range.modulators.nb the value of TAG (300A,0340),
- \$fixation.light.azimuthal.angle the value of TAG (300A,0356),
- \$fixation.light.polar.angle the value of TAG (300A,0358).

- \$brachy.info (in case of brachy treatment): dataframe containing, if they exist,

- \$fraction.id
- \$planned.frac.nb,
- \$brachy.dose the value of TAG (300A,00A4),
- \$brachy.nb the value of TAG (300C,000C),
- \$brachy.specif.pt the value of TAG (300A,00A).

- the "struct" class also includes :

- \$nb.of.roi: number of regions of interest (RoI).
- \$thickness: thickness between two consecutive planes of a contour.
- \$ref.from.contour: reference frame change matrix, from the contour reference frame to the ref.pseudo reference frame
- \$roi.info: dataframe. Information on RoI contours. It includes the followings columns:

- \$number: value of TAG (3006,0084) for the concerned RoI.
- \$name: value of TAG (3006,0026) for the concerned RoI.
- \$description: value of TAG (3006,0028) for the concerned RoI.
- \$generation.algorithm: value of TAG (3006,0036) for the concerned RoI.
- \$color: value of TAG (3006,002A) for the concerned RoI.
- \$dz: z step between planes for the concerned RoI.
- \$roi.pseudo: pseudonym of the RoI \$name. It can be changed by the user.
- \$min.x: minimum value x in mm of the RoI. Absent when data = FALSE.
- \$max.x: maximum value x in mm of the RoI. Absent when data = FALSE.
- \$min.y: minimum value y in mm of the RoI. Absent when data = FALSE.
- \$max.y: maximum value y in mm of the RoI. Absent when data = FALSE.
- \$min.z: minimum value z in mm of the RoI. Absent when data = FALSE.
- \$max.z: maximum value z in mm of the RoI. Absent when data = FALSE.

- \$vol: volume in mm<sup>3</sup> of the RoI. Absent when data = FALSE.
- \$Gx: position x in mm of the RoI center of gravity. Absent when data = FALSE.
- \$Gy: position y in mm of the RoI center of gravity. Absent when data = FALSE.
- \$Gz: position z in mm of the RoI center of gravity. Absent when data = FALSE.
- \$continue: boolean, indicating whether the contours are on adjacent planes.

- \$roi.obs: dataframe. RT RoI observations (sequence TAG (3006,0080)). It includes the followings columns :

- \$nb: value of TAG (3006,0082) for the concerned RoI.
- \$roi.nb: value of TAG (3006,0084) for the concerned RoI.
- \$label: value of TAG (3006,0085) for the concerned RoI.
- \$code.value: value of TAG (0008,0100) in the Identification code sequence.
- \$code.scheme: value of TAG (0008,0102) in the Identification code sequence.
- \$code.scheme.v: value of TAG (0008,0103) in the Identification code sequence.
- \$code.meaning: value of TAG (0008,0104) in the Identification code sequence.
- \$type: value of TAG (3006,00A4) for the concerned RoI.
- \$interpreter: value of TAG (3006,00A6) for the concerned RoI.

- \$roi.data: exists only if the data is loaded. Contains the list of contour coordinates. The RoI of list number i is that of line i of roi.info. Each element of the list is a list giving the contour information for each plane, namely:

- \$type: value of TAG (3006,0042).
- \$pt: dataframe of the coordinates of the contour points.  
If the contour is closed (i.e.\$type = "CLOSED\_PLANAR"), then the first point is repeated at the end.
- \$level: contour inclusion level. If this number is even, the inside of the closed contour belongs to the RoI.  
Otherwise, if odd, the inside of the closed contour is excluded from the RoI.

- the "undef" class : is used for DICOM objects that will not be processed further by **espadon** functions. It can also include what the user wants.

- the "volume" class also includes :

- \$number: sub-object number.
- \$n.ijk: vector defining the number of indices i, j, k. The product prod(...\$n.ijk) represents the number of voxels in the 3D volume.
- \$slice.thickness: thickness in mm of a plane.
- \$min.pixel: minimum value of voxels in the volume.
- \$max.pixel: maximum value of voxels in the volume.
- \$dxyz: x, y, z steps in mm.
- \$patient.orientation: value of TAG (0020,0037). Vector, comprising the vectors i and j defining the orientation of the patient with respect to the volume planes.
- \$patient.xyz0: in the patient frame of reference, position of the first voxel of each plane.
- \$xyz.from.ijk: transfer matrix of the voxels i, j, k indices to the position x, y, z in mm in the patient's frame of reference.
- \$k.idx: index of planes in the 3D volume.

- `$missing.k.idx`: Boolean, indicating if `k` is a continuous sequence of integers.
- `$cube.idx`: 3D volume vertices indices.
- `$vol13D.data`: exists only if the data is loaded. 3D array of the voxel values of the 3D volume.

### See Also

[toy.load.patient](#), [load.patient.from.dicom](#), [load.patient.from.Rdcm](#), [load.T.MAT](#) [histo.DVH](#), [histo.vol](#), [histo.from.roi](#), [histo.from.bin](#), [histo.2D](#), [mesh.from.bin](#), [load.obj.from.Rdcm](#)

### Examples

```
cat ("espadon class names are:", paste (espadon.class(), collapse = ", "))
```

---

get.extreme.pt

*Coordinates of the extreme points*

---

### Description

The `get.extreme.pt` function returns the x, y, z coordinates of the 2 extreme voxels of the rectangular parallelepiped, containing the volume `vol`. These coordinates are given in the `ref.pseudo` frame of reference .

### Usage

```
get.extreme.pt(vol, ref.pseudo = vol$ref.pseudo, T.MAT = NULL)
```

### Arguments

<code>vol</code>	"volume" class object.
<code>ref.pseudo</code>	Pseudonym of the frame of reference in which you want the coordinates.
<code>T.MAT</code>	"t.mat" class object, created by <a href="#">load.patient.from.Rdcm</a> or <a href="#">load.T.MAT</a> . If <code>T.MAT = NULL</code> , <code>ref.pseudo</code> must be equal to <code>vol\$ref.pseudo</code> .

### Value

Returns a dataframe of min and max columns, and x, y and z rows, representing the coordinates of the 2 extreme voxels of the rectangular parallelepiped.

### Examples

```
# loading of toy-patient objects
patient <- toy.load.patient (modality = "ct", roi.name = "", dxyz = c (5, 5, 5))
CT <- patient$ct[[1]]

# xyz extreme coordinate
get.extreme.pt (CT)
```

---

get.ijk.from.index      *Conversion of the indices of a point into ijk vector*

---

## Description

The `get.ijk.from.index` function converts the voxel indices of `vol$vol3D.data` (for example, obtained with the function `which`) into a vector or matrix of DICOM indices `i, j, k`.

## Usage

```
get.ijk.from.index(idx, vol)
```

## Arguments

`idx`                      Index, or matrix of voxel indices of the array `vol$vol3D.data`.  
`vol`                      "volume" class object.

## Value

Returns an `i, j, k` column matrix of the DICOM indices of the points of `vol$vol3D.data`.

## See Also

[get.value.from.ijk](#), [display.kplane](#)

## Examples

```
# loading of toy-patient objects (decrease dxyz and increase beam.nb for
# better result)
step <- 4
patient <- toy.load.patient (modality = "rtdose", roi.name = "",
                             dxyz = rep (step, 3), beam.nb = 3)
D <- patient$rtdose[[1]]

# voxels location where the dose is greater than 99.9% Dmax
Dmax <- max (D$vol3D.data, na.rm = TRUE) # D$max.pixel
get.ijk.from.index (which (D$vol3D.data >= 0.999 * Dmax), D)
# or
get.ijk.from.index (which (D$vol3D.data >= 0.999 * Dmax, arr.ind = TRUE), D)

ijk <- as.numeric (get.ijk.from.index (which.max (D$vol3D.data), D))
display.kplane (D, k = ijk[3])
```

---

get.ijk.from.xyz      *Indices relating to the coordinates of the points*

---

### Description

The `get.ijk.from.xyz` function calculates the *i, j, k* DICOM indices of the points given in the patient's reference frame.

### Usage

```
get.ijk.from.xyz(xyz = matrix(c(0, 0, 0), ncol = 3), vol, verbose = FALSE)
```

### Arguments

<code>xyz</code>	Vector of length 3, corresponding to the <i>x, y, z</i> coordinates (in mm) of a point in the patient's frame of reference, or 3-column matrix of <i>x, y, z</i> coordinates of several points.
<code>vol</code>	"volume" class object.
<code>verbose</code>	Boolean, default to FALSE. If <code>verbose = TRUE</code> , then the <i>xyz</i> coordinates are printed.

### Value

Returns a vector or a matrix of the *i, j, k* DICOM indices of the *x, y, z* coordinate points in the patient's frame of reference.

### Note

The vector or matrix is made up of real numbers. It is up to the user to make the indices as integer. The indices of the first voxel `vol` are 0, 0, 0. WARNING: As *i,j,k* are DICOM indices, they are not directly related to array indices. To get the value of the `vol$vol3D.data`, use the function [get.value.from.ijk](#).

### Examples

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = "ct", roi.name = "",
                             dxyz = rep (step, 3))
CT <- patient$ct[[1]]

get.ijk.from.xyz (xyz = CT$patient.xyz0[1,], vol = CT, verbose = TRUE)
get.ijk.from.xyz (xyz = c (1,1,1), vol = CT, verbose = TRUE)

index <- get.ijk.from.xyz (xyz = c (1,1,1), vol = CT)
floor (index)

index <- get.ijk.from.xyz (xyz = matrix (c (0,0,0,1,1,1), ncol = 3, byrow = TRUE),
                           vol = CT)
floor (index)
```



---

get.line	<i>Image value along an axis</i>
----------	----------------------------------

---

### Description

The `get.line` function calculates the value of the points of a volume `vol` along an axis in any direction.

### Usage

```
get.line(
  vol,
  origin = c(0, 0, 0),
  orientation = c(1, 0, 0),
  grid = seq(-100, 100, 1),
  interpolate = TRUE
)
```

### Arguments

<code>vol</code>	"volume" class object.
<code>origin</code>	Vector of x, y, z coordinates belonging to the line to extract. If <code>interpolate = FALSE</code> , these coordinates are replaced by the coordinates of the voxel closest to origin.
<code>orientation</code>	Directing vector of the line in the <code>vol</code> frame of reference. This vector is internally normalized.
<code>grid</code>	Vector, representing the curvilinear coordinates on the line to extract.
<code>interpolate</code>	Boolean, default to <code>TRUE</code> . If <code>interpolate = TRUE</code> , a trilinear interpolation of the value of the voxels, relative to the values of adjacent voxels, is performed.

### Value

Returns a dataframe, composed of the columns `$x`, `$y`, `$z`, representing the coordinates of the points where the values are taken in `vol` volume, the column `$s` representing the curvilinear abscissa, and the column `$value` representing values along `$s`.

### Examples

```
# loading of toy-patient objects (decrease dxyz and increase beam.nb for
# better result)
step <- 4
patient <- toy.load.patient (modality = "rtdose", roi.name = "",
                             dxyz = rep (step, 3), beam.nb = 3)
D <- patient$rtdose[[1]]

# Dose at maximum dose
origin <- get.xyz.from.index (which.max (D$vol3D.data), D)
display.plane (bottom = D, view.coord = origin[3],
               bg = "#0000ff")

# Dose profile at x = origin[1] and z = origin[3].
```

```

l <- get.line (vol = D, origin = origin,
              orientation = c (0, 1, 0), interpolate = FALSE)
plot (l$y, l$value, type = "l")
grid ()

# Dose profile at y = origin[2] and z = origin[3].
l <- get.line (D, origin = origin,
              orientation = c (1, 0, 0), interpolate = FALSE)
plot (l$s, l$value, type = "l")
grid ()

```

---

get.plane

*Extracting a plane from a volume*


---

### Description

The `get.plane` function extracts a plane from a "volume" class object.

### Usage

```

get.plane(
  vol,
  origin = c(0, 0, 0),
  plane.orientation = c(1, 0, 0, 0, 1, 0),
  alias = "plane.n",
  xgrid = NULL,
  ygrid = NULL,
  interpolate = TRUE
)

```

### Arguments

<code>vol</code>	"volume" class object.
<code>origin</code>	Vector of x, y, z coordinates, representing the origin of the plane to extract. If <code>interpolate = FALSE</code> , these coordinates are replaced by the coordinates of the voxel closest to origin.
<code>plane.orientation</code>	Vector orientation of the plane in the <code>vol</code> frame of reference, composed by the 2 vectors coordinates of the orthonormal basis of the plane. First vector is x-axis, and second one is y-axis.
<code>alias</code>	<code>\$object.alias</code> of the created object.
<code>xgrid</code>	Vector, representing the grid of the plane abscissa. See note.
<code>ygrid</code>	Vector, representing the grid of the plane ordinates. See note. If <code>ygrid = NULL</code> , the ordinate is the line intercepting the volume and the step is set to the projection of <code>vol\$dxzy</code> onto the ordinate orientation.
<code>interpolate</code>	Boolean, default to <code>TRUE</code> . If <code>interpolate = TRUE</code> , a trilinear interpolation of the value of the voxels, relative to the values of adjacent voxels, is performed.

**Value**

Returns a "volume" class object, containing only a single plane, at  $k = 0$ , in the same frame of reference as `vol`. This returned object has 2 new fields `local.xgrid`, and `local.ygrid`, representing the local grids of the abscissa (columns) and ordinate (rows) of the plane.

**Note**

*Determination of axes :*

- the x-axis has `plane.orientation[1:3]` as unit vector.
- the y-axis has `plane.orientation[4:6]` as unit vector.
- If `xgrid` is not NULL, `origin + x.grid * plane.orientation[1:3]` are the coordinates of the points on the x axis.
- If `ygrid` is not NULL, `origin + y.grid * plane.orientation[4:6]` are the coordinates of the points on the y axis.
- If `xgrid` or `ygrid` are NULL, they are determined to represent as closely as possible the initial volume in the required cut.

**Examples**

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = "mr", dxyz = rep (step, 3))
MR <- patient$mr[[1]]

# mid-volume point
mid.point <- apply (get.extreme.pt (MR),1,mean)

plane <- get.plane (MR, origin = mid.point, interpolate = TRUE)
display.kplane (plane, interpolate = FALSE)

plane <- get.plane (MR, origin = mid.point, xgrid = seq (-50, 50, 1),
                  ygrid = seq (-50, 50, 1), interpolate = TRUE)
display.kplane (plane, interpolate = FALSE)

# 3 points on the inclined plane
pts <- t ((MR$xyz.from.ijk %*% MR$cube.idx) [1:3 , c (1, 2, 7)])
orientation <- orientation.create (A = pts[1,], B = pts[2,], C = pts[3,])
origin <- apply (pts, 2, mean)
plane <- get.plane (MR, origin = origin,
                  plane.orientation = orientation, interpolate = TRUE)
display.kplane (plane, interpolate = FALSE)

orientation <- orientation.create (A = c (0, 0, 0) , B = c (1, 1, 0),
                                  C = c (-1, 1, 0))
plane <- get.plane (MR, origin = origin,
                  plane.orientation = orientation, interpolate = TRUE)
display.kplane (plane, interpolate = FALSE)
```

---

get.rigid.M	<i>Transfer matrix between two frames of reference</i>
-------------	--

---

### Description

The function `get.rigid.M` provides, from the `T.MAT` list created by the functions [load.patient.from.Rdcm](#), [load.patient.from.dicom](#) or [load.T.MAT](#), the 4x4 transfer matrix from the FoR (frame of reference) pseudonym `src.ref` to the FoR pseudonym `dest.ref`.

### Usage

```
get.rigid.M(T.MAT, src.ref, dest.ref)
```

### Arguments

<code>T.MAT</code>	"t.mat" class object, created by the functions <a href="#">load.patient.from.Rdcm</a> , <a href="#">load.patient.from.dicom</a> or <a href="#">load.T.MAT</a>
<code>src.ref</code>	Pseudonym of the source frame of reference
<code>dest.ref</code>	Pseudonym of the destination frame of reference

### Value

Returns the 4x4 transfer matrix `dest.ref` from `src.ref`.

### Examples

```
# loading of toy-patient objects
patient <- toy.load.patient (modality = c ("ct", "mr"), roi.name = "",
                             dxyz = c(5, 5, 5))
get.rigid.M (patient$T.MAT, "ref1", "ref2")
```

---

get.value.from.ijk	<i>Value of the volume at a selection of DICOM indices</i>
--------------------	--

---

### Description

The `get.value.from.ijk` function calculates the value of a "volume" class object at DICOM indices `i, j, k`, whether they are integers or not.

### Usage

```
get.value.from.ijk(ijk, vol, interpolate = TRUE)
```

### Arguments

<code>ijk</code>	Vector or 3-column matrix of DICOM indices.
<code>vol</code>	"volume" class object.
<code>interpolate</code>	Boolean, default to TRUE. If <code>interpolate = TRUE</code> , a trilinear interpolation of the value of the voxels, relative to the values of adjacent voxels, is performed.

**Value**

Returns a vector of the values of the volume at the requested DICOM indices.

**See Also**

[get.ijk.from.index.](#)

**Examples**

```
# loading of toy-patient objects (decrease dxyz and increase beam.nb for
# better result)
step <- 4
patient <- toy.load.patient (modality = "rtdose", roi.name = "",
                           dxyz = rep (step, 3), beam.nb = 3)

D <- patient$rtdose[[1]]
# isodose
Dmax <- max (D$vol3D.data, na.rm = TRUE)
Dmax
idx <- which (D$vol3D.data >= (Dmax -1) & D$vol3D.data <= (Dmax - 0.2))
ijk <- get.ijk.from.index (idx, D)
get.value.from.ijk (ijk, vol = D, interpolate = FALSE)
```

---

get.value.from.xyz      *Voxel values on a selection of points*

---

**Description**

The `get.value.from.xyz` function calculates the voxel values at the x, y, z coordinate points in the chosen frame of reference.

**Usage**

```
get.value.from.xyz(
  xyz,
  vol,
  xyz.ref.pseudo = NULL,
  T.MAT = NULL,
  interpolate = TRUE,
  verbose = FALSE
)
```

**Arguments**

xyz	Vector of length 3, corresponding to the x, y, z coordinates (in mm) of a point in xyz.ref.pseudo frame of reference, or 3-column matrix of x, y, z coordinates of several points.
vol	"volume" class object.
xyz.ref.pseudo	ref.pseudo in which the xyz coordinate points are given. This ref.pseudo must exist in the T.MAT list. If ref.pseudo is NULL then the point with coordinates xyz is considered to be in the patient frame of reference vol\$ref.pseudo.

T.MAT	"t.mat" class object, created by <a href="#">load.patient.from.Rdcm</a> , <a href="#">load.patient.from.dicom</a> or <a href="#">load.T.MAT</a> . If T.MAT = NULL, xyz.ref.pseudo must be equal to vol\$ref.pseudo or NULL.
interpolate	Boolean, default to FALSE. If interpolate = TRUE, a trilinear interpolation of the value of the voxels, relative to the values of adjacent voxels, is performed.
verbose	Boolean, default to FALSE. If verbose = TRUE, then the xyz coordinates are printed.

**Value**

Returns a vector of the voxel values at the requested coordinates.

**See Also**

[get.xyz.from.index](#)

**Examples**

```
# loading of toy-patient objects (decrease dxyz and increase beam.nb for
# better result)
step <- 4
patient <- toy.load.patient (modality = "rtdose", roi.name = "",
                           dxyz = rep (step, 3), beam.nb = 3)
D <- patient$rtdose[[1]]
get.value.from.xyz (xyz = matrix (c (0, 0, 0, 10, 10, 10),
                                   ncol = 3, byrow = TRUE), vol = D)

# isodose
Dmax <- max (D$vol3D.data, na.rm = TRUE)
idx <- which (D$vol3D.data >= (Dmax - 1) & D$vol3D.data <= (Dmax - 0.3))
pt <- get.xyz.from.index (idx, D)
get.value.from.xyz (pt, vol = D, interpolate = FALSE, verbose = TRUE)
```

---

get.volume.from.bin      *Volume selected by binary volume*

---

**Description**

The `get.volume.from.bin` function calculates the volume in  $cm^3$  of the selection specified by a "volume" class object of "binary" modality.

**Usage**

```
get.volume.from.bin(bin)
```

**Arguments**

bin                    "volume" class object, of "binary" modality.

**Value**

Returns the volume of the binary selection, in  $cm^3$ .

**See Also**[get.volume.from.roi](#)**Examples**

```
# loading of toy-patient objects
step <- 4
patient <- toy.load.patient (modality = c ("ct", "rtstruct"), roi.name = "brain",
                             dxyz = rep (step, 3))

CT <- patient$ct[[1]]
S <- patient$rtstruct[[1]]

# creation of a binary object
bin.brain <- bin.from.roi (vol = CT, struct = S, roi.sname = "bra")
# Volume calculation
get.volume.from.bin (bin.brain)
```

---

get.volume.from.roi     *Volume of a region of interest (ROI)*

---

**Description**

The `get.volume.from.roi` function extracts the volume in  $cm^3$  of one or more ROI, from the `$roi.info` of the "struct" class object.

**Usage**

```
get.volume.from.roi(struct, roi.name = NULL, roi.sname = NULL, roi.idx = NULL)
```

**Arguments**

<code>struct</code>	"struct" class object.
<code>roi.name</code>	Vector of exact names of the ROI in the struct object. By default <code>roi.name = NULL</code> . See Details.
<code>roi.sname</code>	Vector of names or parts of names of the ROI in the struct object. By default <code>roi.sname = NULL</code> . See Details.
<code>roi.idx</code>	Vector of indices of the ROI that belong to the struct object. By default <code>roi.idx = NULL</code> . See Details.

**Details**

If `roi.name`, `roi.sname`, and `roi.idx` are all set to `NULL`, all ROI are selected.

**Value**

Returns a vector of the volumes in  $cm^3$  of the requested ROI.

**See Also**[get.volume.from.bin](#), [select.names](#)

**Examples**

```
# loading of toy-patient objects
step <- 4
patient <- toy.load.patient (modality = c ("rtstruct"),
                             dxyz = rep (step, 3))
S <- patient$rtstruct[[1]]

# Volume extraction
vol <- get.volume.from.roi (S, roi.sname = "bra", roi.idx = c (1, 3))
names (vol)
vol
```

---

get.xyz.from.index	<i>Conversion of the indices of a point, into xyz coordinate vector in the patient's frame of reference</i>
--------------------	---

---

**Description**

The `get.xyz.from.index` function converts the indices of a voxel of `vol$vol3D.data` (for example, obtained with the function `which`) into a vector or matrix of x, y, z coordinates in the patient's frame of reference.

**Usage**

```
get.xyz.from.index(idx, vol)
```

**Arguments**

<code>idx</code>	Index, or matrix of voxel indices in the array <code>vol\$vol3D.data</code> . The first index of the array is 1.
<code>vol</code>	"volume" class object.

**Value**

Returns a column-matrix of coordinates in the patient's reference frame, corresponding to the indices `idx`.

**Examples**

```
# loading of toy-patient objects (decrease dxyz and increase beam.nb for better
# result)
step <- 4
patient <- toy.load.patient (modality = "rtdose", roi.name = "",
                             dxyz = rep (step, 3), beam.nb = 3)
D <- patient$rtdose[[1]]

# voxels location where the dose is greater than 99.9% Dmax
Dmax <- max (D$vol3D.data, na.rm = TRUE) # D$max.pixel
get.xyz.from.index (which (D$vol3D.data >= 0.99 * Dmax), D)
# or
get.xyz.from.index (which (D$vol3D.data >= 0.99 * Dmax, arr.ind = TRUE), D)
```



---

 grid.equal

*Comparison of the grids of two volume objects*


---

**Description**

The grid.equal function checks that two volumes share the same grid, i.e. the same frame of reference, the same origin point, and the same dx, dy, dz steps.

**Usage**

```
grid.equal(vol1, vol2)
```

**Arguments**

vol1, vol2      "volume" class objects

**Value**

Returns TRUE if the 2 volumes share the same grid.

**Examples**

```
# loading of toy-patient objects
patient <- toy.load.patient (modality = c ("ct","mr","rtdose"), roi.name = "",
                             dxyz = c (4, 4, 4), beam.nb = 1)

# Comparison of the grids
grid.equal (patient$rtdose[[1]], patient$ct[[1]])
grid.equal (patient$mr[[1]], patient$ct[[1]])
```

---

 histo.2D

*2D histograms of 2 volumes*


---

**Description**

The histo.2D function creates a "histo2D" class object, containing the two-dimensional array of histograms of two "volume" class objects that have the same grid.

**Usage**

```
histo.2D(
  x.vol,
  y.vol,
  x.breaks = NULL,
  y.breaks = NULL,
  include.outer = TRUE,
  alias = "",
  description = ""
)
```

**Arguments**

<code>x.vol</code> , <code>y.vol</code>	"volume" class objects. The 2 volumes must have the grid (i.e. share the same voxels location).
<code>x.breaks</code> , <code>y.breaks</code>	Vectors giving the breakpoints of x and y axes. See Details.
<code>include.outer</code>	Boolean. If <code>include.outer = TRUE</code> , the values out the <code>x.breaks</code> and <code>y.breaks</code> of each volume are counted in the first and the last cell of the histograms. They are not taken into account otherwise.
<code>alias</code>	Character string, <code>\$alias</code> of the created object
<code>description</code>	Character string, describing the created object.

**Details**

The arguments `x.breaks` and `y.breaks` represent the scales of the x and y axes of 2D-histogram graph. If they are NULL, the `histo.2D` function defaults to 256 cells between the values `vol$min.pixel` and `vol$max.pixel`.

**Value**

Returns a "histo2D" class object. This is a list including:

- `$patient`: set to `x.vol$patient`.
- `$patient.bd`: set to `x.vol$patient.bd`.
- `$patient.sex`: set to `x.vol$patient.sex`.
- `$file.basename`: set to "".
- `$file.dirname`: set to "".
- `$object.name`: set to "".
- `$object.alias`: alias of the histo2D object.
- `$frame.of.reference`: set to `x.vol$frame.of.reference`.
- `$ref.pseudo`: set to `x.vol$ref.pseudo`.
- `$modality`: set to "histo2D".
- `$description`: description of the histo2D object.
- `$creation.date`: set to `Sys.Date`.
- `$nb.pixels`: number of elements in the `density.map`.
- `$x.file.src`: set to `x.vol$object.alias`
- `$y.file.src`: set to `y.vol$object.alias`
- `x.breaks`: vector of x-axis breakpoints.
- `y.breaks`: vector of y-axis breakpoints.
- `x.mids`: vector of x-axis cell centers.
- `y.mids`: vector of y-axis cell centers.
- `density.map`: array of densities.
- `total.counts`: number of counted voxels.

**See Also**

[display.2D.histo](#).

**Examples**

```

# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = c("ct", "mr", "rtstruct"),
                             roi.name = "brain",
                             dxyz = rep (step, 3))

CT <- patient$ct[[1]]
MR <- patient$mr[[1]]
S <- patient$rtstruct[[1]]
T.MAT <- patient$T.MAT

# restriction of the volume around the RoI
CT.on.roi <- nesting.roi (CT, S, roi.name = "brain", vol.restrict = TRUE,
                          xyz.margin = c (1, 1, 1), alias = CT$description)
MR.on.CT <- vol.regrid (vol = MR, back.vol = CT.on.roi, interpolate = TRUE,
                       T.MAT = T.MAT, alias = CT$description,
                       description = NULL)

# selection of voxels included in the RoI.
roi.bin <- bin.from.roi (vol = CT.on.roi, struct = S, roi.sname = "brain")
MR.select <- vol.from.bin (MR.on.CT, roi.bin, alias = MR$description)
CT.select <- vol.from.bin (CT.on.roi, roi.bin, alias = CT$description)
# 2D histogram
H2D <- histo.2D (MR.select, CT.select, x.breaks = seq (50, 400, 10),
                y.breaks = seq (50, 400, 10), alias = "H2D MR CT")
str (H2D)

```

histo.DVH

*Cumulative Dose Volume Histogram***Description**

The histo.DVH function calculates, for each dose, the volume receiving at least this dose.

**Usage**

```
histo.DVH(histo, alias = "", description = histo$description)
```

**Arguments**

histo	"histo" class object.
alias	Character string, \$alias of the created object.
description	Character string, describing the the created object. If the description = NULL (default value), it will be set to histo\$description.

**Value**

Returns a "dvh" class object. This is a list including:

- \$patient: set to histo\$patient.
- \$patient.bd: set to histo\$patient.bd.
- \$patient.sex: set to histo\$patient.sex.
- \$file.basename: set to "".

- `$file.dirname`: set to "".
- `$object.name`: set to "".
- `$object.alias`: alias of the dvh object..
- `$frame.of.reference`: set to `histo$frame.of.reference`.
- `$ref.pseudo`: set to `histo$ref.pseudo`.
- `$modality`: set to "dvh".
- `$description`: description of the dvh object. By default, set to `histo$description`.
- `$creation.date`: set to `Sys.Date`.
- `$nb.MC`: set to `histo$nb.MC`.
- `$breaks`: vector breakpoints.
- `$mids`: vector of cell centers.
- `$mids.unit`: Character string, representing the unit of the abscissa of the DVH. For instance, "Gy", when `vol` is a `rtdose`.
- `$vol`: cumulative volume receiving at least the doses defined by `$mids`.
- `$pcv`: percentage of the total volume receiving at least the doses defined by `$mids`.
- `$MC.vol`: cumulative volume associated with `histo$MC.dV_dx`, if it exists.
- `$MC.pcv`: percentage of the total volume associated with `histo$MC.dV_dx`, if it exists.
- `$MC.dxyz`: set to `histo$MC.dxyz`, if it exists.

### See Also

[histo.from.roi](#), [histo.from.bin](#), [histo.vol](#), [display.DVH](#), [display.DVH.pc](#)

### Examples

```
# loading of toy-patient objects (decrease dxyz and increase beam.nb for
# better result)
step <- 5
patient <- toy.load.patient (modality = c("rtdose", "rtstruct"),
                           roi.name = "gizzard", dxyz = rep (step, 3),
                           beam.nb = 3)

# Calculation of the histogram
H <- histo.from.roi (patient$rtdose[[1]], patient$rtstruct[[1]],
                   roi.name = "gizzard",
                   breaks = seq (0, 60, by = 1))

# DVH
DVH <- histo.DVH (H)
str (DVH)
```

---

histo.from.bin	<i>Histogram according to a binary</i>
----------------	--

---

### Description

The `histo.from.bin` function computes the voxels histogram of the selection defined by the binary object `sel.bin` of a "volume" class object.

### Usage

```
histo.from.bin(vol, sel.bin, breaks = NULL, alias = "", description = NULL)
```

### Arguments

<code>vol</code>	"volume" class object
<code>sel.bin</code>	"volume" class object, of binary modality
<code>breaks</code>	Vector giving the breakpoints between histogram cells. If <code>breaks = NULL</code> , the chosen breakpoints are those used by the <a href="#">hist</a> function by default. If breaks are specified, outside values of <code>vol\$vol3D.data</code> are not taken into account.
<code>alias</code>	Character string, \$alias of the created object
<code>description</code>	Character string, describing the the created object. If the <code>description = NULL</code> (default value),it will be set to <code>vol\$description</code>

### Value

Returns a "histo" class object. See [histo.vol](#).

### See Also

[histo.from.roi](#), [histo.vol](#), [display.histo](#), [display.dV\\_dx](#)

### Examples

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 5
patient <- toy.load.patient (modality = c("ct","rtstruct"), roi.name = "",
                           dxyz = rep (step, 3))
bin.patient <- bin.from.roi (patient$ct[[1]], struct = patient$rtstruct[[1]],
                           roi.name = "patient")
# ct histogram in patient volume
H <- histo.from.bin (patient$ct[[1]], sel.bin = bin.patient, breaks = NULL,
                   alias = "patient_hist")
str(H)

## Not run:
# Skin dose histogram
patient <- toy.load.patient (modality = c("rtdose", "rtstruct"), roi.name = "",
                           dxyz = c (2, 2, 2), beam.nb = 3)
D <- patient$rtdose[[1]]
S <- patient$rtstruct[[1]]

# Creation of the skin contour of 3 mm
```

```

bin.patient <- bin.from.roi (D, struct = S, roi.name = "patient",
                           alias = "patient")
inverse.patient <- bin.inversion (bin.patient, alias = "inv (patient)")
expansion <- bin.dilation (inverse.patient, radius = 3,
                          alias = "inv (patient) + 3")
contour.3mm <- bin.intersection (bin.patient, expansion,
                                 alias = "contour 3 mm")

# Dose histogram in this volume
H <- histo.from.bin (D, sel.bin = contour.3mm, breaks = NULL,
                   alias = "Skin dose")

str(H)

## End(Not run)

```

---

histo.from.roi	<i>Histogram according to a ROI</i>
----------------	-------------------------------------

---

## Description

The `histo.from.roi` function calculates the histogram of the volume voxels belonging to a ROI.

## Usage

```

histo.from.roi(
  vol,
  struct,
  roi.name = NULL,
  roi.sname = NULL,
  roi.idx = NULL,
  T.MAT = NULL,
  breaks = NULL,
  MC = NULL,
  sd = c(1, 1, 1),
  offset = c(0, 0, 0),
  alias = "",
  description = NULL
)

```

## Arguments

<code>vol</code>	"volume" class object
<code>struct</code>	"struct" class object.
<code>roi.name</code>	Exact name of a ROI in struct object. By default <code>roi.name = NULL</code> . See Details.
<code>roi.sname</code>	Name or part of name of a ROI in struct object. By default <code>roi.sname = NULL</code> . See Details.
<code>roi.idx</code>	Value of the index of a ROI that belong to the struct object. By default <code>roi.idx = NULL</code> . See Details.
<code>T.MAT</code>	"t.mat" class object, created by <a href="#">load.patient.from.Rdcm</a> , <a href="#">load.patient.from.dicom</a> or <a href="#">load.T.MAT</a> . If <code>T.MAT = NULL</code> , <code>struct\$ref.pseudo</code> must be equal to <code>vol\$ref.pseudo</code> .

breaks	Vector giving the breakpoints between histogram cells. If breaks = NULL, the chosen breakpoints are those used by the <a href="#">hist</a> function by default. If breaks are specified, outside values of <code>vol\$vol3D.data</code> are not taken into account.
MC	If different from NULL (default value), number of calculations that will be performed, by Monte-Carlo, by randomly moving the chosen RoI over a random distance, generated according to a normal distribution with mean translation defined by <code>offset</code> and standard deviation <code>sd</code> .
sd	Vector representing the standard deviation of distances in the 3 directions x, y and z.
offset	Vector representing the translation of the RoI in the 3 directions x, y and z.
alias	Character string, <code>\$alias</code> of the created object
description	Character string, describing the the created object. If the <code>description = NULL</code> (default value), it will be set to <code>struct\$roi.info\$roi.pseudo[roi.idx]</code>

### Details

`roi.name`, `roi.sname`, and `roi.idx` must select only one RoI.

### Value

Returns "histo" class object. This is a list including:

- `$alias`: alias of the histo object.
- `$description`: description of the histo object.
- `$breaks`: vector breakpoints
- `$mids`: vector of cell centers.
- `$mids.unit`: Character string, representing the unit of the abscissa of the histogram. For instance, "Gy", when `vol` is a `rtdose`.
- `counts`: count of voxels whose value is included in the limits defined by `$breaks`.
- `dV_dx`: differential histogram, expressed in cm<sup>3</sup> by voxel units, at each `$mids`.
- `MC.counts`: array of MC rows. Each row `i` represents the histogram of the voxels contained in the RoI, whose points have been shifted by `MC.dxyz[i, ]`.
- `MC.dV_dx`: array of MC rows. Each row `i` represents the differential histogram of the voxels contained in the RoI, the points of which have been shifted by `MC.dxyz[i, ]`.
- `MC.dxyz`: array of MC rows, representing the offset applied to the RoI.

### Note

Using Monte-Carlo can be time consuming for large RoI.

If you only want the result just for a translation, use the arguments `MC = 1`, `sd = 0` and `offset =` desired translation vector.

### See Also

[histo.vol](#), [histo.from.bin](#), [display.histo](#), [display.dV\\_dx](#)

**Examples**

```
# loading of toy-patient objects (decrease dxyz and increase beam.nb for better
# result)
step <- 5
patient <- toy.load.patient (modality = c("rtdose", "rtstruct"),
                             roi.name = "gizzard", dxyz = rep (step, 3),
                             beam.nb = 3)

# Calculation of the histogram
H <- histo.from.roi (patient$rtdose[[1]], patient$rtstruct[[1]],
                    roi.name = "gizzard",
                    breaks = seq (0, 60, by = 1))

str (H)
```

histo.vol

*Histogram of a volume***Description**

The `histo.vol` function calculates the voxel values histogram of "volume" class object.

**Usage**

```
histo.vol(vol, breaks = NULL, alias = "", description = NULL)
```

**Arguments**

<code>vol</code>	"volume" class object.
<code>breaks</code>	Vector giving the breakpoints between histogram cells. If <code>breaks = NULL</code> , the chosen breakpoints are those used by the <code>hist</code> function by default. If <code>breaks</code> are specified, outside values of <code>vol\$vol3D.data</code> are not taken into account.
<code>alias</code>	Character string, <code>\$alias</code> of the created object.
<code>description</code>	Character string, describing the the created object. If the <code>description = NULL</code> (default value), it will be set to <code>vol\$description</code> .

**Value**

Returns a "histo" class object. This is a list including:

- `$patient`: set to `vol$patient`.
- `$patient.bd`: set to `vol$patient.bd`.
- `$patient.sex`: set to `vol$patient.sex`.
- `$file.basename`: set to "".
- `$file.dirname`: set to "".
- `$object.name`: set to "".
- `$object.alias`: alias of the histo object.
- `$frame.of.reference`: set to `vol$frame.of.reference`.
- `$ref.pseudo`: set to `vol$ref.pseudo`.



- `$modality`: set to "histo".
- `$description`: description of the histo object.
- `$creation.date`: set to `Sys.Date`.
- `$nb.MC`: set to 0.
- `$breaks`: vector breakpoints
- `$mids`: vector of cell centers.
- `$mids.unit`: Character string, representing the unit of the abscissa of the histogram. For instance, "Gy", when `vol` is a `rtdose`.
- `counts`: count of voxels whose value is included in the limits defined by `$breaks`.
- `dV_dx`: differential histogram, expressed in  $cm^3$  by voxel units, at each `$mids`.

### See Also

[histo.from.roi](#), [histo.from.bin](#), [display.histo](#), [display.dV\\_dx](#)

### Examples

```
# loading of toy-patient objects
step <- 3
patient <- toy.load.patient (modality = "ct", dxyz = rep (step, 3))
CT <- patient$ct[[1]]

# histogram and display
H <- histo.vol (CT, breaks = seq (3, ceiling (CT$max.pixel), 1),
               alias = "CT_hist")
str (H)
```

---

load.obj.data	<i>Load data of an <b>espadon</b> class object</i>
---------------	--

---

### Description

The `load.obj.data` function loads all the data of an **espadon** object of class 'struct' or 'volume'.

### Usage

```
load.obj.data(obj, tag.dictionary = dicom.tag.dictionary())
```

### Arguments

<code>obj</code>	struct or "volume" class object
<code>tag.dictionary</code>	Dataframe, by default equal to <a href="#">dicom.tag.dictionary</a> , whose structure it must keep. This dataframe is used to parse DICOM files in case <code>obj</code> was extracted from DICOM files.

### Value

Returns the **espadon** object with data `$vol3D.data` or `$roi.data`

**See Also**

[load.obj.from.dicom](#) and [load.obj.from.Rdcm](#)

**Examples**

```
# First, save toy patient objects to a temporary file pat.dir for testing.
pat.dir <- file.path (tempdir(), "PM_Rdcm")
dir.create (pat.dir, recursive = TRUE)
patient <- toy.load.patient (modality = c("ct", "mr"), roi.name = "",
                             dxyz = c (4, 4, 4))
save.to.Rdcm (patient$ct[[1]], dirname = pat.dir)
rm( patient)

patient <- load.patient.from.Rdcm (pat.dir, data = FALSE)
CT <- load.obj.data (patient$ct[[1]])
str (CT, max.level = 2)
```

---

load.obj.from.dicom     *Loading an **espadon** object from DICOM files or folder*

---

**Description**

Loading an **espadon** object from DICOM files or folder.

**Usage**

```
load.obj.from.dicom(
  dcm.files,
  data = TRUE,
  ref.pseudo = "ref1",
  tag.dictionary = dicom.tag.dictionary(),
  verbose = TRUE
)
```

**Arguments**

dcm.files	String vector, representing the list of the full names of the DICOM files of the same DICOM object, or its directory.
data	Boolean. Only valid for objects usable by the <b>espadon</b> package, namely ct, mr, rtdose, rtstruct, pt... If data = TRUE, either the values of the voxels when modality is (ct, mr, rtdose, pt), or the coordinates of the RoI when modality is rtstruct, are loaded into memory.
ref.pseudo	String, \$ref.pseudo (i.e. pseudonym of the frame of reference) to assign to the loaded object.
tag.dictionary	Dataframe, by default equal to <a href="#">dicom.tag.dictionary</a> , whose structure it must keep. This dataframe is used to parse DICOM files.
verbose	Boolean. If TRUE, a progress bar indicates the progress of the conversion.

**Value**

Returns an **espadon** object of class "dvh","histo","histo2D","mesh", "rtplan","struct", "undef" or "volume" depending on the object modality. See [espadon.class](#) for class definitions.

**See Also**

[load.obj.data](#) and [load.obj.from.Rdcm](#)

**Examples**

```
# First, save toy.dicom.raw () raw data to a temporary file pat.dir for testing.
pat.dir <- file.path (tempdir(), "PM_dcm")
dir.create (pat.dir, recursive = TRUE)
dcm.filename <- tempfile (pattern = "toyrtplan", tmpdir = pat.dir,
                          fileext = ".dcm")
zz <- file (dcm.filename, "wb")
writeBin (toy.dicom.raw (), zz, size = 1)
close (zz)

# loading of rt-plan object
RTplan <- load.obj.from.dicom (dcm.filename)
str (RTplan)
# Cleaning temporary directory
unlink (pat.dir, recursive = TRUE)
```

---

load.obj.from.Rdcm      *Loading an **espadon** object from \*.Rdcm file*

---

**Description**

The `load.obj.from.Rdcm` function loads a DICOM object into memory, creating a list containing the information necessary for its subsequent use with the **espadon** package.

**Usage**

```
load.obj.from.Rdcm(Rdcm.filename, data = TRUE, nb = NULL)
```

**Arguments**

Rdcm.filename	Character string, representing the full name of a *.Rdcm file created by <a href="#">dicom.to.Rdcm.converter</a> .
data	Boolean. Only works for objects usable by the <b>espadon</b> package, namely ct, mr, rtdose, rtstruct, pt... If data = TRUE, either the values of the voxels when modality is (ct, mr, rtdose), or the coordinates of the RoI when modality is rtstruct, are loaded into memory.
nb	Vector of integers, active only if data = TRUE, and only operating on rtstruct. If nb = NULL, all the RoI of rtstruct are loaded into memory. Otherwise only data of the RoI indices defined by the vector nb are loaded.

**Value**

Returns an **espadon** object of class "dvh","histo","histo2D","mesh", "rtplan","struct", "undef" or "volume" depending on the object modality. See [espadon.class](#) for class definitions.

**See Also**

[load.obj.data](#) and [load.obj.from.dicom](#)

**Examples**

```
# First, save toy patient objects to a temporary file pat.dir for testing.
pat.dir <- file.path (tempdir(), "PM_Rdcm")
dir.create (pat.dir, recursive = TRUE)
patient <- toy.load.patient (modality = c("ct", "mr"), roi.name = "",
                             dxyz = c (4, 4, 4))
save.to.Rdcm (patient$ct[[1]], dirname = pat.dir)
save.to.Rdcm (patient$mr[[1]], dirname = pat.dir)
save.T.MAT (patient$T.MAT, dirname = pat.dir)
# Rdcm files in pat.dir
list.files(pat.dir)

CT <- load.obj.from.Rdcm (file.path (pat.dir,
                                     list.files(pat.dir, pattern="ct1[.]Rdcm")[1]),
                         data=TRUE)
MR <- load.obj.from.Rdcm (file.path (pat.dir,
                                     list.files(pat.dir, pattern="mr1[.]Rdcm")[1]),
                         data=TRUE)
Reg <-load.obj.from.Rdcm (file.path (pat.dir,"ref1_from_ref2.Rdcm"), data=TRUE)
str(Reg)

# Cleaning temporary directory
unlink (pat.dir, recursive = TRUE)
```

---

load.patient.from.dicom

*Loading patient data from DICOM files*

---

**Description**

The `load.patient.from.dicom` function is used to load or pre-load in memory all patient objects from DICOM files.

**Usage**

```
load.patient.from.dicom(
  dcm.files,
  data = FALSE,
  dvh = FALSE,
  tag.dictionary = dicom.tag.dictionary(),
  verbose = TRUE
)
```

**Arguments**

`dcm.files` String vector, representing the list of the full names of the DICOM files of the same patient, or its directories.

data	Boolean. If data = TRUE, the voxels value of the "volume" class objects, or the coordinates of the RoI (region of interest) of the struct class objects, are loaded into memory.
dvh	Boolean. if dvh = TRUE and if they exist, patient DVH are loaded, for convenience. They are not used as is in <b>espadon</b> package.
tag.dictionary	Dataframe, by default equal to <a href="#">dicom.tag.dictionary</a> , whose structure it must keep. This dataframe is used to parse DICOM files.
verbose	Boolean. If TRUE, a progress bar indicates the progress of the conversion.

### Value

Returns an **espadon** object of class "patient", describing the information from dcm.files. See [espadon.class](#) for a description of the "patient" class.

### See Also

[dicom.to.Rdcm.converter](#), [load.patient.from.Rdcm](#), [load.obj.data](#), [load.obj.from.dicom](#), [load.obj.from.Rdcm](#) and [load.T.MAT](#).

### Examples

```
# First, save toy.dicom.raw () raw data to a temporary file pat.dir for testing.
pat.dir <- file.path (tempdir(), "toy_dcm")
dir.create (pat.dir, recursive = TRUE)
dcm.filename <- tempfile (pattern = "toyrtplan", tmpdir = pat.dir,
                          fileext = ".dcm")
zz <- file (dcm.filename, "wb")
writeBin (toy.dicom.raw (), zz, size = 1)
close (zz)

# loading patient. Here the toy patient ha only a unique rt-plan object
patient <- load.patient.from.dicom (pat.dir, data = FALSE)
str (patient, max = 2)
# description of object
patient$description
# transfer matrices :
patient$T.MAT
# rt-plan object
str (patient$rtplan[[1]])
# Cleaning temporary directory
unlink (pat.dir, recursive = TRUE)
```

---

```
load.patient.from.Rdcm
```

*Loading patient data from \*.Rdcm files*

---

### Description

The `load.patient.from.Rdcm` function is used to load or pre-load in memory all patient objects converted in \*.Rdcm files.

**Usage**

```
load.patient.from.Rdcm(dirname, data = FALSE, dvh = FALSE)
```

**Arguments**

dirname	Full paths of the directories of a single patient.
data	Boolean. If data = TRUE, the voxels value of the "volume" class objects, or the coordinates of the RoI (region of interest) of the struct class objects, are loaded into memory.
dvh	Boolean. if dvh = TRUE and if they exist, patient DVH are loaded, for convenience. They are not used as is in <b>espadon</b> package.

**Value**

Returns an **espadon** object of class "patient", describing the information contained in dirname. See [espadon.class](#) for a description of the "patient" class.

**See Also**

[dicom.to.Rdcm.converter](#), [load.patient.from.dicom](#), [load.obj.data](#), [load.obj.from.dicom](#), [load.obj.from.Rdcm](#) and [load.T.MAT](#).

**Examples**

```
# First, save toy patient objects to a temporary file pat.dir for testing.
pat.dir <- file.path(tempdir(), "PM_Rdcm")
dir.create(pat.dir, recursive = TRUE)
patient <- toy.load.patient(modality = c("ct", "mr"), roi.name = "",
                           dxyz = c(4, 4, 4))
save.to.Rdcm(patient$ct[[1]], dirname = pat.dir)
save.to.Rdcm(patient$mr[[1]], dirname = pat.dir)
save.T.MAT(patient$T.MAT, dirname = pat.dir)
# Rdcm files in pat.dir
list.files(pat.dir)

# loading patient from Rdcm files with data:
new.patient <- load.patient.from.Rdcm(pat.dir, data = TRUE)
str(new.patient, max.level = 2)

# Cleaning temporary directory
unlink(pat.dir, recursive = TRUE)
```

---

load.Rdcm.raw.data      *Loading a \*.Rdcm file*

---

**Description**

the load.Rdcm.raw.data function loads the content of a \*.Rdcm file.

**Usage**

```
load.Rdcm.raw.data(Rdcm.filename, address = TRUE, data = TRUE)
```

**Arguments**

Rdcm.filename	Character string, representing the full name of a *.Rdcm file created by <a href="#">dicom.to.Rdcm.converter</a> .
address	boolean. If TRUE, a dataframe with the address of the tags in the raw DICOM data is returned.
data	boolean. If TRUE, the DICOM information are returned as an R list.

**Value**

Returns a list containing the information, converted by **espadon**, of a DICOM object..

**See Also**

[dicom.to.Rdcm.converter](#), [load.obj.from.Rdcm](#).

**Examples**

```
# For testing, save first toy.dicom.raw () raw data to a temporary file, and
# convert it in Rdcm fie
pat.src.dir <- file.path (tempdir(), "PM_dcm")
dir.create (pat.src.dir, recursive = TRUE)
dcm.filename <- tempfile (pattern = "PM_rtplan", tmpdir = pat.src.dir,
                          fileext = ".dcm")
zz <- file (dcm.filename, "wb")
writeBin (toy.dicom.raw (), zz, size = 1)
close (zz)
pat.dir <- file.path (tempdir(), "PM_Rdcm")
dicom.to.Rdcm.converter (pat.src.dir, pat.dir, update = TRUE)
lf <- list.files (pat.dir, pattern = "[.]Rdcm$", full.names = TRUE)
lf

# Inspect Rdcm raw data
L <- load.Rdcm.raw.data (lf)
str (L, max.level =3)
```

---

load.T.MAT

*Loading of information about transfer matrices between frames of reference of patient objects.*

---

**Description**

The load.T.MAT function lists all the frames of reference of the objects included in the patient directory. It concatenates all the information of the reg matrices of a directory, creating, among other things, a list of 4x4 transfer matrices between frames of reference.

**Usage**

```
load.T.MAT(dirname)
```

**Arguments**

dirname	Directory containing a patient's DICOM objects.
---------	---

**Value**

Returns a "t.mat" class object. It is a list that includes :

- `$ref.info`: dataframe giving the correspondence between the frame of reference (column `$ref`) of the DICOM object (TAG (0020,0052) ) and its pseudonym (column `$ref_pseudo`).
- `$reg.info`: list of dataframes : the first one gives the PID, birthday, and sex of the patient, the second one gives the name of the source file of transfer matrices.
- `$matrix.description`: dataframe giving the transfer matrix names (column `$t`), its source frame of reference (column `$src`), the destination frame of reference (column `$dest`), and its type (`$type`). Note: only the RIGID type is supported.
- `$matrix.list`: list of 4X4 transfer matrices. This list contains at least as many Identity matrices as there are `ref.pseudo`.

**Examples**

```
# First, save toy patient objects to a temporary file pat.dir for testing.
pat.dir <- file.path (tempdir(), "PM_Rdcm")
dir.create (pat.dir, recursive = TRUE)
patient <- toy.load.patient (modality = c("ct", "mr"), roi.name = "",
                           dxyz = c (4, 4, 4))
save.to.Rdcm (patient$ct[[1]], dirname = pat.dir)
save.to.Rdcm (patient$mr[[1]], dirname = pat.dir)
save.T.MAT (patient$T.MAT, dirname = pat.dir)
# Rdcm files in pat.dir
list.files(pat.dir)

T.MAT <- load.T.MAT (pat.dir)
T.MAT

# Cleaning temporary directory
unlink (pat.dir, recursive = TRUE)
```

---

mesh.from.bin

*Creation of a mesh according to a binary volume*

---

**Description**

The `mesh.from.bin` function creates a mesh class object from a volume object of "binary" modality.

**Usage**

```
mesh.from.bin(
  bin,
  alias = "",
  tol = 1,
  smooth.iteration = 10,
  smooth.type = c("taubin", "laplace", "HClaplace", "fujiLaplace", "angWeight",
                 "surfPreserveLaplace"),
  smooth.lambda = 0.5,
  smooth.mu = -0.53,
  smooth.delta = 0.1,
  verbose = FALSE
)
```



**Arguments**

bin	"volume" class object of "binary" modality.
alias	Character string, \$alias of the mesh defining the \$alias of the created object.
tol	Tolerance in mm, applied for mesh simplification. See <a href="#">vcgClean</a> .
smooth.iteration	Number of iterations applied in the smoothing algorithm. See <a href="#">vcgSmooth</a> .
smooth.type	character: select smoothing algorithm. Available are "taubin", "laplace", "HClaplace", "fujiLaplace", "angWeight" (and any sensible abbreviations). By default, set to "taubin". See <a href="#">vcgSmooth</a> .
smooth.lambda	numeric: parameter for Taubin smooth. See <a href="#">vcgSmooth</a> .
smooth.mu	numeric: parameter for Taubin smooth. See <a href="#">vcgSmooth</a> .
smooth.delta	numeric: parameter for Scale dependent laplacian smoothing (see reference below).and maximum allowed angle (in radians) for deviation between normals Laplacian (surface preserving). See <a href="#">vcgSmooth</a> .
verbose	Boolean, by default set to FALSE. Allows you to inhibit comments.

**Value**

Returns a "mesh" class object. This is a list including the following 6 elements:

- \$patient: set to bin\$patient.
- \$patient.bd: set to bin\$patient.bd.
- \$patient.sex: set to bin\$patient.sex.
- \$file.basename: set to "".
- \$file.dirname: set to "".
- \$object.name: set to "".
- \$object.alias: set to the alias argument of the function.
- \$frame.of.reference: set to bin\$frame.of.reference.
- \$ref.pseudo: set to bin\$ref.pseudo.
- \$modality: set to "mesh".
- \$description: By default, set to paste (bin\$object.alias, "mesh").
- \$creation.date: set to Sys.Date.
- \$nb.faces: set to the number of faces of the mesh.
- \$mesh: list of 3 elements defining the mesh:
  - \$vb: array made up of the generalized coordinates (x, y, z, 1) of the vertices of the triangles. There are as many columns as there are vertices.
  - \$it: array of the 3 indices of the vertices forming a triangle, arranged by column. There are as many columns as there are triangles in the mesh.
  - \$normals: array made up of the generalized coordinates (x, y, z, 1) of the normal vectors of each triangle. There are as many columns as there are vertices.

**Note**

To compute the mesh, all NA voxels of the binary volume bin are set to FALSE. If all voxels are equal to FALSE, the function returns the code NULL.

**See Also**

[vcgSmooth](#)

**Examples**

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = c("ct", "rtstruct"), roi.name = "",
                             dxyz = rep (step, 3))

CT <- patient$ct[[1]]
S <- patient$rtstruct[[1]]

# creation of the patient mesh
bin <- bin.from.roi (CT, struct = S, roi.name = "patient")
mesh.patient <- mesh.from.bin (bin, alias = "patient", verbose = FALSE)
str (mesh.patient)
```

---

mesh.in.new.ref

*Change of frame of reference of a mesh*

---

**Description**

The mesh.in.new.ref function allows you to change the frame of reference of a mesh.

**Usage**

```
mesh.in.new.ref(mesh, new.ref.pseudo, T.MAT, alias = "", description = NULL)
```

**Arguments**

mesh	"volume" class object.
new.ref.pseudo	pseudonym of the frame of reference in which the mesh should be located. This new.ref.pseudo must exist in the T.MAT list.
T.MAT	"t.mat" class object, created by <a href="#">load.patient.from.Rdcm</a> , <a href="#">load.patient.from.dicom</a> , <a href="#">load.T.MAT</a> or <a href="#">ref.add</a> .
alias	Character string, \$alias of the created object.
description	Character string, describing the created object. If description = NULL (default value), it will be that of the mesh.

**Value**

Returns "mesh" class object in the new frame of reference new.ref.pseudo.

**Examples**

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = c("ct", "rtstruct", "mr"),
                             roi.name = "", dxyz = rep (step, 3))

CT <- patient$ct[[1]]
S <- patient$rtstruct[[1]]

#creation of the patient mesh
bin <- bin.from.roi (CT, struct = S, roi.name = "patient")
mesh.patient <- mesh.from.bin (bin, alias = "patient", verbose = FALSE)

# mesh in the MR frame of reference
new.mesh <- mesh.in.new.ref (mesh.patient, patient$mr[[1]]$ref.pseudo,
                             T.MAT = patient$T.MAT)

str (new.mesh, max.level = 2)
```

---

 mesh.repair

*Repair of a mesh*


---

**Description**

The mesh.repair function repairs holes in a mesh class object.

**Usage**

```
mesh.repair(mesh, verbose = TRUE)
```

**Arguments**

mesh	"mesh" class object.
verbose	Boolean, by default set to FALSE. Allows you to inhibit comments.

**Value**

Returns a mesh, repaired by removing degenerated triangles and filling holes.

**Examples**

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = c("ct", "rtstruct"),
                             roi.name = "gizzard", dxyz = rep (step, 3))

CT <- patient$ct[[1]]
S <- patient$rtstruct[[1]]

# creation of the gizzard mesh
bin <- bin.from.roi (CT, struct = S, roi.name = "gizzard")
mesh.gizzard <- mesh.from.bin (bin, alias = "gizzard", verbose = FALSE)

repair.mesh.gizzard <- mesh.repair (mesh.gizzard, verbose = FALSE)
str (mesh.gizzard)
str (repair.mesh.gizzard)
```

---

mesh.spheric.proj      *Adding spherical coordinates to a mesh*

---

## Description

The `mesh.spheric.proj` function adds latitude and longitude coordinates to a mesh. These features map the mesh surface to a sphere. Latitude and longitude are computed using the heat diffusion approach explained by *Brechbühler and al* [1].

## Usage

```
mesh.spheric.proj(mesh, verbose = TRUE)
```

## Arguments

mesh	"mesh" class object.
verbose	Boolean, by default set to FALSE. Allows you to inhibit comments.

## Value

returns a "mesh" class object in which `$mesh` contains `Lat` and `lon` evaluated at vertices. The function allows to have a parameterized surface for later computations as curvature or shape index, hence, nor the surface, nor the angles are preserved. In the DICOM frame of reference, latitude goes along Z axis (from feet = -1 to head = +1) and longitude turns counter clockwise (from -1 to +1).

## Note

This funtion is time consuming.

## References

[1] Brechbuhler C, Gerig G, Kubler O (1995). "Parametrization of Closed Surfaces for 3-D Shape Description." *Computer Vision and Image Understanding*, **61**(2), 154-170. ISSN 1077-3142, doi:[10.1006/cviu.1995.1013](https://doi.org/10.1006/cviu.1995.1013).

## Examples

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 5
patient <- toy.load.patient (modality = c("ct", "rtstruct"), roi.name = "",
                             dxyz = rep (step, 3))

CT <- patient$ct[[1]]
S <- patient$rtstruct[[1]]

#creation of the patient mesh
bin <- bin.from.roi (CT, struct = S, roi.name = "patient")
m.patient <- mesh.from.bin (bin)
m.skin <- mesh.repair (m.patient, verbose = FALSE)

m.proj <- mesh.spheric.proj (m.skin, verbose = FALSE)

library (rgl)
```

```

col <- hcl.colors (12, "Blue-Red 3")
open3d()
shade3d (m.proj$mesh, meshColors = "vertices",
         color = col[round ((m.proj$mesh$Lat/2 + 0.5) * 11) + 1],
         specular = "#404040")
open3d()
shade3d (m.proj$mesh, meshColors = "vertices",
         color = col[round ((m.proj$mesh$Lon/2 + 0.5) * 11) + 1],
         specular = "#404040")

```

---

nesting.cube

*Restriction of a volume to a rectangular parallelepiped*


---

### Description

The `nesting.cube` function restricts or increases a volume to the rectangular parallelepiped defined by its 2 extreme vertices.

### Usage

```
nesting.cube(vol, pt.min, pt.max, alias = "", description = NULL)
```

### Arguments

<code>vol</code>	"volume" class object.
<code>pt.min</code>	minimum x, y, z coordinates of the rectangular parallelepiped vertex.
<code>pt.max</code>	maximum x, y, z coordinates of the rectangular parallelepiped vertex.
<code>alias</code>	Character string, \$alias of the created object.
<code>description</code>	Character string, describing the the created object. If the <code>description = NULL</code> (default value), it will be set to <code>vol\$description</code> .

### Value

Returns a "volume" class object, in which 3D volume is restricted or increased to be circumscribed to the requested rectangular parallelepiped. If the created volume exceeds the initial volume, new voxels are set to NA.

### See Also

[add.margin.](#)

### Examples

```

# loading of toy-patient objects (decrease dxyz for better result)
step <- 5
patient <- toy.load.patient (modality = "ct", roi.name = "",
                           dxyz = rep (step, 3))
CT <- patient$ct[[1]]
# Calculation of the new CT restricted to the parallelepiped reduced by 10 mm.
pt.CT <- get.extreme.pt (CT) # extreme points of CT
new.pt.CT <- pt.CT + matrix (rep (c (+ 12, -12), 3), ncol = 2, byrow = TRUE)

```

```

new.CT <- nesting.cube (CT, new.pt.CT$min, new.pt.CT$max, alias = "new CT")
## Not run:
# check for change
display.3D.stack (CT)
display.3D.stack (new.CT, line.col="red")

## End(Not run)

```

---

nesting.roi

*Restrict volume to RoI*


---

## Description

The `nesting.roi` function restricts a "volume" class object to the rectangular parallelepiped circumscribed to the chosen RoI.

## Usage

```

nesting.roi(
  vol,
  struct,
  roi.name = NULL,
  roi.sname = NULL,
  roi.idx = NULL,
  xyz.margin = c(0, 0, 0),
  vol.restrict = FALSE,
  T.MAT = NULL,
  alias = "",
  description = NULL
)

```

## Arguments

<code>vol</code>	"volume" class object
<code>struct</code>	"struct" class object.
<code>roi.name</code>	Vector of exact names of the RoI in the struct object. By default <code>roi.name = NULL</code> . See Details.
<code>roi.sname</code>	Names or parts of names of the RoI in the struct object. By default <code>roi.sname = NULL</code> . See Details.
<code>roi.idx</code>	Index of the RoI that belong to the struct object. By default <code>roi.idx = NULL</code> . See Details.
<code>xyz.margin</code>	Vector of length 3, representing the distances in mm to be added to the x, y and z directions of the rectangular parallelepiped circumscribed to the chosen RoI, in the cutting planes frame of reference. By default <code>xyz.margin = c(0, 0, 0)</code> .
<code>vol.restrict</code>	Boolean. If <code>vol.restrict = TRUE</code> , the rectangular parallelepiped circumscribed to the chosen RoI, enlarged by <code>xyz.margin</code> cannot exceed the initial volume.
<code>T.MAT</code>	"t.mat" class object, created by <a href="#">load.patient.from.dicom</a> , <a href="#">load.patient.from.Rdcm</a> or <a href="#">load.T.MAT</a> . If <code>T.MAT = NULL</code> , <code>struct\$ref.pseudo</code> must be equal to <code>vol\$ref.pseudo</code> .
<code>alias</code>	Character string, \$alias of the created object.
<code>description</code>	Character string, describing the the created object. If <code>description = NULL</code> , it will be that of the vol.

**Details**

If `roi.name`, `roi.sname`, and `roi.idx` are all set to `NULL`, all ROI are selected.

**Value**

Returns a "volume" class object, in which 3D volume is limited to the rectangular parallelepiped circumscribed to the chosen ROI, increased by the requested margins.

**Examples**

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = c("ct", "rtstruct"),
                             roi.name = "brain", dxyz = rep (step, 3))

CT <- patient$ct[[1]]
S <- patient$rtstruct[[1]]

CT.brain <- nesting.roi (CT, S, roi.sname = "brain")
CT.brain.with.margin <- nesting.roi (CT, S, roi.sname = "brain",
                                     xyz.margin = c (10,10,10))

# display at the center of gravity of the cerebellum Gz
Gz <- S$roi.info [grep("^brain",S$roi.info$roi.pseudo),]$Gz
display.plane (bottom = CT.brain, view.coord = Gz,
               struct = S, bottom.col = pal.RVV (1000),
               bottom.breaks = seq (-1000, 1000, length.out = 1001),
               bg = "#00ff00", interpolate = FALSE, legend.shift = -20)
display.plane (bottom = CT.brain.with.margin,view.coord = Gz,
               struct = S, bottom.col = pal.RVV (1000),
               bottom.breaks = seq(-1000, 1000, length.out = 1001),
               bg = "#00ff00", interpolate = FALSE, legend.shift = -20)
```

---

orientation.create      *Creation of orientation*

---

**Description**

The `orientation.create` function creates the orientation vectors of a plane:

- from 3 points A, B and C (see details),
- or from 2 vectors B and C, resp. defining x and y-axis (see details),
- or from 2 points A, B defining x-axis, and the normal vector to the plane (see details),
- or from a vector B defining x-axis, and the normal vector to the plane (see details).

**Usage**

```
orientation.create(A = c(0, 0, 0), B = NULL, C = NULL, normal = NULL)
```

**Arguments**

A	Vector of the x, y and z coordinates of point A, by default equal to $c(0, 0, 0)$ in the case where B and C are vectors.
B	Vector of x, y and z coordinates of point or vector B.
C	Vector of x, y and z coordinates of point or vector C.
normal	Vector of x, y and z coordinates of normal vector.

**Details**

When using B and C, B-A define the x-axis unit vector. The unit vector of the y-axis is orthonormal to the x-axis, coplanar with A, B and C, and in the direction of A to C.

When using B and normal, the unit vector of the x-axis is orthonormal to the normal vector, in the direction of A to B. The unit vector of the y-axis is defined so as to constitute a direct orthonormal basis with the unit vector of the x-axis and the normal vector of the plane.

**Value**

Returns the orientation of the plane. That means the concatenation of 2 vectors, defining an orthonormal basis of the plane.

**Examples**

```
A <- c (-29.93, 18.85, 4.34)
B <- c (28.73, 15.36, 4.46)
C <- c (1.53, 75.21, 13.51)
orientation.create (A, B, C)
```

---

pal.RVV	<i>Conversion of Hounsfield Units to Realistic Volume Vizualization colors</i>
---------	--

---

**Description**

The RVV.pal function produces a color palette where Hounsfield Units in the range -1000 HU to 1000 HU are converted into realistically colorized virtual anatomy (for use with CT), developed by *J.C. Silverstein and al* [1]

**Usage**

```
pal.RVV(n, alpha = NULL, min.col = "#000000", max.col = "#FFFFFF")
```

**Arguments**

n	Integer, number of colors to be in the palette
alpha	Vector representing the opacity, in the range of 0 (transparent) to 1 (opaque). If alpha = NULL (default), all colors are opaque, and no alpha channel is added to the colors.
min.col, max.col	respectively the color below -1000HU (by default, black, i.e. "#000000") and above +1000HU (by default, white, i.e. "#FFFFFF")



**Value**

Returns a vector of colors of size n.

**References**

[1] Silverstein JC, Parsad NM, Tsirlina V (2008). "Automatic perceptual color map generation for realistic volume visualization." *Journal of Biomedical Informatics*, **41**(6), 927-935. ISSN 1532-0464, doi:[10.1016/j.jbi.2008.02.008](https://doi.org/10.1016/j.jbi.2008.02.008).

**Examples**

```
pal <- pal.RVV (256)

image (x = seq (-1000, 1000, length.out = 1024), y = 1,
       z = matrix (seq (-1100, 1100, length.out = 1024), ncol = 1),
       col = pal,
       main = "Realistic Volume Vizualization colors")
```

---

Rdcm.inventory	<i>Inventory of <b>espadon</b> objects from Rdcm files</i>
----------------	--

---

**Description**

The Rdcm.inventory function creates, from Rdcm files in a patient's directory, a dataframe describing objects.

**Usage**

```
Rdcm.inventory(dirname)
```

**Arguments**

dirname            Character string, representing the full name of patient directory, including Rdcm files.

**Value**

Returns a dataframe, providing information of DICOM objects.

**Examples**

```
# First, save toy patient objects to a temporary file pat.dir for testing.
pat.dir <- file.path (tempdir(), "PM_Rdcm")
dir.create (pat.dir, recursive = TRUE)
patient <- toy.load.patient (modality = c("ct", "mr"), roi.name = "",
                             dxyz = c (4, 4, 4))
save.to.Rdcm (patient$ct[[1]], dirname = pat.dir)
save.to.Rdcm (patient$mr[[1]], dirname = pat.dir)
save.T.MAT (patient$T.MAT, dirname = pat.dir)
```

```
Rdcm.inventory (pat.dir)
```

```
# Cleaning temporary directory
unlink (pat.dir, recursive = TRUE)
```

---

ref.add *Adding a frame of reference in T.MAT*

---

### Description

The `ref.add` function adds the transfer matrices from or to a new frame of reference defined from 2 unit vectors and an origin point.

### Usage

```
ref.add(
  src.ref,
  orientation = c(1, 0, 0, 0, 1, 0),
  origin = c(0, 0, 0),
  new.ref.pseudo = "newref",
  T.MAT = NULL
)
```

### Arguments

<code>src.ref</code>	Character string, pseudonym of the frame of reference in which the orientation vector and the origin point <code>origin</code> are defined.
<code>orientation</code>	Vector of 6 or 9 elements, composed of the coordinates of the 2 orthonormal vectors (i, j), or of the 3 orthonormal vectors (i, j, k) of the new coordinate system, in the <code>src.ref</code> frame of reference.
<code>origin</code>	Vector of the x, y, z coordinates of the origin point of the new frame of reference in the <code>src.ref</code> frame of reference. Default to <code>c(0, 0, 0)</code> .
<code>new.ref.pseudo</code>	Character string, pseudonym of the new frame of reference to add.
<code>T.MAT</code>	"t.mat" class object created by <a href="#">load.patient.from.dicom</a> , <a href="#">load.patient.from.Rdcm</a> or <a href="#">load.T.MAT</a> . If <code>T.MAT = NULL</code> , then only the link between <code>src.ref</code> and <code>new.ref.pseudo</code> is computed.

### Value

Returns a "t.mat" class object, which contains the transfer matrices from or to `new.ref.pseudo` pseudonym of the new frame of reference. If the `T.MAT` is `NULL`, then the returned object will contain only 4 matrices: "`src.ref<-src.ref`", "`src.ref<-new.ref.pseudo`", "`new.ref.pseudo<- new.ref.pseudo`", "`new.ref.pseudo<-src.ref`".

Returns a `NULL` if `orientation` is not well defined.

### See Also

[ref.cutplane.add](#), [ref.remove](#).

**Examples**

```
# Adding of the reference frame "ref1_60", which is a 60 degree rotation of
# reference frame "ref1".
orientation <- c (cos (pi / 3), sin (pi / 3), 0,
                 -sin (pi / 3), cos (pi / 3), 0)

local.Tmat <- ref.add (src.ref = "ref1", orientation = orientation,
                     new.ref.pseudo = "ref1_60")

str(local.Tmat)
```

---

ref.cutplane.add	<i>Adding volume's cutting planes frame of reference in T.MAT</i>
------------------	---

---

**Description**

The `ref.cutplane.add` function adds in T.MAT the transfer matrices from or to volume's cutting planes frame of reference.

**Usage**

```
ref.cutplane.add(
  vol,
  origin = vol$patient.xyz0[1, ],
  ref.cutplane = paste0(vol$ref.pseudo, "m"),
  T.MAT = NULL
)
```

**Arguments**

vol	"volume" class object.
origin	Vector of the x, y, z coordinates of the origin point of the cut planes frame of reference.
ref.cutplane	Name of the volume's cutting planes frame of reference. By default <code>ref.cutplane = paste0 (vol\$ref.pseudo, ".m")</code> .
T.MAT	"t.mat" class object created by <a href="#">load.patient.from.dicom</a> , <a href="#">load.patient.from.Rdcm</a> or <a href="#">load.T.MAT</a> . If T.MAT = NULL, then only the link between <code>vol\$ref.pseudo</code> and <code>ref.name</code> is established.

**Value**

Returns a "t.mat" class object, which contains the transfer matrices from or to volume's cutting planes frame of reference. If the T.MAT is NULL, then the returned object will contain only 4 matrices: "src.ref<-src.ref", "src.ref<-ref.cutplane", "ref.cutplane<-ref.cutplane", "ref.cutplane<-src.ref".

**See Also**

[ref.add](#), [ref.remove](#).

**Examples**

```
# loading of toy-patient objects
patient <- toy.load.patient (modality = "mr", roi.name = "", dxyz = c (4, 4, 4))
MR <- patient$mr[[1]]
MR$xyz.from.ijk

# creation of t.mat, containing the transfer matrix to the frame of reference
# of the MR cutting planes
t.mat <- ref.cutplane.add (MR)

# Change of frame of reference
MR.m <- vol.in.new.ref (MR, paste0 (MR$ref.pseudo, "m"), t.mat)

MR.m$xyz.from.ijk
```

---

ref.remove

*Deletion of a frame of reference in T.MAT*


---

**Description**

The `ref.remove` function removes the management of a frame of reference in T.MAT.

**Usage**

```
ref.remove(ref.name, T.MAT)
```

**Arguments**

<code>ref.name</code>	Character string, pseudonym of the frame of reference to delete.
<code>T.MAT</code>	"t.mat" class object in which the <code>ref.name</code> frame of reference is to be deleted.

**Value**

Returns a "t.mat" class object, which no longer contains transfer matrices from or to the `ref.pseudo` `ref.name`.

**See Also**

[ref.add](#)

**Examples**

```
# Adding of the reference frame "ref1_60", which is a 60 degree rotation of
# reference frame "ref1".
orientation <- c (cos (pi / 3), sin (pi / 3), 0,
                 -sin (pi / 3), cos (pi / 3), 0)

local.Tmat <- ref.add (src.ref = "ref1", orientation = orientation,
                    new.ref.pseudo = "ref1_60")
str(local.Tmat)

# Removal of "ref1_60"
local.Tmat <- ref.remove (ref.name = "ref1_60", T.MAT = local.Tmat)
str(local.Tmat)
```



---

rt.indices.from.bin     *Dosimetry, volume, conformity, homogeneity indices from binary selection*

---

## Description

The `rt.indices.from.bin` function calculates, from a "volume" class object of modality "rtdose", all the standard indicators of radiotherapy, as long as their options are transmitted, for the target and healthy "volume" object of modality "binary".

## Usage

```
rt.indices.from.bin(
  vol,
  target.bin.list = NULL,
  healthy.bin.list = NULL,
  T.MAT = NULL,
  presc.dose = NA,
  healthy.tol.dose = NA,
  healthy.weight = 1,
  dosimetry = c("D.min", "D.max", "D.mean", "STD"),
  volume.indices = c("V.tot", "area", "V.prescdose"),
  conformity.indices = c("PITV", "CI.lomax2003", "CN", "NCI", "DSC", "CI.distance",
    "CI.abs_distance", "CDI", "CS3", "ULF", "OHTF", "gCI", "COIN", "G_COSI", "COSI"),
  homogeneity.indices = c("HI.RTOG.max_ref", "HI.RTOG.5_95", "HI.ICRU.max_min",
    "HI.ICRU.2.98_ref", "HI.ICRU.2.98_50", "HI.ICRU.5.95_ref", "HI.mayo2010",
    "HI.heufelder"),
  gradient.indices = c("GI.ratio.50"),
  D.xpc = NULL,
  V.xGy = NULL,
  verbose = TRUE
)
```

## Arguments

<code>vol</code>	"volume" class object, of "rtdose" modality.
<code>target.bin.list</code>	list of "volume" class objects, of "binary" modality. The <code>\$object.alias</code> field of each <code>target.bin.list</code> object represents the name of the selected region of interest of the target volume.
<code>healthy.bin.list</code>	list of "volume" class objects, of "binary" modality. The <code>\$object.alias</code> field of each <code>healthy.bin.list</code> object represents the name of the selected region of interest of the healthy tissues.
<code>T.MAT</code>	"t.mat" class object, created by <a href="#">load.patient.from.Rdcm</a> or <a href="#">load.T.MAT</a> . If <code>T.MAT = NULL</code> , all <code>\$ref.pseudo</code> of <code>bin.list</code> elements must be equal to <code>vol\$ref.pseudo</code> .
<code>presc.dose</code>	vector of prescription doses that serve as reference doses for the target RoI.
<code>healthy.tol.dose</code>	vector of tolerance dose of each healthy RoI.
<code>healthy.weight</code>	Vector of weight, indicating the importance of the healthy RoI.



```

})
names (healthy.bin.list) <- struct$roi.info$name[healthy.roi.idx]

indices <- rt.indices.from.bin (D, target.bin.list, healthy.bin.list,
                             presc.dose = 50,
                             conformity.indices = c("PITV", "PDS", "CI.lomax2003",
                                                    "CN", "NCI", "DSC", "COIN"),
                             verbose = FALSE)

indices

```

---

rt.indices.from.roi     *Dosimetry, volume, conformity, homogeneity indices from RoI*

---

### Description

The `rt.indices.from.roi` function calculates, from a "volume" class object of modality "rtdose", standard indicators of radiotherapy in relation to the target and healthy RoI, as long as their options are transmitted.

### Usage

```

rt.indices.from.roi(
  vol,
  struct = NULL,
  T.MAT = NULL,
  target.roi.name = NULL,
  target.roi.sname = NULL,
  target.roi.idx = NULL,
  healthy.roi.name = NULL,
  healthy.roi.sname = NULL,
  healthy.roi.idx = NULL,
  presc.dose = NA,
  healthy.tol.dose = NA,
  healthy.weight = 1,
  dosimetry = c("D.min", "D.max", "D.mean", "STD"),
  volume.indices = c("V.tot", "area", "V.prescdose"),
  conformity.indices = c("PITV", "PDS", "CI.lomax2003", "CN", "NCI", "DSC",
                        "CI.distance", "CI.abs_distance", "CDI", "CS3", "ULF", "OHTF", "gCI", "COIN",
                        "G_COSI", "COSI"),
  homogeneity.indices = c("HI.RTOG.max_ref", "HI.RTOG.5_95", "HI.ICRU.max_min",
                          "HI.ICRU.2.98_ref", "HI.ICRU.2.98_50", "HI.ICRU.5.95_ref", "HI.mayo2010",
                          "HI.heufelder"),
  gradient.indices = c("GI.ratio.50", "mGI"),
  D.xpc = NULL,
  V.xGy = NULL,
  verbose = TRUE
)

```

### Arguments

<code>vol</code>	"volume" class object, of "rtdose" modality.
<code>struct</code>	"struct" class object.



T.MAT	"t.mat" class object, created by <code>load.patient.from.Rdcm</code> or <code>load.T.MAT</code> . If T.MAT = NULL, <code>struct\$ref.pseudo</code> must be equal to <code>vol\$ref.pseudo</code> .
target.roi.name	Exact name of target RoI in struct object. By default <code>target.roi.name = NULL</code> . See Details.
target.roi.sname	Name or part of name of target RoI in struct object. By default <code>target.roi.sname = NULL</code> . See Details.
target.roi.idx	Value of the index of target RoI that belong to the struct object. By default <code>target.roi.idx = NULL</code> . See Details.
healthy.roi.name	Exact name of healthy RoI in struct object. By default <code>healthy.roi.name = NULL</code> .
healthy.roi.sname	Name or part of name of healthy RoI in struct object. By default <code>healthy.roi.sname = NULL</code> .
healthy.roi.idx	Value of the index of healthy RoI that belong to the struct object. By default <code>healthy.roi.idx = NULL</code> .
presc.dose	Vector of prescription doses that serve as reference doses for the target RoI.
healthy.tol.dose	Vector of tolerance doses of each healthy RoI.
healthy.weight	Vector of weights, indicating the importance of the healthy RoI.
dosimetry	Vector indicating the requested dose indicators from among 'D.min', 'D.max', 'D.mean' and 'STD.' If <code>D.xpc</code> is different from NULL, it will be added.
volume.indices	Vector indicating the requested volume indices from among 'V.tot', 'V.prescdose' (i.e. volume over <code>presc.dose</code> ) and 'area'. If <code>V.xGy</code> is different from NULL, it will be added.
conformity.indices	Vector. Requested conformity indices from among 'PITV', 'PDS', 'CI.lomax2003', 'CN', 'NCI', 'DSC', 'CI.distance', 'CI.abs_distance', 'CDI', 'CS3', 'ULF', 'OHTF', 'gCI', 'COIN', 'COSI' and 'G_COSI'.
homogeneity.indices	Vector. Requested homogeneity indices from among 'HIRTog.max_ref', 'HIRTog.5_95', 'HICRU.max_min', 'HICRU.2.98_ref', 'HICRU.2.98_50', 'HICRU.5.95_ref', 'Hl.mayo2010' and 'Hl.heufelder.'
gradient.indices	Vector. Requested gradient indices from among 'GI.ratio.50', 'mGI'.
D.xpc	Vector of the percentage of the volume, for which the dose coverage is requested.
V.xGy	Vector of the minimum dose in Gy, received by the volume to be calculated.
verbose	Boolean. if TRUE (default) a progress bar is displayed.

### Details

If `target.roi.name`, `target.roi.sname`, and `target.roi.idx` are all set to NULL, all RoI containing 'ptv' (if they exist) are selected.

If `target.roi.name`, `target.roi.sname`, and `target.roi.idx` are all set to NULL, all RoI that include 'ptv', if they exist, are selected by default.

If `healthy.roi.name`, `healthy.roi.sname`, and `healthy.roi.idx` are all set to NULL, no healthy RoI are selected.

**Value**

Return a list containing (if requested)

– *dosimetry* : dataframe containing, for all target and healthy structures:

- the requested *dosimetry* : D.min (Gy), D.max (Gy), D.mean (Gy) and STD (Gy), respectively the minimum, maximum, mean and standard deviation of the dose in the regions of interest.
- the requested *D.x%* : (Gy) Dose covering x percent of structure volume.

– *volume* : dataframe containing, for all target and healthy structures, and isodoses:

- the requested *volume.indices* : *V\_tot* ( $cm^3$ ) (except for isodose) the total volume of the regions of interest, *area* ( $cm^2$ ) (except for isodose) their surface areas, *V.prescdose* ( $cm^3$ ) the volumes receiving at least *presc.dose* Gy,
- the requested *V.xGy* ( $cm^3$ ): volumes receiving at least x Gy.

– *conformity* : dataframe containing, if requested,

- PITV : (1) Prescription Isodose Target Volume, or conformity index defined by *E.Shaw* [1]

$$PITV = \frac{V_{presc.dose}}{V_{target}}$$

- PDS : (1) Prescription Dose Spillage defined by *SABR UK Consortium 2019* [2]

$$PDS = \frac{V_{presc.dose}}{V_{target \geq presc.dose}} = \frac{V_{presc.dose}}{V_{target} \cap V_{presc.dose}}$$

- *CI.lomax2003* : (1) Conformity Index defined by *Lomax and al* [3]

$$CI_{lomax2003} = \frac{V_{target \geq presc.dose}}{V_{presc.dose}} = \frac{V_{target} \cap V_{presc.dose}}{V_{presc.dose}}$$

- *CN* : (1) Conformation Number defined by *Van't Riet and al* [4]. It corresponds to conformity index defined by *Paddick* [5]

$$CN = CI_{paddick2000} = \frac{V_{target \geq presc.dose}^2}{V_{target} \cdot V_{presc.dose}} = \frac{(V_{target} \cap V_{presc.dose})^2}{V_{target} \cdot V_{presc.dose}}$$

- *NCI* : (1) New conformity index, inverse of *CN*, defined by *Nakamura and al* [6]

$$NCI = \frac{1}{CN}$$

- *DSC* : (1) Dice Similarity Coefficient [7]

$$DSC = 2 \cdot \frac{V_{target \geq presc.dose}}{V_{target} + V_{presc.dose}} = 2 \cdot \frac{V_{target} \cap V_{presc.dose}}{V_{target} + V_{presc.dose}}$$

- *CI.distance* : (1) Conformity Index based on distance defined by *Park and al* [8]

$$CI.distance = \frac{100}{N} \sum \frac{dist_{S_{presc.dose} \rightarrow G_{target}} - dist_{S_{target} \rightarrow G_{target}}}{dist_{S_{target} \rightarrow G_{target}}}$$

where  $dist_{S_{presc.dose} \rightarrow G_{target}}$  is the distance between the surface of the prescription dose volume and the centroid of the target, and  $dist_{S_{target} \rightarrow G_{target}}$  the surface of the target volume and the centroid of the target.  $N$  is the number of directions where the distances are calculated. These directions are computed every  $1^\circ$ . If the centroid is not within the target volume, then *CI.distance* = NA.

- `CI.abs_distance` : (1) Conformity Index based on distance defined by *Park and al* [8]

$$CI.abs\_distance = \frac{100}{N} \sum \frac{|dist_{S_{presc.dose} \rightarrow G_{target}} - dist_{S_{target} \rightarrow G_{target}}|}{dist_{S_{target} \rightarrow G_{target}}}$$

- `CDI` : (1) Conformity Distance Index defined by *Wu and al* [9]

$$CDI = 2 \frac{V_{presc.dose} + V_{target} - 2 V_{target \geq presc.dose}}{S_{target} + S_{presc.dose}} = \frac{V_{presc.dose} + V_{target} - 2 \cdot V_{target \cap V_{presc.dose}}}{S_{target} + S_{presc.dose}}$$

where  $S_{target}$  is the surface of the target volume and  $S_{presc.dose}$  is the surface of the prescription dose volume.

- `CS3` : (1) Triple Point Conformity Scale defined by *Ansari and al* [10]

$$CS3 = \frac{V_{0.95 \cdot presc.dose} + V_{presc.dose} + V_{1.05 \cdot presc.dose}}{3 \cdot V_{target}}$$

- `ULF` : (1) Underdosed lesion factor defined by *Lefkopoulos and al* [11]

$$ULF = \frac{V_{target < presc.dose}}{V_{target}} = \frac{V_{target} \cap \bar{V}_{presc.dose}}{V_{target}}$$

- `OHTF` : (1) Overdosed healthy tissues factor defined by *Lefkopoulos and al* [11]

$$OHTF = \frac{\sum V_{healthy \geq presc.dose}}{V_{target}} = \frac{\sum V_{healthy \cap V_{presc.dose}}}{V_{target}}$$

- `gCI` : (1) Geometric Conformity Index defined by *Lefkopoulos and al* [11]

$$gCI = ULF + OHTF$$

- `COIN` : Conformity Index defined by *Baltas and al* [12]

$$COIN = \frac{V_{target \geq presc.dose}^2}{V_{target} \cdot V_{presc.dose}} \cdot \prod^{N_{healthy}} \left( 1 - \frac{V_{healthy \geq presc.dose}}{V_{healthy}} \right)$$

- `gCOSI` : generalized COSI, defined by *Menhel and al* [13].

$$gCOSI = 1 - \sum^{N_{healthy}} healthy.weight \cdot \frac{\frac{V_{healthy \geq healthy.tol.dose}}{V_{healthy}}}{\frac{V_{target \geq presc.dose}}{V_{target}}}$$

– `COSI` : if "COSI" is requested in conformity indices, it returns a dataframe of Critical Organ Scoring Index for each healthy organ, at each presc. dose, and for each target. COSI is defined by *Menhel and al* [13]

$$COSI = 1 - \frac{\frac{V_{healthy \geq healthy.tol.dose}}{V_{healthy}}}{\frac{V_{target \geq presc.dose}}{V_{target}}}$$

– `homogeneity` : dataframe containing

- `HI.RTOG.max_ref` : (1) Homogeneity Index from RTOG defined by *E.Shaw* [1]

$$HI.RTOG.max\_ref = \frac{D_{max}}{presc.dose}$$

where  $D_{max}$  is the maximum dose in the target volume.

- HI.RTOG.5\_95 : (1) Homogeneity Index from RTOG [1]

$$HI.RTOG.5_95 = \frac{D.5pc}{D.95pc}$$

where  $D.5pc$  and  $D.95pc$  are respectively the doses at 5% and 95% of the target volume in cumulative dose-volume histogram.

- HI.ICRU.max\_min : (1) Homogeneity Index from ICRU report 62 [14]

$$HI.ICRU.max\_min = \frac{D_{max}}{D_{min}}$$

where  $D_{max}$  and  $D_{min}$  are respectively the maximum and the minimum dose in the target volume.

- HI.ICRU.2.98\_ref : (1) Homogeneity Index from ICRU report 83 [15]

$$HI.ICRU.2.98\_ref = 100 \frac{D.2pc - D.98pc}{presc.dose}$$

where  $D.2pc$  and  $D.98pc$  are respectively the doses at 2% and 98% of the target volume in cumulative dose-volume histogram.

- HI.ICRU.2.98\_50 : (1) Homogeneity Index from ICRU report 83 [15]

$$HI.ICRU.2.98\_50 = 100 \frac{D.2pc - D.98pc}{D.50pc}$$

where  $D.2pc$ ,  $D.98pc$  and  $D.50pc$  are respectively the doses at 2%, 98% and 50% of the target volume in cumulative dose-volume histogram.

- HI.ICRU.5.95\_ref : (1) Homogeneity Index from ICRU report 83 [15]

$$HI.ICRU.5.95\_ref = 100 \frac{D.5pc - D.95pc}{presc.dose}$$

where  $D.5pc$  and  $D.95pc$  are respectively the doses at 5% and 95% of the target volume in cumulative dose-volume histogram.

- HI.mayo2010 : (1) Homogeneity Index defined by Mayo and al [16]

$$HI.mayo2010 = \sqrt{\frac{D_{max}}{presc.dose} \cdot \left(1 + \frac{\sigma_D}{presc.dose}\right)}$$

where  $D_{max}$  is the maximum dose in the target volume, and  $\sigma_D$  the standard deviation of the dose in the target volume.

- HI.heufelder : (1) Homogeneity Index defined by Heufelder and al [17]

$$HI.heufelder = e^{-0.01 \cdot \left(1 - \frac{\mu_D}{presc.dose}\right)^2} \cdot e^{-0.01 \cdot \left(\frac{\sigma_D}{presc.dose}\right)^2}$$

where  $\mu_D$  and  $\sigma_D$  are respectively the mean and the standard deviation of the dose in the target volume.

– *gradient* : dataframe containing

- GI.ratio.50: Gradient Index based on volumes ratio defined by Paddick and Lippitz [18]

$$GI.ratio.50 = \frac{V_{0.5} \cdot presc.dose}{V_{presc.dose}}$$

- mGI: Modified Gradient Index defined by SABR UK Consortium 2019 [2]

$$mGI = \frac{V_{0.5} \cdot presc.dose}{V_{target \geq presc.dose}} = \frac{V_{0.5} \cdot presc.dose}{V_{target} \cap V_{presc.dose}}$$

## References

- [1] Shaw E, Kline R, Gillin M, Souhami L, Hirschfeld A, Dinapoli R, Martin L (1993). "Radiation therapy oncology group: Radiosurgery quality assurance guidelines." *International journal of radiation oncology, biology, physics*, **27**(5), 1231-1239. ISSN 0360-3016, doi:10.1016/0360-3016(93)90548A.
- [2] UK SABR Consortium (Online; accessed 2022-04-01). "Stereotactic Ablative Radiation Therapy (SABR): a resource. v6.1, January 2019." <https://www.sabr.org.uk/wp-content/uploads/2019/04/SABRconsortium-guidelines-2019-v6.1.0.pdf>.
- [3] Lomax NJ, Scheib SG (2003). "Quantifying the degree of conformity in radiosurgery treatment planning." *International journal of radiation oncology, biology, physics*, **55**(5), 1409-1419. ISSN 0360-3016, doi:10.1016/S03603016(02)045996.
- [4] Riet AV, Mak AC, Moerland MA, Elders LH, Van der Zee W (1997). "A conformation number to quantify the degree of conformality in brachytherapy and external beam irradiation: Application to the prostate." *International journal of radiation oncology, biology, physics*, **37**(3), 731-736. ISSN 0360-3016, doi:10.1016/S03603016(96)006013.
- [5] Paddick I (2000). "A simple scoring ratio to index the conformity of radiosurgical treatment plans. Technical note." *Journal of neurosurgery*, **93 Suppl 3**, 219-222.
- [6] Nakamura J, Verhey L, Smith V, Petti P, Lamborn K, Larson D, Wara W, Mcdermott M, Sneed P (2002). "Dose conformity of Gamma Knife radiosurgery and risk factors for complications." *International journal of radiation oncology, biology, physics*, **51**, 1313-9. doi:10.1016/S0360-3016(01)017576.
- [7] Dice LR (1945). "Measures of the Amount of Ecologic Association Between Species." *Ecology*, **26**(3), 297-302. ISSN 00129658, 19399170.
- [8] Park JM, Park S, Ye S, Kim J, Carlson J, Wu H (2014). "New conformity indices based on the calculation of distances between the target volume and the volume of reference isodose." *The British journal of radiology*, **87**, 20140342. doi:10.1259/bjr.20140342.
- [9] Wu Q, Wessels BW, Einstein DB, Maciunas RJ, Kim EY, Kinsella TJ (2003). "Quality of coverage: Conformity measures for stereotactic radiosurgery." *Journal of Applied Clinical Medical Physics*, **4**, 374-381.
- [10] Ansari S, Satpathy S, Singh P, Lad S, Thappa N, Singh B (2018). "A new index: Triple Point Conformity Scale (CS3) and its implication in qualitative evaluation of radiotherapy plan." *Journal of Radiotherapy in Practice*, **17**, 1-4. doi:10.1017/S1460396917000772.
- [11] Lefkopoulos D, Dejean C, bala ZE, Platoni K, Grandjean P, Foulquier J, Schlienger M (2000). "Determination of dose-volumes parameters to characterise the conformity of stereotactic treatment plans." In chapter XIII, 356-358. Springer Berlin Heidelberg. ISBN 978-3-540-67176-3, doi:10.1007/9783642597589\_135.
- [12] Baltas D, Kolotas C, Geramani KN, Mould RF, Ioannidis G, Kekchidi M, Zamboglou N (1998). "A conformal index (COIN) to evaluate implant quality and dose specification in brachytherapy." *International journal of radiation oncology, biology, physics*, **40 2**, 515-24. doi:10.1016/s0360-3016(97)007323.
- [13] Menhel J, Levin D, Alezra D, Symon Z, Pfeffer R (2006). "Assessing the quality of conformal treatment planning: a new tool for quantitative comparison." *Physics in Medicine and Biology*, **51**(20), 5363-5375.
- [14] Landberg T, Chavaudra J, Dobbs J, Gerard J, Hanks G, Horiot J, Johansson K, Möller T, Purdy J, Suntharalingam N, Svensson H (1999). "ICRU Report 62: Prescribing, Recording and Reporting Photon Beam Therapy (Supplement to ICRU Report 50),3. Absorbed Doses." *Reports of the International Commission on Radiation Units and Measurements*, **os-32**(1), 21-25.

[15] ICRU (2010). “Report 83 : Prescribing, Recording, and Reporting Photon-Beam Intensity-Modulated Radiation Therapy (IMRT).” *Reports of the International Commission on Radiation Units and Measurements*, **10**(1), 1-3.

[16] Mayo CS, Ding L, Addesa A, Kadish S, Fitzgerald TJ, Moser R (2010). “Initial Experience With Volumetric IMRT (RapidArc) for Intracranial Stereotactic Radiosurgery.” *International Journal of Radiation Oncology\*Biophysics\*Physics*, **78**(5), 1457-1466. ISSN 0360-3016, doi:10.1016/j.ijrobp.2009.10.005.

[17] Heufelder J, Zink K, Scholz M, Kramer K, Welker K (2003). “Eine Methode zur automatisierten Bewertung von CT-basierten Bestrahlungsplänen in der perkutanen Strahlentherapie.” *Zeitschrift für Medizinische Physik*, **13**(4), 231-239. ISSN 0939-3889, doi:10.1078/0939388900175.

[18] Paddick I, Lippitz BE (2006). “A simple dose gradient measurement tool to complement the conformity index.” *Journal of neurosurgery*, **105 Suppl**, 194-201.

All this references are compiled by

- Kaplan LP, Korreman SS (2021). “A systematically compiled set of quantitative metrics to describe spatial characteristics of radiotherapy dose distributions and aid in treatment planning.” *Physica Medica*, **90**, 164-175. ISSN 1120-1797, doi:10.1016/j.ejmp.2021.09.014. and
- Patel G, Mandal A, Choudhary S, Mishra R, Shende R (2020). “Plan evaluation indices: A journey of evolution.” *Reports of Practical Oncology & Radiotherapy*, **25**. doi:10.1016/j.rpor.2020.03.002..

## See Also

[rt.indices.from.bin.](#)

## Examples

```
# loading of toy-patient objects (decrease dxyz and increase beam.nb
# for better result)
step <- 5
patient <- toy.load.patient (modality = c("rtdose", "rtstruct"), roi.name = "eye",
                           dxyz = rep (step, 3), beam.nb = 3)
indices <- rt.indices.from.roi (patient$rtdose[[1]], patient$rtstruct[[1]],
                              healthy.roi.sname = "eye", presc.dose = 50,
                              conformity.indices = c("PITV", "PDS", "CI.lomax2003",
                                                    "CN", "NCI", "DSC", "COIN"),
                              verbose = FALSE)

indices
```

---

save.T.MAT

*Save a T.MAT class object*

---

## Description

The save.T.MAT function saves the data required by [load.T.MAT](#), [load.patient.from.dicom](#) or [load.patient.from.Rdcm](#) to generate T.MAT, as pre-formatted Rdcm files.

## Usage

```
save.T.MAT(T.MAT, dirname)
```

**Arguments**

T.MAT "t.mat" class object to save.  
 dirname Directory where new reg .Rdcm files will be saved.

**Details**

Reg files from DICOM files cannot be updated with the save.T.MAT function. Only transfer matrices added with [ref.add](#) or [ref.cutplane.add](#) will be saved.

**Value**

Returns TRUE, if all reg files generating T.MAT are saved.

**Examples**

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 5
patient <- toy.load.patient (modality = c("ct", "mr"), roi.name = "",
                             dxyz = rep (step, 3))

# Save T.MAT to a temporary file pat.dir
pat.dir <- file.path (tempdir(), "PM_Rdcm")
dir.create (pat.dir, recursive = TRUE)
save.T.MAT (patient$T.MAT, dirname = pat.dir)
list.files(pat.dir)

# Cleaning temporary directory
unlink (pat.dir, recursive = TRUE)
```

---

 save.to.Rdcm

---

*Save a **espadon** object in a pre-formatted \*.Rdcm file*


---

**Description**

The function save.to.Rdcm allows you to save an object created by **espadon** in a pre-formatted \*.Rdcm file. This object will also be accessible by the load.patient.from.Rdcm function.

**Usage**

```
save.to.Rdcm(obj, object.name = obj$object.alias, dirname = obj$file.dirname)
```

**Arguments**

obj **espadon** object of class "volume", "struct", "mesh", "histo", "dvh", "histo2D".  
 object.name Character string, representing the name of the object, default to obj\$object.alias.  
 dirname Directory where new files from obj will be saved.

**Value**

Returns TRUE, if paste0(object.name, ".Rdcm") exists in dirname.

Returns FALSE, if object.name is not a valid file name, or if the file that is created would replace a \*.Rdcm file created by [dicom.to.Rdcm.converter](#).

**Note**

save.to.Rdcm can not replace an \*.Rdcm file created by [dicom.to.Rdcm.converter](#).

**Examples**

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 5
patient <- toy.load.patient (modality = c("ct", "mr"), roi.name = "",
                           dxyz = rep (step, 3))

# Save T.MAT to a temporary file pat.dir
pat.dir <- file.path (tempdir(), "PM_Rdcm")
dir.create (pat.dir, recursive = TRUE)
save.to.Rdcm (patient$ct[[1]], dirname = pat.dir)
save.to.Rdcm (patient$mr[[1]], dirname = pat.dir)
list.files(pat.dir)

# Cleaning temporary directory
unlink (pat.dir, recursive = TRUE)
```

---

select.names	<i>Regions of Interest (RoI) indices</i>
--------------	--

---

**Description**

The select.names function allows you to select words from a vector of words, according to several criteria, eliminating spaces and case.

**Usage**

```
select.names(names, roi.name = NULL, roi.sname = NULL, roi.idx = NULL)
```

**Arguments**

names	Words vector
roi.name	Vector of words to compare to names. By default roi.name = NULL. See Details
roi.sname	Vector of words or parts of words to compare. By default roi.sname = NULL. See Details
roi.idx	Index vector. By default roi.idx = NULL. See Details.

**Details**

If roi.name, roi.sname, and roi.idx are all NULL, then all RoI are selected.

**Value**

Returns the indices of the elements of the word vector names satisfying one or more of the following conditions:

- ASCII // TRANSLIT transcriptions, without spaces, of names and roi.name, are identical.
- ASCII // TRANSLIT transcriptions, without spaces of roi.sname are identical to part of ASCII // TRANSLIT transcriptions, without spaces of names.
- names indices belong to the index vector roi.idx.



**Examples**

```
# loading patient objects
names <- c("Eye left", "EyeR", "OPTICAL nerve L", "opical nervR", "chiasma")

# RoI selection.
select.names (names = names, roi.name = c("eye left", "eye right"))
select.names (names = names, roi.sname = c("eye", "ner"))
select.names (names = names, roi.idx = 4:9)
```

---

struct.from.bin

*Creation of struct class object from a binary volume*


---

**Description**

The `struct.from.bin` function creates a struct object with a unique RoI, defined by the contours of binary volume.

**Usage**

```
struct.from.bin(
  vol,
  roi.name = vol$description,
  roi.nb = 1,
  roi.color = "#379DA2",
  roi.type = c("", "EXTERNAL", "PTV", "CTV", "GTV", "TREATED_VOLUME", "IRRAD_VOLUME",
    "OAR", "BOLUS", "AVOIDANCE", "ORGAN", "MARKER", "REGISTRATION", "ISOCENTER",
    "CONTRAST_AGENT", "CAVITY", "BRACHY_CHANNEL", "BRACHY_ACCESSORY", "BRACHY_SRC_APP",
    "BRACHY_CHNL_SHLD", "SUPPORT", "FIXATION", "DOSE_REGION", "CONTROL",
    "DOSE_MEASUREMENT"),
  external.only = FALSE,
  alias = "",
  description = paste("RoI from", vol$object.alias)
)
```

**Arguments**

<code>vol</code>	"volume" class object, of binary modality.
<code>roi.name</code>	Character string, representing the name of created RoI.
<code>roi.nb</code>	Positive integer, representing the number of created RoI.
<code>roi.color</code>	Color of the created RoI, in hex code format ("#RRGGBB").
<code>roi.type</code>	Type of RoI, from among "", "EXTERNAL", "PTV", "CTV", "GTV", "TREATED_VOLUME", "IRRAD_VOLUME", "OAR", "BOLUS", "AVOIDANCE", "ORGAN", "MARKER", "REGISTRATION", "ISOCENTER", "CONTRAST_AGENT", "CAVITY", "BRACHY_CHANNEL", "BRACHY_ACCESSORY", "BRACHY_SRC_APP", "BRACHY_CHNL_SHLD", "SUPPORT", "FIXATION", "DOSE_REGION", "CONTROL" and "DOSE_MEASUREMENT"
<code>external.only</code>	Boolean. If TRUE, only external contours are kept.
<code>alias</code>	Character string, \$alias of the created object.
<code>description</code>	Character string, describing the created object.

**Value**

Returns a "struct" class object (see [espadon.class](#) for class definition), including the unique `roi.name` as region of interest.

**Examples**

```
# Contours of a sphere of 10 mm radius
b.sphere <- vol.create (n.ijk = c (40, 40, 40), dxyz = c(1,1,1),
                        mid.pt = c (0, 0, 0), modality = "binary",
                        default.value = FALSE)
xyz <- expand.grid (-20:19, -20:19, -20:19)
R <- 10
Sphere.flag <- (xyz[, 1]^2 + xyz[, 2]^2 + xyz[, 3]^2) <= R^2
b.sphere$vol3D.data[Sphere.flag] <- TRUE
b.sphere$max.pixel <- TRUE
S.sphere <- struct.from.bin (b.sphere, roi.name = "sphere", external.only = TRUE)
str (S.sphere$roi.info)
```

---

struct.in.new.ref      *Change of frame of reference of a "struct" class object.*

---

**Description**

The `struct.in.new.ref` function allows you to change the frame of reference of a struct.

**Usage**

```
struct.in.new.ref(struct, new.ref.pseudo, T.MAT, alias = "")
```

**Arguments**

<code>struct</code>	"struct" class object.
<code>new.ref.pseudo</code>	pseudonym of the frame of reference in which the struct should be located. This <code>new.ref.pseudo</code> must exist in the <code>T.MAT</code> list.
<code>T.MAT</code>	"t.mat" class object, created by <a href="#">load.patient.from.dicom</a> , <a href="#">load.patient.from.Rdcm</a> , <a href="#">load.T.MAT</a> or <a href="#">ref.add</a> .
<code>alias</code>	Character string, <code>\$alias</code> of the created object.

**Value**

Returns "struct" class object in the new frame of reference `new.ref.pseudo`.

**See Also**

[vol.in.new.ref](#)

**Examples**

```
# loading of toy-patient objects (decrease dxyz for better result)
step <- 4
patient <- toy.load.patient (modality = c("mr", "rtstruct"), roi.name = "",
                             dxyz = rep (step, 3))
S <- patient$rtstruct[[1]]
S.in.new.ref <- struct.in.new.ref (S, patient$mr[[1]]$ref.pseudo, patient$T.MAT)
```

---

 struct.merge

*Merging of structures into a new structure*


---

**Description**

The struct.merge function merges two structures into a new one. It is useful for comparing contours, for example.

**Usage**

```
struct.merge(
  ref.struct,
  add.struct,
  roi.name = NULL,
  roi.sname = NULL,
  roi.idx = NULL,
  suffix = "",
  alias = "",
  description = ""
)
```

**Arguments**

ref.struct	struct class object. All RoI of this structure are kept.
add.struct	struct class object. Only the selected RoI are kept for merging.
roi.name	Vector of exact names of the RoI in the add.struct object. By default roi.name = NULL. See Details.
roi.sname	Vector of names or parts of names of the RoI in the add.struct object. By default roi.sname = NULL. See Details.
roi.idx	Vector of indices of the RoI that belong to the add.struct object. By default roi.idx = NULL. See Details.
suffix	Character string. '-suffix' is added to RoI name.
alias	Character string, \$alias of the resulted object.
description	Character string, describing the the resulted object.

**Details**

If roi.name, roi.sname, and roi.idx are all NULL, then all RoI of add.struct are selected.

**Value**

Returns a struct class object. See [espadon.class](#) for class definitions.

**Note**

Beware that, when merging structures, some ROI may have same name or `roi.info$roi.pseudo`. In this case `struct.merge` prints a warning message. Consider changing suffix to avoid the ambiguity.

**See Also**

[struct.from.bin](#).

**Examples**

```
# loading of toy-patient objects (decrease dxyz and increase beam.nb for
# better result)
step <- 5
patient <- toy.load.patient (modality = c("rtdose"),
                             dxyz = rep (step, 3), beam.nb = 3)
D <- patient$rtdose[[1]]

# isodose 50% Dmax Gy and 90% Dmax
bin50 <- bin.from.vol (D, min = 0.5 * D$max.pixel)
bin90 <- bin.from.vol (D, min = 0.9 * D$max.pixel)
S.isodose50 <- struct.from.bin (bin50, roi.name = "50pc" ,
                               roi.color = "#00FFFF")
S.isodose90 <- struct.from.bin (bin90, roi.name = "90pc" ,
                               roi.color = "#FFFF00")
S <- struct.merge (S.isodose50, S.isodose90, alias = "isodose",
                  description = paste ("isodose of", D$object.alias))

# Dmax location :
z.dmax <- get.xyz.from.index(which (D$vol3D.data == D$max.pixel), D)[1,3]
display.plane(top = D, struct = S, view.coord = z.dmax, legend.shift = -50)
```

---

toy.dicom.raw

*toy DICOM raw data*

---

**Description**

The `toy.dicom.raw` loads raw data from a dummy DICOM file. It is used for the test.

**Usage**

```
toy.dicom.raw()
```

**Value**

Returns the raw data of a dummy DICOM file of rtplan modality.

**Examples**

```
toy.dicom.raw ()
```

---

toy.load.patient	<i>Load a toy patient for test</i>
------------------	------------------------------------

---

## Description

The `toy.load.patient` creates a dummy "patient" class object. It is used for the test.

## Usage

```
toy.load.patient(  
  modality = c("ct", "mr", "rtdose", "rtstruct"),  
  roi.name = c("eye", "optical nerve", "brain", "labyrinth processing unit",  
    "energy unit", "gizzard", "ghost container", "exhaust valve"),  
  dxyz = c(1, 1, 1),  
  beam.nb = 7  
)
```

## Arguments

<code>modality</code>	String vector, whose elements are chosen among the modalities "ct", "mr", "rtstruct" and "rtdose".
<code>roi.name</code>	String vector, whose elements are chosen among the regions of interest (RoI) "eye", "optical nerve", "brain", "labyrinth processing unit", "energy unit", "gizzard", "ghost container" and "exhaust valve". Note that the RoI "couch", "patient" and "ptv" are still present.
<code>dxyz</code>	Vector of length 3, representing the x, y, z steps in mm, between ct, mr and rtdose voxels.
<code>beam.nb</code>	Positive integer. Number of radiotherapy beams in rtdose modality.

## Value

Returns an toy object of "patient" class, containing the modalities defined in `modality`. See [espadon.class](#) for class definitions.

## Examples

```
# loading of toy-patient objects (decrease dxyz for better result)  
step <- 5  
pat <- toy.load.patient (dxyz = rep (step, 3), beam.nb = 1)  
str (pat, max.level = 2)
```

---

vector.product	<i>Vector product of two vectors</i>
----------------	--------------------------------------

---

**Description**

Vector product of two vectors

**Usage**

```
vector.product(v1, v2)
```

**Arguments**

v1	Vector of x, y, z coordinates
v2	Vector of x, y, z coordinates

**Value**

Returns the x, y, z coordinates of the vector product of v1 and v2

**Examples**

```
vector.product(c(1, 0, 0), c(0, 1, 0))
```

---

vol.copy	<i>Creating a volume from another one</i>
----------	---

---

**Description**

The vol.copy function creates a "volume" class object, with the same grid as the vol volume object.

**Usage**

```
vol.copy(vol, alias = "", modality = NULL, description = NULL, number = NULL)
```

**Arguments**

vol	"volume" class object, template of the created object.
alias	Character string, \$object.alias of the created object.
modality	Character string, modality of the created volume. If modality = NULL, then the created object will have the modality of vol.
description	Character string, description of the returned object. If description = NULL, then the created object will have the description of vol.
number	number of the returned volume. If number = NULL, then the returned object will have the number of vol.

**Value**

Returns a "volume" class object (see [espadon.class](#) for class definitions), with the same grid as vol, in which \$vol3D.data is initialized to NA.

**Examples**

```
# loading of toy-patient objects (decrease dxyz for better result)
patient <- toy.load.patient (modality = "ct", roi.name = "", dxyz = c (4, 4, 4))
CT <- patient$ct[[1]]

# creating a volume
vol.from.CT <- vol.copy (CT, alias = "ct reference")
str (vol.from.CT)
```

---

vol.create	<i>Volume creating</i>
------------	------------------------

---

**Description**

The vol.create function creates a volume object from a user-defined grid.

**Usage**

```
vol.create(
  n.ijk,
  dxyz,
  mid.pt = NULL,
  pt000 = NULL,
  default.value = NA,
  ref.pseudo = "",
  frame.of.reference = "",
  alias = "",
  modality = "",
  description = "",
  number = 0
)
```

**Arguments**

n.ijk	Vector of length 3, representing the number of elements on the i, j and k axes.
dxyz	Vector of length 3, representing the x, y, z steps in mm, between voxels. See details.
mid.pt	Vector of length 3, representing the x, y, z coordinates of the midpoint of the volume. See details.
pt000	Vector of length 3, representing the x, y, z coordinates of the first voxel of the first plane.
default.value	Numerical or boolean value, representing the default value of the voxels.
ref.pseudo	Character string, frame of reference pseudonym of the created object.
frame.of.reference	Character string, frame of reference of the created object.

alias	Character string, \$alias of the created object.
modality	Character string, \$modality of the created object.
description	Character string, describing the the created object.
number	Integer, by default set to 0, number of the created object.

### Details

If mid.pt and pt000 are both equal to NULL, then mid.pt = c(0, 0, 0) by default. If mid.pt and pt000 are both different from NULL, then only mid.pt is taken into account.

### Value

Returns a "volume" class object (see [espadon.class](#) for class definitions), in which the grid is defined by pt000 or mid.pt, dxyz n.ijk. If default.value are initialized to FALSE, then modality = "binary". The orientation of the patient is orthonormal to the grid.

### Examples

```
new.vol <- vol.create (pt000 = c(1,10,10), dxyz = c(1, 1, 1),
                     n.ijk = c(100, 100, 100),
                     ref.pseudo = "ref1",
                     frame.of.reference = "toyref1",
                     alias = "new ct", modality = "ct",
                     description = "")
str (new.vol)
```

---

vol.from.bin	<i>Volume class object according to binary selection</i>
--------------	--

---

### Description

The vol.from.bin function selects a part of a "volume" class object of "binary" modality which has the same grid. It is especially useful to restrict voxel data in region of interest.

### Usage

```
vol.from.bin(vol, sel.bin, alias = "", description = NULL)
```

### Arguments

vol	"volume" class object, containing data to restrict.
sel.bin	"volume" class object, of "binary" modality. vol and sel.bin must have the same grid.
alias	Character string, \$alias of the created object
description	Character string, describing the created object. If description = NULL (default value), it will be set to paste (vol\$object.alias, "from", sel.bin\$object.alias)

### Value

Returns a "volume" class object (see [espadon.class](#) for class definitions), in which non-selected voxels have the value NA, and selected voxels have the original value of vol.



**Examples**

```
# loading of toy-patient objects (decrease dxyz for better result)
patient <- toy.load.patient (modality = c ("ct", "rtstruct"),
                           roi.name = "brain", dxyz = c (4, 4, 4))

CT <- patient$ct[[1]]
S <- patient$rtstruct[[1]]

# select the brain in the volume
bin.brain <- bin.from.roi (vol = CT, struct = S, roi.name = "brain")
vol.brain <- vol.from.bin (CT, bin.brain)
# display at the center of gravity of the brain Gz
Gz <- S$roi.info [grep("^brain", S$roi.info$roi.pseudo),]$Gz
display.plane (bottom = vol.brain, view.coord = Gz, struct = S,
              roi.sname = "brain", bg = "#00ff00", interpolate = FALSE)
```

---

vol.gradient	<i>Gradient of a volume</i>
--------------	-----------------------------

---

**Description**

The `vol.gradient` function calculates the 3D gradient of a "volume" class object

**Usage**

```
vol.gradient(vol, alias = "", description = NULL)
```

**Arguments**

vol	"volume" class object.
alias	Character string, \$alias of the created object.
description	Character string, describing the created object. If description = NULL (default value), it will be set to paste (vol\$object.alias, "gradient").

**Value**

Returns a "volume" class object (see [espadon.class](#) for class definitions), with the same grid and modality as vol, gradient of vol.

**Examples**

```
# loading of toy-patient objects (decrease dxyz and increase beam.nb for
# better result)
step <- 3
pat <- toy.load.patient (modality = c ("ct"), dxyz = rep (step, 3))
CT.gradient <- vol.gradient (pat$ct[[1]])

display.plane (CT.gradient, view.type = "sagi", view.coord = 61,
              interpolate = FALSE)
```

---

vol.in.new.ref	<i>Change of frame of reference of a volume</i>
----------------	---

---

### Description

The `vol.in.new.ref` function allows you to change the frame of reference of a volume.

### Usage

```
vol.in.new.ref(vol, new.ref.pseudo, T.MAT, alias = "", description = NULL)
```

### Arguments

<code>vol</code>	"volume" class object.
<code>new.ref.pseudo</code>	pseudonym of the frame of reference in which the volume should be located. This <code>new.ref.pseudo</code> must exist in the <code>T.MAT</code> list.
<code>T.MAT</code>	"t.mat" class object, created by <a href="#">load.patient.from.dicom</a> , <a href="#">load.patient.from.Rdcm</a> , <a href="#">load.T.MAT</a> or <a href="#">ref.add</a> .
<code>alias</code>	Character string, <code>\$alias</code> of the created object.
<code>description</code>	Character string, describing the created object. If <code>description = NULL</code> (default value), it will be that of the <code>vol</code> volume.

### Value

Returns "volume" class object in the new frame of reference `new.ref.pseudo`.

### See Also

[struct.in.new.ref](#)

### Examples

```
# loading of toy-patient objects (decrease dxyz for better result)
patient <- toy.load.patient (modality = c("ct", "mr"), roi.name = "",
                           dxyz = c (4, 4, 4))

CT <- patient$ct[[1]]
CT.in.new.ref <- vol.in.new.ref (CT, patient$mr[[1]]$ref.pseudo, patient$T.MAT)
```

---

vol.regrid	<i>Transform the grid of a volume class object into the grid of another</i>
------------	---

---

### Description

The `vol.regrid` function transforms the grid of a volume according to the grid of another.

**Usage**

```
vol.regrid(
  vol,
  back.vol,
  T.MAT = NULL,
  interpolate = TRUE,
  alias = "",
  description = NULL,
  verbose = TRUE
)
```

**Arguments**

vol	"volume" class object to regrid.
back.vol	"volume" class object whose grid will be used for regriding. Its \$ref.pseudo must exist in the T.MAT list.
T.MAT	"t.mat" class object, created by <a href="#">load.patient.from.dicom</a> , <a href="#">load.patient.from.Rdcm</a> , <a href="#">load.T.MAT</a> or <a href="#">ref.add</a> . If T.MAT = NULL, back.vol\$ref.pseudo must be equal to vol\$ref.pseudo.
interpolate	Boolean, default to TRUE. If interpolate = TRUE, a trilinear interpolation of the value of the voxels, relative to the values of adjacent voxels, is performed.
alias	Character string, \$alias of the created object.
description	Character string, describing the the created object. If description = NULL, it will be that of vol.
verbose	Boolean. if TRUE (default) a progress bar is displayed.

**Value**

Returns a copy of vol, in which grid is that of back.vol.

**Examples**

```
# loading of toy-patient objects (decrease dxyz and increase beam.nb for
# better result)
step <- 5
patient <- toy.load.patient (modality = c ("mr", "rtdose"),
                             dxyz = rep (step, 3), beam.nb = 4)

MR <- patient$mr[[1]]
D <- patient$rtdose[[1]]

# change grid
D.on.MR <- vol.regrid (vol = D, back.vol = MR, interpolate = TRUE,
                      T.MAT = patient$T.MAT, alias = "",
                      description = NULL, verbose = FALSE)

# maximum dose location
max.dose.in.MR <- get.xyz.from.index (which.max (D.on.MR$vol3D.data), D.on.MR)
display.plane (bottom = MR, view.coord = max.dose.in.MR[3],
              top = D.on.MR, bottom.col = grey.colors(255, start = 0, end = 1),
              bottom.breaks = seq (0, 500, length.out = 256),
              bg = "#00ff00", interpolate = FALSE)
```

---

vol.sum	<i>Sum of 2 volumes</i>
---------	-------------------------

---

### Description

The `vol.sum` function adds two "volume" class objects of the same grid and of the same modality.

### Usage

```
vol.sum(vol1, vol2, alias = "", description = NULL)
```

### Arguments

<code>vol1, vol2</code>	"volume" class objects. The 2 volumes must have the same modality, and the same grid (i.e. share the same position of the voxels).
<code>alias</code>	Character string, \$alias of the created object.
<code>description</code>	Character string, describing the created object. If <code>description = NULL</code> (default value), it will be set to paste ( <code>vol1\$object.alias, "+", vol2\$object.alias</code> ).

### Value

Returns a "volume" class object (see [espadon.class](#) for class definitions), with the same grid and modality as `vol1` and `vol2`, sum of `vol1` and `vol2`.

### Examples

```
# loading of toy-patient objects (decrease dxyz and increase beam.nb for
# better result)
step <- 5
pat<- toy.load.patient (modality = c ( "rtdose"), dxyz = rep (step, 3),
                        beam.nb = 3)

# Double dose
D <- vol.sum (pat$rtdose[[1]], pat$rtdose[[1]])
pat$rtdose[[1]]$max.pixel
D$max.pixel
```

---

xlsx.from.dcm	<i>Converting DICOM files to .xlsx files</i>
---------------	--

---

### Description

The `xlsx.from.dcm` function creates an Excel file from DICOM files.

**Usage**

```

xlsx.from.dcm(
  dcm.filesnames,
  xlsx.filesnames,
  multipage = TRUE,
  txt.sep = "\\ ",
  txt.length = 100,
  tag.dictionary = dicom.tag.dictionary()
)

```

**Arguments**

`dcm.filesnames` String vector, representing the list of full names of DICOM files.

`xlsx.filesnames` String vector, representing the list of full names of created \*.xlsx files. If `multipage = TRUE`, only the `xlsx.filesnames[1]` is used.

`multipage` Boolean. If `TRUE`, all `dcm.filesnames` are converted into multiple pages of the same \*.xlsx file.

`txt.sep` String. Used if `as.txt = TRUE`. Separator of the tag value elements.

`txt.length` Positive integer. Used if `as.txt = TRUE`. Maximum number of letters in the representation of the TAG value.

`tag.dictionary` Dataframe, by default equal to [dicom.tag.dictionary](#), whose structure it must keep. This dataframe is used to parse DICOM files.

**Value**

Returns a boolean vector, establishing the existence of the created Excel files.

**Examples**

```

# First, save toy.dicom.raw () raw data to a temporary file pat.dir for testing.
pat.dir <- file.path (tempdir(), "PM_dcm")
dir.create (pat.dir, recursive = TRUE)
dcm.filename <- tempfile (pattern = "PMrtplan", tmpdir = pat.dir, fileext = ".dcm")
zz <- file (dcm.filename, "wb")
writeBin (toy.dicom.raw (), zz, size = 1)
close (zz)
list.files (pat.dir)

# Creating an Excel file
xlsx.fnames <- file.path (pat.dir,
  paste (basename (dcm.filename), "xlsx", sep = "."))
xlsx.from.dcm (dcm.filename, xlsx.fnames)
list.files (pat.dir)

# Cleaning temporary directory
unlink (pat.dir, recursive = TRUE)

```



```
xlsx.from.Rdcm (Rdcm.fileNames)  
list.files (pat.dir)  
  
# Cleaning temporary directory  
unlink (pat.dir, recursive = TRUE)
```

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