dicompyler-core Documentation

Release 0.5.7

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CHAPTER

ONE

DICOMPYLER-CORE

A library of core radiation therapy modules for DICOM / DICOM RT used by dicompyler. This package includes:

- `dicomparser`: parse DICOM objects in an easy-to-use manner
- `dvh`: Pythonic access to dose volume histogram (DVH) data
- `dvhcalc`: Independent DVH calculation using DICOM RT Dose & RT Structure Set
- `dose`: Pythonic access to RT Dose data including dose summation

1.1 Other information

- Free software: BSD license
- Documentation: Read the docs
- Tested on Python 3.7+

1.2 Dependencies

- numpy 1.2 or higher
- pydicom 0.9.9 or higher (pydicom 1.0 compatible)
- matplotlib 1.3.0 or higher (for DVH calculation)
- Optional:
  - Pillow (for image display)
  - Shapely (for structure volume calculation)
  - scikit-image (for DVH interpolation)
  - scipy (for dose grid summation using interpolation)

1.3 Basic Usage

```
from dicompylercore import dicomparser, dvh, dvhcalc
dp = dicomparser.DicomParser("rtss.dcm")

# i.e. Get a dict of structure information
structures = dp.GetStructures()

>>> structures[5]
{'color': array([255, 128, 0]), 'type': 'ORGAN', 'id': 5, 'empty': False, 'name': 'Heart
↪'}

# Access DVH data
rtdose = dicomparser.DicomParser("rtdose.dcm")
heartdvh = dvh.DVH.from_dicom_dvh(rtdose.ds, 5)

>>> heartdvh.describe()
Structure: Heart
DVH Type:  cumulative, abs dose: Gy, abs volume: cm3
Volume:    437.46 cm3
Max Dose:  3.10 Gy
Min Dose:  0.02 Gy
Mean Dose: 0.64 Gy
D100:      0.00 Gy
D98:       0.03 Gy
D95:       0.03 Gy
D2cc:      2.93 Gy

# Calculate a DVH from DICOM RT data
calcdvh = dvhcalc.get_dvh("rtss.dcm", "rtdose.dcm", 5)

>>> calcdvh.max, calcdvh.min, calcdvh.D2cc
(3.0899999999999999, 0.029999999999999999, dvh.DVHValue(2.96, 'Gy'))
```

Advanced Usage and Examples can be found in Binder:

1.4 Citing dicompyler-core

A DOI for dicompyler-core with various citation styles can be found at Zenodo:

1.5 Credits

This package was created with Cookiecutter and the audreyr/cookiecutter-pypackage project template.

CHAPTER

TWO

INSTALLATION

At the command line:

```
$ pip install dicompyler-core
```

Or, if you have virtualenvwrapper installed:

```
$ mkvirtualenv dicompylercore
$ pip install dicompyler-core
```

CHAPTER

THREE

USAGE

To use dicompyler-core in a project:

DICOM data can be easily accessed using convenience functions using the *dicompylercore.dicomparser.DicomParser* class:

```
from dicompylercore import dicomparser, dvh, dvhcalc
dp = dicomparser.DicomParser("rtss.dcm")

# i.e. Get a dict of structure information
structures = dp.GetStructures()

>>> structures[5]
{'color': array([255, 128, 0]), 'type': 'ORGAN', 'id': 5, 'empty': False, 'name': 'Heart
↪'}
```

Dose volume histogram (DVH) data can be accessed in a Pythonic manner using the *dicompylercore.dvh.DVH* class:

```
rtdose = dicomparser.DicomParser("rtdose.dcm")
heartdvh = dvh.DVH.from_dicom_dvh(rtdose.ds, 5)

>>> heartdvh.describe()
Structure: Heart
-----
DVH Type:  cumulative, abs dose: Gy, abs volume: cm3
Volume:    437.46 cm3
Max Dose:  3.10 Gy
Min Dose:  0.02 Gy
Mean Dose: 0.64 Gy
D100:      0.00 Gy
D98:       0.03 Gy
D95:       0.03 Gy
D2cc:      2.93 Gy

>>> heartdvh.max, heartdvh.min, heartdvh.D2cc
(3.0999999999999779, 0.02, dvh.DVHValue(2.9299999999999815, 'Gy'))
```

Dose volume histograms (DVHs) can be independently calculated using the *dicompylercore.dvhcalc* module:

```
# Calculate a DVH from DICOM RT data
calcdvh = dvhcalc.get_dvh("rtss.dcm", "rtdose.dcm", 5)
```

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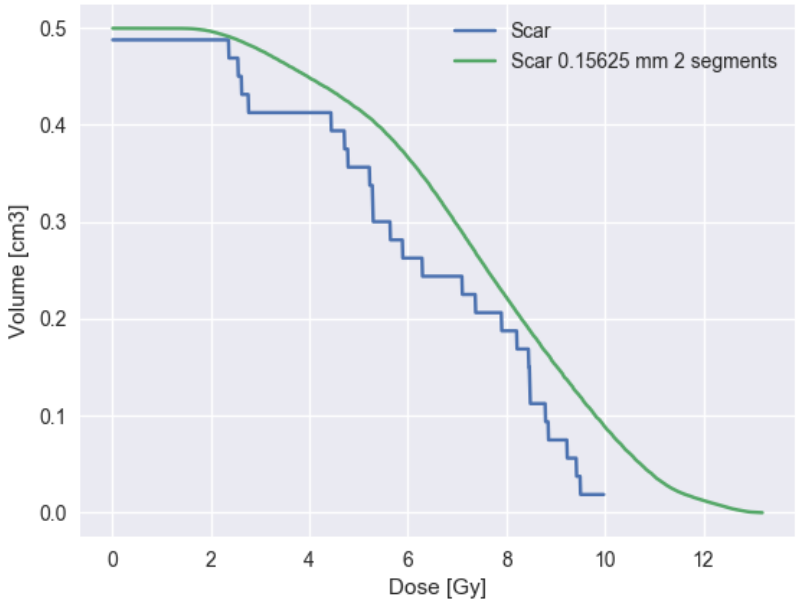
```
>>> calcdvh.max, calcdvh.min, calcdvh.D2cc
(3.0899999999999999, 0.029999999999999999, dvh.DVHValue(2.96, 'Gy'))
```

Structure and dose data for independently calculated DVHs can also be interpolated in-plane and between planes:

```
# Calculate a DVH using interpolation to super-sample the dose grid in plane,
# interpolate dose between planes and restrict calculation to the structure
# extents
interpscar = dvhcalc.get_dvh("rtss.dcm", "rtdose.dcm", 8,
    interpolation_resolution=(2.5/16),
    interpolation_segments_between_planes=2,
    use_structure_extents=True)
interpscar.name += ' interp'

# Compare against un-interpolated DVH
origscar = dvhcalc.get_dvh("rtss.dcm", "rtdose.dcm", 8)

>>> origscar.compare(interpscar)
Structure:          Scar            Scar interp       Rel Diff       Abs diff
-----
DVH Type:  cumulative, abs dose: Gy, abs volume: cm3
Volume:             0.47 cm3          0.50 cm3         +6.55 %          +0.03
Max:                9.50 Gy          13.18 Gy         +38.74 %          +3.68
Min:                2.36 Gy           1.23 Gy         -47.88 %          -1.13
Mean:               6.38 Gy           7.53 Gy         +18.02 %          +1.15
D100:               0.00 Gy           0.00 Gy          +0.00 %          +0.00
D98:                2.36 Gy           2.44 Gy          +3.39 %          +0.08
D95:                2.36 Gy           3.09 Gy         +30.93 %          +0.73
D2cc:               0.00 Gy           0.00 Gy          +0.00 %          +0.00
```



Dose grids can be summed and scaled using the *dicompylercore.dose* module:

```
from dicompylercore import dose

# Dose grid summation with (tri-linear) interpolation if dose grids are not spatially␣
↪coincident
grid_1 = dose.DoseGrid(dose_file_1)
grid_2 = dose.DoseGrid(dose_file_2)
grid_sum = grid_1 + grid_2
grid_sum.save_dcm("grid_sum.dcm")  # save to file

# Dose grid scaling
grid_scaled = grid_1 * 2  # Scale grid_1 by a factor of 2
grid_scaled.save_dcm("grid_scaled.dcm")  # save to file

# Dose grid subtraction may be performed, however, negative doses are not currently
# DICOM compliant (i.e., the pixel_array of RTDOSE datasets are unsigned integer arrays).
# dicompyler-core users must work with the DoseGrid's numpy array directly (DoseGrid.dose_
↪grid)
dose_diff_direct = grid_1.dose_grid - grid_2.dose_grid
dose_diff_interp = grid_1.dose_grid - grid_1.interp_entire_grid(grid_2)
```

CHAPTER

FOUR

DICOMPYLERCORE

4.1 dicomparser module

Class that parses and returns formatted DICOM RT data.

class dicompylercore.dicomparser.**DicomParser**(*dataset*, *memmap_pixel_array=False*)

Bases: object

Class to parse DICOM / DICOM RT files.

Initialize DicomParser from a pydicom Dataset or DICOM file.

Parameters

- **dataset** (*pydicom Dataset or filename*) – pydicom dataset object or DICOM file location
- **memmap_pixel_array** (*bool, optional*) – Enable pixel array access via memory mapping, by default False

Raises

- **AttributeError** – Raised if SOPClassUID is not present in the pydicom Dataset
- **AttributeError** – Raised if the DICOM file or pydicom Dataset cannot be read

GetSOPClassUID()

Determine the SOP Class UID of the current file.

GetSOPInstanceUID()

Determine the SOP Class UID of the current file.

GetStudyInfo()

Return the study information of the current file.

GetSeriesDateTime()

Return the series date/time information.

GetSeriesInfo()

Return the series information of the current file.

GetReferencedSeries()

Return the SOP Class UID of the referenced series.

GetFrameOfReferenceUID()

Determine the Frame of Reference UID of the current file.

GetReferencedStructureSet()

Return the SOP Class UID of the referenced structure set.

GetReferencedRTPlan()

Return the SOP Class UID of the referenced RT plan.

GetDemographics()

Return the patient demographics from a DICOM file.

GetImageData()

Return the image data from a DICOM file.

GetPixelArray()

Generate a memory mapped numpy accessor to the pixel array.

property get_pixel_array

Generate a memory mapped numpy accessor to the pixel array.

GetImageLocation()

Calculate the location of the current image slice.

GetImageOrientationType()

Get the orientation of the current image slice.

GetNumberOfFrames()

Return the number of frames in a DICOM image file.

GetRescaleInterceptSlope()

Return the rescale intercept and slope if present.

GetImage(*window=0*, *level=0*, *size=None*, *background=False*, *frames=0*)

Return the image from a DICOM image storage file.

Parameters

- **window** (*int, optional*) – Image window, by default 0
- **level** (*int, optional*) – Image level or width, by default 0
- **size** (*tuple, optional*) – Image size tuple in pixels, by default None
- **background** (*bool, optional*) – Enable a black image background, by default False
- **frames** (*int, optional*) – If multi-frame, use requested frame to generate image, by default 0

Returns
A Pillow Image object

Return type
Pillow Image

GetDefaultImageWindowLevel()

Determine the default window/level for the DICOM image.

GetLUTValue(*data*, *window*, *level*)

Apply the RGB Look-Up Table for the data and window/level value.

Parameters

- **data** (*numpy array*) – Pixel data array from pydicom dataset

- **window** (*float*) – Image window value
- **level** (*float*) – Image window level or width

Returns
Modified numpy array with RGB LUT applied

Return type
numpy array

`GetPatientToPixelLUT()`

Get image transformation matrix from the DICOM standard.

Referenced matrix can be found in Part 3 Section C.7.6.2.1.1

`GetStructureInfo()`

Return the patient demographics from a DICOM file.

`GetStructures()`

Return a dictionary of structures (ROIs).

`GetStructureCoordinates(roi_number)`

Get the list of coordinates for each plane of the structure.

Parameters
roi_number (*integer*) – ROI number used to index structure from RT Struct

Returns
Dict of structure coordinates sorted by slice position (z)

Return type
dict

`GetContourPoints(array)`

Unflatten a flattened list of xyz point triples.

Parameters
array (*list*) – Flattened list of xyz point triples

Returns
Unflattened list of xyz point triples

Return type
list

`CalculatePlaneThickness(planesDict)`

Calculate the plane thickness for each structure.

Parameters
planesDict (*dict*) – Output from GetStructureCoordinates

Returns
Thickness of the structure in mm

Return type
float

`CalculateStructureVolume(coords, thickness)`

Calculate the volume of the given structure.

Parameters

- **coords** (*dict*) – Coordinates of each plane of the structure

- **thickness** (*float*) – Thickness of the structure in mm

Returns
Volume of structure in cm3

Return type
float

`HasDVHs()`

Return whether dose-volume histograms (DVHs) exist.

`GetDVHs()`

Return cumulative dose-volume histograms (DVHs).

`GetDoseGrid`(*z=0*, *threshold=0.5*)

Return the 2d dose grid for the given slice position (mm).

Parameters

- **z** (*int, optional*) – Slice position in mm, by default 0
- **threshold** (*float, optional*) – Threshold in mm to determine the max difference from z to the closest dose slice without using interpolation, by default 0.5

Returns
An numpy 2d array of dose points

Return type
np.array

`InterpolateDosePlanes`(*uplane*, *lplane*, *fz*)

Interpolate a dose plane between two bounding planes.

Parameters

- **uplane** (*float*) – Upper dose plane boundary in mm
- **lplane** (*float*) – Lower dose plane boundary in mm
- **fz** (*float*) – Fractional distance from the bottom to the top, where the new plane is located. E.g. if fz = 1, the plane is at the upper plane, fz = 0, it is at the lower plane.

Returns
An numpy 2d array of the interpolated dose plane

Return type
numpy array

`is_head_first_orientation()`

Return True if self.orientation is head-first.

Raises
NotImplementedError – Raised if orientation is not one of head/feet-first and supine/prone/decubitus

Returns
True if orientation is head-first, else False

Return type
bool

`x_lut_index()`

Return LUT index for real-world X direction.

Raises
`NotImplementedError` – Raised if orientation is not one of head/feet-first and supine/prone/decubitus

Returns
0 if real-world X across columns 1 if real-world X along rows

Return type
X direction LUT index, matching 'lut' from GetDoseData

`GetIsodosePoints(z=0, level=100, threshold=0.5)`

Return dose grid points from an isodose level & slice position.

Parameters

- `z` (*int, optional*) – Slice position in mm., by default 0
- `level` (*int, optional*) – Isodose level in scaled form (multiplied by self.ds.DoseGridScaling), by default 100
- `threshold` (*float, optional*) – Threshold in mm to determine the max difference from z to the closest dose slice without using interpolation, by default 0.5

Returns
An list of tuples representing isodose points

Return type
list

`GetDoseData()`

Return the dose data from a DICOM RT Dose file.

`GetReferencedBeamNumber()`

Return the referenced beam number (if it exists) from RT Dose.

`GetPlan()`

Return the plan information.

`GetReferencedBeamsInFraction(fx=0)`

Return the referenced beams from the specified fraction.

Parameters
`fx` (*int, optional*) – FractionGroupSequence number, by default 0

Returns
Dictionary of referenced beam data

Return type
dict

4.2 dvh module

Class that stores dose volume histogram (DVH) data.

class dicompylercore.dvh.**DVH**(*counts*, *bins*, *dvh_type='cumulative'*, *dose_units='Gy'*, *volume_units='cm3'*, *rx_dose=None*, *name=None*, *color=None*, *notes=None*)

Bases: object

Class that stores dose volume histogram (DVH) data.

Initialization for a DVH from existing histogram counts and bins.

Parameters

- **counts** (*iterable or numpy array*) – An iterable of volume or percent count data
- **bins** (*iterable or numpy array*) – An iterable of dose bins
- **dvh_type** (*str, optional*) – Choice of 'cumulative' or 'differential' type of DVH
- **dose_units** (*str, optional*) – Absolute dose units, i.e. 'gy' or relative units '%'
- **volume_units** (*str, optional*) – Absolute volume units, i.e. 'cm3' or relative units '%'
- **rx_dose** (*number, optional*) – Prescription dose value used to normalize dose bins (in Gy)
- **name** (*String, optional*) – Name of the structure of the DVH
- **color** (*numpy array, optional*) – RGB color triplet used for plotting the DVH
- **notes** (*String, optional*) – Additional notes about the DVH instance

classmethod from_dicom_dvh(*dataset*, *roi_num*, *rx_dose=None*, *name=None*, *color=None*)

Initialization for a DVH from a pydicom RT Dose DVH sequence.

classmethod from_data(*data*, *binsize=1*)

Initialization for a DVH from raw data.

Parameters

- **data** (*iterable or numpy array*) – An iterable of dose data that is used to create the histogram
- **binsize** (*int, optional*) – Bin width size (in cGy used to create the histogram)

property bincenters

Return a numpy array containing the bin centers.

property differential

Return a differential DVH from a cumulative DVH.

property cumulative

Return a cumulative DVH from a differential DVH.

absolute_dose(*rx_dose=None*, *dose_units='Gy'*)

Return an absolute dose DVH.

Parameters

- **rx_dose** (*number, optional*) – Prescription dose value used to normalize dose bins
- **dose_units** (*str, optional*) – Units for the absolute dose

Raises
AttributeError – Description

relative_dose(*rx_dose=None*)

Return a relative dose DVH based on a prescription dose.

Parameters
rx_dose (*number, optional*) – Prescription dose value used to normalize dose bins

Raises
AttributeError – Raised if prescription dose was not present either during class initialization or passed via argument.

absolute_volume(*volume*, *volume_units='cm3'*)

Return an absolute volume DVH.

Parameters

- **volume** (*number*) – Absolute volume of the structure
- **volume_units** (*str, optional*) – Units for the absolute volume

property relative_volume

Return a relative volume DVH.

property max

Return the maximum dose.

property min

Return the minimum dose.

property mean

Return the mean dose.

property volume

Return the volume of the structure.

describe()

Describe a summary of DVH statistics in a text based format.

compare(*dvh*)

Compare the DVH properties with another DVH.

Parameters
dvh (DVH) – DVH instance to compare against

Raises
AttributeError – If DVHs do not have equivalent dose & volume units

plot()

Plot the DVH using Matplotlib if present.

volume_constraint(*dose*, *dose_units=None*)

Calculate the volume that receives at least a specific dose.

i.e. V100, V150 or V20Gy

Parameters
dose (*number*) – Dose value used to determine minimum volume that receives this dose. Can either be in relative or absolute dose units.

Returns
Volume in self.volume_units units.

Return type
number

`dose_constraint`(*volume*, *volume_units=None*)

Calculate the maximum dose that a specific volume receives.

i.e. D90, D100 or D2cc

Parameters
volume (*number*) – Volume used to determine the maximum dose that the volume receives. Can either be in relative or absolute volume units.

Returns
Dose in self.dose_units units.

Return type
number

`statistic`(*name*)

Return a DVH dose or volume statistic.

Parameters
name (*str*) – DVH statistic in the form of D90, D100, D2cc, V100 or V20Gy, etc.

Returns
Value from the dose or volume statistic calculation.

Return type
number

`class dicompylercore.dvh.DVHValue`(*value*, *units=''*)

Bases: `object`

Class that stores DVH values with the appropriate units.

Initialization for a DVH value that will also store units.

4.3 dvhcalc module

Calculate dose volume histogram (DVH) from DICOM RT Structure/Dose data.

`dicompylercore.dvhcalc.get_dvh`(*structure*, *dose*, *roi*, *limit=None*, *calculate_full_volume=True*, *use_structure_extents=False*, *interpolation_resolution=None*, *interpolation_segments_between_planes=0*, *thickness=None*, *memmap_rtdose=False*, *callback=None*)

Calculate a cumulative DVH in Gy from a DICOM RT Structure Set & Dose.

Parameters

- **structure** (*pydicom Dataset or filename*) – DICOM RT Structure Set used to determine the structure data.
- **dose** (*pydicom Dataset or filename*) – DICOM RT Dose used to determine the dose grid.
- **roi** (*int*) – The ROI number used to uniquely identify the structure in the structure set.
- **limit** (*int, optional*) – Dose limit in cGy as a maximum bin for the histogram.

- **calculate_full_volume** (*bool, optional*) – Calculate the full structure volume including contours outside of the dose grid.
- **use_structure_extents** (*bool, optional*) – Limit the DVH calculation to the in-plane structure boundaries.
- **interpolation_resolution** (*tuple or float, optional*) – Resolution in mm (row, col) to interpolate structure and dose data to. If float is provided, original dose grid pixel spacing must be square.
- **interpolation_segments_between_planes** (*integer, optional*) – Number of segments to interpolate between structure slices.
- **thickness** (*float, optional*) – Structure thickness used to calculate volume of a voxel.
- **memmap_rtdose** (*bool, optional*) – Use memory mapping to access the pixel array of the DICOM RT Dose. This reduces memory usage at the expense of increased calculation time.
- **callback** (*function, optional*) – A function that will be called at every iteration of the calculation.

Returns
An instance of dvh.DVH in cumulative dose. This can be converted to different formats using the attributes and properties of the DVH class.

Return type
dvh.DVH

dicompylercore.dvhcalc.**calculate_plane_histogram**(*plane*, *doseplane*, *dosegridpoints*, *maxdose*, *dd*, *id*, *structure*, *hist*)

Calculate the DVH for the given plane in the structure.

dicompylercore.dvhcalc.**get_contour_mask**(*dd*, *id*, *dosegridpoints*, *contour*)

Get the mask for the contour with respect to the dose plane.

dicompylercore.dvhcalc.**calculate_contour_dvh**(*mask*, *doseplane*, *maxdose*, *dd*, *id*, *structure*)

Calculate the differential DVH for the given contour and dose plane.

dicompylercore.dvhcalc.**structure_extents**(*coords*)

Determine structure extents in patient coordinates.

Parameters
coords (*dict*) – Structure coordinates from dicomparser.GetStructureCoordinates.

Returns
Structure extents in patient coordintes: [xmin, ymin, xmax, ymax].

Return type
list

dicompylercore.dvhcalc.**dosegrid_extents_indices**(*extents*, *dd*, *padding=1*)

Determine dose grid extents from structure extents as array indices.

Parameters

- **extents** (*list*) – Structure extents in patient coordinates: [xmin, ymin, xmax, ymax]. If an empty list, no structure extents will be used in the calculation.
- **dd** (*dict*) – Dose data from dicomparser.GetDoseData.
- **padding** (*int, optional*) – Pixel padding around the structure extents.

Returns
Dose grid extents in pixel coordinates as array indices: [col_min, row_min, col_max, row_max].

Return type
list

dicompylercore.dvhcalc.**dosegrid_extents_positions**(*extents*, *dd*)

Determine dose grid extents in patient coordinate indices.

Parameters

- **extents** (*list*) – Dose grid extents in pixel coordintes: [col_pos_min, row_pos_min, col_pos_max, row_pos_max].
- **dd** (*dict*) – Dose data from dicomparser.GetDoseData.

Returns
Dose grid extents in patient coordintes: [xmin, ymin, xmax, ymax].

Return type
list

dicompylercore.dvhcalc.**get_resampled_lut**(*index_extents*, *extents*, *new_pixel_spacing*, *min_pixel_spacing*)

Determine the patient to pixel LUT based on new pixel spacing.

Parameters

- **index_extents** (*list*) – Dose grid extents as array indices.
- **extents** (*list*) – Dose grid extents in patient coordinates: [col_pos_min, row_pos_min, col_pos_max, row_pos_max].
- **new_pixel_spacing** (*tuple or float*) – New pixel spacing in mm (row, column). If float is provided, original dose grid pixel spacing must be square.
- **min_pixel_spacing** (*tuple*) – Min pixel spacing used to determine new pixel spacing (row, column).

Returns
A tuple of lut lists (col lut, row lut) with the coordinates of the dose grid in patient coordinates

Return type
tuple

Raises
AttributeError – Raised if the new pixel_spacing is not a factor of the minimum pixel spacing.

Notes

The new pixel spacing must be a factor of the original (minimum) pixel spacing. For example if the original pixel spacing was 3 mm, the new pixel spacing should be: `3 / (2^n)` mm, where `n` is an integer. This applies independently to both the row and column pixel spacing.

If a single float value is provided it will be applied to both row and column. Additionally, the original dose grid pixel spacing must be square.

Examples

Original pixel spacing: 3 mm, new pixel spacing: 0.375 mm Derived via: (3 / 2^16) == 0.375

dicompylercore.dvhcalc.**get_interpolated_dose**(*dose*, *z*, *resolution*, *extents*)

Get interpolated dose for the given z, resolution & array extents.

Parameters

- **dose** (DicomParser) – A DicomParser instance of an RT Dose.
- **z** (*float*) – Index in mm of z plane of dose grid.dose
- **resolution** (*tuple*) – Interpolation resolution less than or equal to dose grid pixel spacing. Provided in (row, col) format.
- **extents** (*list*) – Dose grid index extents.

Returns
Interpolated dose grid with a shape larger than the input dose grid.

Return type
ndarray

dicompylercore.dvhcalc.**interpolate_between_planes**(*planes*, *n=2*)

Interpolate n additional structure planes (segments) in between planes.

Parameters

- **planes** (*dict*) – RT Structure plane data from dicomparser.GetStructureCoordinates.
- **n** (*int, optional*) – Number of planes to interpolate in between the existing planes.

Returns
Plane data with additional keys representing interpolated planes.

Return type
dict

4.4 dose module

Routines to access and modify DICOM RT Dose.

class dicompylercore.dose.**DoseGrid**(*rt_dose*, *order=1*, *mode='constant'*, *cval=0.0*)

Bases: object

Class that stores DICOM-RT dose grids, performs addition/scaling.

Initialization of a DoseGrid from a DICOM-RT Dose file or dataset.

Parameters

- **rt_dose** (*pydicom Dataset or filename*) – DICOM RT Dose used to determine the structure dose grid data.
- **order** (*int, optional*) – The order of the spline interpolation (if needed), default is 1. The order has to be in the range 0-5. 0: the nearest grid point, 1: trilinear, 2 to 5: spline See scipy.ndimage.map_coordinates documentation for more details
- **mode** (*'constant' or 'nearest', optional*) – The mode parameter determines how the other dose grid is extended beyond its boundaries. Default is 'constant'. Behavior for these values is as follows:

'constant' (k k k k | a b c d | k k k k)
The other dose grid is extended by filling all values beyond the edge with the same constant value, defined by the cval parameter.

'nearest' (a a a a | a b c d | d d d d)
The input is extended by replicating the last pixel.

Additional modes are available, see scipy.ndimage.map_coordinates documentation for more details.

- **cval** (*scalar, optional*) – Value to fill past edges of input if mode is 'constant'. Default is 0.0.

property shape

Get the x, y, z dimensions of the dose grid

property axes

Get the x, y, z axes of the dose grid (in mm)

property scale

Get the dose grid resolution (xyz)

property offset

Get the coordinates of the dose grid origin (mm)

property max_boundary_dose

Get the max boundary dose

property max_boundary_relative_dose

multiply(*factor*)

Scale the dose grid.

Parameters
factor (*int, float*) – Multiply the dose grid by this factor.

dose_grid_post_processing(*other=None*)

Set the pixel data and store UIDs from other DoseGrid

is_coincident(*other*)

Check dose grid spatial coincidence.

Parameters
other (DoseGrid) – Another DoseGrid object.

set_pixel_data()

Update the PixelData with the current dose_grid

save_dcm(*file_path*)

Save the pydicom.FileDataset to file

get_ijk_points(*other_axes*)

Convert axes from another DoseGrid into ijk of this DoseGrid.

Parameters
other_axes (*list*) – The x, y, and z axis arrays.

Returns
Array of other_axes in this ijk space.

Return type
np.vstack

add(*other*, *force=False*)

Add another dose grid to this dose grid, with interpolation if needed

Parameters

- **other** (DoseGrid) – Another DoseGrid object.
- **force** (*bool*) – Set to True to ignore differences in DoseSummationType, DoseType, DoseUnits, ImageOrientationPatient

interp_entire_grid(*other*)

Interpolate the other dose grid to this dose grid's axes in one operation

Parameters
other (DoseGrid) – Another DoseGrid object.

Returns
The other dose grid interpolated to this dose grid's axes

Return type
np.array

update_dicom_tags()

Update DICOM UIDs, Content Date/Time, and Dose Comment

show(*z=None*)

Show the dose grid using Matplotlib if present.

Parameters
z (*float, optional*) – slice position to display initially, by default None

dicompylercore.dose.**set_dicom_tag_value**(*ds*, *tag*, *value*)

Set or update a DICOM tag value in the pydicom dataset.

Parameters

- **ds** (*pydicom Dataset*) – The pydicom dataset for the tag to be added/updated to.
- **tag** (*str, int or tuple*) – DICOM tag or keyword to be added.
- **value** (*any*) – New value for the tag's element.

dicompylercore.dose.**add_dicom_sequence**(*ds*, *seq_keyword*, *data_set_dict*)

Add a sequence to a data set.

Parameters

- **ds** (*pydicom Dataset*) – The pydicom dataset for the sequence to be added to.
- **seq_keyword** (*str*) – The DICOM keyword for the sequence.
- **data_set_dict** (*dict*) – Dictionary of tags and values for the sequence element.

dicompylercore.dose.**validate_attr_equality**(*obj_1*, *obj_2*, *attr*)

Assess the equality of the provided attr between two objects. Send warning if unequal.

Parameters

- **obj_1** (*object*) – Any object with an *attr* attribute that is comparable by !=
- **obj_2** (*object*) – Any object with an *attr* attribute that is comparable by !=

- **attr** (*str*) – The attribute to be compared between obj_1 and obj_2

dicompylercore.dose.**max_boundary_value**(*arr*)

Get the greatest value on the boundary of a 3D numpy array

Parameters
arr (*numpy.array*) – Any 3-dimensional array-like object

Returns
Maximum value along any side of the input array

Return type
float

CHAPTER

FIVE

CONTRIBUTING

Contributions are welcome, and they are greatly appreciated! Every little bit helps, and credit will always be given.

You can contribute in many ways:

5.1 Types of Contributions

5.1.1 Report Bugs

Report bugs at https://github.com/dicompyler/dicompyler-core/issues.

If you are reporting a bug, please include:

- Your operating system name and version.
- Any details about your local setup that might be helpful in troubleshooting.
- Detailed steps to reproduce the bug.

5.1.2 Fix Bugs

Look through the GitHub issues for bugs. Anything tagged with "bug" is open to whoever wants to implement it.

5.1.3 Implement Features

Look through the GitHub issues for features. Anything tagged with "feature" is open to whoever wants to implement it.

5.1.4 Write Documentation

dicompyler-core could always use more documentation, whether as part of the official dicompyler-core docs, in docstrings, or even on the web in blog posts, articles, and such.

5.1.5 Submit Feedback

The best way to send feedback is to file an issue at https://github.com/dicompyler/dicompyler-core/issues.

If you are proposing a feature:

- Explain in detail how it would work.
- Keep the scope as narrow as possible, to make it easier to implement.
- Remember that this is a volunteer-driven project, and that contributions are welcome :)

5.2 Get Started!

Ready to contribute? Here's how to set up *dicompyler-core* for local development.

1. Fork the *dicompyler-core* repo on GitHub.
2. Clone your fork locally:

```
$ git clone git@github.com:your_name_here/dicompyler-core.git
```

3. Install your local copy into a virtualenv. Assuming you have virtualenvwrapper installed, this is how you set up your fork for local development:

```
$ mkvirtualenv dicompyler-core
$ cd dicompyler-core/
$ python setup.py develop
```

4. Create a branch for local development:

```
$ git checkout -b name-of-your-bugfix-or-feature
```

   Now you can make your changes locally.

5. When you're done making changes, check that your changes pass flake8 and the tests, including testing other Python versions with tox:

```
$ flake8 dicompyler-core tests
$ python -m unittest discover -v
$ tox
```

   To get flake8 and tox, just pip install them into your virtualenv.

6. Commit your changes and push your branch to GitHub:

```
$ git add .
$ git commit -m "Your detailed description of your changes."
$ git push origin name-of-your-bugfix-or-feature
```

7. Submit a pull request through the GitHub website.

5.3 Pull Request Guidelines

Before you submit a pull request, check that it meets these guidelines:

1. The pull request should include tests.
2. If the pull request adds functionality, the docs should be updated. Put your new functionality into a function with a docstring, and add the feature to the list in *README.rst*.
3. The pull request should work for Python versions listed in *README.rst*. Check that your pull request passes for all supported Python versions.

5.4 Tips

To run a subset of tests:

```
$ python -m unittest tests.test_dicompyler-core
```

CHAPTER

SIX

CREDITS

6.1 Development Lead

- Aditya Panchal

6.2 Contributors

- Roy Keyes (Original co-author of dicompyler)
- See *History* for additional contributors

CHAPTER

SEVEN

HISTORY

7.1 0.5.7 (unreleased)

- Dropped support for Python 2.

7.2 0.5.6 (2023-05-08)

Warning: This version will be the last version to support Python 2.x and support will be dropped in version 0.5.7.

- Dropped support for Python 3.5 & 3.6 and added support for Python 3.9 & 3.10.
- Made changes to codebase to support recent versions of numpy, Shapely and scikit-image dependencies.
- Added `dose` module with `DVH` class for Pythonic access to RT Dose. (#164) [Dan Cutright]
- Added decubitus orientation and related changes. (#285) [Darcy Mason]
- Fix a bug if Pixel Data attribute was set for non image based SOP Classes (i.e. RT Structure Set). (#214) [Dan Cutright]

7.2.1 dvhcalc

- Implement interpolation for non square pixels in DVH calculation. (#124)
- Fix a bug where the DVHDoseScaling attribute was not applied properly to RT Dose DVHs. (#301) [Christian Velten]
- Fix a bug where floating point pixel spacing wasn't rounded in DVH calculations. (#318) [Samuel Ouellet]

7.2.2 dose

- Added RT Dose grid summmation with interpolation (from DVHA). (#164) [Dan Cutright]

7.2.3 dicomparser

- Initial implementation of memory mapped access to pixel data. (#131)
- Ensure that all files read have a valid File Meta header.

7.3 0.5.5 (2019-05-31)

7.3.1 dvhcalc

- Refactored bounding & resampling set up code to only execute if conditions are met.
- Fix a bug where the resampled LUT was not calculated correctly for DVH interpolation.

7.3.2 dvh

- Differential DVH calculation modified. (#60) [Hideki Nakamoto]
- Fix an issue with D100 not returning 0 Gy. (#74) [Gabriel Couture]
- Preserve global maximum dose. (#106) [Akihisa Wakita]

7.3.3 dicomparser

- Remove the test for existence of *ContourImageSequence* in *GetStructureCoordinates*. (#81) [Gabriel Couture]
- Utilize integer division when generating a background for an image.
- Return a string for the patient's name as *PersonName3* cannot be serialized.
- Fix a bug to return a referenced FoR if the FrameOfReference is blank.
- Fix a bug in *GetPlan* where the wrong object names were used. (#43) [gertsikkema]
- Ensure that Rx Dose from RT Plan is rounded instead of truncated.
- Account for holes and bifurcated structures for structure volume calculation.
- Implement structure volume calculation using Shapely.
- Fix window calculation if not present in header.
- Add checks in max, mean, min and dose_constraint for case where counts array is empty or all 0's. (#96) [Nicolas Galler]

7.4 0.5.4 (2018-04-02)

7.4.1 dvhcalc

- Implemented DVH interpolation. (#39)
- Implemented optional user-specified structure thickness for DVH calculation.

7.4.2 dvh

- Fix a bug in absolute_volume if a DVH instance's volume units don't use default of Gy.
- Fix a bug in absolute_dose if a DVH instance's dose units don't use default of Gy. (#19)
- Support decimal values for volume constraints (i.e.V71.6).
- Support decimal values for dose constraints (i.e. D0.03cc).

7.4.3 dicomparser

- Ensure that Rx Dose from RT Plan is rounded instead of truncated.
- Account for holes and bifurcated structures for structure volume calculation.
- Implement structure volume calculation using Shapely. (#28)

7.5 0.5.3 (2017-08-03)

- Added support for plotting structure colors.
- Support Python 2 unicode filenames in dicomparser.
- Support DVH calculation of structures partially covered by the dose grid.

7.6 0.5.2 (2016-07-25)

- Added `DVH` class for Pythonic access to dose volume histogram data.
- Refactored and added unit tests for dvhcalc.
- Added examples and usage for `dvh` and `dvhcalc` modules.
- Jupyter notebook of examples can be found in Binder:

7.7 0.5.1 (2016-02-17)

- Added support for pydicom 0.9.9 so releases from PyPI can be built.

7.8 0.5.0 (2016-02-11)

- First release on PyPI.

CHAPTER

EIGHT

INDICES AND TABLES

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PYTHON MODULE INDEX

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