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Technical note

Espadon, an R package for automation, exploitation and processing of DICOM files in medical physics and clinical research



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ABSTRACT

Introduction: One of the main issues in the field of clinical research is to enhance clinical databases with information from imaging (CT, MR, PET-scan), contouring (RTstruct), or produced by TPS such as dose distribution (RTdose) or treatment plans (RTplan). To perform these analyses automatically, we propose the new open-source package “espadon”, developed in R environment. This package also opens up numerous perspectives for TPS-independent calculation, automation and processing of DICOM data.

Results: The espadon package converts DICOM objects into espadon objects. Several tools have been developed to manipulate these objects and extract the desired information. In addition to decode DICOM files and pseudonymize them, the great advantage of espadon is that it presents the links between patient data (images, structures, treatment plans) in a didactic way, respecting the dates of the examinations. It can visualize volumes or structures in 2D or 3D, resample volumes, segment them, and change geometric frames of reference. It integrates dose-volume histogram functions on a selection, with Monte Carlo calculations of random shifts of contours. It offers the automatic calculation of several usual radiotherapy indices, as well as the calculation of Gamma and Chi indices.

Conclusions: Espadon is a toolkit designed to be easily used by radiotherapists, medical physicists or students. Espadon’s functions are implemented in an R script, and allow the automatic extraction or calculation of data from DICOM files, which can be used for statistical modelling or machine-learning in the R environment. This package is available on the Comprehensive R Archive Network (CRAN) repository.

1. Introduction

Cancer research is focused on answering an important question: what treatment can kill cancer cells while preserving healthy organs? [1,2] Indeed, finding the influencing factors of the responses to a treatment is one of the key issues to optimize the treatment proposed for a specific patient and its post-treatment management. Espadon (acronym of Easy Study of PATient Dicom data in ONcology) has been developed in the framework of this research. Its objective is to enhance clinical databases, generally containing the outcomes and pathways of patients, with objective data from imaging, dose distribution and treatment geometry or organ location in relation to the tumor.

Espadon is a package proposed under the R [3] environment, which is also a very suitable language for statistical studies, data mining, machine learning and database creation. It is available for free on the Comprehensive R Archive Network (CRAN) repository [4]. Espadon is a coherent and logical set of functions that can be easily implemented in a study automation script. It allows to manipulate and visualize DICOM

objects, and to systematically calculate most of the usual radiotherapy indices. Espadon can also manipulate the raw data of DICOM files: for example, it has been used in ArDCore [5] software that automatically pseudonymizes and sorts patient DICOM files.

In this article, we will use simple examples to illustrate how the espadon package can be used to access or compute information of interest to research actors in radiotherapy.

2. Methods

Espadon was designed and authored by Cathy Fontbonne and Jean-Marc Fontbonne, with Nathan Azemar as contributor. It is a package written in R language, with some functions using C++ for better performances. The package uses the capabilities offered by other packages: for example qs [6] for data storage, rgl [7] for 3D visualization, Rvcg [8] for area calculation, stats [3] for statistical functions, but also sp [9], grDevices, graphics [3]...

As the objective of espadon is to study DICOM exports related to

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radiotherapy, the package is first able to decode a DICOM file into an R data.frame or R list. It also includes a function to modify the ASCII fields of the DICOM file.

Espadon incorporates a tag dictionary, which can be called using the `dicom.tag.dictionary()` function. The tag dictionary is defined by the nema standard [10]. It can be completed, as needed, by constructor dictionaries. In addition to the NEMA standard dictionary, the espadon package provides the Raysearch Laboratories dictionary [11] by default.

Espadon then interprets all the DICOM files by creating espadon objects that belong to specific classes. The class of an object ensures how the object is used by the espadon functions, and thus simplifies their use. Each object of a specific class contains information (fields) that are necessary for the use of that object. For example, RTdose dose distribution, CT and MRI scans create objects of the volume class. This class necessarily includes the number of voxels in the three dimensions of space, the size of the voxel in millimeters, the value (if requested) and the unit of each voxel, as well as the information to locate this volume in space. The DICOM RTstruct files form struct class objects that necessarily include a table of information about the regions of interest (name, color of the RoI in the DICOM file, but also calculated data such as volume, barycenter, coordinates of the end points) and a list with the coordinates of the contours in space.

In the current version there are other object classes, which are listed by calling the `espadon.class()` function and explained in the help page accessible by the command `help(espadon.class)`. One of the important classes is the “patient” class. A patient object contains not only a description of all the patient’s examinations, the examinations themselves sorted by modality, but also a `t.mat` class object managing the spatial registrations. To simplify the management of geometric reference frames, the espadon package automatically assigns to each reference frame defined by the DICOM tag (0020,0052) a pseudonym “ref1” then “ref2”... Each DICOM object loaded is then assigned a new alias by default, consisting of, among other things, its study date, the pseudonym of its reference frame, and its modality. This new alias makes it possible to quickly visualize the chronology of a patient’s examinations, as well as the links that exist between them.

As the interpretation of DICOM data to create an espadon object can be a long process, the package proposes to convert DICOM files into *.Rdcm files with the function `dicom.to.Rdcm.converter()`. The backup of the object being performed with the `qs` package, the speed of access to the data as well as the amount of memory necessary for the backup are considerably improved. As a comparison, a database including the imaging and dose distribution data of 441 patients uses 239 GB of memory for 324,164 DICOM files, and uses only 79.5 GB for 4499 Rdcm files. Considering now the data of a single patient including 2 CT-scan, 5 RTdose, 2 RTplan, 2 RTstruct, the data are loaded entirely in 130 s from the 907 DICOM files (717 MB) with the function `load.patient.from.dicom()`, compared to 21 s from the 11 Rdcm files (248 MB) with the function `load.patient.from.Rdcm()`. In this second case, it is nevertheless necessary to perform a one-time 114 s conversion from DICOM files to Rdcm files beforehand with the function `dicom.to.Rdcm.converter()`. The measurements were performed on computer with Intel Core i9 CPU (2.40 GHz) and 64 GB of system memory, running 64-bit Microsoft Windows 10 Professional. The complete content of a *.Rdcm file can be accessed with the function `load.Rdcm.raw.data()`. It is a list composed of, among other things, a “header” list containing interpreted data (e.g. name of the patient, number of voxels or number of contours, etc.), an “address” list giving the addresses of the content of the DICOM tags in the raw data of the DICOM file, and a “data” list giving the list of exports in the R-list of the various DICOM files making up the object.

Espadon’s primary objective is to facilitate quality control of patient data. Several display functions with palette management and view overlays are available.

Espadon will also allow the creation of new objects that have not been created by the TPS: RTstruct, differential histogram, dose-volume histogram (DVH), and meshes. It has several tools for resampling

imaging volumes or reducing volumes to focus on the area of interest and speed up calculations. Binary volumes can define regions of interest, creating a new “binary” modality. Operations on binary volumes such as logical, morpho-mathematical or segmentation operations are proposed, allowing the user to make new selections undefined in the original data.

Finally, espadon will allow the calculation of most of the radiotherapy indices such as Prescription Isodose Target Volume (PITV), Prescription Dose Spillage (PDS), Conformity Index (CI), Conformity Number (CN), New conformity index (NCI), Dice Similarity Coefficient (DSC), Conformity Distance Index (CDI), Triple Point Conformity Scale (CS3), Underdosed lesion factor (ULF), Overdosed healthy tissues factor (OHTF), Geometric Conformity Index (gCI), COIN Conformity Index, generalized COSI, several Homogeneity Index (HI), Gradient Index (GI) and modified Gradient Index (mGI). All these indices are compiled by Kaplan et al. [12] and Patel et al. [13] and referenced in the reference manual of espadon package.

With the functions `rt.gamma.index()` and `rt.chi.index()`, the espadon package can also compute, on a 3D volume or 2D image, the γ -index and χ -index, as defined by Low et al. [14] and Bakai et al. [15] respectively.

3. Results

In this section, we will focus on a few example applications that provide a quick understanding of how to exploit espadon features to understand and control a patient’s imaging and dose distribution data, and to calculate the usual indicators in radiation therapy. We have the DICOM data of patient A, consisting of a CT scan, an MRI, three RTdose, an RTplan, two RTstruct, and a registration matrix.

The DICOM files of patient A are pseudonymised data, generated by the `dicom.raw.data.anonymizer()` function of the espadon package. This function replaced the patient’s name and identifier with a user-selected string, removed all other patient data except age, weight, height, gender, and birthday, shifted all dates by a selected number of days, removed all address, phone, physician, operator, author, reviewer, and department data. More generally, the `dicom.set.tag.value()` function can be used to modify the content of any tag, provided that this content is a character string.

Appendix A provides the instructions that were used to generate the CT, MR, RTdose displays, DVH numbers and index calculations in this paper.

3.1. Loading and displaying patient imaging and dose distribution data

The data from patient A is loaded into memory by creating a “patient” class object, either by the simple function `load.patient.from.dicom()`, or, if it is preferable to convert the data into pre-formatted Rdcm data for faster later use, by using the functions `dicom.to.Rdcm.converter()` followed by `load.patient.from.Rdcm()`. To manage memory space, objects can only be partially loaded, depending on whether the data argument is TRUE or FALSE. If FALSE, the objects of the volume class, for example, will be missing the values of the voxels (`$vol3D.data` field), which can then be loaded using the `load.obj.data()` function. In all cases, the links between the objects contained in the espadon class object “patient” can be represented using the `display.obj.links()` function, taking into account the spatial registrations (Fig. 1a) or not (Fig. 1b).

The loaded objects can easily be represented by espadon in any reference frame. For example, patient A has a CT scan and an MRI scan with different geometric reference frames. Fig. 2 shows different views obtained with the `display.plane()` function of the CT or MRI, with superposition of the dose and PTV contour.

Fig. 3 shows the use of espadon 3D functions: the display of the PTV contours (`display.3D.contour()` function), the stacking of the selected MRI planes in space (`display.3D.stack()` function), and the three cross-sections, frontal and sagittal at a given point (`display.3D.sections()` function).

The user has the choice to create his/her own color palette. However

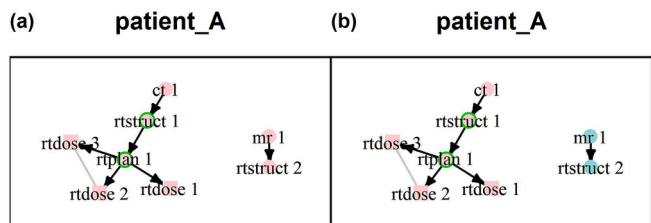


Fig. 1. Links between the different objects, defined by the `display.obj.link()` function. The arrows indicate the objects that have been used to build another object. The lines indicate that the objects are sub-objects belonging to the same object. The objects with a green outline are approved for treatment. (a) The argument `group.by.connected.For` is set to `TRUE`: all the objects that are connected by a spatial registration are represented with the same color. (b) The argument `group.by.connected.For` is set to `FALSE`: the objects having a different frame of reference have a different color. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

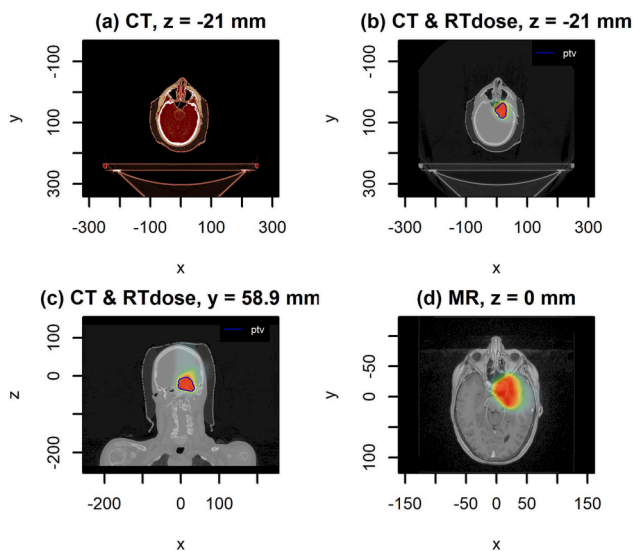


Fig. 2. (a) Display of the CT transverse view with palette `pal.RVV` [16]. Display of transverse (b) and frontal (c) overlap of CT, RTdose, and the PTV contour. (d) Overlap of transverse view of the MR, and RTdose in the MR frame of reference.

espadon also proposes the use of the `pal.RVV` palette in which Hounsfield units in the range -1000 HU to 1000 HU are converted to realistic colors, as defined by J.C. Silverstein et al [16].

3.2. Histograms computation and radiotherapy indices

Espadon allows to compute very quickly differential histograms of volume class objects in predefined areas either by a region of interest (RoI) coming from an `RTstruct` file with the function `histo.from.roi()`, or by a selection by binary volume with the `histo.from.bin()` function. In addition, the `histo.from.roi()` function can simulate random displacements of the contours according to a normal distribution, by Monte Carlo method.

Fig. 4 illustrates the result of computing the dose-volume histogram of a small RoI in the `RTstruct` file of patient A: the chiasma. In this example, the `histo.from.roi()` function first calculates the differential histogram with a Monte Carlo simulation on 100 samples (argument `MC`). The cumulative histogram, called in this case the dose-volume histogram or DVH, is then calculated using the `histo.DVH()` function. The `display.DVH()` and `display.DVH.pc()` functions are used to display clear graphs of the DVH, including the 100%, 95% and 50% quantile areas of the Monte Carlo data.

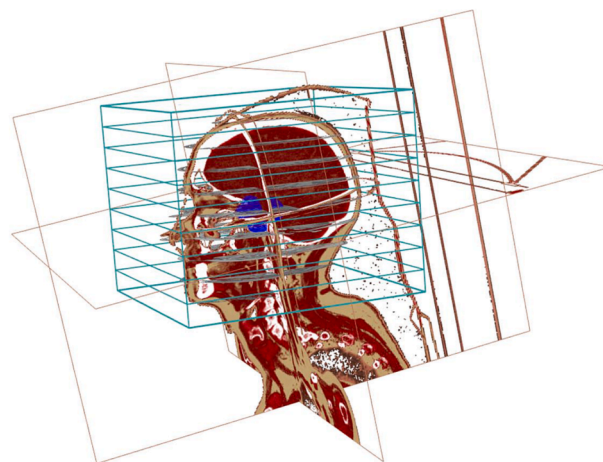


Fig. 3. 3D Display in CT frame of reference using three espadon functions: - `display.3D.contour` for the PTV contour display in blue, - `display.3D.sections` for transverse, frontal and sagittal views, with palette `pal.RVV` [16] and transparency management, - `display.3D.stack` for display of some MR slices in the default grayscale palette. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

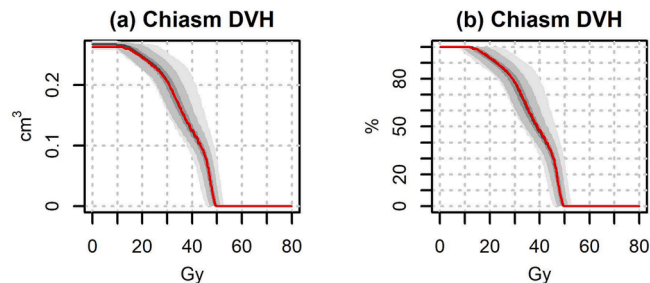


Fig. 4. Use of the `display.DVH()` and `display.DVH.pc()` functions to display the optic chiasm DVH in cm^3 (a) or % (b), with a simulation of a shift of 1 mm in all directions. The grey areas represent from lightest to darkest, respectively, the 100%, 95% and 50% quantiles of the MC data.

It may be convenient to compute only a few dose points in the DVH. This is done by means of the `rt.indices.from.roi()` function. Table 1 gives for example the mean dose and D.5%, D.95%, D0.1cc and D0.2cc dose point values:

The `rt.indices.from.roi()` and `rt.indices.from.bin()` functions actually provide the ability to compute many more radiotherapy indices. By providing the RTdose volume, the prescription dose, the target volumes to be treated (e.g., the different PTVs, depending on which function is used either as RoI in an `RTstruct` or as a binary volume), and the healthy volumes to be protected, it is possible, as shown in Table 2, to compute the Prescription Isodose Target Volume (PITV) as defined by E.Shaw [17], and the Prescription Dose Spillage (PDS) as defined by the SABR UK Consortium 2019 [18].

The available conformity, homogeneity and gradient indices are all defined and referenced in the reference manual of espadon package.

Table 1

Field `$dosimetry` obtained with `rt.indices.from.roi()` fonction, with arguments `healthy.roi.sname = "chiasm"`, `dosimetry = "D.mean"`, `D.xpc = c(5,95)`, `D.xcc = c(0.1,0.2)`, `volume.indices = ""`, `conformity.indices = ""`, `homogeneity.indices = ""` and `gradient.indices = ""`.

<code>\$dosimetry</code>	D.mean	D.5%	D.95%	D0.1cc	D0.2cc
Chiasma	37.46	48.59	18.83	43.34	30.85

Table 2

Use of the function `rt.indices.from.roi()`, with the PTV as target region of interest (RoI), chiasma as healthy RoI, and 48.77 Gy as prescription dose. The function provides the requested dose data, volume, conformity and gradient table.

<u>\$dosimetry</u>					
	D.min	D.max	D.mean	D.95%	D0.2 cc
PTV	44.56	56.46	53.77	51.82	55.38
Chiasma	11.86	49.55	37.46	18.83	30.85
<u>\$volume</u>					
	V_tot	area	V_48.77 Gy		
isodose	NA	NA	47.95		
PTV	32.52	54.83	32.43		
Chiasma	0.26	3.13	0.01		
<u>\$conformity</u>					
	presc.dose	target	PITV	PDS	
	48.77	PTV	1.47	1.48	
<u>\$gradient</u>					
	presc.dose	target	PITV		
	48.77	PTV	5.06		

3.3. Geometric tools

The available geometrical tools are used to simplify the manipulation of volume objects. First, it is possible to increase or reduce a volume. The `add.margin()` function adds or removes a margin to the volume, the `nesting.cube()` function restricts the volume to a volume defined by the two vertices, the `nesting.bin()` function reduces the volume to a binary selection and `nesting.roi()` reduces the volume to the selection defined by a region of interest defined in an RTstruct, as illustrated in Fig. 5:

In order to add volumes together (`vol.sum()` function), it is also possible to regrid a volume, thanks to the `vol.regrid()` function. One of the applications is, for example, to cumulate two dose distributions from different treatments. Fig. 6 shows, for example, the total dose of a patient who received a proton treatment and a boost with a CyberKnife machine. Each dose distribution was built from the contours of two different RTstruct files. The barycenters of the common Regions of Interest (RoI) were used to connect the two dose distributions, as explained in the manual `Dose-cumulation.pdf` available on the `espadon` website [19].

3.4. Binary objects

Binary volumes are important tools for selecting only the desired part of a volume. They work like masks. The values of the voxels are either TRUE, FALSE or NA (i.e. indeterminate). Fig. 7 illustrates how to select the MRI region of patient A bounded by the brain. Only three functions were used: `nesting.bin()` to limit the working area and thus to reduce the computation time, `bin.from.roi()` to select the brain from the RoI provided by the RTstruct file, and `vol.from.bin()`, to select the relevant area in the MRI.

In the `espadon` toolkit, several mathematical morphology functions allow to increase (`bin.dilation()`), decrease (`bin.erosion()`), merge and fill holes (`bin.closing()`), and smooth (`bin.opening()`) binary volumes.

One of the applications of binary volumes is the definition of isodoses. A simple binary selection on the voxel value of a dose distribution (`bin.from.vol()` function) followed by an export to a `espadon` struct object (`struct.from.bin()` function) builds a network of isodoses (`struct.merge()` function), as illustrated in Fig. 8.

4. Conclusions

The `espadon` open-source code is an R package available for free on the Comprehensive R Archive Network (CRAN) [4]. It allows

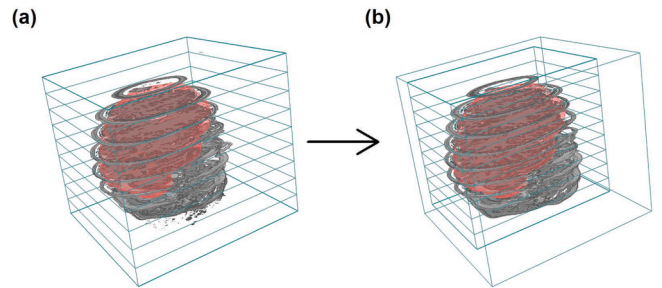


Fig. 5. (a) 3D view of MRI and brain RoI. (b) 3D view of the reduction of the MRI volume around the contours of the “brain”.

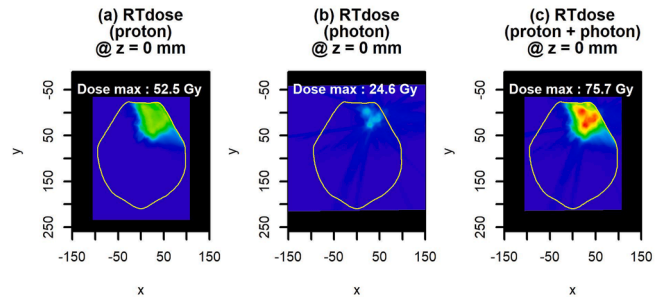


Fig. 6. (a) Transverse view of the RTdose from proton treatment machine. (b) Transverse view of the boost RTdose from CyberKnife machine. (c) Sum of the two dose distributions.

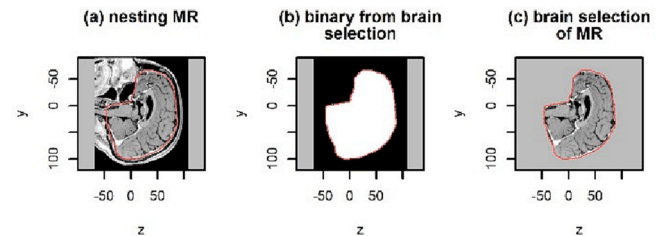


Fig. 7. Selection of the brain from the patient A MRI. (a) MRI reduced to the brain (with a 2 cm margin). (b) Binary selection of the brain. (c) Selection of the brain in the MRI.

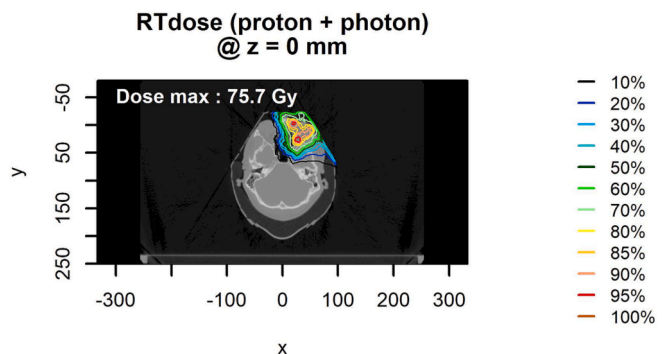


Fig. 8. Isodoses from dose distribution, using `espadon` functions `bin.from.vol()`, `struct.from.bin()` and `struct.merge()`.

radiotherapists, medical physicists and students to access an R tool, independent of the treatment planning system (TPS), to extract data from DICOM files in order to enhance clinical data a posteriori.

By forming a coherent set of functions, it allows users to write their

own script in R, which may eventually enrich the package. The applications are numerous: from the creation of new contours to the automatic calculation of indices, it opens the way to multi-TPS analysis, the analysis of inter-operator practices, intra- and inter-centric comparisons and dose calculation or contouring challenges.

The *espadon* package will improve and develop over time: we plan to include TCP/NTCP and geometric index calculations.

Like all R packages, help is available for each *espadon* function in the reference manual, or with the simple “help (function)” instruction: the input parameters are explained and an example of use is proposed. Other explanations and use cases are available on the *espadon* website [19].

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.ejmp.2023.102580>.

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