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Working with the DICOM and NIfTI Data Standards in R

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Abstract

Two packages (**oro.dicom** and **oro.nifti**) are provided for the interaction with and manipulation of medical imaging data that conform to the DICOM standard or ANALYZE/NIfTI formats. DICOM data, from a single file or single directory or directory tree, may be uploaded into R using basic data structures: a data frame for the header information and a matrix for the image data. A list structure is used to organize multiple DICOM files. The S4 class framework is used to develop basic ANALYZE and NIfTI classes, where NIfTI extensions may be used to extend the fixed-byte NIfTI header. One example of this, that has been implemented, is an XML-based "audit trail" that tracks the history of operations applied to a dataset. The conversion from DICOM to ANALYZE/NIfTI is straightforward using the capabilities of both packages. The S4 classes have been developed to provide a user-friendly interface to the ANALYZE/NIfTI data formats; allowing easy data input, data output, image processing and visualization.

Keywords: export, imaging, import, medical, visualization.

1. Introduction

Medical imaging is well established in both the clinical and research areas with numerous equipment manufacturers supplying a wide variety of modalities. The DICOM (Digital Imaging and Communications in Medicine; http://medical.nema.org) standard was developed from earlier standards and released in 1993. It is the data format for clinical imaging equipment and a variety of other devices whose complete specification is beyond the scope of this paper. All major manufacturers of medical imaging equipment (e.g., GE, Siemens, Philips)

have so-called DICOM conformance statements that explicitly state how their hardware implements DICOM. The DICOM standard provides interoperability across hardware, but was not designed to facilitate efficient data manipulation and image processing. Hence, additional data formats have been developed over the years to accommodate data analysis and image processing.

The ANALYZE format was developed at the Mayo Clinic (in the 1990s) to store multidimensional biomedical images. It is fundamentally different from the DICOM standard since it groups all images from a single acquisition (typically three- or four-dimensional) into a pair of binary files, one containing header information and one containing the image information. The DICOM standard groups the header and image information, typically a single two-dimensional image, into a single file. Hence, a single acquisition will contain multiple DICOM files but only a pair of ANALYZE files.

The NIfTI format was developed in the early 2000s by the DFWG (Data Format Working Group) in an effort to improve upon the ANALYZE format. The resulting NIfTI-1 format adheres to the basic header/image combination from the ANALYZE format, but allows the pair of files to be combined into a single file and re-defines the header fields. In addition, NIfTI extension allow to store any additional information.

The material presented here provides users with a method of interacting with DICOM, ANALYZE and NIfTI files in R (R Development Core Team 2010). Real-world datasets, that are publicly available, are used to illustrate the basic functionality of the two packages: **oro.dicom** and **oro.nifti**. Major features include data input/output, visualization and conversion from DICOM to ANALYZE/NIfTI. These packages should appeal not only to other R package developers, but also to scientists who want to manipulate medical imaging data using R without writing and validating basic data input/output functionality. Packages already available on CRAN that utilize **oro.dicom** and **oro.nifti** include **cudaBayesreg** (Ferreira da Silva 2010a), **dcemriS4** (Whitcher and Schmid 2010) and **dpmixsim** (Ferreira da Silva 2010b).

2. oro.dicom: DICOM Data Input/Output in R

The DICOM "standard" for data acquired using a clinical imaging device is very broad and complex. Roughly speaking each DICOM-compliant file is a collection of fields organized into two two-byte sequences (group,element) that are represented as hexadecimal numbers and form a tag. The (group,element) combination establishes what type of information is forthcoming in the file. There is no fixed number of bytes for a DICOM header. The final (group,element) tag should be the "pixel data" tag (7FE0,0010), such that all subsequent information is related to the image(s).

All attributes in the DICOM standard require different data types for correct representation. These are known as value representations (VRs) in DICOM, which may be encoded explicitly or implicitly. There are 27 explicit VRs defined in the DICOM standard, and provided in Table 1. Detailed explanations of these data types are provided in the Section 6.2 (part 5) of the DICOM standard (`http://medical.nema.org`). The first column provides the two-character string that is present in each entry of the header field and the second column provides a descriptive name for the abbreviated code. The third column provides the maximum length of the data associated with the VR (in bytes), where a length of zero bytes may be interpreted as having an unknown or unlimited number of bytes associated with the VR. The fourth

Code	Name	Bytes	Fixed
AE	ApplicationEntity	16	0
AS	AgeString	4	1
AT	AttributeTag	4	1
CS	CodeString	16	0
DA	Date	8	1
DS	DecimalString	16	0
DT	DateTime	26	0
FL	FloatingPointSingle	4	1
FD	FloatingPointDouble	8	1
IS	IntegerString	12	0
LO	LongStrong	64	0
LT	LongText	10240	0
OB	OtherByteString	0	0
OW	OtherWordString	0	0
PN	PersonName	64	0
SH	ShortString	16	0
SL	SignedLong	4	1
SQ	SequenceOfItems	0	0
SS	SignedShort	2	1
ST	ShortText	1024	0
TM	Time	16	0
UI	UniqueIdentifierUID	64	0
UL	UnsignedLong	4	1
UN	Unknown	0	0
US	UnsignedShort	2	1
UT	UnlimitedText	0	0

Table 1: Value representations in the DICOM standard. A value of zero bytes may be interpreted as having an unknown or unlimited number of bytes associated with the VR.

```
Data element with explicit VR of OB, OF, OW, SQ, UT or UN:

+-----------------------------------------------------------+
|  0 |  1 |  2 |  3 |  4 |  5 |  6 |  7 |  8 |  9 | 10 | 11 |
+----+----+----+----+----+----+----+----+----+----+----+----+
|<Group-->|<Element>|<VR----->|<0x0000->|<Length----------->|<Value->

Data element with explicit VR other than as shown above:

+---------------------------------------+
|  0 |  1 |  2 |  3 |  4 |  5 |  6 |  7 |
+----+----+----+----+----+----+----+----+
|<Group-->|<Element>|<VR----->|<Length->|<Value->

Data element with implicit VR:

+---------------------------------------+
|  0 |  1 |  2 |  3 |  4 |  5 |  6 |  7 |
+----+----+----+----+----+----+----+----+
|<Group-->|<Element>|<Length----------->|<Value->
```

Figure 1: Byte ordering for a single (group,element) tag in the DICOM standard. Explicit VRs store the VR as text characters in two bytes. More information is provided in Section 7, Part 3.5-2009 of the DICOM standard (http://medical.nema.org).

column is not used in the current implementation of the **oro.dicom** package. Internal functions have been written to manipulate each of the value representations and are beyond the scope of this article. The functions `str2date` and `str2time` are useful for converting from the DICOM `Datetime` and `Time` value representations to R date and time objects, respectively.

2.1. The DICOM Header

Accessing the information stored in a single DICOM file is provided using the `dicomInfo` function. The basic structure of a DICOM file is summarized in Figure 1, for both explicit and implicit value representations. The first two bytes represent the `group` tag and the second two bytes represent the `element` tag, regardless of the type of VR. The third set of two bytes contains the characters of the VR on which a decision about being implicit or explicit is made. Explicit VRs of type `(OB, OF, OW, SQ, UT, UN)` skip bytes six and seven (counting from zero), convert the next four bytes into an integer `length` and read `length` number of objects from the DICOM file. All other explicit VRs follow a slightly different path where bytes six and seven (counting from zero) provide an integer `length` and all remaining bytes are read in as the `value`. If the character string in bytes four and five do not correspond to a known VR (Figure 1), then the (`group`,`element`) tag is declared to be implicit, the `length` is taken from bytes four through seven and all remaining bytes contribute to the `value`.

The basic structure of the resulting object is a list with two elements: the DICOM header (`hdr`) and the DICOM image (`img`). The header information is organized in a data frame

with six columns and an unknown number of rows depending on the input parameters.

```
R> fname <- system.file(file.path("dcm", "Abdo.dcm"), package = "oro.dicom")
R> abdo <- dicomInfo(fname)
R> names(abdo)

[1] "hdr" "img"

R> abdo$hdr[1:5, ]

  group element                        name code length
1  0002    0000                 GroupLength   UL      4
2  0002    0001 FileMetaInformationVersion   OB      2
3  0002    0002    MediaStorageSOPClassUID   UI     26
4  0002    0003 MediaStorageSOPInstanceUID   UI     38
5  0002    0010           TransferSyntaxUID   UI     20
                                  value sequence
1                                   166
2                                skipped
3             1.2.840.10008.5.1.4.1.1.4
4 1.3.46.670589.11.0.4.1996082307380007
5                   1.2.840.10008.1.2.1

R> abdo$hdr[nrow(abdo$hdr) - 4:0, ]

   group element                name code length value sequence
80  0028    0102             HighBit   US      2    11
81  0028    0103 PixelRepresentation   US      2     0
82  0028    1050        WindowCenter   DS      4   530
83  0028    1051         WindowWidth   DS      4  1052
84  7FE0    0010           PixelData   OW 131072
```

The ordering of the rows is identical to the ordering in the original DICOM file. Hence, the first five tags in the DICOM header of `Abdo.dcm` are: `GroupLength`, `FileMetaInformationVersion`, `MediaStorageSOPClassUID`, `MediaStorageSOPInstanceUID` and `TransferSyntaxUID`. The last five tags in the DICOM header are also shown, with the very last tag indicating the start of the image data for that file and the number of bytes (131072) involved. When additional tags in the DICOM header information are queried (via `extractHeader`)

```
R> extractHeader(abdo$hdr, "BitsAllocated")

[1] 16

R> extractHeader(abdo$hdr, "Rows")

[1] 256
```

```
R> extractHeader(abdo$hdr, "Columns")

[1] 256
```

it is clear that the data are consistent with the header information in terms of the number of bytes ($256 \times 256 \times (16/8) = 131072$).

The first five columns are taken directly from the DICOM header information (`group`, `element`, `code`, `length` and `value`) or inferred from that information (`name`). Note, the (`group`,`element`) values are stored as character strings even though they are hexadecimal numbers. All aspects of the data frame may be interrogated in R in order to extract relevant information from the DICOM header; e.g., `"BitsAllocated"` as above. The `sequence` column is used to keep track of tags that are embedded in a fixed-length SequenceItems tag or between a SequenceItem-SequenceDelimitationItem pair.

When multiple DICOM files are located in a single directory, or spread across multiple directories, one may use the function `dicomSeparate` (applied here to the directory `hk-40`).

```
R> fname <- system.file("hk-40", package = "oro.dicom")
R> hk40 <- dicomSeparate(fname, verbose = TRUE, counter = 10)

   40 files to be processed!
   10 files processed...
   20 files processed...
   30 files processed...
   40 files processed...

R> unlist(lapply(hk40, length))

hdr img
 40  40
```

The object associated with `dicomSeparate` is now a nested set of lists, where the `hdr` element is a list of data frames and the `img` element is a list of matrices. These two lists are associated in a pairwise sense; i.e., `hdr[[1]]` is the header information for the image `img[[1]]`. Default parameters `recursive = TRUE` and `pixelData = TRUE` (which is actually an input parameter for `dicomInfo`) allow the user to search down all possible sub-directories and upload the image in addition to the header information, respectively. Also, by default all files are treated as DICOM files unless the `exclude` parameter is set to the unwanted file extension; e.g., `exclude = "xml"`.

The list of DICOM header information across multiple files may be converted to a single data frame using `dicomTable`, and written to disc for further analysis; e.g., using `write.csv`.

```
R> hk40.info <- dicomTable(hk40$hdr)
R> write.csv(hk40.info, file = "hk40_header.csv")
R> sliceloc.col <- which(hk40$hdr[[1]]$name == "SliceLocation")
R> sliceLocation <- as.numeric(hk40.info[, sliceloc.col])
R> sliceLocation[1:5]
```

```
[1] 160.9315 157.8315 154.7315 151.6315 148.5315

R> diff(sliceLocation[1:5])

[1] -3.1 -3.1 -3.1 -3.1

R> unique(extractHeader(hk40$hdr, "SliceThickness"))

[1] 3.125
```

The tag `SliceLocation` is extracted from the DICOM header information (at the first element in the list) and processed using the `diff` function, and should agree with the `SliceThickness` tag. Single DICOM fields may also be extracted from the list of DICOM header information that contain attributes that are crucial for further image processing; e.g., extracting relevant MR sequences or acquisition timings.

```
R> extractHeader(hk40$hdr, "SliceLocation")[1:5]

[1] 160.9315 157.8315 154.7315 151.6315 148.5315

R> modality <- extractHeader(hk40$hdr, "Modality", numeric = FALSE)
R> matchHeader(modality, "mr")[1:5]

[1] TRUE TRUE TRUE TRUE TRUE

R> (seriesTime <- extractHeader(hk40$hdr, "SeriesTime", numeric = FALSE))

 [1] "113751.966000" "113751.966000" "113751.966000" "113751.966000"
 [5] "113751.966000" "113751.966000" "113751.966000" "113751.966000"
 [9] "113751.966000" "113751.966000" "113751.966000" "113751.966000"
[13] "113751.966000" "113751.966000" "113751.966000" "113751.966000"
[17] "113751.966000" "113751.966000" "113751.966000" "113751.966000"
[21] "113751.966000" "113751.966000" "113751.966000" "113751.966000"
[25] "113751.966000" "113751.966000" "113751.966000" "113751.966000"
[29] "113751.966000" "113751.966000" "113751.966000" "113751.966000"
[33] "113751.966000" "113751.966000" "113751.966000" "113751.966000"
[37] "113751.966000" "113751.966000" "113751.966000" "113751.966000"

R> str2time(seriesTime[1:5])

$txt
[1] "11:37:51.96600" "11:37:51.96600" "11:37:51.96600" "11:37:51.96600"
[5] "11:37:51.96600"

$time
[1] 41871.97 41871.97 41871.97 41871.97 41871.97
```

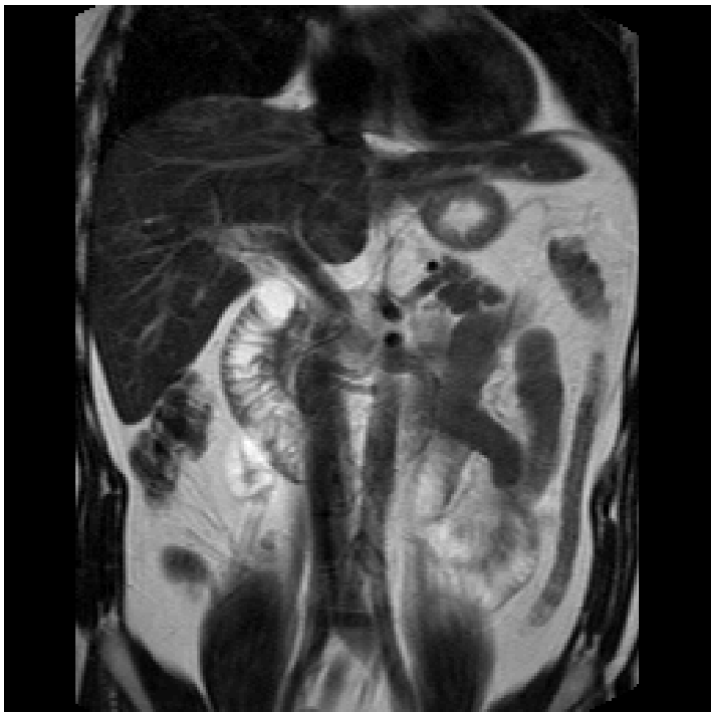


Figure 2: Coronal slice of the abdomen viewed in *neurological* convention (left is right and right is left).

2.2. The DICOM Image

Most DICOM files involve a single slice from an acquisition – the image. A notable exception is the Siemens MOSAIC format (addressed in Section 2.2.1). The **oro.dicom** package assumes the image is stored as a flat file of two-byte integers without compression. A variety of additional image formats are possible within the DICOM standard; for example, RGB-colorized, JPEG, JPEG Lossless, JPEG 2000 and run-length encoding (RLE). Going back to the `Abdo.dcm` example, the image is accessed via

```
R> image(t(abdo$img), col = grey(0:64/64), axes = FALSE, xlab = "",
+     ylab = "")
```

where the transpose operation is necessary for proper visualization of the image. Figure 2 displays a coronal slice through the abdomen from an MRI acquisition. All information from the original data acquisition should accompany the image through the DICOM header, and this information is utilized as much as possible by **oro.dicom** to simplify the manipulation of DICOM data. As previously shown, this information is easily available to the user by matching DICOM header fields with valid strings. Note, the function `extractHeader` assumes the output should be coerced via `as.numeric` but this may be disabled setting the input parameter `numeric=FALSE`.

```
R> extractHeader(abdo$hdr, "Manufacturer", numeric = FALSE)

[1] "Philips"
```

```
R> extractHeader(abdo$hdr, "RepetitionTime")

[1] 2000

R> extractHeader(abdo$hdr, "EchoTime")

[1] 100
```

The basic DICOM file structure does not encourage the analysis of multi-dimensional imaging data (e.g., 3D or 4D) commonly acquired on clinical scanners. Hence, the **oro.dicom** package has been developed to access DICOM files and facilitate their conversion to the NIfTI or ANALYZE formats. The conversion process requires the **oro.nifti** package and will be outlined in Section 4.

Siemens MOSAIC Format

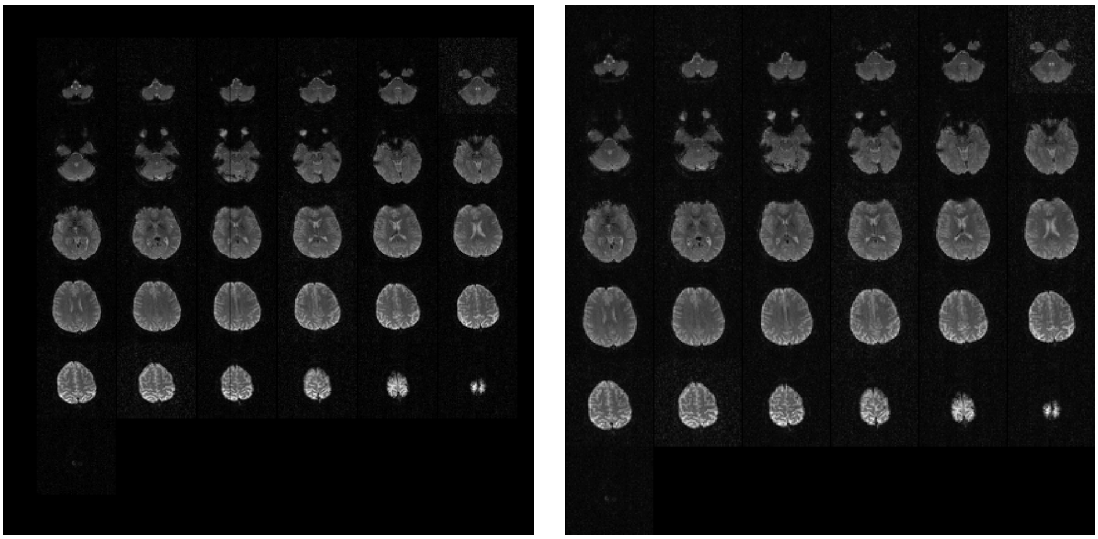
Siemens multi-slice EPI (echo planar imaging) data may be collected as a "mosaic" image; i.e., all slices acquired in a single TR (repetition time) frame of a dynamic run are stored in a single DICOM file. The images are stored in an $M \times N$ array of images. The function `create3D` will try to guess the number of images embedded within the single DICOM file using the `AcquisitionMatrix` field. If this doesn't work, one may enter the (M, N) doublet explicitly.

```
R> fname <- system.file(file.path("dcm", "MR-sonata-3D-as-Tile.dcm"),
+     package = "oro.dicom")
R> dcm <- dicomInfo(fname)
R> dim(dcm$img)

[1] 384 384

R> dcmImage <- create3D(dcm, mosaic = TRUE)
R> dim(dcmImage)

[1] 64 64 36
```

Figure 3a is taken from the raw DICOM file, in mosaic format, and displayed with the default margins in R. Figure 3b is displayed after re-organizing the original DICOM file into a three-dimensional array (it was also converted to the NIfTI format for ease of visualization using the overloaded `image` function in **oro.nifti**).

3. oro.nifti: NIfTI-1 Data Input/Output in R

Although the industry standard for medical imaging data is DICOM, another format has come to be heavily used in the image analysis community. The ANALYZE format was originally developed in conjunction with an image processing system (of the same name) at the Mayo Foundation. A common version of the format, although not the most recent, is called



(a) **(b)**

Figure 3: **(a)** Single MOSAIC image as read in from `dicomInfo`. **(b)** Lightbox display of three-dimensional array of images after processing via `create3D`.

ANALYZE 7.5. A copy of the file ANALYZE75.pdf has been included in **oro.nifti** (accessed via `system.file("doc/ANALYZE75.pdf", package="oro.dicom")`) since it does not appear to be available from `www.mayo.edu` any longer. An ANALYZE 7.5 format image is comprised of two files, the ".hdr" and ".img" files, that contain information about the acquisition and the acquisition itself, respectively. A more recent adaption of this format is known as NIfTI-1 and is a product of the Data Format Working Group (DFWG) from the Neuroimaging Informatics Technology Initiative (NIfTI; `http://nifti.nimh.nih.gov`). The NIfTI-1 data format is almost identical to the ANALYZE format, but offers a few improvements

- merging of the header and image information into one file (.nii)
- re-organization of the 348-byte fixed header into more relevant categories
- possibility of extending the header information.

3.1. The NIfTI Header

The NIfTI header inherits its structure (348 bytes in length) from the ANALYZE data format. The last four bytes in the NIfTI header correspond to the "magic" field and denote whether or not the header and image are contained in a single file (`magic = "n+1\0"`) or two separate files (`magic = "ni1\0"`), the latter being identical to the structure of the ANALYZE data format. The NIfTI data format added an additional four bytes to allow for "extensions" to the header. By default these four bytes are set to zero.

The first example of reading in, and displaying, medical imaging data in NIfTI format `avg152T1_LR_nifti.nii.gz` was obtained from the NIfTI website (`http://nifti.nimh.nih.gov/nifti-1/`). Successful execution of the commands

```
R> fname <- system.file(file.path("nifti", "mniLR.nii.gz"),
+     package = "oro.nifti")
R> (mniLR <- readNIfTI(fname))

NIfTI-1 format
  Type            : niftiAuditTrail
  Data Type       : 2 (UINT8)
  Bits per Pixel  : 8
  Slice Code      : 0 (Unknown)
  Intent Code     : 0 (None)
  Qform Code      : 0 (Unknown)
  Sform Code      : 4 (MNI_152)
  Dimension       : 91 x 109 x 91
  Pixel Dimension : 2 x 2 x 2
  Voxel Units     : mm
  Time Units      : sec

R> aux.file(mniLR)

[1] "none                    "

R> descrip(mniLR)

[1] "FSL3.2beta"
```

produces an S4 `"nifti"` object (or `"niftiAuditTrail"` if the audit trail option is set). Two accessor functions are also provided: `aux.file` and `descrip`. The former is used to access the original name of the file (if it has been provided) and the latter is the name of a valid NIfTI header field used to hold a "description" (up to 80 characters in length).

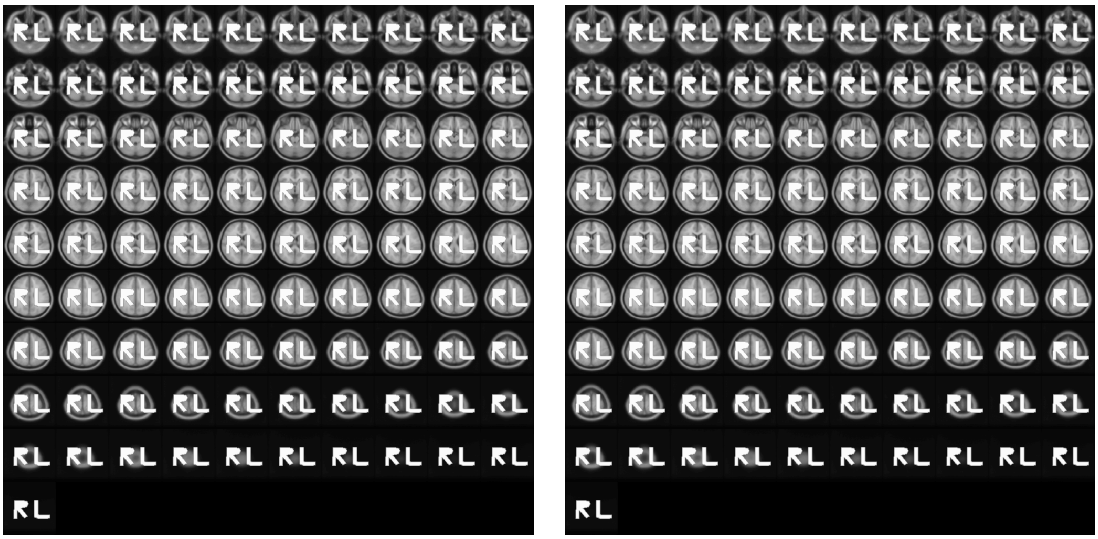
3.2. The NIfTI Image

Image information begins at the byte position determined by the `voxoffset` slot. In a single NIfTI file (`magic = "n+1\0"`), this is by default after the first 352 bytes. Header extensions extend the size of the header and come before the image information leading to a consequent increase of `voxoffset` for single NIfTI files. Split NIfTI files do not have this problem and `voxoffset` is set at 0.

The `image` function has been overloaded so that it behaves differently when dealing with medical image objects (`nifti` and `anlz`). The command

```
R> image(mniLR)
```

produces a three-dimensional array of the MNI brain, with the default NIfTI axes, and is displayed on a 10×10 grid of images (Figure 4a). The `image` function for medical image S4 objects is an attempt to balance minimal user input with enough flexibility to customize the display when necessary. For example, single slices may be viewed by using the option `plot.type="single"` in conjuction with the option `z=` to specify the slice.



(a) **(b)**

Figure 4: **(a)** Axial slices of MNI volume `mniLR_nifti` stored in the *neurological* convention (right-is-right), but displayed in the *radiological* convention (right-is-left). **(b)** Axial slices of MNI volume `mniRL_nifti` stored and displayed in the *radiological* convention.

The second example of reading in and displaying medical imaging data in the NIfTI format `avg152T1_RL_nifti.nii.gz` was also obtained from the NIfTI website (http://nifti.nimh.nih.gov/nifti-1/). Successful execution of the commands

```
R> fname <- system.file(file.path("nifti", "mniRL.nii.gz"),
+     package = "oro.nifti")
R> (mniRL <- readNIfTI(fname))

NIfTI-1 format
  Type            : niftiAuditTrail
  Data Type       : 2 (UINT8)
  Bits per Pixel  : 8
  Slice Code      : 0 (Unknown)
  Intent Code     : 0 (None)
  Qform Code      : 0 (Unknown)
  Sform Code      : 4 (MNI_152)
  Dimension       : 91 x 109 x 91
  Pixel Dimension : 2 x 2 x 2
  Voxel Units     : mm
  Time Units      : sec

R> image(mniRL)
```

produces a three-dimensional array of the MNI brain that is displayed in a 10×10 grid of images (Figure 4b). The two sets of data in Figure 4 are stored in two different orientations,

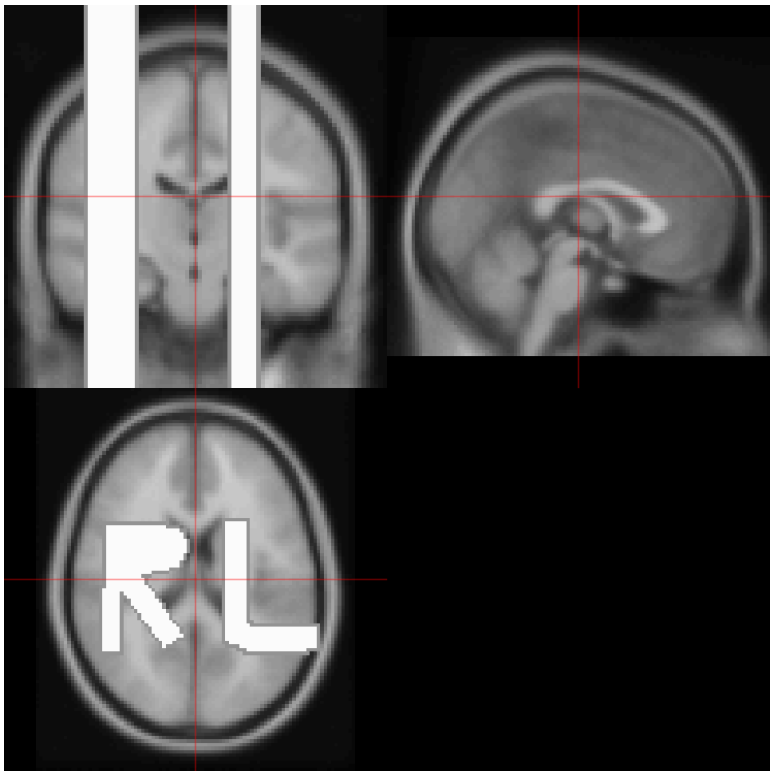


Figure 5: Orthographic display of the MNI volume `mniRL_nifti`. By default the mid-axial, mid-saggital and mid-coronal planes are chosen.

commonly referred to as the *radiological* and *neurological* conventions. The neurological convention is where "right is right" and one is essentially looking through the subject. The radiological convention is where "right is left" and one is looking at the subject.

An additional graphical display function has been added for `nifti` and `anlz` objects that allows a so-called orthographic visualization of the data.

```
R> orthographic(mniRL)
```

As seen in Figure 5 the mid-axial, mid-saggital and mid-coronal planes are displayed by default. The slices used may be set using `xyz = c(I,J,K)`, where (I, J, K) are appropriate indices, and the crosshairs will provide a spatial reference in each plane relative to the other two.

3.3. A Note on Axes and Orientation

The NIfTI format contains an implicit generalized spatial transformation from the data co-ordinate system (i, j, k) into a real-space "right-handed" co-ordinate system. In this real-space system, the (x, y, z) axes are *usually* set such that x increases from left to right, y increases from posterior to anterior and z increases from inferior to superior.

At this point in time the **oro.nifti** package cannot apply an arbitrary transform to the imaging data into (x, y, z) space – such a transform may require non-integral indices and interpolation

steps. The package does accommodate straightforward transformations of imaging data; e.g., setting the i-axis to increase from right to left (the neurological convention). Future versions of **oro.nifti** will attempt to address more complicated spatial transformations and provide functionality to display the (x, y, z) axes on orthographic plots.

3.4. NIfTI and ANALYZE Data in S4

A major improvement in the **oro.nifti** package is the fact that standard medical imaging formats are stored in unique classes under the S4 system (Chambers 2008). Essentially, NIfTI and ANALYZE data are stored as multi-dimensional arrays with extra slots created that capture the format-specific header information; e.g., for a `nifti` object

```
R> slotNames(mniRL)
```

```
 [1] ".Data"          "trail"          "extensions"     "sizeof_hdr"
 [5] "data_type"      "db_name"        "extents"        "session_error"
 [9] "regular"        "dim_info"       "dim_"           "intent_p1"
[13] "intent_p2"      "intent_p3"      "intent_code"    "datatype"
[17] "bitpix"         "slice_start"    "pixdim"         "vox_offset"
[21] "scl_slope"      "scl_inter"      "slice_end"      "slice_code"
[25] "xyzt_units"     "cal_max"        "cal_min"        "slice_duration"
[29] "toffset"        "glmax"          "glmin"          "descrip"
[33] "aux_file"       "qform_code"     "sform_code"     "quatern_b"
[37] "quatern_c"      "quatern_d"      "qoffset_x"      "qoffset_y"
[41] "qoffset_z"      "srow_x"         "srow_y"         "srow_z"
[45] "intent_name"    "magic"          "extender"       "reoriented"
```

```
R> c(mniRL@cal_min, mniRL@cal_max)
```

```
[1]   0 255
```

```
R> range(mniRL)
```

```
[1]   0 255
```

```
R> mniRL@datatype
```

```
[1] 2
```

```
R> convert.datatype(mniRL@datatype)
```

```
[1] "UINT8"
```

Note, an ANALYZE object has a slightly different set of slots. Slots 4–47 are taken verbatim from the definition of the NIfTI format and are read directly from a file. The slot `.Data` is the multidimensional array (since class `nifti` inherits from class `array`) and the slots `trail`,

`extensions` and `reoriented` are used for internal bookkeeping. In the code above we have accessed the min/max values of the imaging data using the `"cal_min"` and `"cal_max"` slots and matches a direct interrogation of the `.Data` slot using the `range` function. Looking at the `datatype` slot provides a numeric code that may be converted into a value that indicates the type of byte structure used (in this case an 8-bit or 1-byte unsigned integer).

As introduced in Section 3.1 there are currently only two accessor functions to slots in the NIfTI header (`aux.file` and `descrip`) – all other slots are either ignored or used inside of functions that operate on ANALYZE/NIfTI objects. The NIfTI class also has the ability to read and write extensions that conform to the NIfTI data format. Customized printing and validity-checking functions are available to the user and every attempt has been made to ensure that the information from the multi-dimensional array is in agreement with the header values.

The constructor function `nifti` produces valid NIfTI objects, including a consistent header, from an arbitrary array.

```
R> (random.image <- nifti(array(runif(100 * 100), c(100, 100,
+     1)), datatype = 16))

NIfTI-1 format
  Type            : niftiAuditTrail
  Data Type       : 16 (FLOAT32)
  Bits per Pixel  : 32
  Slice Code      : 0 (Unknown)
  Intent Code     : 0 (None)
  Qform Code      : 0 (Unknown)
  Sform Code      : 0 (Unknown)
  Dimension       : 100 x 100 x 1
  Pixel Dimension : 1 x 1 x 1
  Voxel Units     : Unknown
  Time Units      : Unknown

R> random.image@dim

[1] 100 100   1

R> dim(random.image)

[1] 100 100   1
```

Data types used for NIfTI formats can be achieved from the `convert.datatype` function.

```
R> cbind(convert.datatype())

          [,1]
UINT8     2
INT16     4
```

```
INT32      8
FLOAT32    16
COMPLEX64  32
FLOAT64    64
RGB24      128
INT8       256
UINT16     512
UINT32     768
INT64      1024
UINT64     1280
FLOAT128   1536
COMPLEX128 1792
COMPLEX256 2048
RGBA32     2304
```

The function `writeNIfTI` outputs valid NIfTI class files, which can be opened in other medical imaging software. Files can either be stored as standard `.nii` files or compressed with gnuzip.

```
R> writeNIfTI(random.image, "random", gzipped = TRUE)
R> system("ls random*", intern = TRUE)
```

```
[1] "random.nii.gz"
```

3.5. Audit Trail

Following on from the S4 implementation of both the NIfTI and ANALYZE data formats, the ability to extend the NIfTI data format header is utilized in the **oro.nifti** package. First, extensions are properly handled when reading and writing NIfTI data. Second, users are allowed to add extensions to newly-created NIfTI objects by casting them as `niftiExtension` objects and adding `niftiExtensionSection` objects to the `extensions` slot. Third, by default all operations that are performed on a NIfTI object will generate what we call an *audit trail* that consists of an XML-based log. Each log entry contains information not only about the function applied to the NIfTI object, but also various system-level information; e.g., version of R, user name, date, time, etc. When writing NIfTI-class objects to disk, the XML-based NIfTI extension is converted into plain text and saved using `ecode = 6` to denote plain ASCII text only. The user may control the tracking of data manipulation via the audit trail using a global option. For example, please use the command

```
R> options(niftiAuditTrail = FALSE)
```

to turn off the "audit trail" option in **oro.nifti**. Table 2 displays output from the accessor function `audit.trail(mniLR)`, the XML-based audit trail that is stored as a NIfTI header extension.

3.6. Interactive visualization

Basic visualization of `nifti` and `anlz` class images can be achieved with any visualization for arrays in R. For example, the **EBImage** package provides functions `display` and `animate` for

Table 2: XML-based audit trail obtained via `audit.trail(mniLR)`.

```
R> audit.trail(mniLR)

<audit-trail xmlns="http://www.dcemri.org/namespaces/audit-trail/1.0">
  <created>
    <workingDirectory>/mnt/sonne/projects/rigorous/papers/jss_dicom_nifti</workingDirectory>
    <filename>/home/schmid/R/i486-pc-linux-gnu-library/2.12/oro.nifti/nifti/mniLR.nii.gz</filename>
    <call>readNIfTI(fname = fname)</call>
    <system>
      <r-version.version.string>R version 2.12.2 (2011-02-25)</r-version.version.string>
      <date>Di MÃd'r 01 15:15:46 2011 CET</date>
      <user.LOGNAME>schmid</user.LOGNAME>
      <package-version.Version>0.2.5</package-version.Version>
    </system>
  </created>
</audit-trail>
```

visualization (Sklyar *et al.* 2010). Please note that functions in **EBImage** expect greyscale values in the range $[0, 1]$, hence the display of `nifti` data may be performed using

```
R> mniLR.range <- range(mniLR)
R> display((mniLR - min(mniLR))/diff(mniLR.range))
```

Interactive visualization of multi-dimensional arrays, stored in NIfTI or ANALYZE format, is however best performed outside of R at this point in time. Popular viewers, especially for neuroimaging data, are

- FSLView (`http://www.fmrib.ox.ac.uk/fsl/fslview/`),
- MRIcron (`http://cabiatl.com/mricron/`).

The **mritc** package provides basic interactive visualization of ANALYZE/NIfTI data using a Tcl/Tk interface (Feng and Tierney 2010).

3.7. fMRI example

Simple Time-series or Multi-volume Image

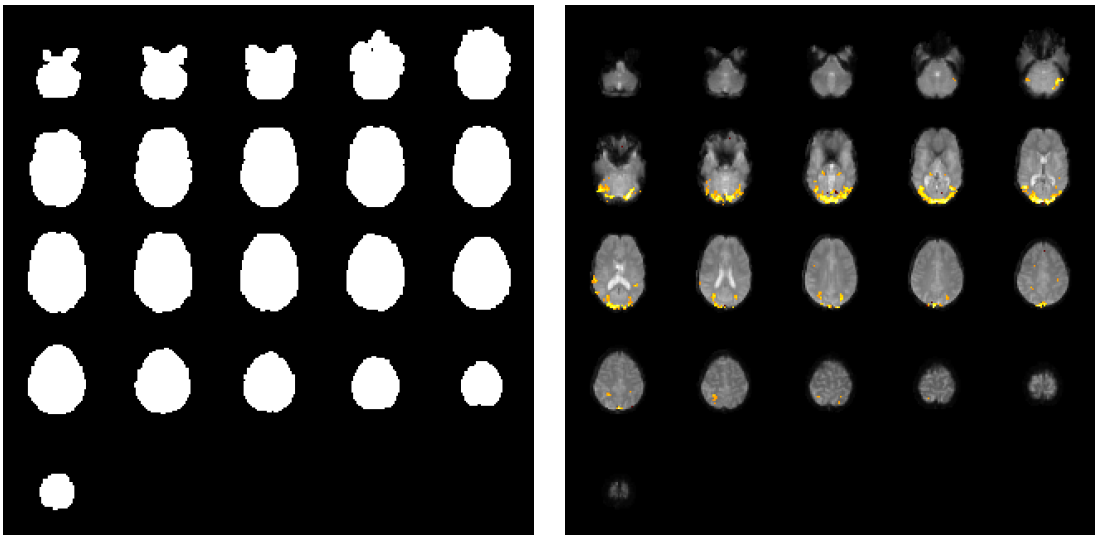
This is an example of reading in, and displaying, a four-dimensional medical imaging data set in NIfTI format `filtered_func_data.nii.gz` obtained from the FSL evaluation and example data suite (`http://www.fmrib.ox.ac.uk/fsl/fsl/feeds.html`). Successful execution of the commands

```
R> (ffd <- readNIfTI("filtered_func_data.nii.gz"))
```

```
NIfTI-1 format
  Type            : niftiAuditTrail
  Data Type       : 16 (FLOAT32)
  Bits per Pixel  : 32
  Slice Code      : 0 (Unknown)
  Intent Code     : 0 (None)
  Qform Code      : 0 (Unknown)
  Sform Code      : 0 (Unknown)
  Dimension       : 64 x 64 x 21 x 180
  Pixel Dimension : 4 x 4 x 6 x 3
  Voxel Units     : mm
  Time Units      : sec
```

```
R> image(ffd)
```

produces a four-dimensional (4D) array of imaging data that may be displayed in a 5×5 grid of images (Figure 6a). The first three dimensions are spatial locations of the voxel (volume element) and the fourth dimension is time for this functional MRI (fMRI) acquisition. As seen from the summary of object, there are 21 axial slices of fairly coarse resolution (4×4×6 mm)



(a) **(b)**

Figure 6: **(a)** Axial slices of the functional MRI "volume" `filtered_func_data` from the first acquisition. **(b)** Axial slices of the functional MRI data with the statistical image overlayed. The test statistics were thresholded at $|Z| \geq 5$ for all voxel.

and reasonable temporal resolution (3 s). Figure 8 depicts the orthographic display of the `filtered_func_data` using the axial plane containing the left-and-right thalamus to approximately center the crosshair.

```
R> orthographic(ffd, xyz = c(34, 29, 10))
```

Statistical analysis

R provides virtually any statistical method for the analysis of imaging data. For example, fMRI data are typically analysed by fitting a general linear model (GLM) with using the stimuli to construct a design matrix. This leads to a resulting statistical image, e.g., Z-

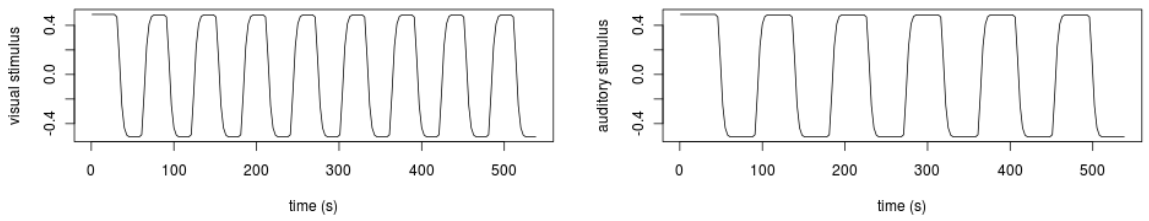


Figure 7: Visual (30 seconds on/off) and auditory (45 seconds on/off) stimulus convolved with a Gamma haemodynamic response function, used in the GLM fMRI analysis.

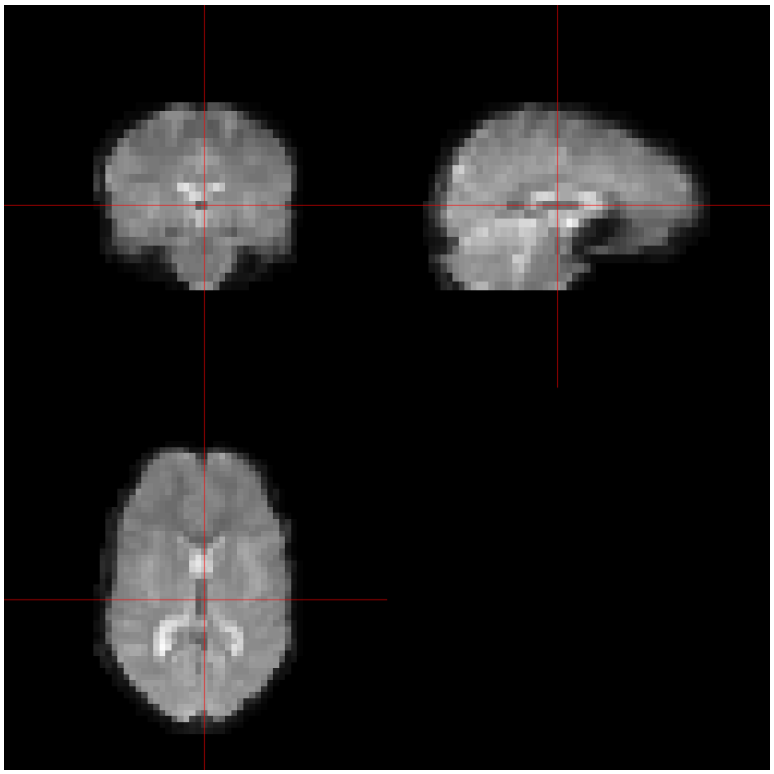


Figure 8: Orthographic display of the first volume from the functional MRI dataset `filtered_func_data`.

statistics for a voxel-wise hypothesis test on activation in fMRI experiments (Friston *et al.* 1994).

The `filtered_func_data.nii.gz` image was acquired in an experiment with $TR = 3s$ and both visual and auditory stimulus. The visual stimulus was a on/off with an amplitude of 60 seconds and the auditory stimulus was on/off with an amplitude of 90 seconds. We use a Gamma haemodynamic respone function (HRF) with mean 6 and standard deviation 3, similar to the default values in FSL. Figure 8 depicts the convolved visual and auditory stimuli.

```
R> visual <- rep(c(rep(-0.5, 30), rep(0.5, 30)), 12)
R> auditory <- rep(c(rep(-0.5, 45), rep(0.5, 45)), 12)
R> hrf <- c(dgamma(1:15, 4, scale = 1.5))
R> visual.hrf <- rep(NA, 540)
R> for (k in 60:599) visual.hrf[k - 59] <- sum(visual[k - (1:15)] *
+     hrf)
R> auditory.hrf <- rep(NA, 540)
R> for (k in 90:629) auditory.hrf[k - 89] <- sum(auditory[k -
+     (1:15)] * hrf)
R> visual.hrf <- c(rep(0.5, 30), visual.hrf)
R> auditory.hrf <- c(rep(0.5, 45), auditory.hrf)
R> visual.hrf <- visual.hrf[seq(3, 540, by = 3)]
R> auditory.hrf <- auditory.hrf[seq(3, 540, by = 3)]
R> visual.hrf <- visual.hrf - mean(visual.hrf)
R> auditory.hrf <- auditory.hrf - mean(auditory.hrf)
```

The design matrix is than used in a voxel-wise GLM using the the standard `lm()` R function for (general) linear models. From this, for each voxel, e.g., t-statistics and p-values for a hypothesis test on no effect of each stimulus along with a F-statistic for a hypothesis test on no effect of any stimuli can be computed.

```
R> thresh <- 0.1 * max(ffd)
R> local.lm <- function(x) {
+     if (max(x) < thresh)
+         return(rep(NA, 5))
+     model <- lm(x ~ visual.hrf + auditory.hrf)
+     sum.model <- summary(model)
+     return(c(as.vector(sum.model$coeff[2:3, 3:4]), sum.model$fstatistic[1]))
+ }
R> flim <- apply(ffd, 1:3, local.lm)
```

For anatomical context, statistical images are displayed as an overlay on top of a reference image. Successful execution of the command allows one to display the statistical image (of voxel-wise activations) overlayed on the original EPI (echo planar imaging) data taken from the functional MRI experiment.

```
R> t.visual <- nifti(flim[1, , , ])
R> t.auditory <- nifti(flim[2, , , ])
```

```
R> p.visual <- nifti(flim[3, , , ])
R> p.auditoy <- nifti(flim[4, , , ])
R> F <- nifti(flim[5, , , ])
R> Z.visual <- nifti(qnorm(pt(t.visual, 179, log.p = TRUE),
+     log.p = TRUE))
R> Z.auditory <- nifti(qnorm(pt(t.auditory, 179, log.p = TRUE),
+     log.p = TRUE))

R> overlay(ffd, ifelse(abs(Z.visual) > 5, Z.visual, NA), zlim.x = range(ffd),
+     zlim.y = range(Z.visual, na.rm = TRUE))

R> overlay(ffd, ifelse(abs(Z.auditory) > 5, Z.auditory, NA),
+     zlim.x = range(ffd), zlim.y = range(Z.auditory, na.rm = TRUE))
```

The four-dimensional array of parameter estimates are overlayed on the original data for anatomical reference in Figure 6b. The function `overlay` extends the capabilities of displaying "images" by allowing one to add a statistical image to a structural image of the same dimension.

4. Converting DICOM to NIfTI

The **oro.dicom** and **oro.nifti** packages have been specifically designed to use as much information as possible from the metadata-rich DICOM format and use that information in the construction of the NIfTI data volume. The function `dicom2nifti` converts a list of DICOM images into an `nifti` object, and likewise `dicom2analyze` converts them into an `anlz` object.

Historically, data conversion from DICOM to NIfTI (or ANALYZE) has been provided outside of R using one of several standalone software packages:

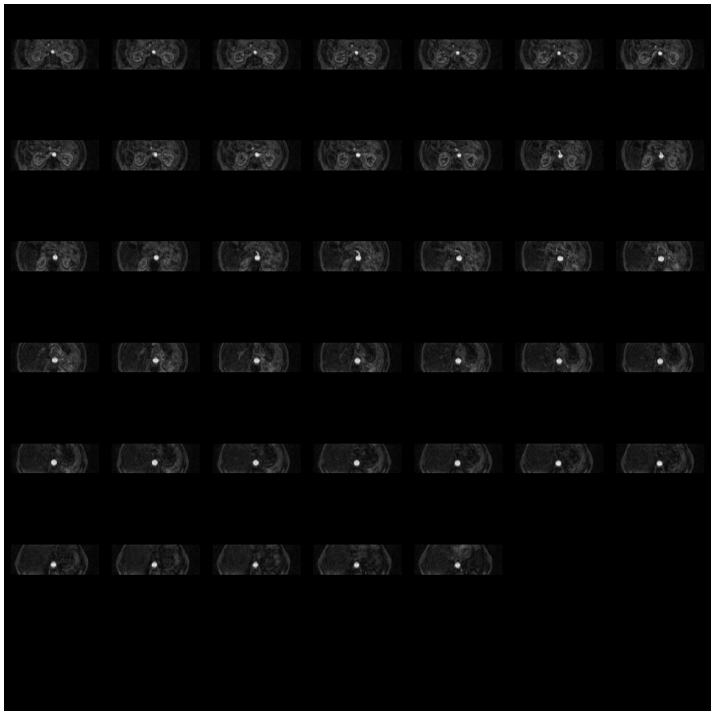
- Xmedcon (Nolf 2003),
- FreeSurfer (`http://surfer.nmr.mgh.harvard.edu`),
- MRIConvert (`http://lnci.oregon.edu/~jolinda/MRIConvert`).

This is by no means an exhaustive list of software packages available for DICOM conversion. In addition there are several other R packages with the ability to process DICOM data

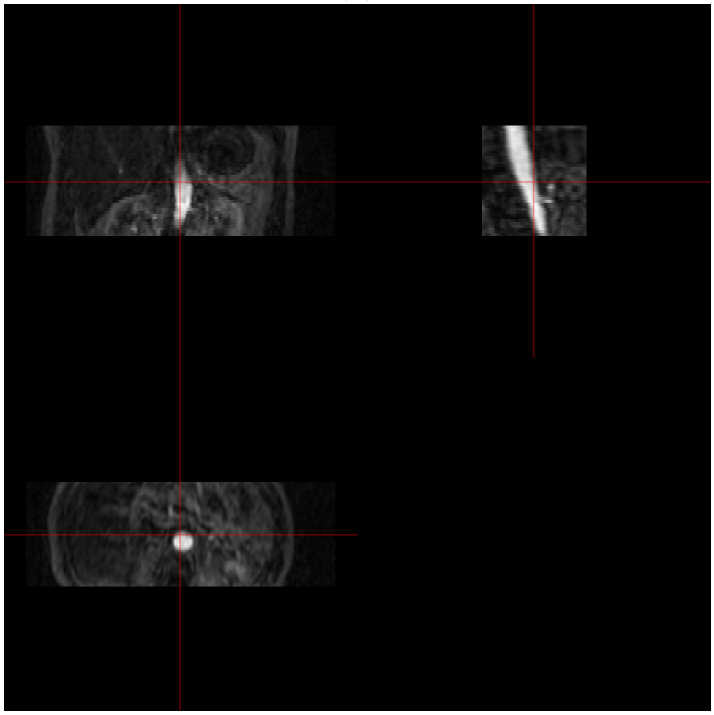
- **fmri** (Polzehl and Tabelow 2007),
- **tractor.base** (Clayden 2010) (part of the tractor project `http://code.google.com/p/tractor`).

4.1. Single-Series Example

Using the 40 images from the `hk40` object (previously defined in Section 2.1) it is straightforward to perform DICOM-to-NIfTI conversion using only default settings and plot the results in either lightbox or orthographic displays.



(a)



(b)

Figure 9: **(a)** Lightbox display of three-dimensional array of images. **(b)** Orthographic display of the same three-dimensional array (using the default settings for `orthographic`).

```
R> dput(formals(dicom2nifti))

list(dcm = , datatype = 4, units = c("mm", "sec"), rescale = FALSE, reslice = TRUE, DIM =

R> (hk40n <- dicom2nifti(hk40))

NIfTI-1 format
  Type            : niftiAuditTrail
  Data Type       : 4 (INT16)
  Bits per Pixel  : 16
  Slice Code      : 0 (Unknown)
  Intent Code     : 0 (None)
  Qform Code      : 0 (Unknown)
  Sform Code      : 0 (Unknown)
  Dimension       : 256 x 256 x 40
  Pixel Dimension : 1.56 x 1.56 x 3.12
  Voxel Units     : mm
  Time Units      : sec

R> image(hk40n)
R> orthographic(hk40n)
```

At default `dicom2nifti` takes all image data from the DICOM list and creates a 3D image. Four-dimensional image volumes (three in space plus one in time) are also converted automatically by specifying `DIM=4`, where slice positions are taken from the `ImagePositionPatient` DICOM header field. For example, using `DIM=4` on the `hk40` DICOM data,

```
R> (hk40n <- dicom2nifti(hk40, DIM = 4))

NIfTI-1 format
  Type            : niftiAuditTrail
  Data Type       : 4 (INT16)
  Bits per Pixel  : 16
  Slice Code      : 0 (Unknown)
  Intent Code     : 0 (None)
  Qform Code      : 0 (Unknown)
  Sform Code      : 0 (Unknown)
  Dimension       : 256 x 256 x 40
  Pixel Dimension : 1.56 x 1.56 x 3.12
  Voxel Units     : mm
  Time Units      : sec
```

will also produce a three-dimensional volume of images, since the `ImagePositionPatient` field is unique for each single slice of the volume.

The functions `dicom2nifti` and `dicom2analyze` will fail when the dimensions of the individual images in the DICOM list do not match. However, they do not check for different series

numbers or patient IDs so caution should be exercised when scripting automated workflows for DICOM-to-NIfTI conversion. In cases where a DICOM file includes images from more than one series, the corresponding slices have to be chosen before conversion, using `dicomTable`, `extractHeader`, and `matchHeader`.

4.2. Multiple-Series Example

The National Biomedical Imaging Archive (NBIA) is a searchable, national repository integrating *in vivo* cancer images with clinical and genomic data. The NBIA provides the scientific community with public access to DICOM images, image markup, annotations, and rich metadata.[1] The multiple MRI sequences processed here were downloaded from the "RIDER Neuro MRI" collection.[2] A small `for` loop has been written to operate on a subset of the DICOM directory structure, where the `SeriesInstanceUID` DICOM header field is assumed to be 100% accurate in series differentiation.

```
R> subject <- "1086100996"
R> DCM <- dicomSeparate(subject, verbose = TRUE, counter = 100)

   564 files to be processed!
   100 files processed...
   200 files processed...
   300 files processed...
   400 files processed...
   500 files processed...

R> seriesInstanceUID <- extractHeader(DCM$hdr, "SeriesInstanceUID",
+     FALSE)
R> for (uid in unique(seriesInstanceUID)) {
+     index <- which(unlist(lapply(DCM$hdr, function(x) uid %in%
+         x$value)))
+     uid.dcm <- list(hdr = DCM$hdr[index], img = DCM$img[index])
+     patientsName <- extractHeader(uid.dcm$hdr, "PatientsName",
+         FALSE)
+     studyDate <- extractHeader(uid.dcm$hdr, "StudyDate",
+         FALSE)
+     seriesDescription <- extractHeader(uid.dcm$hdr, "SeriesDescription",
+         FALSE)
+     fname <- paste(gsub("[^0-9A-Za-z]", "", unique(c(patientsName,
+         studyDate, seriesDescription))), collapse = "_")
+     cat("##  ", fname, fill = TRUE)
+     if (gsub("[^0-9A-Za-z]", "", unique(seriesDescription)) ==
+         "axtensor") {
+         D <- 4
+         reslice <- FALSE
+     }
```

[1] http://cabig.nci.nih.gov/tools/NCIA
[2] http://wiki.nci.nih.gov/display/CIP/RIDER

```
+     else {
+         D <- 3
+         reslice <- TRUE
+     }
+     uid.nifti <- dicom2nifti(uid.dcm, DIM = D, reslice = reslice,
+         descrip = c("PatientID", "SeriesDescription"))
+     writeNIfTI(uid.nifti, fname)
+ }
```

```
##   281949_19040720_axtensor
##   281949_19040720_ax30flip
##   281949_19040720_ax15flip
##   281949_19040720_ax25flip
##   281949_19040720_ax20flip
##   281949_19040720_ax10flip
##   281949_19040720_ax5flip
```

Note, the diffusion tensor imaging (DTI) data `axtensor` is assumed to be four dimensional and all other series (the multiple flip-angle acquisitions) are assumed to be three dimensional. There is always a balance between what information should be pre-specified versus what can easily be extracted from the DICOM headers or images.

5. Conclusion

Medical image analysis depends on the efficient manipulation and conversion of DICOM data. The **oro.dicom** and **oro.nifti** packages have been developed to provide the user with a set of functions that mask as many of the background details as possible while still providing flexible and robust performance.

The future of medical image analysis in R will benefit from a unified view of the imaging data standards: DICOM, NIfTI and ANALYZE. The existence of a single package for handling imaging data formats would facilitate interoperability between the ever increasing number of R packages devoted to medical image analysis. We do not assume that the data structures in **oro.dicom** or **oro.nifti** are best-suited for this purpose and we welcome an open discussion around how best to provide this standardization to the end user.

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References

Chambers JM (2008). *Software for Data Analysis: Programming in R*. Springer, New York.

Clayden J (2010). *tractor.base: A package for reading, manipulating and visualising magnetic resonance images*. R package version 1.5.0, URL http://CRAN.R-project.org/package=tractor.base.

Feng D, Tierney L (2010). *mritc: MRI tissue classification*. R package version 0.3-1, URL http://CRAN.R-project.org/package=mritc.

Ferreira da Silva A (2010a). *cudaBayesreg: CUDA parallel implementation of a Bayesian multilevel model for fMRI data analysis*. R package version 0.3-9, URL http://CRAN.R-project.org/package=cudaBayesreg.

Ferreira da Silva A (2010b). *dpmixsim: Dirichlet process mixture model simulation for clustering and image segmentation*. R package version 0.0-5, URL http://CRAN.R-project.org/package=dpmixsim.

Friston K, Holmes AP, Worsley KJ, Poline JP, Frith CD, Frackowiak RSJ (1994). "Statistical Parametric Maps in Functional Imaging: A General Linear Approach." *Human Brain Mapping*, **2**, 189–210.

Nolf E (2003). "XMedCon - An open-source medical image conversion toolkit." *European Journal of Nuclear Medicine*, **30**(Suppl. 2), S246. URL http://xmedcon.sourceforge.net.

Polzehl J, Tabelow K (2007). "fmri: A package for analyzing fMRI data." *RNews*, **7**(2), 13–17. URL http://www.r-project.org/doc/Rnews/Rnews_2007-2.pdf.

R Development Core Team (2010). *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL http://www.R-project.org.

Sklyar O, Pau G, Smith M, Huber W (2010). *EBImage: Image processing toolbox for R*. R package version 3.5.5.

Whitcher B, Schmid VJ (2010). *dcemriS4: A package for medical image analysis*. R package version 0.41, URL http://CRAN.R-project.org/package=dcemriS4.

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Journal of Statistical Software http://www.jstatsoft.org/
published by the American Statistical Association http://www.amstat.org/
Volume VV, Issue II *Submitted:* yyyy-mm-dd
MMMMMM YYYY *Accepted:* yyyy-mm-dd