NiBabel Documentation

Release 2.0.2

NiBabel Authors

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CONTENTS

Read / write access to some common neuroimaging file formats

This package provides read +/- write access to some common medical and neuroimaging file formats, including: ANALYZE (plain, SPM99, SPM2 and later), GIFTI, NIfTI1, NIfTI2, MINC1, MINC2, MGH and ECAT as well as Philips PAR/REC. We can read and write Freesurfer geometry, and read Freesurfer morphometry and annotation files. There is some very limited support for DICOM. NiBabel is the successor of PyNIfTI.

The various image format classes give full or selective access to header (meta) information and access to the image data is made available via NumPy arrays.

CHAPTER

ONE

WEBSITE

Current documentation on nibabel can always be found at the NIPY nibabel website.

CHAPTER

TWO

MAILING LISTS

Please see the nipy devel list. The nipy devel list is fine for user and developer questions about nibabel.

CHAPTER

THREE

CODE

You can find our sources and single-click downloads:

- Main repository on Github;
- Documentation for all releases and current development tree;
- Download the current release from pypi;
- Download current development version as a zip file;
- Downloads of all available releases.

CHAPTER

FOUR

LICENSE

Nibabel is licensed under the terms of the MIT license. Some code included with nibabel is licensed under the BSD license. Please see the COPYING file in the nibabel distribution.

CHAPTER

FIVE

DOCUMENTATION

- *User Documentation* (manual)
- *Tutorials* (relevant tutorials on imaging)
- *API Documentation* (comprehensive reference)
- *Developer Guidelines* (for those who want to contribute)
- *Development Changelog* (see what has changed)
- *DICOM concepts* (details about implementing DICOM reading)
- genindex (access by keywords)
- search (online and offline full-text search)

See also the *Developer documentation page* for development discussions, release procedure and more.

CHAPTER

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CHAPTER

SEVEN

LICENSE REPRISE

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CHAPTER

EIGHT

DOWNLOAD AND INSTALLATION

Please find detailed *download and installation instructions* in the manual.

CHAPTER

NINE

SUPPORT

If you have problems installing the software or questions about usage, documentation or anything else related to NiBabel, you can post to the NiPy mailing list.

Mailing list neuroimaging@python.org [subscription, archive]

We recommend that anyone using NiBabel subscribes to the mailing list. The mailing list is the preferred way to announce changes and additions to the project. You can also search the mailing list archive using the *mailing list archive search* located in the sidebar of the NiBabel home page.

9.1 NiBabel Manual

9.1.1 Installation

NiBabel is a pure Python package at the moment, and it should be easy to get NiBabel running on any system. For the most popular platforms and operating systems there should be packages in the respective native packaging format (DEB, RPM or installers). On other systems you can install NiBabel using pip or by downloading the source package and running the usual `python setup.py install`.

Installer and packages

pip and the Python package index

If you are not using a Linux package manager, then best way to install NiBabel is via pip. If you don't have pip already, follow the pip install instructions.

Then open a terminal (`Terminal.app` on OSX, `cmd` or `Powershell` on Windows), and type:

```
pip install nibabel
```

This will download and install NiBabel.

If you really like doing stuff manually, you can install NiBabel by downoading the source from NiBabel pypi . Go to the pypi page and select the source distribution you want. Download the distribution, unpack it, and then, from the unpacked directory, run:

```
python setup.py install
```

or (if you need root permission to install on a unix system):

```
sudo python setup.py install
```

Debian/Ubuntu

Our friendas at NeuroDebian have packaged NiBabel at NiBabel NeuroDebian. Please follow the instructions on the NeuroDebian website on how to access their repositories. Once this is done, installing NiBabel is:

```
apt-get update
apt-get install python-nibabel
```

Install from source

If no installer or package is provided for your platfom, you can install NiBabel from source.

Requirements

- Python 2.6 or greater
- NumPy 1.5 or greater
- SciPy (for full SPM-ANALYZE support)
- PyDICOM 0.9.7 or greater (for DICOM support)
- Python Imaging Library (for PNG conversion in DICOMFS)
- nose 0.11 or greater (to run the tests)
- sphinx (to build the documentation)

Get the sources

The latest release is always available from NiBabel pypi.

Alternatively, you can download a tarball of the latest development snapshot (i.e. the current state of the *master* branch of the NiBabel source code repository) from the NiBabel github page.

If you want to have access to the full NiBabel history and the latest development code, do a full clone (aka checkout) of the NiBabel repository:

```
git clone git://github.com/nipy/nibabel.git
```

or:

```
git clone https://github.com/nipy/nibabel.git
```

(The first may be faster, the second more likely to work behind a firewall).

Installation

Just install the modules by invoking:

```
sudo python setup.py install
```

If sudo is not configured (or even installed) you might have to use `su` instead.

Validating your install

For a basic test of your installation, fire up Python and try importing the module to see if everything is fine. It should look something like this:

```
Python 2.7.8 (v2.7.8:ee879c0ffa11, Jun 29 2014, 21:07:35)
[GCC 4.2.1 (Apple Inc. build 5666) (dot 3)] on darwin
Type "help", "copyright", "credits" or "license" for more information.
>>> import nibabel
>>>
```

To run the nibabel test suite, from the terminal run `nosetests nibabel` or `python -c "import nibabel; nibabel.test()`.

To run an extended test suite that validates `nibabel` for long-running and resource-intensive cases, please see *Advanced Testing*.

9.1.2 Getting Started

NiBabel supports an ever growing collection of neuroimaging file formats. Every file format format has its own features and pecularities that need to be taken care of to get the most out of it. To this end, NiBabel offers both high-level format-independent access to neuroimages, as well as an API with various levels of format-specific access to all available information in a particular file format. The following examples show some of NiBabel's capabilities and give you an idea of the API.

For more detail on the API, see Nibabel images.

When loading an image, NiBabel tries to figure out the image format from the filename. An image in a known format can easily be loaded by simply passing its filename to the `load` function.

To start the code examples, we load some useful libraries:

```
>>> import os
>>> import numpy as np
```

Then we fine the nibabel directory containing the example data:

```
>>> from nibabel.testing import data_path
```

There is a NIfTI file in this directory called `example4d.nii.gz`:

```
>>> example_filename = os.path.join(data_path, 'example4d.nii.gz')
```

Now we can import nibabel and load the image:

```
>>> import nibabel as nib
>>> img = nib.load(example_filename)
```

A NiBabel image knows about its shape:

```
>>> img.shape
(128, 96, 24, 2)
```

It also records the data type of the data as stored on disk. In this case the data on disk are 16 bit signed integers:

```
>>> img.get_data_dtype() == np.dtype(np.int16)
True
```

The image has an affine transformation that determines the world-coordinates of the image elements (see Coordinate systems and affines):

```
>>> img.affine.shape
(4, 4)
```

This information is available without the need to load anything of the main image data into the memory. Of course there is also access to the image data as a NumPy array

```
>>> data = img.get_data()
>>> data.shape
(128, 96, 24, 2)
>>> type(data)
<type 'numpy.ndarray'>
```

The complete information embedded in an image header is available via a format-specific header object.

```
>>> hdr = img.header
```

In case of this NIfTI file it allows accessing all NIfTI-specific information, e.g.

```
>>> hdr.get_xyzt_units()
('mm', 'sec')
```

Corresponding "setter" methods allow modifying a header, while ensuring its compliance with the file format specifications.

In some situations we need even more flexibility, and for with great courage, NiBabel also offers access to the raw header information

```
>>> raw = hdr.structarr
>>> raw['xyzt_units']
array(10, dtype=uint8)
```

This lowest level of the API is designed for people who know the file format well enough to work with its internal data, and comes without any safety-net.

Creating a new image in some file format is also easy. At a minimum it only needs some image data and an image coordinate transformation (affine):

```
>>> import numpy as np
>>> data = np.ones((32, 32, 15, 100), dtype=np.int16)
>>> img = nib.Nifti1Image(data, np.eye(4))
>>> img.get_data_dtype() == np.dtype(np.int16)
True
>>> img.header.get_xyzt_units()
('unknown', 'unknown')
```

In this case, we used the identity matrix as the affine transformation. The image header is initialized from the provided data array (i.e. shape, dtype) and all other values are set to resonable defaults.

Saving this new image to a file is trivial. We won't do it here, but it looks like:

```
img.to_filename(os.path.join('build','test4d.nii.gz'))
```

or:

```
nib.save(img, os.path.join('build','test4d.nii.gz'))
```

This short introduction only gave a quick overview of NiBabel's capabilities. Please have a look at the *API Documentation* for more details about supported file formats and their features.

9.1.3 Nibabel images

A nibabel image object is the association of three things:

- an N-D array containing the image *data*;
- a (4, 4) *affine* matrix mapping array coordinates to coordinates in some RAS+ world coordinate space (Coordinate systems and affines);
- image metadata in the form of a *header*.

The image object

First we load some libraries we are going to need for the examples:

```
>>> import os
>>> import numpy as np
```

There is an example image in the nibabel distribution.

```
>>> from nibabel.testing import data_path
>>> example_file = os.path.join(data_path, 'example4d.nii.gz')
```

We load the file to create a nibabel *image object*:

```
>>> import nibabel as nib
>>> img = nib.load(example_file)
```

The object `img` is an instance of a nibabel image. In fact it is an instance of a nibabel *`nibabel.nifti1.Nifti1Image`*:

```
>>> img
<nibabel.nifti1.Nifti1Image object at ...>
```

As with any Python object, you can inspect `img` to see what attributes it has. We recommend using IPython tab completion for this, but here are some examples of interesting attributes:

`dataobj` is the object pointing to the image array data:

```
>>> img.dataobj
<nibabel.arrayproxy.ArrayProxy object at ...>
```

See *Array proxies and proxy images* for more on why this is an array *proxy*.

`affine` is the affine array relating array coordinates from the image data array to coordinates in some RAS+ world coordinate system (Coordinate systems and affines):

```
>>> # Set numpy to print only 2 decimal digits for neatness
>>> np.set_printoptions(precision=2, suppress=True)
```

```
>>> img.affine
array([[  -2.  ,    0.  ,    0.  ,  117.86],
       [  -0.  ,    1.97,   -0.36,  -35.72],
       [   0.  ,    0.32,    2.17,   -7.25],
       [   0.  ,    0.  ,    0.  ,    1.  ]])
```

`header` contains the metadata for this inage. In this case it is specifically NIfTI metadata:

```
>>> img.header
<nibabel.nifti1.Nifti1Header object at ...>
```

The image header

The header of an image contains the image metadata. The information in the header will differ between different image formats. For example, the header information for a NIfTI1 format file differs from the header information for a MINC format file.

Our image is a NIfTI1 format image, and it therefore has a NIfTI1 format header:

```
>>> header = img.header
>>> print(header)
<class 'nibabel.nifti1.Nifti1Header'> object, endian='<'
sizeof_hdr      : 348
data_type       :
db_name         :
extents         : 0
session_error   : 0
regular         : r
dim_info        : 57
dim             : [  4 128  96  24   2   1   1   1]
intent_p1       : 0.0
intent_p2       : 0.0
intent_p3       : 0.0
intent_code     : none
datatype        : int16
bitpix          : 16
slice_start     : 0
pixdim          : [   -1.      2.      2.      2.2  2000.      1.      1.      1. ]
vox_offset      : 0.0
scl_slope       : nan
scl_inter       : nan
slice_end       : 23
slice_code      : unknown
xyzt_units      : 10
cal_max         : 1162.0
cal_min         : 0.0
slice_duration  : 0.0
toffset         : 0.0
glmax           : 0
glmin           : 0
descrip         : FSL3.3\ v2.25 NIfTI-1 Single file format
aux_file        :
qform_code      : scanner
sform_code      : scanner
quatern_b       : -1.94510681403e-26
quatern_c       : -0.996708512306
quatern_d       : -0.081068739295
qoffset_x       : 117.855102539
qoffset_y       : -35.7229423523
qoffset_z       : -7.24879837036
srow_x          : [  -2.      0.      0.    117.86]
srow_y          : [ -0.     1.97  -0.36 -35.72]
srow_z          : [ 0.    0.32  2.17 -7.25]
intent_name     :
magic           : n+1
```

The header of any image will normally have the following methods:

- `get_data_shape()` to get the output shape of the image data array:

```
>>> print(header.get_data_shape())
(128, 96, 24, 2)
```

- `get_data_dtype()` to get the numpy data type in which the image data is stored (or will be stored if you save the image):

```
>>> print(header.get_data_dtype())
int16
```

- `get_zooms()` to get the voxel sizes in millimeters:

```
>>> print(header.get_zooms())
(2.0, 2.0, 2.1999991, 2000.0)
```

  The last value of `header.get_zooms()` is the time between scans in milliseconds; this is the equivalent of voxel size on the time axis.

The image data array

The image data array is a little more complicated, because the image array can be stored in the image object as a numpy array or stored on disk for you to access later via an *array proxy*.

Array proxies and proxy images

When you load an image from disk, as we did here, the data is likely to be accessible via an array proxy. An array proxy is not the array itself but something that represents the array, and can provide the array when we ask for it.

Our image does have an array proxy, as we have already seen:

```
>>> img.dataobj
<nibabel.arrayproxy.ArrayProxy object at ...>
```

The array proxy allows us to create the image object without immediately loading all the array data from disk.

Images with an array proxy object like this one are called *proxy images* because the image data is not yet an array, but the array proxy points to (proxies) the array data on disk.

You can test if the image has a array proxy like this:

```
>>> nib.is_proxy(img.dataobj)
True
```

Array images

We can also create images from numpy arrays. For example:

```
>>> array_data = np.arange(24, dtype=np.int16).reshape((2, 3, 4))
>>> affine = np.diag([1, 2, 3, 1])
>>> array_img = nib.Nifti1Image(array_data, affine)
```

In this case the image array data is already a numpy array, and there is no version of the array on disk. The `dataobj` property of the image is the array itself rather than a proxy for the array:

```
>>> array_img.dataobj
array([[[ 0,  1,  2,  3],
        [ 4,  5,  6,  7],
        [ 8,  9, 10, 11]],
```

```
       [[12, 13, 14, 15],
        [16, 17, 18, 19],
        [20, 21, 22, 23]]], dtype=int16)
>>> array_img.dataobj is array_data
True
```

`dataobj` is an array, not an array proxy, so:

```
>>> nib.is_proxy(array_img.dataobj)
False
```

Getting the image data the easy way

For either type of image (array or proxy) you can always get the data with the *`get_data()`* method.

For the array image, `get_data()` just returns the data array:

```
>>> image_data = array_img.get_data()
>>> image_data.shape
(2, 3, 4)
>>> image_data is array_data
True
```

For the proxy image, the `get_data()` method fetches the array data from disk using the proxy, and returns the array.

```
>>> image_data = img.get_data()
>>> image_data.shape
(128, 96, 24, 2)
```

The image `dataobj` property is still a proxy object:

```
>>> img.dataobj
<nibabel.arrayproxy.ArrayProxy object at ...>
```

Proxies and caching

You may not want to keep loading the image data off disk every time you call `get_data()` on a proxy image. By default, when you call `get_data()` the first time on a proxy image, the image object keeps a cached copy of the loaded array. The next time you call `img.get_data()`, the image returns the array from cache rather than loading it from disk again.

```
>>> data_again = img.get_data()
```

The returned data is the same (cached) copy we returned before:

```
>>> data_again is image_data
True
```

See Images and memory for more details on managing image memory and controlling the image cache.

Loading and saving

The `save` and `load` functions in nibabel should do all the work for you:

```
>>> nib.save(array_img, 'my_image.nii')
>>> img_again = nib.load('my_image.nii')
>>> img_again.shape
(2, 3, 4)
```

You can also use the `to_filename` method:

```
>>> array_img.to_filename('my_image_again.nii')
>>> img_again = nib.load('my_image_again.nii')
>>> img_again.shape
(2, 3, 4)
```

You can get and set the filename with `get_filename()` and `set_filename()`:

```
>>> img_again.set_filename('another_image.nii')
>>> img_again.get_filename()
'another_image.nii'
```

Details of files and images

If an image can be loaded or saved on disk, the image will have an attribute called `file_map`. `img.file_map` is a dictionary where the keys are the names of the files that the image uses to load / save on disk, and the values are `FileHolder` objects, that usually contain the filenames that the image has been loaded from or saved to. In the case of a NiFTI1 single file, this is just a single image file with a `.nii` or `.nii.gz` extension:

```
>>> list(img_again.file_map)
['image']
>>> img_again.file_map['image'].filename
'another_image.nii'
```

Other file types need more than one file to make up the image. The NiFTI1 pair type is one example. NIfTI pair images have one file containing the header information and another containing the image array data:

```
>>> pair_img = nib.Nifti1Pair(array_data, np.eye(4))
>>> nib.save(pair_img, 'my_pair_image.img')
>>> sorted(pair_img.file_map)
['header', 'image']
>>> pair_img.file_map['header'].filename
'my_pair_image.hdr'
>>> pair_img.file_map['image'].filename
'my_pair_image.img'
```

The older Analyze format also has a separate header and image file:

```
>>> ana_img = nib.AnalyzeImage(array_data, np.eye(4))
>>> sorted(ana_img.file_map)
['header', 'image']
```

It is the contents of the `file_map` that gets changed when you use `set_filename` or `to_filename`:

```
>>> ana_img.set_filename('analyze_image.img')
>>> ana_img.file_map['image'].filename
'analyze_image.img'
>>> ana_img.file_map['header'].filename
'analyze_image.hdr'
```

9.1.4 Images and memory

We saw in Nibabel images that images loaded from disk are usually *proxy images*. Proxy images are images that have a `dataobj` property that is not a numpy array, but an *array proxy* that can fetch the array data from disk.

```
>>> import os
>>> import numpy as np
>>> from nibabel.testing import data_path
>>> example_file = os.path.join(data_path, 'example4d.nii.gz')
```

```
>>> import nibabel as nib
>>> img = nib.load(example_file)
>>> img.dataobj
<nibabel.arrayproxy.ArrayProxy object at ...>
```

Nibabel does not load the image array from the proxy when you `load` the image. It waits until you ask for the array data. The standard way to ask for the array data is to call the `get_data()` method:

```
>>> data = img.get_data()
>>> data.shape
(128, 96, 24, 2)
```

We also saw in *Proxies and caching* that this call to `get_data()` will (by default) load the array data into an internal image cache. The image returns the cached copy on the next call to `get_data()`:

```
>>> data_again = img.get_data()
>>> data is data_again
True
```

This behavior is convenient if you want quick and repeated access to the image array data. The down-side is that the image keeps a reference to the image data array, so the array can't be cleared from memory until the image object gets deleted. You might prefer to keep loading the array from disk instead of keeping the cached copy in the image.

This page describes ways of using the image array proxies to save memory and time.

Using `in_memory` to check the state of the cache

You can use the `in_memory` property to check if the image has cached the array.

The `in_memory` property is always True for array images, because the image data is always an array in memory:

```
>>> array_data = np.arange(24, dtype=np.int16).reshape((2, 3, 4))
>>> affine = np.diag([1, 2, 3, 1])
>>> array_img = nib.Nifti1Image(array_data, affine)
>>> array_img.in_memory
True
```

For a proxy image, the `in_memory` property is False when the array is not in cache, and True when it is in cache:

```
>>> img = nib.load(example_file)
>>> img.in_memory
False
>>> data = img.get_data()
>>> img.in_memory
True
```

Using `uncache`

As y'all know, the proxy image has the array in cache, `get_data()` returns the cached array:

```
>>> data_again = img.get_data()
>>> data_again is data  # same array returned from cache
True
```

You can uncache a proxy image with the `uncache()` method:

```
>>> img.uncache()
>>> img.in_memory
False
>>> data_once_more = img.get_data()
>>> data_once_more is data  # a new copy read from disk
False
```

`uncache()` has no effect if the image is an array image, or if the cache is already empty.

You need to be careful when you modify arrays returned by `get_data()` on proxy images, because `uncache` will then change the result you get back from `get_data()`:

```
>>> proxy_img = nib.load(example_file)
>>> data = proxy_img.get_data()  # array cached and returned
>>> data[0, 0, 0, 0]
0
>>> data[0, 0, 0, 0] = 99  # modify returned array
>>> data_again = proxy_img.get_data()  # return cached array
>>> data_again[0, 0, 0, 0]  # cached array modified
99
```

So far the proxy image behaves the same as an array image. `uncache()` has no effect on an array image, but it does have an effect on the returned array of a proxy image:

```
>>> proxy_img.uncache()  # cached array discarded from proxy image
>>> data_once_more = proxy_img.get_data()  # new copy of array loaded
>>> data_once_more[0, 0, 0, 0]  # array modifications discarded
0
```

Saving memory

Uncache the array

If you do not want the image to keep the array in its internal cache, you can use the `uncache()` method:

```
>>> img.uncache()
```

Use the array proxy instead of `get_data()`

The `dataobj` property of a proxy image is an array proxy. We can ask the proxy to return the array directly by passing `dataobj` to the numpy `asarray` function:

```
>>> proxy_img = nib.load(example_file)
>>> data_array = np.asarray(proxy_img.dataobj)
>>> type(data_array)
<type 'numpy.ndarray'>
```

This also works for array images, because `np.asarray` returns the array:

```
>>> array_img = nib.Nifti1Image(array_data, affine)
>>> data_array = np.asarray(array_img.dataobj)
>>> type(data_array)
<type 'numpy.ndarray'>
```

If you want to avoid caching you can avoid `get_data()` and always use `np.asarray(img.dataobj)`.

Use the `caching` keyword to `get_data()`

The default behavior of the `get_data()` function is to always fill the cache, if it is empty. This corresponds to the default `'fill'` value to the `caching` keyword. So, this:

```
>>> proxy_img = nib.load(example_file)
>>> data = proxy_img.get_data()  # default caching='fill'
>>> proxy_img.in_memory
True
```

is the same as this:

```
>>> proxy_img = nib.load(example_file)
>>> data = proxy_img.get_data(caching='fill')
>>> proxy_img.in_memory
True
```

Sometimes you may want to avoid filling the cache, if it is empty. In this case, you can use `caching='unchanged'`:

```
>>> proxy_img = nib.load(example_file)
>>> data = proxy_img.get_data(caching='unchanged')
>>> proxy_img.in_memory
False
```

`caching='unchanged'` will leave the cache full if it is already full.

```
>>> data = proxy_img.get_data(caching='fill')
>>> proxy_img.in_memory
True
>>> data = proxy_img.get_data(caching='unchanged')
>>> proxy_img.in_memory
True
```

See the *get_data() docstring* for more detail.

Saving time and memory

You can use the array proxy to get slices of data from disk in an efficient way.

The array proxy API allows you to do slicing on the proxy. In most cases this will mean that you only load the data from disk that you actually need, often saving both time and memory.

For example, let us say you only wanted the second volume from the example dataset. You could do this:

```
>>> proxy_img = nib.load(example_file)
>>> data = proxy_img.get_data()
>>> data.shape
(128, 96, 24, 2)
>>> vol1 = data[..., 1]
```

```
>>> vol1.shape
(128, 96, 24)
```

The problem is that you had to load the whole data array into memory before throwing away the first volume and keeping the second.

You can use array proxy slicing to do this more efficiently:

```
>>> proxy_img = nib.load(example_file)
>>> vol1 = proxy_img.dataobj[..., 1]
>>> vol1.shape
(128, 96, 24)
```

The slicing call in `proxy_img.dataobj[..., 1]` will only load the data from disk that you need to fill the memory of `vol1`.

9.1.5 Working with NIfTI images

This page describes some features of the nibabel implementation of the NIfTI format. Generally all these features apply equally to the NIfTI 1 and the NIfTI 2 format, but we will note the differences when they come up. NIfTI 1 is much more common than NIfTI 2.

Preliminaries

We first set some display parameters to print out numpy arrays in a compact form:

```
>>> import numpy as np
>>> # Set numpy to print only 2 decimal digits for neatness
>>> np.set_printoptions(precision=2, suppress=True)
```

Example NIfTI images

```
>>> import os
>>> import nibabel as nib
>>> from nibabel.testing import data_path
```

This is the example NIfTI 1 image:

```
>>> example_ni1 = os.path.join(data_path, 'example4d.nii.gz')
>>> n1_img = nib.load(example_ni1)
>>> n1_img
<nibabel.nifti1.Nifti1Image object at ...>
```

Here is the NIfTI 2 example image:

```
>>> example_ni2 = os.path.join(data_path, 'example_nifti2.nii.gz')
>>> n2_img = nib.load(example_ni2)
>>> n2_img
<nibabel.nifti2.Nifti2Image object at ...>
```

The NIfTI header

The NIfTI 1 header is a small C structure of size 352 bytes. It contains the following fields:

```
>>> n1_header = n1_img.header
>>> print(n1_header)
<class 'nibabel.nifti1.Nifti1Header'> object, endian='<'
sizeof_hdr      : 348
data_type       :
db_name         :
extents         : 0
session_error   : 0
regular         : r
dim_info        : 57
dim             : [  4 128  96  24   2   1   1   1]
intent_p1       : 0.0
intent_p2       : 0.0
intent_p3       : 0.0
intent_code     : none
datatype        : int16
bitpix          : 16
slice_start     : 0
pixdim          : [   -1.      2.      2.      2.2  2000.      1.      1.      1. ]
vox_offset      : 0.0
scl_slope       : nan
scl_inter       : nan
slice_end       : 23
slice_code      : unknown
xyzt_units      : 10
cal_max         : 1162.0
cal_min         : 0.0
slice_duration  : 0.0
toffset         : 0.0
glmax           : 0
glmin           : 0
descrip         : FSL3.3\ v2.25 NIfTI-1 Single file format
aux_file        :
qform_code      : scanner
sform_code      : scanner
quatern_b       : -1.94510681403e-26
quatern_c       : -0.996708512306
quatern_d       : -0.081068739295
qoffset_x       : 117.855102539
qoffset_y       : -35.7229423523
qoffset_z       : -7.24879837036
srow_x          : [  -2.      0.      0.    117.86]
srow_y          : [ -0.     1.97  -0.36 -35.72]
srow_z          : [ 0.    0.32  2.17 -7.25]
intent_name     :
magic           : n+1
```

The NIfTI 2 header is similar, but of length 540 bytes, with fewer fields:

```
>>> n2_header = n2_img.header
>>> print(n2_header)
    <class 'nibabel.nifti2.Nifti2Header'> object, endian='<'
    sizeof_hdr      : 540
    magic           : n+2
    eol_check       : [13 10 26 10]
    datatype        : int16
    bitpix          : 16
    dim             : [ 4 32 20 12  2  1  1  1]
```

```
    intent_p1       : 0.0
    intent_p2       : 0.0
    intent_p3       : 0.0
    pixdim          : [   -1.      2.      2.      2.2  2000.      1.      1.      1. ]
    vox_offset      : 0
    scl_slope       : nan
    scl_inter       : nan
    cal_max         : 1162.0
    cal_min         : 0.0
    slice_duration  : 0.0
    toffset         : 0.0
    slice_start     : 0
    slice_end       : 23
    descrip         : FSL3.3\ v2.25 NIfTI-1 Single file format
    aux_file        :
    qform_code      : scanner
    sform_code      : scanner
    quatern_b       : -1.94510681403e-26
    quatern_c       : -0.996708512306
    quatern_d       : -0.081068739295
    qoffset_x       : 117.855102539
    qoffset_y       : -35.7229423523
    qoffset_z       : -7.24879837036
    srow_x          : [  -2.      0.      0.    117.86]
    srow_y          : [ -0.     1.97  -0.36 -35.72]
    srow_z          : [ 0.    0.32  2.17 -7.25]
    slice_code      : unknown
    xyzt_units      : 10
    intent_code     : none
    intent_name     :
    dim_info        : 57
    unused_str      :
```

You can get and set individual fields in the header using dict (mapping-type) item access. For example:

```
>>> n1_header['cal_max']
array(1162.0, dtype=float32)
>>> n1_header['cal_max'] = 1200
>>> n1_header['cal_max']
array(1200.0, dtype=float32)
```

Check the attributes of the header for `get_` / `set_` methods to get and set various combinations of NIfTI header fields.

The `get_` / `set_` methods should check and apply valid combinations of values from the header, whereas you can do anything you like with the dict / mapping item access. It is safer to use the `get_` / `set_` methods and use the mapping item access only if the `get_` / `set_` methods will not do what you want.

The NIfTI affines

Like other nibabel image types, NIfTI images have an affine relating the voxel coordinates to world coordinates in RAS+ space:

```
>>> n1_img.affine
array([[  -2.  ,    0.  ,    0.  ,  117.86],
       [  -0.  ,    1.97,   -0.36,  -35.72],
       [   0.  ,    0.32,    2.17,   -7.25],
       [   0.  ,    0.  ,    0.  ,    1.  ]])
```

Unlike other formats, the NIfTI header format can specify this affine in one of three ways — the *sform* affine, the *qform* affine and the *fall-back header* affine.

Nibabel uses an *algorithm* to chose which of these three it will use for the overall image `affine`.

The sform affine

The header stores the three first rows of the 4 by 4 affine in the header fields `srow_x`, `srow_y`, `srow_z`. The header does not store the fourth row because it is always `[0, 0, 0, 1]` (see Coordinate systems and affines).

You can get the sform affine specifically with the `get_sform()` method of the image or the header.

For example:

```
>>> print(n1_header['srow_x'])
[  -2.      0.      0.    117.86]
>>> print(n1_header['srow_y'])
[ -0.     1.97  -0.36 -35.72]
>>> print(n1_header['srow_z'])
[ 0.    0.32  2.17 -7.25]
>>> print(n1_header.get_sform())
[[  -2.      0.      0.    117.86]
 [  -0.      1.97   -0.36  -35.72]
 [   0.      0.32    2.17   -7.25]
 [   0.      0.      0.      1.  ]]
```

This affine is valid only if the `sform_code` is not zero.

```
>>> print(n1_header['sform_code'])
1
```

The different sform code values specify which RAS+ space the sform affine refers to, with these interpretations:

Code	Label	Meaning
0	unknown	sform not defined
1	scanner	RAS+ in scanner coordinates
2	aligned	RAS+ aligned to some other scan
3	talairach	RAS+ in Talairach atlas space
4	mni	RAS+ in MNI atlas space

In our case the code is 1, meaning "scanner" alignment.

You can get the affine and the code using the `coded=True` argument to `get_sform()`:

```
>>> print(n1_header.get_sform(coded=True))
(array([[  -2.  ,    0.  ,    0.  ,  117.86],
       [  -0.  ,    1.97,   -0.36,  -35.72],
       [   0.  ,    0.32,    2.17,   -7.25],
       [   0.  ,    0.  ,    0.  ,    1.  ]]), array(1, dtype=int16))
```

You can set the sform with with the `get_sform()` method of the header and the image.

```
>>> n1_header.set_sform(np.diag([2, 3, 4, 1]))
>>> n1_header.get_sform()
array([[ 2.,  0.,  0.,  0.],
       [ 0.,  3.,  0.,  0.],
       [ 0.,  0.,  4.,  0.],
       [ 0.,  0.,  0.,  1.]])
```

Set the affine and code using the `code` parameter to `set_sform()`:

```
>>> n1_header.set_sform(np.diag([3, 4, 5, 1]), code='mni')
>>> n1_header.get_sform(coded=True)
(array([[ 3.,  0.,  0.,  0.],
       [ 0.,  4.,  0.,  0.],
       [ 0.,  0.,  5.,  0.],
       [ 0.,  0.,  0.,  1.]]), array(4, dtype=int16))
```

The qform affine

This affine can be calculated from a combination of the voxel sizes (entries 1 through 4 of the `pixdim` field), a sign flip called `qfac` stored in entry 0 of `pixdim`, and a quaternion that can be reconstructed from fields `quatern_b`, `quatern_c`, `quatern_d`.

See the code for the *`get_qform() method`* for details.

You can get and set the qform affine using the equivalent methods to those for the sform: `get_qform()`, `set_qform()`.

```
>>> n1_header.get_qform(coded=True)
(array([[  -2.  ,    0.  ,    0.  ,  117.86],
       [  -0.  ,    1.97,   -0.36,  -35.72],
       [   0.  ,    0.32,    2.17,   -7.25],
       [   0.  ,    0.  ,    0.  ,    1.  ]]), array(1, dtype=int16))
```

The qform also has a corresponding `qform_code` with the same interpretation as the *sform_code*.

The fall-back header affine

This is the affine of last resort, constructed only from the `pixdim` voxel sizes. The NIfTI specification says that this should set the first voxel in the image as [0, 0, 0] in world coordinates, but we nibabblers follow SPM in preferring to set the central voxel to have [0, 0, 0] world coordinate. The NIfTI spec also implies that the image should be assumed to be in RAS+ *voxel* orientation for this affine (see Coordinate systems and affines). Again like SPM, we prefer to assume LAS+ voxel orientation by default.

You can always get the fall-back affine with `get_base_affine()`:

```
>>> n1_header.get_base_affine()
array([[  -2. ,    0. ,    0. ,  127. ],
       [   0. ,    2. ,    0. ,  -95. ],
       [   0. ,    0. ,    2.2,  -25.3],
       [   0. ,    0. ,    0. ,    1. ]])
```

Choosing the image affine

Given there are three possible affines defined in the NIfTI header, nibabel has to chose which of these to use for the image `affine`.

The algorithm is defined in the `get_best_affine()` method. It is:

1. If `sform_code` != 0 ('unknown') use the sform affine; else
2. If `qform_code` != 0 ('unknown') use the qform affine; else
3. Use the fall-back affine.

Data scaling

NIfTI uses a simple scheme for data scaling.

By default, nibabel will take care of this scaling for you, but there may be times that you want to control the data scaling yourself. If so, the next section describes how the scaling works and the nibabel implementation of same.

There are two scaling fields in the header called `scl_slope` and `scl_inter`.

The output data from a NIfTI image comes from:

1. Loading the binary data from the image file;
2. Casting the numbers to the binary format given in the header and returned by `get_data_dtype()`;
3. Reshaping to the output image shape;
4. Multiplying the result by the header `scl_slope` value, if both of `scl_slope` and `scl_inter` are defined;
5. Adding the value header `scl_slope` value to the result, if both of `scl_slope` and `scl_inter` are defined;

'Defined' means, the value is not NaN (not a number).

All this gets built into the array proxy when you load a NIfTI image.

When you load an image, the header scaling values automatically get set to NaN (undefined) to mark the fact that the scaling values have been consumed by the read. The scaling values read from the header on load only appear in the array proxy object.

To see how this works, let's make a new image with some scaling:

```
>>> array_data = np.arange(24, dtype=np.int16).reshape((2, 3, 4))
>>> affine = np.diag([1, 2, 3, 1])
>>> array_img = nib.Nifti1Image(array_data, affine)
>>> array_header = array_img.header
```

The default scaling values are NaN (undefined):

```
>>> array_header['scl_slope']
array(nan, dtype=float32)
>>> array_header['scl_inter']
array(nan, dtype=float32)
```

You can get the scaling values with the `get_slope_inter()` method:

```
>>> array_header.get_slope_inter()
(None, None)
```

None corresponds to the NaN scaling value (undefined).

We can set them in the image header, so they get saved to the header when the image is written. We can do this by setting the fields directly, or with `set_slope_inter()`:

```
>>> array_header.set_slope_inter(2, 10)
>>> array_header.get_slope_inter()
(2.0, 10.0)
>>> array_header['scl_slope']
array(2.0, dtype=float32)
>>> array_header['scl_inter']
array(10.0, dtype=float32)
```

Setting the scale factors in the header has no effect on the image data before we save and load again:

```
>>> array_img.get_data()
array([[[ 0,  1,  2,  3],
        [ 4,  5,  6,  7],
        [ 8,  9, 10, 11]],

       [[12, 13, 14, 15],
        [16, 17, 18, 19],
        [20, 21, 22, 23]]], dtype=int16)
```

Now we save the image and load it again:

```
>>> nib.save(array_img, 'scaled_image.nii')
>>> scaled_img = nib.load('scaled_image.nii')
```

The data array has the scaling applied:

```
>>> scaled_img.get_data()
memmap([[[ 10.,  12.,  14.,  16.],
        [ 18.,  20.,  22.,  24.],
        [ 26.,  28.,  30.,  32.]],

       [[ 34.,  36.,  38.,  40.],
        [ 42.,  44.,  46.,  48.],
        [ 50.,  52.,  54.,  56.]]])
```

The header for the loaded image has had the scaling reset to undefined, to mark the fact that the scaling has been "consumed" by the load:

```
>>> scaled_img.header.get_slope_inter()
(None, None)
```

The original slope and intercept are still accessible in the array proxy object:

```
>>> scaled_img.dataobj.slope
2.0
>>> scaled_img.dataobj.inter
10.0
```

If the header scaling is undefined when we save the image, nibabel will try to find an optimum slope and intercept to best preserve the precision of the data in the output data type. Because nibabel will set the scaling to undefined when loading the image, or creating a new image, this is the default behavior.

9.1.6 Image voxel orientation

It is sometimes useful to know the approximate world-space orientations of the image voxel axes.

See Coordinate systems and affines for background on voxel and world axes.

For example, let's say we had an image with an identity affine:

```
>>> import numpy as np
>>> import nibabel as nib
>>> affine = np.eye(4)  # identity affine
>>> voxel_data = np.random.normal(size=(10, 11, 12))
>>> img = nib.Nifti1Image(voxel_data, affine)
```

Because the affine is an identity affine, the voxel axes align with the world axes. By convention, nibabel world axes are always in RAS+ orientation (left to Right, posterior to Anterior, inferior to Superior).

Let's say we took a single line of voxels along the first voxel axis:

```
>>> single_line_axis_0 = voxel_data[:, 0, 0]
```

The first voxel axis is aligned to the left to Right world axes. This means that the first voxel is towards the left of the world, and the last voxel is towards the right of the world.

Here is a single line in the second axis:

```
>>> single_line_axis_1 = voxel_data[0, :, 0]
```

The first voxel in this line is towards the posterior of the world, and the last towards the anterior.

```
>>> single_line_axis_2 = voxel_data[0, 0, :]
```

The first voxel in this line is towards the inferior of the world, and the last towards the superior.

This image therefore has RAS+ *voxel* axes.

In other cases, it is not so obvious what the orientations of the axes are. For example, here is our example NIfTI 1 file again:

```
>>> import os
>>> from nibabel.testing import data_path
>>> example_file = os.path.join(data_path, 'example4d.nii.gz')
>>> img = nib.load(example_file)
```

Here is the affine (to two digits decimal precision):

```
>>> np.set_printoptions(precision=2, suppress=True)
>>> img.affine
array([[  -2.  ,    0.  ,    0.  ,  117.86],
       [  -0.  ,    1.97,   -0.36,  -35.72],
       [   0.  ,    0.32,    2.17,   -7.25],
       [   0.  ,    0.  ,    0.  ,    1.  ]])
```

What are the orientations of the voxel axes here?

Nibabel has a routine to tell you, called `aff2axcodes`.

```
>>> nib.aff2axcodes(img.affine)
('L', 'A', 'S')
```

The voxel orientations are nearest to:

1. First voxel axis goes from right to Left;
2. Second voxel axis goes from posterior to Anterior;
3. Third voxel axis goes from inferior to Superior.

Sometimes you may want to rearrange the image voxel axes to make them as close as possible to RAS+ orientation. We refer to this voxel orientation as *canonical* voxel orientation, because RAS+ is our canonical world orientation. Rearranging the voxel axes means reversing and / or reordering the voxel axes.

You can do the arrangement with `as_closest_canonical`:

```
>>> canonical_img = nib.as_closest_canonical(img)
>>> canonical_img.affine
array([[   2.  ,    0.  ,    0.  , -136.14],
       [   0.  ,    1.97,   -0.36,  -35.72],
       [  -0.  ,    0.32,    2.17,   -7.25],
       [   0.  ,    0.  ,    0.  ,    1.  ]])
>>> nib.aff2axcodes(canonical_img.affine)
('R', 'A', 'S')
```

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NiBabel

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NetCDF

The netcdf IO module has been taken from SciPy.

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Sphinx autosummary extension

This extension has been copied from NumPy (Jul 16, 2010) as the one shipped with Sphinx 0.6 doesn't work properly.

```
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Ordereddict

In `nibabel/externals/ordereddict.py`

Copied from: https://pypi.python.org/packages/source/o/ordereddict/ordereddict-1.1.tar.gz#md5=a0ed854ee442051b249bfad0f638bbec

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mni_icbm152_t1_tal_nlin_asym_09a

The file `doc/source/someone.nii.gz` is a subsampled version of the file `mni_icbm152_t1_tal_nlin_asym_09a.nii` from the MNI non-linear templates archive `mni_icbm152_t1_tal_nlin_asym_09a`. The original image has the following license (where 'softwware' refers to the image):

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Philips PAR/REC data

The files:

```
nibabel/tests/data/phantom_EPI_asc_CLEAR_2_1.PAR
nibabel/tests/data/phantom_EPI_asc_CLEAR_2_1.REC
nibabel/tests/data/Phantom_EPI_3mm_cor_20APtrans_15RLrot_SENSE_15_1.PAR
nibabel/tests/data/Phantom_EPI_3mm_cor_SENSE_8_1.PAR
nibabel/tests/data/Phantom_EPI_3mm_sag_15AP_SENSE_13_1.PAR
nibabel/tests/data/Phantom_EPI_3mm_sag_15FH_SENSE_12_1.PAR
nibabel/tests/data/Phantom_EPI_3mm_sag_15RL_SENSE_11_1.PAR
nibabel/tests/data/Phantom_EPI_3mm_sag_SENSE_7_1.PAR
nibabel/tests/data/Phantom_EPI_3mm_tra_-30AP_10RL_20FH_SENSE_14_1.PAR
nibabel/tests/data/Phantom_EPI_3mm_tra_15FH_SENSE_9_1.PAR
nibabel/tests/data/Phantom_EPI_3mm_tra_15RL_SENSE_10_1.PAR
nibabel/tests/data/Phantom_EPI_3mm_tra_SENSE_6_1.PAR
```

are from http://psydata.ovgu.de/philips_achieva_testfiles, and released under the PDDL version 1.0 available at http://opendatacommons.org/licenses/pddl/1.0/

The files:

```
nibabel/nibabel/tests/data/DTI.PAR
nibabel/nibabel/tests/data/NA.PAR
nibabel/nibabel/tests/data/T1.PAR
nibabel/nibabel/tests/data/T2-interleaved.PAR
nibabel/nibabel/tests/data/T2.PAR
nibabel/nibabel/tests/data/T2_-interleaved.PAR
```

```
nibabel/nibabel/tests/data/T2_.PAR
nibabel/nibabel/tests/data/fieldmap.PAR
```

are from https://github.com/yarikoptic/nitest-balls1, also released under the the PDDL version 1.0 available at http://opendatacommons.org/licenses/pddl/1.0/

nibabel/nibabel/tests/data/umass_anonymized.PAR

is courtesy of the University of Massachusetts Medical School, also released under the PDDL.

9.1.8 NiBabel Development Changelog

NiBabel is the successor to the much-loved PyNifti package. Here we list the releases for both packages.

The full VCS changelog is available here:

http://github.com/nipy/nibabel/commits/master

Releases

NiBabel

Most work on NiBabel so far has been by Matthew Brett (MB), Michael Hanke (MH) and Stephan Gerhard (SG).

References like "pr/298" refer to github pull request numbers.

- 2.0.2 (Monday 23 November 2015)
  - Fix for integer overflow on large images (pr/325) (MB);
  - Fix for Freesurfer nifti files with unusual dimensions (pr/332) (Chris Markiewicz);
  - Fix typos on benchmarks and tests (pr/336, pr/340, pr/347) (Chris Markiewicz);
  - Fix Windows install script (pr/339) (MB);
  - Support for Python 3.5 (pr/363) (MB) and numpy 1.10 (pr/358) (Chris Markiewicz);
  - Update pydicom imports to permit version 1.0 (pr/379) (Chris Markiewicz);
  - Workaround for Python 3.5.0 gzip regression (pr/383) (Ben Cipollini).
  - tripwire.TripWire object now raises subclass of AttributeError when trying to get an attribute, rather than a direct subclass of Exception. This prevents Python 3.5 triggering the tripwire when doing inspection prior to running doctests.
  - Minor API change for tripwire.TripWire object; code that checked for AttributeError will now also catch TripWireError.
- 2.0.1 (Saturday 27 June 2015)

  Contributions from Ben Cipollini, Chris Markiewicz, Alexandre Gramfort, Clemens Bauer, github user freec84.
  - Bugfix release with minor new features;
  - Added `axis` parameter to `concat_images` (pr/298) (Ben Cipollini);
  - Fix for unsigned integer data types in ECAT images (pr/302) (MB, test data and issue report from Github user freec84);
  - Added new ECAT and Freesurfer data files to automated testing;
  - Fix for Freesurfer labels error on early numpies (pr/307) (Alexandre Gramfort);

- Fixes for PAR / REC header parsing (pr/312) (MB, issue reporting and test data by Clemens C. C. Bauer);
- Workaround for reading Freesurfer ico7 surface files (pr/315) (Chris Markiewicz);
- Changed to github pages for doc hosting;
- Changed docs to point to neuroimaging@python.org mailing list.

- 2.0.0 (Tuesday 9 December 2014)

  This release had large contributions from Eric Larson, Brendan Moloney, Nolan Nichols, Basile Pinsard, Chris Johnson and Nikolaas N. Oosterhof.

  - New feature, bugfix release with minor API breakage;
  - Minor API breakage: default write of NIfTI / Analyze image data offset value. The data offset is the number of bytes from the beginning of file to skip before reading the image data. Nibabel behavior changed from keeping the value as read from file, to setting the offset to zero on read, and setting the offset when writing the header. The value of the offset will now be the minimum value necessary to make room for the header and any extensions when writing the file. You can override the default offset by setting value explicitly to some value other than zero. To read the original data offset as read from the header, use the `offset` property of the image `dataobj` attribute;
  - Minor API breakage: data scaling in NIfTI / Analyze now set to NaN when reading images. Data scaling refers to the data intercept and slope values in the NIfTI / Analyze header. To read the original data scaling you need to look at the `slope` and `inter` properties of the image `dataobj` attribute. You can set scaling explicitly by setting the slope and intercept values in the header to values other than NaN;
  - New API for managing image caching; images have an `in_memory` property that is true if the image data has been loaded into cache, or is already an array in memory; `get_data` has new keyword argument `caching` to specify whether the cache should be filled by `get_data`;
  - Images now have properties `dataobj`, `affine`, `header`. We will slowly phase out the `get_affine` and `get_header` image methods;
  - The image `dataobj` can be sliced using an efficient algorithm to avoid reading unnecessary data from disk. This makes it possible to do very efficient reads of single volumes from a time series;
  - NIfTI2 read / write support;
  - Read support for MINC2;
  - Much extended read support for PAR / REC, largely due to work from Eric Larson and Gregory R. Lee on new code, advice and code review. Thanks also to Jeff Stevenson and Bennett Landman for helpful discussion;
  - `parrec2nii` script outputs images in LAS voxel orientation, which appears to be necessary for compatibility with FSL `dtifit` / `fslview` diffusion analysis pipeline;
  - Preliminary support for Philips multiframe DICOM images (thanks to Nolan Nichols, Ly Nguyen and Brendan Moloney);
  - New function to save Freesurfer annotation files (by Github user ohinds);
  - Method to return MGH format `vox2ras_tkr` affine (Eric Larson);
  - A new API for reading unscaled data from NIfTI and other images, using `img.dataobj.get_unscaled()`. Deprecate previous way of doing this, which was to read data with the `read_img_data` function;
  - Fix for bug when replacing NaN values with zero when writing floating point data as integers. If the input floating point data range did not include zero, then NaN would not get written to a value corresponding to zero in the output;

  - Improvements and bug fixes to image orientation calculation and DICOM wrappers by Brendan Moloney;
  - Bug fixes writing GIfTI files. We were using a base64 encoding that didn't match the spec, and the wrong field name for the endian code. Thanks to Basile Pinsard and Russ Poldrack for diagnosis and fixes;
  - Bug fix in `freesurfer.read_annot` with `orig_ids=False` when annot contains vertices with no label (Alexandre Gramfort);
  - More tutorials in the documentation, including introductory tutorial on DICOM, and on coordinate systems;
  - Lots of code refactoring, including moving to common code-base for Python 2 and Python 3;
  - New mechanism to add images for tests via git submodules.

- 1.3.0 (Tuesday 11 September 2012)

  Special thanks to Chris Johnson, Brendan Moloney and JB Poline.

  - New feature and bugfix release
  - Add ability to write Freesurfer triangle files (Chris Johnson)
  - Relax threshold for detecting rank deficient affines in orientation detection (JB Poline)
  - Fix for DICOM slice normal numerical error (issue #137) (Brendan Moloney)
  - Fix for Python 3 error when writing zero bytes for offset padding

- 1.2.2 (Wednesday 27 June 2012)
  - Bugfix release
  - Fix longdouble tests for Debian PPC (thanks to Yaroslav Halchecko for finding and diagnosing these errors)
  - Generalize longdouble tests in the hope of making them more robust
  - Disable saving of float128 nifti type unless platform has real IEEE binary128 longdouble type.

- 1.2.1 (Wednesday 13 June 2012)

  Particular thanks to Yaroslav Halchecko for fixes and cleanups in this release.

  - Bugfix release
  - Make compatible with pydicom 0.9.7
  - Refactor, rename nifti diagnostic script to `nib-nifti-dx`
  - Fix a bug causing an error when analyzing affines for orientation, when the affine contained all 0 columns
  - Add missing `dicomfs` script to installation list and rename to `nib-dicomfs`

- 1.2.0 (Sunday 6 May 2012)

  This release had large contributions from Krish Subramaniam, Alexandre Gramfort, Cindee Madison, Félix C. Morency and Christian Haselgrove.

  - New feature and bugfix release
  - Freesurfer format support by Krish Subramaniam and Alexandre Gramfort.
  - ECAT read write support by Cindee Madison and Félix C. Morency.
  - A DICOM fuse filesystem by Christian Haselgrove.
  - Much work on making data scaling on read and write more robust to rounding error and overflow (MB).
  - Import of nipy functions for working with affine transformation matrices.

  - Added methods for working with nifti sform and qform fields by Bago Amirbekian and MB, with useful discussion by Brendan Moloney.
  - Fixes to read / write of RGB analyze images by Bago Amirbekian.
  - Extensions to `concat_images` by Yannick Schwartz.
  - A new `nib-ls` script to display information about neuroimaging files, and various other useful fixes by Yaroslav Halchenko.

- 1.1.0 (Thursday 28 April 2011)

  Special thanks to Chris Burns, Jarrod Millman and Yaroslav Halchenko.

  - New feature release
  - Python 3.2 support
  - Substantially enhanced gifti reading support (SG)
  - Refactoring of trackvis read / write to allow reading and writing of voxel points and mm points in tracks. Deprecate use of negative voxel sizes; set voxel_order field in trackvis header. Thanks to Chris Filo Gorgolewski for pointing out the problem and Ruopeng Wang in the trackvis forum for clarifying the coordinate system of trackvis files.
  - Added routine to give approximate array orientation in form such as 'RAS' or 'LPS'
  - Fix numpy dtype hash errors for numpy 1.2.1
  - Other bug fixes as for 1.0.2

- 1.0.2 (Thursday 14 April 2011)
  - Bugfix release
  - Make inference of data type more robust to changes in numpy dtype hashing
  - Fix incorrect thresholds in quaternion calculation (thanks to Yarik H for pointing this one out)
  - Make parrec2nii pass over errors more gracefully
  - More explicit checks for missing or None field in trackvis and other classes - thanks to Marc-Alexandre Cote
  - Make logging and error level work as expected - thanks to Yarik H
  - Loading an image does not change qform or sform - thanks to Yarik H
  - Allow 0 for nifti scaling as for spec - thanks to Yarik H
  - nifti1.save now correctly saves single or pair images

- 1.0.1 (Wednesday 23 Feb 2011)
  - Bugfix release
  - Fix bugs in tests for data package paths
  - Fix leaks of open filehandles when loading images (thanks to Gael Varoquaux for the report)
  - Skip rw tests for SPM images when scipy not installed
  - Fix various windows-specific file issues for tests
  - Fix incorrect reading of byte-swapped trackvis files
  - Workaround for odd numpy dtype comparisons leading to header errors for some loaded images (thanks to Cindee Madison for the report)

- 1.0.0 (Thursday, 13, Oct 2010)
  - This is the first public release of the NiBabel package.
  - NiBabel is a complete rewrite of the PyNifti package in pure python. It was designed to make the code simpler and easier to work with. Like PyNifti, NiBabel has fairly comprehensive NIfTI read and write support.
  - Extended support for SPM Analyze images, including orientation affines from matlab `.mat` files.
  - Basic support for simple MINC 1.0 files (MB). Please let us know if you have MINC files that we don't support well.
  - Support for reading and writing PAR/REC images (MH)
  - `parrec2nii` script to convert PAR/REC images to NIfTI format (MH)
  - Very preliminary, limited and highly experimental DICOM reading support (MB, Ian Nimmo Smith).
  - Some functions (*nibabel.funcs*) for basic image shape changes, including the ability to transform to the image with data closest to the cononical image orientation (first axis left-to-right, second back-to-front, third down-to-up) (MB, Jonathan Taylor)
  - Gifti format read and write support (preliminary) (Stephen Gerhard)
  - Added utilities to use nipy-style data packages, by rip then edit of nipy data package code (MB)
  - Some improvements to release support (Jarrod Millman, MB, Fernando Perez)
  - Huge downward step in the quality and coverage by the docs, caused by MB, mostly fixed by a lot of good work by MH.
  - NiBabel will not work with Python < 2.5, and we haven't even tested it with Python 3. We will get to it soon...

PyNifti

Modifications are done by Michael Hanke, if not indicated otherwise. 'Closes' statement IDs refer to the Debian bug tracking system and can be queried by visiting the URL:

```
http://bugs.debian.org/<bug id>
```

- 0.20100706.1 (Tue, 6 Jul 2010)
  - Bugfix: NiftiFormat.vx2s() used the qform not the sform. Thanks to Tom Holroyd for reporting.
- 0.20100412.1 (Mon, 12 Apr 2010)
  - Bugfix: Unfortunate interaction between Python garbage collection and C library caused memory problems. Thanks to Yaroslav Halchenko for the diagnose and fix.
- 0.20090303.1 (Tue, 3 Mar 2009)
  - Bugfix: Updating the NIfTI header from a dictionary was broken.
  - Bugfix: Removed left-over print statement in extension code.
  - Bugfix: Prevent saving of bogus 'None.nii' images when the filename was previously assign, before calling NiftiImage.save() (Closes: #517920).
  - Bugfix: Extension length was to short for all *edata* whos length matches n*16-8, for all integer n.
- 0.20090205.1 (Thu, 5 Feb 2009)

- This release is the first in a series that aims stabilize the API and finally result in PyNIfTI 1.0 with full support of the NIfTI1 standard.
- The whole package was restructured. The included renaming *nifti.nifti(image,format,clibs)* to *nifti.(image,format,clibs)*. Redirect modules make sure that existing user code will not break, but they will issue a DeprecationWarning and will be removed with the release of PyNIfTI 1.0.
- Added a special extension that can embed any serializable Python object into the NIfTI file header. The contents of this extension is automatically expanded upon request into the *.meta* attribute of each NiftiImage. When saving files to disk the content of the dictionary is also automatically dumped into this extension. Embedded meta data is not loaded automatically, since this has security implications, because code from the file header is actually executed. The documentation explicitely mentions this risk.
- Added `NiftiExtensions`. This is a container-like handler to access and manipulate NIfTI1 header extensions.
- Exposed `MemMappedNiftiImage` in the root module.
- Moved `cropImage()` into the `utils` module.
- From now on Sphinx is used to generate the documentation. This includes a module reference that replaces that old API reference.
- Added methods `vx2q()` and `vx2s()` to convert voxel indices into coordinates defined by qform or sform respectively.
- Updating the *cal_min* and *cal_max* values in the NIfTI header when saving a file is now conditional, but remains enabled by default.
- Full set of methods to query and modify axis units. This includes expanding the previous *xyzt_units* field in the header dictionary into editable *xyz_unit* and *time_unit* fields. The former *xyzt_units* field is no longer available. See: `getXYZUnit()`, `setXYZUnit()`, `getTimeUnit()`, `setTimeUnit()`, `xyz_unit`, `time_unit`
- Full set of methods to query and manuipulate qform and sform codes. See: `getQFormCode()`, `setQFormCode()`, `getSFormCode()`, `setSFormCode()`, `qform_code`, `sform_code`
- Each image instance is now able to generate a human-readable dump of its most important header information via *__str__()*.
- `NiftiImage` objects can now be pickled.
- Switched to NumPy's distutils for building the package. Cleaned and simplified the build procedure. Added optimization flags to SWIG call.
- `nifti.image.NiftiImage.filename` can now also be used to assign a filename.
- Introduced `nifti.__version__` as canonical version string.
- Removed *updateQFormFromQuarternion()* from the list of public methods of `NiftiFormat`. This is an internal method that should not be used in user code. However, a redirect to the new method will remain in-place until PyNIfTI 1.0.
- Bugfix: `getScaledData()` returns a unmodified data array if *slope* is set to zero (as required by the NIfTI standard). Thanks to Thomas Ross for reporting.
- Bugfix: Unicode filenames are now handled properly, as long as they do not contain pure-unicode characters (since the NIfTI library does not support them). Thanks to Gaël Varoquaux for reporting this issue.

- 0.20081017.1 (Fri, 17 Oct 2008)
  - Updated included minimal copy of the nifticlibs to version 1.1.0.
  - Few changes to the Makefiles to enhance Posix compatibility. Thanks to Chris Burns.

  - When building on non-Debian systems, only add include and library paths pointing to the local nifticlibs copy, when it is actually built. On Debian system the local copy is still not used at all, as a proper nifticlibs package is guaranteed to be available.
  - Added minimal setup_egg.py for setuptools users. Thanks to Gaël Varoquaux.
  - PyNIfTI now does a proper wrapping of the image data with NumPy arrays, which no longer leads to accidental memory leaks, when accessing array data that has not been copied before (e.g. via the *data* property of NiftiImage). Thanks to Gaël Varoquaux for mentioning this possibility.
- 0.20080710.1 (Thu, 7 Jul 2008)
  - Bugfix: Pointer bug introduced by switch to new NumPy API in 0.20080624 Thanks to Christopher Burns for fixing it.
  - Bugfix: Honored DeprecationWarning: sync() -> flush() for memory mapped arrays. Again thanks to Christopher Burns.
  - More unit tests and other improvements (e.g. fixed circular imports) done by Christopher Burns.
- 0.20080630.1 (Tue, 30 Jun 2008)
  - Bugfix: NiftiImage caused a memory leak by not calling the NiftiFormat destructor.
  - Bugfix: Merged bashism-removal patch from Debian packaging.
- 0.20080624.1 (Tue, 24 Jun 2008)
  - Converted all documentation (including docstrings) into the restructured text format.
  - Improved Makefile.
  - Included configuration and Makefile support for profiling, API doc generation (via epydoc) and code quality checks (with PyLint).
  - Consistently import NumPy as N.
  - Bugfix: Proper handling of [qs]form codes, which previously have not been handled at all. Thanks to Christopher Burns for pointing it out.
  - Bugfix: Make NiftiFormat work without setFilename(). Thanks to Benjamin Thyreau for reporting.
  - Bugfix: setPixDims() stored meaningless values.
  - Use new NumPy API and replace deprecated function calls (*PyArray_FromDimsAndData*).
  - Initial support for memory mapped access to uncompressed NIfTI files (*MemMappedNiftiImage*).
  - Add a proper Makefile and setup.cfg for compiling PyNIfTI under Windows with MinGW.
  - Include a minimal copy of the most recent nifticlibs (just libniftiio and znzlib; version 1.0), to lower the threshold to build PyNIfTI on systems that do not provide a developer package for those libraries.
- 0.20070930.1 (Sun, 30 Sep 2007)
  - Relicense under the MIT license, to be compatible with SciPy license. http://www.opensource.org/licenses/mit-license.php
  - Updated documentation.
- 0.20070917.1 (Mon, 17 Sep 2007)
  - Bugfix: Can now update NIfTI header data when no filename is set (Closes: #442175).
  - Unloading of image data without a filename set is no checked and prevented as it would damage data integrity and the image data could not be recovered.
  - Added 'pixdim' property (Yaroslav Halchenko).

- 0.20070905.1 (Wed, 5 Sep 2007)
  - Fixed a bug in the qform/quaternion handling that caused changes to the qform to vanish when saving to file (Yaroslav Halchenko).
  - Added more unit tests.
  - 'dim' vector in the NIfTI header is now guaranteed to only contain non-zero elements. This caused problems with some applications.
- 0.20070803.1 (Fri, 3 Aug 2007)
  - Does not depend on SciPy anymore.
  - Initial steps towards a unittest suite.
  - pynifti_pst can now print the peristimulus signal matrix for a single voxel (onsets x time) for easier processing of this information in external applications.
  - utils.getPeristimulusTimeseries() can now be used to compute mean and variance of the signal (among others).
  - pynifti_pst is able to compute more than just the mean peristimulus timeseries (e.g. variance and standard deviation).
  - Set default image description when saving a file if none is present.
  - Improved documentation.
- 0.20070425.1 (Wed, 25 Apr 2007)
  - Improved documentation. Added note about the special usage of the header property. Also added notes about the relevant properties in the docstring of the corresponding accessor methods.
  - Added property and accessor methods to access/modify the repetition time of timeseries (dt).
  - Added functions to manipulate the pixdim values.
  - Added utils.py with some utility functions.
  - Added functions/property to determine the bounding box of an image.
  - Fixed a bug that caused a corrupted sform matrix when converting a NumPy array and a header dictionary into a NIfTI image.
  - Added script to compute peristimulus timeseries (pynifti_pst).
  - Package now depends on python-scipy.
- 0.20070315.1 (Thu, 15 Mar 2007)
  - Removed functionality for "NiftiImage.save() raises an IOError exception when writing the image file fails." (Yaroslav Halchenko)
  - Added ability to force a filetype when setting the filename or saving a file.
  - Reverse the order of the 'header' and 'load' argument in the NiftiImage constructor. 'header' is now first as it seems to be used more often.
  - Improved the source code documentation.
  - Added getScaledData() method to NiftiImage that returns a copy of the data array that is scaled with the slope and intercept stored in the NIfTI header.
- 0.20070301.2 (Thu, 1 Mar 2007)
  - Fixed wrong link to the source tarball in README.html.

- 0.20070301.1 (Thu, 1 Mar 2007)
  - Initial upload to the Debian archive. (Closes: #413049)
  - NiftiImage.save() raises an IOError exception when writing the image file fails.
  - Added extent, volextent, and timepoints properties to NiftiImage class (Yaroslav Halchenko).
- 0.20070220.1 (Tue, 20 Feb 2007)
  - NiftiFile class is renamed to NiftiImage.
  - SWIG-wrapped libniftiio functions are no available in the nifticlib module.
  - Fixed broken NiftiImage from Numpy array constructor.
  - Added initial documentation in README.html.
  - Fulfilled a number of Yarik's wishes ;)
- 0.20070214.1 (Wed, 14 Feb 2007)
  - Does not depend on libfslio anymore.
  - Up to seven-dimensional dataset are supported (as much as NIfTI can do).
  - The complete NIfTI header dataset is modifiable.
  - Most image properties are accessable via class attributes and accessor methods.
  - Improved documentation (but still a long way to go).
- 0.20061114 (Tue, 14 Nov 2006)
  - Initial release.

9.2 General tutorials

9.2.1 Coordinate systems and affines

A nibabel (and nipy) image is the association of three things:

- The *image data array*: a 3D or 4D *array* of image data
- An *affine array* that tells you the position of the image array data in a *reference space*.
- *image metadata* (data about the data) describing the image, usually in the form of an image *header*.

This document describes how the *affine array* describes the position of the image data in a reference space. On the way we will define what we mean by reference space, and the reference spaces that Nibabel uses.

Introducing Someone

We have scanned someone called "Someone", and we have a two MRI images of their brain, a single EPI volume, and a structural scan. In general we never use the person's name in the image filenames, but we make an exception in this case:

- `somones_epi.nii.gz`.
- `somones_anatomy.nii.gz`.

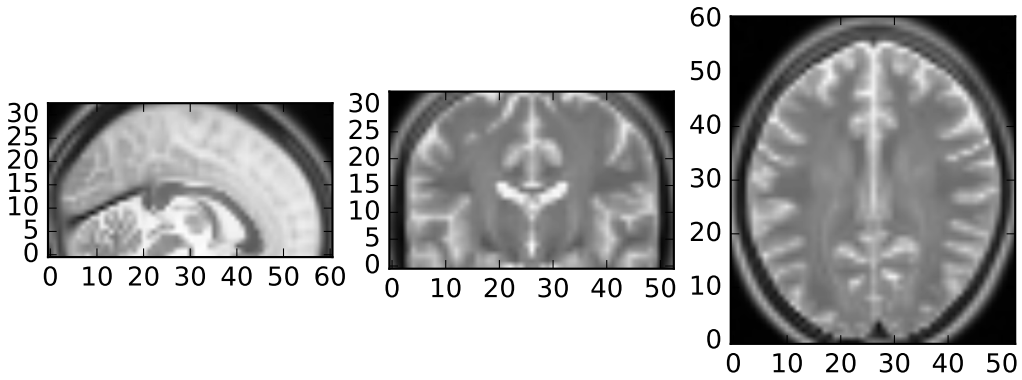
We can load up the EPI image to get the image data array:

```
>>> import nibabel as nib
>>> epi_img = nib.load('downloads/someones_epi.nii.gz')
>>> epi_img_data = epi_img.get_data()
>>> epi_img_data.shape
(53, 61, 33)
```

Then we have a look at slices over the first, second and third dimensions of the array.

```
>>> import matplotlib.pyplot as plt
>>> def show_slices(slices):
...     """ Function to display row of image slices """
...     fig, axes = plt.subplots(1, len(slices))
...     for i, slice in enumerate(slices):
...         axes[i].imshow(slice.T, cmap="gray", origin="lower")
>>>
>>> slice_0 = epi_img_data[26, :, :]
>>> slice_1 = epi_img_data[:, 30, :]
>>> slice_2 = epi_img_data[:, :, 16]
>>> show_slices([slice_0, slice_1, slice_2])
>>> plt.suptitle("Center slices for EPI image")
```

Center slices for EPI image

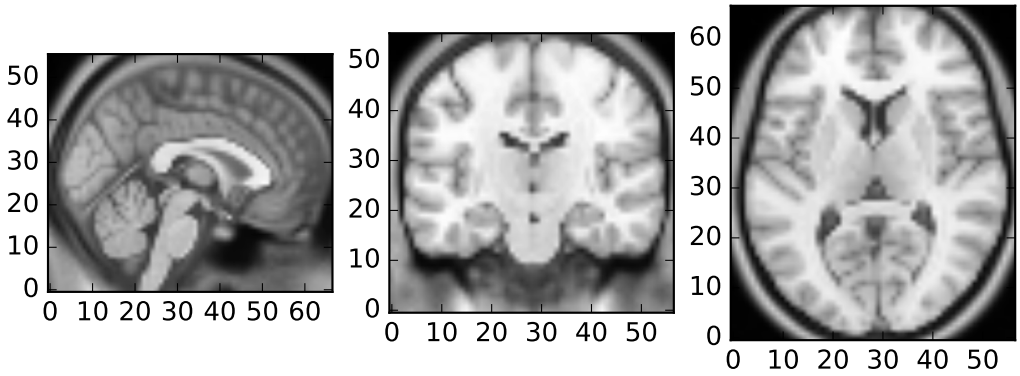


We collected an anatomical image in the same session. We can load that image and look at slices in the three axes:

```
>>> anat_img = nib.load('downloads/someones_anatomy.nii.gz')
>>> anat_img_data = anat_img.get_data()
>>> anat_img_data.shape
(57, 67, 56)
```

```
>>> show_slices([anat_img_data[28, :, :],
...              anat_img_data[:, 33, :],
...              anat_img_data[:, :, 28]])
>>> plt.suptitle("Center slices for anatomical image")
```

Center slices for anatomical image



As is usually the case, we had a different field of view for the anatomical scan, and so the anatomical image has a different shape, size, and orientation in the magnet.

Voxel coordinates are coordinates in the image data array

As y'all know, a voxel is a pixel with volume.

In the code above, `slice_0` from the EPI data is a 2D slice from a 3D image. The plot of the EPI slices displays the slices in grayscale (graded between black for the minimum value, white for the maximum). Each pixel in the slice grayscale image also represents a voxel, because this 2D image represents a slice from the 3D image with a certain thickness.

The 3D array is therefore also a voxel array. As for any array, we can select particular values by indexing. For example, we can get the value for the middle voxel in the EPI data array like this:

```
>>> n_i, n_j, n_k = epi_img_data.shape
>>> center_i = (n_i - 1) / 2.
>>> center_j = (n_j - 1) / 2.
>>> center_k = (n_k - 1) / 2.
>>> center_i, center_j, center_k
(26.0, 30.0, 16.0)
```

```
>>> center_vox_value = epi_img_data[center_i, center_j, center_k]
>>> center_vox_value
81.549287796020508
```

The values (26, 30, 16) are indices into the data array `epi_img_data`. (26, 30, 16) is therefore a 'voxel coordinate' - a coordinate into the voxel array.

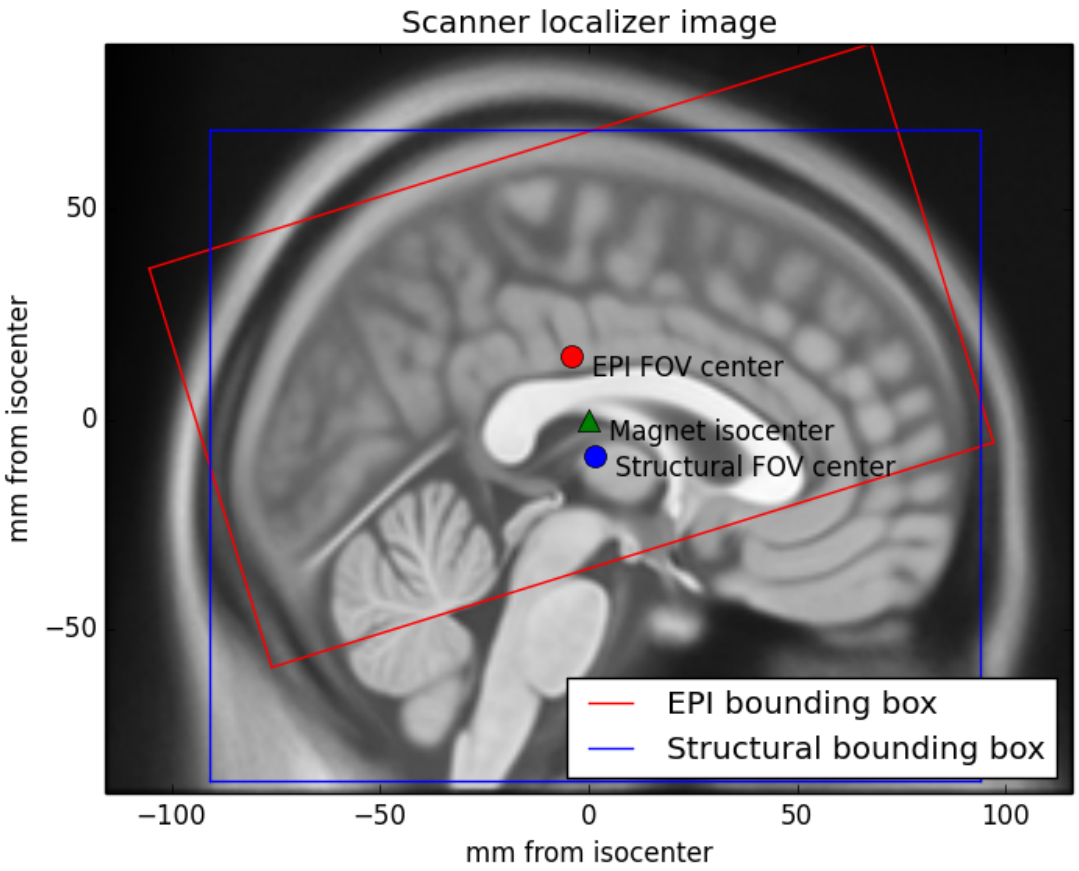
A coordinate is a set of numbers giving positions relative to a set of *axes*. In this case 26 is a position on the first array axis, where the axis is of length `epi_img_data.shape[0]`, and therefore goes from 0 to 52 (`epi_img_data.shape == (53, 61, 33)`). Similarly 30 gives a position on the second axis (0 to 60) and 16 is the position on the third axis (0 to 32).

Voxel coordinates and points in space

The voxel coordinate tells us almost nothing about where the data came from in terms of position in the scanner. For example, let's say we have the voxel coordinate (26, 30, 16). Without more information we have no idea whether this voxel position is on the left or right of the brain, or came from the left or right of the scanner.

This is because the scanner allows us to collect voxel data in almost any arbitrary position and orientation within the magnet.

In the case of Someone's EPI, we took transverse slices at a moderate angle to the floor to ceiling direction. This localizer image from the scanner console has a red box that shows the position of the slice block for `someones_epi.nii.gz` and a blue box for the slice block of `someones_anatomy.nii.gz`:



The localizer is oriented to the magnet, so that the left and right borders of the image are parallel to the floor of the scanner room, with the left border being towards the floor and the right border towards the ceiling.

You will see from the labels on the localizer that the center of the EPI voxel data block (at 26, 30, 16 in `epi_img_data`) is not quite at the center of magnet bore (the magnet *isocenter*).

We have an anatomical and an EPI scan, and later on we will surely want to be able to relate the data from `someones_epi.nii.gz` to `someones_anatomy.nii.gz`. We can't easily do this at the moment, because we collected the anatomical image with a different field of view and orientation to the EPI image, so the voxel coordinates in the EPI image refer to different locations in the magnet to the voxel coordinates in the anatomical image.

We solve this problem by keeping track of the relationship of voxel coordinates to some *reference space*. In particular, the *affine array* stores the relationship between voxel coordinates in the image data array and coordinates in the reference space. We store the relationship of voxel coordinates from `someones_epi.nii.gz` and the reference space, and also the (different) relationship of voxel coordinates in `someones_anatomy.nii.gz` to the *same* reference space. Because we know the relationship of (voxel coordinates to the reference space) for both images, we can use this information to relate voxel coordinates in `someones_epi.nii.gz` to spatially equivalent voxel coordinates in `someones_anatomy.nii.gz`.

The scanner-subject reference space

What does "space" mean in the phrase "reference space"? The space is defined by an ordered set of axes. For our 3D spatial world, it is a set of 3 independent axes.

We can decide what space we want to use, by choosing these axes. We need to choose the origin of the axes, their direction and their units.

To start with, we define a set of three orthogonal *scanner axes*.

The scanner axes

- The origin of the axes is at the magnet isocenter. This is coordinate (0, 0, 0) in our reference space. All three axes pass through the isocenter.
- The units for all three axes are millimeters.
- Imagine an observer standing behind the scanner looking through the magnet bore towards the end of the scanner bed. Imagine a line traveling towards the observer through the center of the magnet bore, parallel to the bed, with the zero point at the magnet isocenter, and positive values closer to the observer. Call this line the *scanner-bore* axis.
- Draw a line traveling from the scanner room floor up through the magnet isocenter towards the ceiling, at right angles to the scanner bore axis. 0 is at isocenter and positive values are towards the ceiling. Call this the *scanner-floor/ceiling* axis.
- Draw a line at right angles to the other two lines, traveling from the observer's left, parallel to the floor, and through the magnet isocenter to the observer's right. 0 is at isocenter and positive values are to the right. Call this the *scanner-left/right*.

If we make the axes have order (scanner left-right; scanner floor-ceiling; scanner bore) then we have an ordered set of 3 axes and therefore the definition of a 3D *space*. Call the first axis the "X" axis, the second "Y" and the third "Z". A coordinate of $(x, y, z) = (10, -5, -3)$ in this space refers to the point in space 10mm to the (fictional observer's) right of isocenter, 5mm towards the floor from the isocenter, and 3mm towards the foot of the scanner bed. This reference space is sometimes known as "scanner XYZ". It was the standard reference space for the predecessor to DICOM, called ACR / NEMA 2.0.

From scanner to subject

If the subject is lying in the usual position for a brain scan, face up and head first in the scanner, then scanner-left/right is also the left-right axis of the subject's head, scanner-floor/ceiling is the anterior-posterior axis of the head and scanner-bore is the inferior-posterior axis of the head.

Sometimes the subject is not lying in the standard position. For example, the subject may be lying with their face pointing to the right (in terms of the scanner-left/right axis). In that case "scanner XYZ" will not tell us about the subject's left and right, but only the scanner left and right. We might prefer to know where we are in terms of the subject's left and right.

To deal with this problem, most reference spaces use subject- or patient- centered scanner coordinate systems. In these systems, the axes are still the scanner axes above, but the ordering and direction of the axes comes from the position of the subject. The most common subject-centered scanner coordinate system in neuroimaging is called "scanner RAS" (right, anterior, superior). Here the scanner axes are reordered and flipped so that the first axis is the scanner axis that is closest to the left to right axis of the subject, the second is the closest scanner axis to the anterior-posterior axis of the subject, and the third is the closest scanner axis to the inferior-superior axis of the subject. For example, if the subject was lying face to the right in the scanner, then the first (X) axis of the reference system would be scanner-floor/ceiling, but reversed so that positive values are towards the floor. This axis goes from left to right in the subject, with positive values to the right. The second (Y) axis would be scanner-left/right (anterior-posterior in the subject), and the Z axis would be scanner-bore (inferior-posterior).

Naming reference spaces

Reading names of reference spaces can be confusing because of different meanings that authors use for the same terms, such as 'left' and 'right'.

We are using the term "RAS" to mean that the axes are (in terms of the subject): left to Right; posterior to Anterior; and inferior to Superior, respectively. Although it is common to call this convention "RAS", it is not quite universal, because some use "R", "A" and "S" in "RAS" to mean that the axes *starts* on the right, anterior, superior of the subject, rather than *ending* on the right, anterior, superior. In other words, they would use "RAS" to refer to a coordinate system we would call "LPI". To be safe, we'll call our interpretation of the RAS convention "RAS+", meaning that Right, Anterior, Posterior are all positive values on these axes.

Some people also use "right" to mean the right hand side when an observer looks at the front of the scanner, from the foot the scanner bed. Unfortunately, this means that you have to read coordinate system definitions carefully if you are not familiar with a particular convention. We nibabel / nipy folks agree with most of our brain imaging friends and many of our enemies in that we always use "right" to mean the subject's right.

Voxel coordinates are in voxel space

We have not yet made this explicit, but voxel coordinates are also in a space. In this case the space is defined by the three voxel axes (first axis, second axis, third axis), where 0, 0, 0 is the center of the first voxel in the array and the units on the axes are voxels. Voxel coordinates are therefore defined in a reference space called *voxel space*.

The affine matrix as a transformation between spaces

We have voxel coordinates (in voxel space). We want to get scanner RAS+ coordinates corresponding to the voxel coordinates. We need a *coordinate transform* to take us from voxel coordinates to scanner RAS+ coordinates.

In general, we have some voxel space coordinate (i, j, k), and we want to generate the reference space coordinate (x, y, z).

Imagine we had solved this, and we had a coordinate transform function f that accepts a voxel coordinate and returns a coordinate in the reference space:

$$(x, y, z) = f(i, j, k)$$

f accepts a coordinate in the *input* space and returns a coordinate in the *output* space. In our case the input space is voxel space and the output space is scanner RAS+.

In theory f could be a complicated non-linear function, but in practice, we know that the scanner collects data on a regular grid. This means that the relationship between (i, j, k) and (x, y, z) is linear (actually *affine*), and can be encoded with linear (actually affine) transformations comprising translations, rotations and zooms (wikipedia linear transform, wikipedia affine transform).

Scaling (zooming) in three dimensions can be represented by a diagonal 3 by 3 matrix. Here's how to zoom the first dimension by p, the second by q and the third by r units:

$$\begin{bmatrix} x \\ y \\ z \end{bmatrix} = \begin{bmatrix} pi \\ qj \\ rk \end{bmatrix} = \begin{bmatrix} p & 0 & 0 \\ 0 & q & 0 \\ 0 & 0 & r \end{bmatrix} \begin{bmatrix} i \\ j \\ k \end{bmatrix}$$

A rotation in three dimensions can be represented as a 3 by 3 *rotation matrix* (wikipedia rotation matrix). For example, here is a rotation by θ radians around the third array axis:

$$\begin{bmatrix} x \\ y \\ z \end{bmatrix} = \begin{bmatrix} \cos(\theta) & -\sin(\theta) & 0 \\ \sin(\theta) & \cos(\theta) & 0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} i \\ j \\ k \end{bmatrix}$$

This is a rotation by ϕ radians around the second array axis:

$$\begin{bmatrix} x \\ y \\ z \end{bmatrix} = \begin{bmatrix} \cos(\phi) & 0 & \sin(\phi) \\ 0 & 1 & 0 \\ -\sin(\phi) & 0 & \cos(\phi) \end{bmatrix} \begin{bmatrix} i \\ j \\ k \end{bmatrix}$$

A rotation of γ radians around the first array axis:

$$\begin{bmatrix} x \\ y \\ z \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 & \\ 0 & \cos(\gamma) & 0 & -\sin(\gamma) \\ 0 & \sin(\gamma) & 0 & \cos(\gamma) \end{bmatrix} \begin{bmatrix} i \\ j \\ k \end{bmatrix}$$

Zoom and rotation matrices can be combined by matrix multiplication.

Here's a scaling of p, q, r units followed by a rotation of θ radians around the third axis followed by a rotation of ϕ radians around the second axis:

$$\begin{bmatrix} x \\ y \\ z \end{bmatrix} = \begin{bmatrix} \cos(\phi) & 0 & \sin(\phi) \\ 0 & 1 & 0 \\ -\sin(\phi) & 0 & \cos(\phi) \end{bmatrix} \begin{bmatrix} \cos(\theta) & -\sin(\theta) & 0 \\ \sin(\theta) & \cos(\theta) & 0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} p & 0 & 0 \\ 0 & q & 0 \\ 0 & 0 & r \end{bmatrix} \begin{bmatrix} i \\ j \\ k \end{bmatrix}$$

This can also be written:

$$M = \begin{bmatrix} \cos(\phi) & 0 & \sin(\phi) \\ 0 & 1 & 0 \\ -\sin(\phi) & 0 & \cos(\phi) \end{bmatrix} \begin{bmatrix} \cos(\theta) & -\sin(\theta) & 0 \\ \sin(\theta) & \cos(\theta) & 0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} p & 0 & 0 \\ 0 & q & 0 \\ 0 & 0 & r \end{bmatrix}$$

$$\begin{bmatrix} x \\ y \\ z \end{bmatrix} = M \begin{bmatrix} i \\ j \\ k \end{bmatrix}$$

This might be obvious because the matrix multiplication is the result of applying each transformation in turn on the coordinates output from the previous transformation. Combining the transformations into a single matrix M works because matrix multiplication is associative – $ABCD = (ABC)D$.

A translation in three dimensions can be represented as a length 3 vector to be added to the length 3 coordinate. For example, a translation of a units on the first axis, b on the second and c on the third might be written as:

$$\begin{bmatrix} x \\ y \\ z \end{bmatrix} = \begin{bmatrix} i \\ j \\ k \end{bmatrix} + \begin{bmatrix} a \\ b \\ c \end{bmatrix}$$

We can write our function f as a combination of matrix multiplication by some 3 by 3 rotation / zoom matrix M followed by addition of a 3 by 1 translation vector (a, b, c)

$$\begin{bmatrix} x \\ y \\ z \end{bmatrix} = M \begin{bmatrix} i \\ j \\ k \end{bmatrix} + \begin{bmatrix} a \\ b \\ c \end{bmatrix}$$

We could record the parameters necessary for f as the 3 by 3 matrix, M and the 3 by 1 vector (a, b, c).

In fact, the 4 by 4 image *affine array* does include exactly this information. If m_{ij} is the value in row i column j of matrix M, then the image affine matrix A is:

$$A = \begin{bmatrix} m_{11} & m_{12} & m_{13} & a \\ m_{21} & m_{22} & m_{23} & b \\ m_{31} & m_{32} & m_{33} & c \\ 0 & 0 & 0 & 1 \end{bmatrix}$$

Why the extra row of $[0, 0, 0, 1]$? We need this row because we have rephrased the combination of rotations / zooms and translations as a transformation in *homogenous coordinates* (see wikipedia homogenous coordinates). This is a trick that allows us to put the translation part into the same matrix as the rotations / zooms, so that both translations and rotations / zooms can be applied by matrix multiplication. In order to make this work, we have to add an extra 1 to our input and output coordinate vectors:

$$\begin{bmatrix} x \\ y \\ z \\ 1 \end{bmatrix} = \begin{bmatrix} m_{11} & m_{12} & m_{13} & a \\ m_{21} & m_{22} & m_{23} & b \\ m_{31} & m_{32} & m_{33} & c \\ 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} i \\ j \\ k \\ 1 \end{bmatrix}$$

This results in the same transformation as applying M and (a, b, c) separately. One advantage of encoding transformations this way is that we can combine two sets of [rotations, zooms, translations] by matrix multiplication of the two corresponding affine matrices.

In practice, although it is common to combine 3D transformations using 4 by 4 affine matrices, we usually *apply* the transformations by breaking up the affine matrix into its component M matrix and (a, b, c) vector and doing:

$$\begin{bmatrix} x \\ y \\ z \end{bmatrix} = M \begin{bmatrix} i \\ j \\ k \end{bmatrix} + \begin{bmatrix} a \\ b \\ c \end{bmatrix}$$

As long as the last row of the 4 by 4 is $[0, 0, 0, 1]$, applying the transformations in this way is mathematically the same as using the full 4 by 4 form, without the inconvenience of adding the extra 1 to our input and output vectors.

The inverse of the affine gives the mapping from scanner to voxel

The affine arrays we have described so far have another pleasant property — they are usually invertible. As y'all know, the inverse of a matrix A is the matrix A^{-1} such that $I = A^{-1}A$, where I is the identity matrix. Put another way:

$$\begin{bmatrix} x \\ y \\ z \\ 1 \end{bmatrix} = A \begin{bmatrix} i \\ j \\ k \\ 1 \end{bmatrix}$$

$$\begin{bmatrix} i \\ j \\ k \\ 1 \end{bmatrix} = A^{-1} \begin{bmatrix} x \\ y \\ z \\ 1 \end{bmatrix}$$

That means that the inverse of the affine matrix gives the transformation from scanner RAS+ coordinates to voxel coordinates in the image data.

Now imagine we have affine array A for `someones_epi.nii.gz`, and affine array B for `someones_anatomy.nii.gz`. A gives the mapping from voxels in the image data array of `someones_epi.nii.gz` to millimeters in scanner RAS+. B gives the mapping from voxels in image data array of `someones_anatomy.nii.gz` to *the same* scanner RAS+. Now let's say we have a particular voxel coordinate (i, j, k) in the data array of `someones_epi.nii.gz`, and we want to find the voxel in `someones_anatomy.nii.gz` that is in the same spatial position. Call this matching voxel coordinate (i', j', k'). We first apply the transform from `someones_epi.nii.gz` voxels to scanner RAS+ (A) and then apply the transform from scanner RAS+ to voxels in `someones_anatomy.nii.gz` (B^{-1}):

$$\begin{bmatrix} i' \\ j' \\ k' \\ 1 \end{bmatrix} = B^{-1}A \begin{bmatrix} i \\ j \\ k \\ 1 \end{bmatrix}$$

The affine by example

We can get the affine from the nibabel image object. Here is the affine for the EPI scan:

```
>>> # Set numpy to print 3 decimal points and suppress small values
>>> import numpy as np
>>> np.set_printoptions(precision=3, suppress=True)
>>> # Print the affine
>>> epi_img.affine
array([[  3.   ,   0.   ,   0.   , -78.   ],
       [  0.   ,   2.866,  -0.887, -76.   ],
       [  0.   ,   0.887,   2.866, -64.   ],
       [  0.   ,   0.   ,   0.   ,   1.   ]])
```

As you see, the last row is $[0, 0, 0, 1]$

Applying the affine

To make the affine simpler to apply, we split it into M and (a, b, c):

```
>>> M = epi_img.affine[:3, :3]
>>> abc = epi_img.affine[:3, 3]
```

Then we can define our function f:

```
>>> def f(i, j, k):
...     """ Return X, Y, Z coordinates for i, j, k """
...     return M.dot([i, j, k]) + abc
```

The labels on the *localizer image* give the impression that the center voxel of `someones_epi.nii.gz` was a little above the magnet isocenter. Now we can check:

```
>>> epi_vox_center = (np.array(epi_img_data.shape) - 1) / 2.
>>> f(epi_vox_center[0], epi_vox_center[1], epi_vox_center[2])
array([ 0.   , -4.205,  8.453])
```

That means the center of the image field of view is at the isocenter of the magnet on the left to right axis, and is around 4.2mm posterior to the isocenter and ~8.5 mm above the isocenter.

The parameters in the affine array can therefore give the position of any voxel coordinate, relative to the scanner RAS+ reference space.

We get the same result from applying the affine directly instead of using M and (a, b, c) in our function. As above, we need to add a 1 to the end of the vector to apply the 4 by 4 affine matrix.

```
>>> epi_img.affine.dot(list(epi_vox_center) + [1])
array([ 0.   , -4.205,  8.453,  1.   ])
```

In fact nibabel has a function `apply_affine` that applies an affine to an (i, j, k) point by splitting the affine into M and abc then multiplying and adding as above:

```
>>> from nibabel.affines import apply_affine
>>> apply_affine(epi_img.affine, epi_vox_center)
array([ 0.   , -4.205,  8.453])
```

Now we can apply the affine, we can use matrix inversion on the anatomical affine to map between voxels in the EPI image and voxels in the anatomical image.

```
>>> import numpy.linalg as npl
>>> epi_vox2anat_vox = npl.inv(anat_img.affine).dot(epi_img.affine)
```

What is the voxel coordinate in the anatomical corresponding to the voxel center of the EPI image?

```
>>> apply_affine(epi_vox2anat_vox, epi_vox_center)
array([ 28.364,  31.562,  36.165])
```

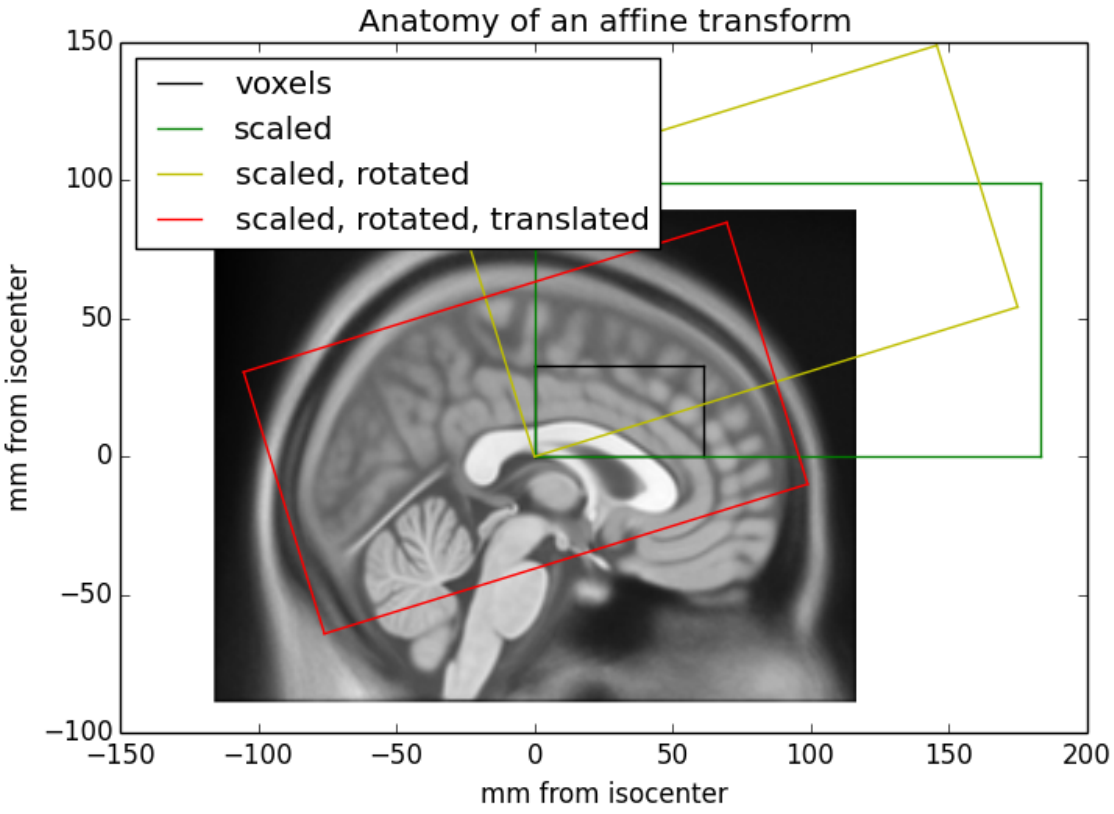
The voxel coordinate of the center voxel of the anatomical image is:

```
>>> anat_vox_center = (np.array(anat_img_data.shape) - 1) / 2.
>>> anat_vox_center
array([ 28. ,  33. ,  27.5])
```

The voxel location in the anatomical image that matches the center voxel of the EPI image is nearly exactly half way across the first axis, a voxel or two back from the anatomical voxel center on the second axis, and about 9 voxels above the anatomical voxel center. We can check the *localizer image* by eye to see whether this makes sense, by seeing how the red EPI field of view center relates to the blue anatomical field of view center and the blue anatomical image field of view.

The affine as a series of transformations

You can think of the image affine as a combination of a series of transformations to go from voxel coordinates to mm coordinates in terms of the magnet isocenter. Here is the EPI affine broken down into a series of transformations, with the results shown on the localizer image:



We start by putting the voxel grid onto the isocenter coordinate system, so a translation of one voxel equates to a translation of one millimeter in the isocenter coordinate system. Our EPI image would then have the black bounding box in the image above. Next we scale the voxels to millimeters by scaling by the voxel size (green bounding box). We could do this with an affine:

```
>>> scaling_affine = np.array([[3, 0, 0, 0],
...                            [0, 3, 0, 0],
...                            [0, 0, 3, 0],
...                            [0, 0, 0, 1]])
```

After applying this affine, when we move one voxel in any direction, we are moving 3 millimeters in that direction:

```
>>> one_vox_axis_0 = [1, 0, 0]
>>> apply_affine(scaling_affine, one_vox_axis_0)
array([3, 0, 0])
```

Next we rotate the scaled voxels around the first axis by 0.3 radians (see *rotate around first axis*):

```
>>> cos_gamma = np.cos(0.3)
>>> sin_gamma = np.sin(0.3)
>>> rotation_affine = np.array([[1, 0, 0, 0],
...                            [0, cos_gamma, -sin_gamma, 0],
...                            [0, sin_gamma, cos_gamma, 0],
...                            [0, 0, 0, 1]])
>>> affine_so_far = rotation_affine.dot(scaling_affine)
>>> affine_so_far
array([[ 3.   ,  0.   ,  0.   ,  0.   ],
```

```
       [ 0.   ,  2.866, -0.887,  0.   ],
       [ 0.   ,  0.887,  2.866,  0.   ],
       [ 0.   ,  0.   ,  0.   ,  1.   ]])
```

The EPI voxel block coordinates transformed by `affine_so_far` are at the position of the yellow box on the figure.

Finally we translate the 0, 0, 0 coordinate at the bottom, posterior, left corner of our array to be at its final position relative to the isocenter, which is -78, -76, -64:

```
>>> translation_affine = np.array([[1, 0, 0, -78],
...                                [0, 1, 0, -76],
...                                [0, 0, 1, -64],
...                                [0, 0, 0, 1]])
>>> whole_affine = translation_affine.dot(affine_so_far)
>>> whole_affine
array([[  3.   ,   0.   ,   0.   , -78.   ],
       [  0.   ,   2.866,  -0.887, -76.   ],
       [  0.   ,   0.887,   2.866, -64.   ],
       [  0.   ,   0.   ,   0.   ,   1.   ]])
```

This brings the affine-transformed voxel coordinates to the red box on the figure, matching the position on the *localizer*.

Other reference spaces

The scanner RAS+ reference space is a "real-world" space, in the sense that a coordinate in this space refers to a position in the real world, in a particular scanner in a particular room.

Imagine that we used some fancy software to register `someones_epi.nii.gz` to a template image, such as the Montreal Neurological Institute (MNI) template brain. The registration has moved the voxels around in complicated ways — the image has changed shape to match the template brain. We probably do not want to know how the voxel locations relate to the original scanner, but how they relate to the template brain. So, what reference space should we use?

In this case we use a space defined in terms of the template brain — the MNI reference space.

- The origin (0, 0, 0) point is defined to be the point that the anterior commissure of the MNI template brain crosses the midline (the AC point).
- Axis units are millimeters.
- The Y axis follows the midline of the MNI brain between the left and right hemispheres, going from posterior (negative) to anterior (positive), passing through the AC point. The template defines this line.
- The Z axis is at right angles to the Y axis, going from inferior (negative) to superior (positive), with the superior part of the line passing between the two hemispheres.
- The X axis is a line going from the left side of the brain (negative) to right side of the brain (positive), passing through the AC point, and at right angles to the Y and Z axes.

These axes are defined with reference to the template. The exact position of the Y axis, for example, is somewhat arbitrary, as is the definition of the origin. Left and right are left and right as defined by the template. These are the axes and the space that MNI defines for its template.

A coordinate in this reference system gives a position relative to the particular brain template. It is not a real-world space because it does not refer to any particular place but to a position relative to a template.

The axes are still left to right, posterior to anterior and inferior to superior in terms of the template subject. This is still an RAS+ space — the MNI RAS+ space.

An image aligned to this template will therefore have an affine giving the relationship between voxels in the aligned image and the MNI RAS+ space.

There are other reference spaces. For example, we might align an image to the Talairach atlas brain. This brain has a different shape and size than the MNI brain. The origin is the AC point, but the Y axis passes through the point that the posterior commissure crosses the midline (the PC point), giving a slightly different trajectory from the MNI Y axis. Like the MNI RAS+ space, the Talairach axes also run left to right, posterior to anterior and inferior superior, so this is the Talairach RAS+ space.

There are conventions other than RAS+ for the reference space. For example, DICOM files map input voxel coordinates to coordinates in scanner LPS+ space. Scanner LPS+ space uses the same scanner axes and isocenter as scanner RAS+, but the X axis goes from right to the subject's Left, the Y axis goes from anterior to Posterior, and the Z axis goes from inferior to Superior. A positive X coordinate in this space would mean the point was to the subject's *left* compared to the magnet isocenter.

Nibabel always uses an RAS+ output space

Nibabel images always use RAS+ output coordinates, regardless of the preferred output coordinates of the underlying format. For example, we convert affines for DICOM images to output RAS+ coordinates instead of LPS+ coordinates. We chose this convention because it is the most popular in neuroimaging; for example, it is the standard used by NIfTI and MINC formats.

Nibabel does not enforce a particular RAS+ space. For example, NIfTI images contain codes that specify whether the affine maps to scanner or MNI or Talairach RAS+ space. For the moment, you have to consult the specifics of each format to find which RAS+ space the affine maps to.

See also Radiological vs neurological conventions

9.2.2 Radiological vs neurological conventions

It is relatively common to talk about images being in "radiological" compared to "neurological" convention, but the terms can be used in different and confusing ways.

See Coordinate systems and affines for background on voxel space, reference space and affines.

Neurological and radiological display convention

Radiologists like looking at their images with the patient's left on the right of the image. If they are looking at a brain image, it is as if they were looking at the brain slice from the point of view of the patient's feet. Neurologists like looking at brain images with the patient's right on the right of the image. This perspective is as if the neurologist is looking at the slice from the top of the patient's head. The convention is one of image display. The image can have any voxel arrangement on disk or memory, and any output reference space; it is only necessary for the software displaying the image to know the reference space and the (probably affine) mapping between voxel space and reference space; then the software can work out which voxels are on the left or right of the subject and flip the images to the taste of the viewer. We could unpack these uses as *neurological display convention* and *radiological display convention*.

Alignment of world and voxel axes

As we will see in the next section, radiological and neurological are sometimes used to refer to particular alignments of the voxel input axes to scanner RAS+ output axes. If we look at the affine mapping between voxel space and scanner RAS+, we may find that moving along the first voxel axis by one unit results in a equivalent scanner RAS+ movement that is mainly left to right. This can happen with a diagonal 3x3 part of the affine mapping to scanner RAS+ (see Coordinate systems and affines):

```
>>> import numpy as np
>>> from nibabel.affines import apply_affine
>>> diag_affine = np.array([[3., 0,  0,  0],
...                         [0,  3., 0,  0],
...                         [0,  0, 4.5, 0],
...                         [0,  0,  0,  1]])
>>> ijk = [1, 0, 0] # moving one unit on the first voxel axis
>>> apply_affine(diag_affine, ijk)
array([ 3.,  0.,  0.])
```

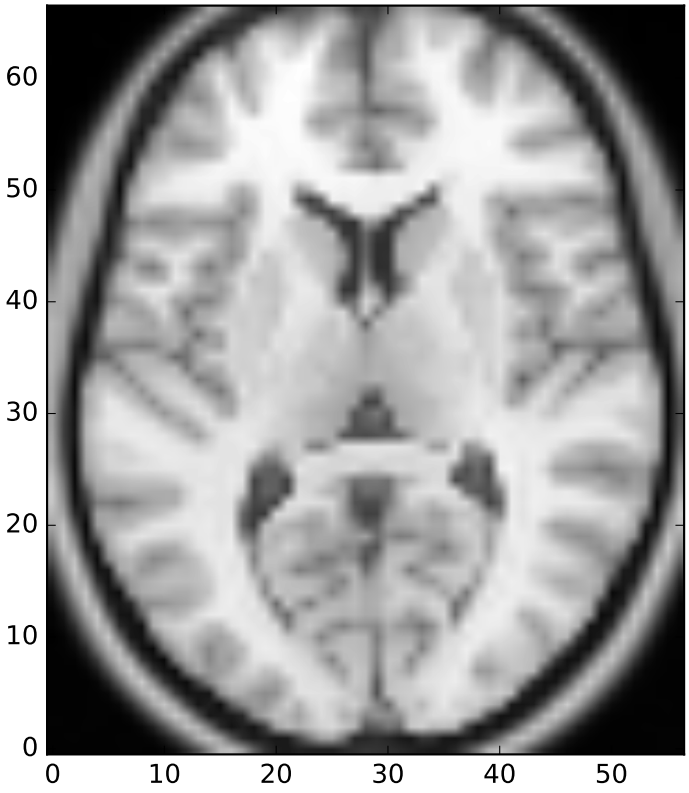
In this case the voxel axes are aligned to the output axes, in the sense that moving in a positive direction on the first voxel axis results in increasing values on the "R+" output axis, and similarly for the second voxel axis with output "A+" and the third voxel axis with output "S+".

Some people therefore refer to this alignment of voxel and RAS+ axes as *RAS voxel axes*.

Neurological / radiological voxel layout

Very confusingly, some people refer to images with RAS voxel axes as having "neurological" voxel layout. This is because the simplest way to display slices from this voxel array will result in the left of the subject appearing towards the left hand side of the screen and therefore neurological display convention. If we take a slice k over the third axis of the image data array (`img_data[:, :, k]`), the resulting slice will have a first array axis going from left to right in terms of spatial position and the second array axis going from posterior to anterior. If we display this image with the first axis going from left to right on screen and the second from bottom to top, it will have the subject's right towards the right of the screen, and anterior towards the top of the screen, as neurologists like it. Here we are showing the middle slice of `an image` with RAS voxel axes:

```
>>> import nibabel as nib
>>> import matplotlib.pyplot as plt
>>> img = nib.load('downloads/someones_anatomy.nii.gz')
>>> # The 3x3 part of the affine is diagonal with all +ve values
>>> img.affine
array([[  2.75,   0.  ,   0.  , -78.  ],
       [  0.  ,   2.75,   0.  , -91.  ],
       [  0.  ,   0.  ,   2.75, -91.  ],
       [  0.  ,   0.  ,   0.  ,   1.  ]])
>>> img_data = img.get_data()
>>> a_slice = img_data[:, :, 28]
>>> # Need transpose to put first axis left-right, second bottom-top
>>> plt.imshow(a_slice.T, cmap="gray", origin="lower")
```



This slice does have the voxels from the right of isocenter towards the right of the screen, neurology style.

Similarly, an "LAS" alignment of voxel axes to RAS+ axes would result in an image with the left of the subject towards the right of the screen, as radiologists like it. "LAS" voxel axes can also be called "radiological" voxel layout for this reason [1].

Over time it has become more common for the scanner to generate images with almost any orientation of the voxel axes relative to the reference axes. Maybe for this reason, the terms "radiological" and "neurological" are less commonly used as applied to voxel layout. We nipyers try to avoid the terms neurological or radiological for voxel layout because they can make it harder to separate the idea of voxel and reference space axes and the affine as a mapping between them.

9.2.3 Introduction to DICOM

DICOM defines standards for storing data in memory and on disk, and for communicating this data between machines over a network.

We are interested here in DICOM data. Specifically we are interested in DICOM files.

[1] We have deliberately not fully defined what we mean by "voxel layout" in the text. Conceptually, an image array could be stored in any layout on disk; the definition of the image format specifies how the image reader should interpret the data on disk to return the right array value for a given voxel coordinate. The relationship of the values on disk to the coordinate values in the array has no bearing on the fact that the voxel axes align to the output axes. In practice the terms RAS / neurological and LAS / radiogical as applied to voxel layout appear to refer exclusively to the situation where image arrays are stored in "Fortran array layout" on disk. Imagine an image array of shape (I, J, K) with values of length v. For an image of 64-bit floating point values, $v = 8$. An image array is stored in Fortran array layout only if the value for voxel coordinate (1, 0, 0) is v bytes on disk from the value for (0, 0, 0); (0, 1, 0) is $I * v$ bytes from (0, 0, 0); and (0, 0, 1) is $I * J * v$ bytes from (0, 0, 0). Analyze and NIfTI images use Fortran array layout.

DICOM files are binary dumps of the objects in memory that DICOM sends across the network.

We need to understand the format that DICOM uses to send messages across the network to understand the terms the DICOM uses when storing data in files.

For example, I hope, by the time you reach the end of this document, you will understand the following complicated and confusing statement from section 7 of the DICOM standards document PS 3.10:

> 7 DICOM File Format
>
> The DICOM File Format provides a means to encapsulate in a file the Data Set representing a SOP Instance related to a DICOM IOD. As shown in Figure 7-1, the byte stream of the Data Set is placed into the file after the DICOM File Meta Information. Each file contains a single SOP Instance.

DICOM is messages

The fundamental task of DICOM is to allow different computers to send messages to one another. These messages can contain data, and the data is very often medical images.

The messages are in the form of requests for an operation, or responses to those requests.

Let's call the requests and the responses - services.

Every DICOM message starts with a stream of bytes containing information about the service. This part of the message is called the DICOM Message Service Element or DIMSE. Depending on what the DIMSE was, there may follow some data related to the request.

For example, there is a DICOM service called "C-ECHO". This asks for a response from another computer to confirm it has seen the echo request. There is no associated data following the "C-ECHO" DIMSE part. So, the full message is the DIMSE "C-ECHO".

There is another DICOM service called "C-STORE". This is a request for the other computer to store some data, such as an image. The data to be stored follows the "C-STORE" DIMSE part.

We go into more detail on this later in the page.

Both the DIMSE and the subsequent data have a particular binary format - consisting of DICOM elements (see below).

Here we will cover:

- what DICOM elements are;
- how DICOM elements are arranged to form complicated data structures such as images;
- how the service part and the data part go together to form whole messages
- how these parts relate to DICOM files.

The DICOM standard

The documents defining the standard are:

Number	Name
PS 3.1	Introduction and Overview
PS 3.2	Conformance
PS 3.3	Information Object Definitions
PS 3.4	Service Class Specifications
PS 3.5	Data Structure and Encoding
PS 3.6	Data Dictionary
PS 3.7	Message Exchange
PS 3.8	Network Communication Support for Message Exchange
PS 3.9	Retired
PS 3.10	Media Storage / File Format for Media Interchange
PS 3.11	Media Storage Application Profiles
PS 3.12	Media Formats / Physical Media for Media Interchange
PS 3.13	Retired
PS 3.14	Grayscale Standard Display Function
PS 3.15	Security and System Management Profiles
PS 3.16	Content Mapping Resource
PS 3.17	Explanatory Information
PS 3.18	Web Access to DICOM Persistent Objects (WADO)
PS 3.19	Application Hosting
PS 3.20	Transformation of DICOM to and from HL7 Standards

DICOM data format

DICOM data is stored in memory and on disk as a sequence of *DICOM elements* (section 7 of PS 3.5).

DICOM elements

A DICOM element is made up of three or four fields. These are (Attribute Tag, [Value Representation,], Value Length, Value Field), where *Value Representation* may be present or absent, depending on the type of "Value Representation Encoding" (see below)

Attribute Tag The attribute tag is a pair of 16-bit unsigned integers of form (Group number, Element number). The tag uniquely identifies the element.

The *Element number* is badly named, because the element number does not give a unique number for the element, but only for the element within the group (given by the *Group number*).

The (Group number, Element number) are nearly always written as hexadecimal numbers in the following format: `(0010, 0010)`. The decimal representation of hexadecimal 0010 is 16, so this tag refers to group number 16, element number 16. If you look this tag up in the DICOM data dictionary (PS 3.6) you'll see this must be the element called "PatientName".

These tag groups have special meanings:

Tag group	Meaning
0000	Command elements
0002	File meta elements
0004	Directory structuring elements
0006	(not used)

See Annex E (command dictionary) of PS 3.7 for details on group 0000. See sections 7 and 8 of PS 3.6 for details of groups 2 and 4 respectively.

Tags in groups 0000, 0002, 0004 are therefore not *data* elements, but Command elements; File meta elements; directory structuring elements.

Tags with groups from 0008 are *data* element tags.

Standard attribute tags *Standard* tags are tags with an even group number (see below). There is a full list of all *standard* data element tags in the DICOM data dictionary in section 6 of DICOM standard PS 3.6.

Even numbered groups are defined in the DICOM standard data dictionary. Odd numbered groups are "private", are *not* defined in the standard data dictionary and can be used by manufacturers as they wish (see below).

Quoting from section 7.1 of PS 3.5:

> Two types of Data Elements are defined:
>
> —Standard Data Elements have an even Group Number that is not (0000,eeee), (0002,eeee), (0004,eeee), or (0006,eeee).
>
> Note: Usage of these groups is reserved for DIMSE Commands (see PS 3.7) and DICOM File Formats.
>
> —Private Data Elements have an odd Group Number that is not (0001,eeee), (0003,eeee), (0005,eeee), (0007,eeee), or (FFFF,eeee). Private Data Elements are discussed further in Section 7.8.

Private attribute tags Private attribute tags are tags with an odd group number. A private element is an element with a private tag.

Private elements still use the (Tag, [Value Representation,] Value Length, Value Field) DICOM data format.

The same odd group may be used by different manufacturers in different ways.

To try and avoid collisions of private tags from different manufacturers, there is a mechanism by which a manufacturer can tell other users of a DICOM dataset that it has reserved a block in the (Group number, Element number) space for their own use. To do this they write a "Private Creator" element where the tag is of the form `(gggg, 00xx)`, the Value Representation (see below) is "LO" (Long String) and the Value Field is a string identifying what the space is reserved for. Here `gggg` is the odd group we are reserving a portion of and the `xx` is the block of elements we are reserving. A tag of `(gggg, 00xx)` reserves the 256 elements in the range `(gggg, xx00)` to `(gggg, xxFF)`.

For example, here is a real data element from a Siemens DICOM dataset:

```
(0019, 0010) Private Creator                    LO: 'SIEMENS MR HEADER'
```

This reserves the tags from `(0019, 1000)` to `(0019, 10FF)` for information on the "SIEMENS MR HEADER"

The odd group `gggg` must be greater than `0008` and the block reservation `xx` must be greater than or equal to `0010` and less than `0100`.

Here is the start of the relevant section from PS 3.5:

> 7.8.1 PRIVATE DATA ELEMENT TAGS
>
> It is possible that multiple implementors may define Private Elements with the same (odd) group number. To avoid conflicts, Private Elements shall be assigned Private Data Element Tags according to the following rules.
>
> a) Private Creator Data Elements numbered (gggg,0010-00FF) (gggg is odd) shall be used to reserve a block of Elements with Group Number gggg for use by an individual implementor. The implementor shall insert an identification code in the first unused (unassigned) Element in this series to reserve a block of Private Elements. The VR of the private identification code shall be LO (Long String) and the VM shall be equal to 1.

b) Private Creator Data Element (gggg,0010), is a Type 1 Data Element that identifies the implementor reserving element (gggg,1000-10FF), Private Creator Data Element (gggg,0011) identifies the implementor reserving elements (gggg,1100-11FF), and so on, until Private Creator Data Element (gggg,00FF) identifies the implementor reserving elements (gggg,FF00- FFFF).

c) Encoders of Private Data Elements shall be able to dynamically assign private data to any available (unreserved) block(s) within the Private group, and specify this assignment through the blocks corresponding Private Creator Data Element(s). Decoders of Private Data shall be able to accept reserved blocks with a given Private Creator identification code at any position within the Private group specified by the blocks corresponding Private Creator Data Element.

Value Representation Value Representation is often abbreviated to VR.

The VR is a two byte character string giving the code for the encoding of the subsequent data in the Value Field (see below).

The VR appears in DICOM data that has "Explicit Value Representation", and is absent for data with "Implicit Value Representation". "Implicit Value Representation" uses the fact that the DICOM data dictionary gives VR values for each tag in the standard DICOM data dictionary, so the VR value is implied by the tag value, given the data dictionary.

Most DICOM data uses "Explicit Value Representation" because the DICOM data dictionary only gives VRs for standard (even group number, not private) data elements. Each manufacturer writes their own private data elements, and the VR of these elements is not defined in the standard, and therefore may not be known to software not from that manufacturer.

The VR codes have to be one of the values from this table (section 6.2 of DICOM standard PS 3.5):

Value Representation	Description
AE	Application Entity
AS	Age String
AT	Attribute Tag
CS	Code String
DA	Date
DS	Decimal String
DT	Date/Time
FL	Floating Point Single (4 bytes)
FD	Floating Point Double (8 bytes)
IS	Integer String
LO	Long String
LT	Long Text
OB	Other Byte
OF	Other Float
OW	Other Word
PN	Person Name
SH	Short String
SL	Signed Long
SQ	Sequence of Items
SS	Signed Short
ST	Short Text
TM	Time
UI	Unique Identifier
UL	Unsigned Long
UN	Unknown
US	Unsigned Short
UT	Unlimited Text

Value length Value length gives the length of the data contained in the Value Field tag, or is a flag specifying the Value Field is of undefined length, and thus must be terminated later in the data stream with a special Item or Sequence Delimitation tag.

Quoting from section 7.1.1 of PS 3.5:

> Value Length: Either:
>
> a 16 or 32-bit (dependent on VR and whether VR is explicit or implicit) unsigned integer containing the Explicit Length of the Value Field as the number of bytes (even) that make up the Value. It does not include the length of the Data Element Tag, Value Representation, and Value Length Fields.
>
> a 32-bit Length Field set to Undefined Length (FFFFFFFFH). Undefined Lengths may be used for Data Elements having the Value Representation (VR) Sequence of Items (SQ) and Unknown (UN). For Data Elements with Value Representation OW or OB Undefined Length may be used depending on the negotiated Transfer Syntax (see Section 10 and Annex A).

Value field An even number of bytes storing the value(s) of the data element. The exact format of this data depends on the Value Representation (see above) and the Value Multiplicity (see next section).

Data element tags and data dictionaries

We can look up data element tags in a *data dictionary*.

As we've seen, data element tags with even group numbers are *standard* data element tags. We can look these up in the standard data dictionary in section 6 of PS 3.6.

Data element tags with odd group numbers are *private* data element tags. These can be used by manufacturers for information that may be specific to the manufacturer. To look up these tags, we need the private data dictionary of the manufacturer.

A data dictionary lists (Attribute tag, Attribute name, Attribute Keyword, Value Representation, Value Multiplicity) for all tags.

For example, here is an excerpt from the table in PS 3.6 section 6:

Tag	Name	Keyword	VR	VM
(0010,0010)	Patient's Name	PatientName	PN	1
(0010,0020)	Patient ID	PatientID	LO	1
(0010,0021)	Issuer of Patient ID	IssuerOfPatientID	LO	1
(0010,0022)	Type of Patient ID	TypeOfPatientID	CS	1
(0010,0024)	Issuer of Patient ID Qualifiers Sequence	IssuerOfPatientIDQualifiersSequence	SQ	1
(0010,0030)	Patient's Birth Date	PatientBirthDate	DA	1
(0010,0032)	Patient's Birth Time	PatientBirthTime	TM	1

The "Name" column gives a standard name for the tag. "Keyword" gives a shorter equivalent to the name without spaces that can be used as a variable or attribute name in code.

Value Representation in the data dictionary The "VR" column in the data dictionary gives the Value Representation. There is usually only one possible VR for each tag [1].

[1] Actually, it is not quite true that there can be only one VR associated with a particular tag. A small number of tags have VRs which can be either Unsigned Short (US) or Signed Short (SS). An even smaller number of tags can be either Other Byte (OB) or Other Word (OW). For all the relevant tags the VM is a set number (1, 3, or 4). So, in the OB / OW cases you can tell which of OB or OW you have by the Value Length. The US / SS cases seem to refer to pixel values; presumably they are US if the Pixel Representation (tag 0028, 0103) is 0 (for unsigned) and SS if the Pixel Representation is 1 (for signed)

If a particular stream of data elements is using "Implicit Value Representation Encoding" then the data elements consist of (tag, Value Length, Value Field) and the Value Representation is implicit. In this case we have to get the Value Representation from the data dictionary. If a stream is using "Explicit Value Representation Encoding", the elements consist of (tag, Value Representation, Value Length, Value Field) and the Value Representation is therefore already specified along with the data.

Value Multiplicity in the data dictionary The "VM" column in the dictionary gives the Value Multiplicity for this tag. Quoting from PS 3.5 section 6.4:

> The Value Multiplicity of a Data Element specifies the number of Values that can be encoded in the Value Field of that Data Element. The VM of each Data Element is specified explicitly in PS 3.6. If the number of Values that may be encoded in an element is variable, it shall be represented by two numbers separated by a dash; e.g., "1-10" means that there may be 1 to 10 Values in the element.

The most common values for Value Multiplicity in the standard data dictionary are (in decreasing frequency) '1', '1-n', '3', '2', '1-2', '4' with other values being less common.

The data dictionary is the only way to know the Value Multiplicity of a particular tag. This means that we need the manufacturer's private data dictionary to know the Value Multiplicity of private attribute tags.

DICOM data structures

A data set A DICOM *data set* is a ordered list of data elements. The order of the list is the order of the tags of the data elements. Here is the definition from section 3.10 of PS 3.5:

> DATA SET: Exchanged information consisting of a structured set of Attribute values directly or indirectly related to Information Objects. The value of each Attribute in a Data Set is expressed as a Data Element. A collection of Data Elements ordered by increasing Data Element Tag number that is an encoding of the values of Attributes of a real world object.

Background - the DICOM world DICOM has abstract definitions of a set of entities (objects) in the "Real World". These real world objects have relationships between them. Section 7 of PS 3.3 has the title "DICOM model of the real world". Examples of Real World entities are Patient, Study, Series.

Here is a selected list of real world entities compiled from section 7 of PS 3.3:

- Patient
- Visit
- Study
- Modality Performed Procedure Steps
- Frame of Reference
- Equipment
- Series
- Registration
- Fiducials
- Image
- Presentation State
- SR Document
- Waveform

- MR Spectroscopy
- Raw Data
- Encapsulated Document
- Real World Value Mapping
- Stereometric Relationship
- Surface
- Measurements

DICOM refers to its model of the entities and their relationships in the real world as the DICOM Application Model. PS 3.3:

> 3.8.5 DICOM application model: an Entity-Relationship diagram used to model the relationships between Real-World Objects which are within the area of interest of the DICOM Standard.

DICOM Entities and Information Object Definitions This is rather confusing.

PS 3.3 gives definitions of fundamental DICOM objects called *Information Object Definitions* (IODs). Here is the definition of an IOD from section 3.8.7 of PS 3.3:

> 3.8.7 Information object definition (IOD): a data abstraction of a class of similar Real-World Objects which defines the nature and Attributes relevant to the class of Real-World Objects represented.

IODs give lists of attributes (data elements) that refer to one or more objects in the DICOM Real World.

A single IOD is the usual atom of data sent in a single DICOM message.

An IOD that contains attributes (data elements) for only one object in the DICOM Real World is a *Normalized IOD*. From PS 3.3:

> 3.8.10 Normalized IOD: an Information Object Definition which represents a single entity in the DICOM Application Model. Such an IOD includes Attributes which are only inherent in the Real-World Object that the IOD represents.

Annex B of PS 3.3 defines the normalized IODs.

Many DICOM Real World objects do not have corresponding normalized IODs, presumably because there is no common need to send data only corresponding to - say - a patient - without also sending related information like - say - an image. If you do want to send information relating to a patient with information relating to an image, you need a *composite IOD*.

An IOD that contains attributes from more than one object in the DICOM Real World is a *Composite IOD*. PS 3.3 again:

> 3.8.2 Composite IOD: an Information Object Definition which represents parts of several entities in the DICOM Application Model. Such an IOD includes Attributes which are not inherent in the Real-World Object that the IOD represents but rather are inherent in related Real-World Objects

Annex A of PS 3.3 defines the composite IODs.

DICOM MR or CT image IODs are classic examples of composite IODs, because they contain information not just about the image itself, but also information about the patient, the study, the series, the frame of reference and the equipment.

The term *Information Entity* (IE) refers to a part of a composite IOD that relates to a single DICOM Real World object. PS 3.3:

> 3.8.6 Information entity: that portion of information defined by a Composite IOD which is related to one specific class of Real-World Object. There is a one-to-one correspondence between Information Entities and entities in the DICOM Application Model.

IEs are names of DICOM Real World objects that label parts of a composite IOD. IEs have no intrinsic content, but serve as meaningful labels for a group of *modules* (see below) that refer to the same Real World object.

Annex A 1.2, PS 3.3 lists all the IEs used in composite IODs.

For example, section A.4 in PD 3.3 defines the composite IOD for an MR Image - the Magnetic Resonance Image Object Definition. The definition looks like this (table A.4-1 of PS 3.3)

IE	Module	Reference	Usage
Patient	Patient	C.7.1.1	M
	Clinical Trial Subject	C.7.1.3	U
Study	General Study	C.7.2.1	M
	Patient Study	C.7.2.2	U
	Clinical Trial Study	C.7.2.3	U
Series	General Series	C.7.3.1	M
	Clinical Trial Series	C.7.3.2	U
Frame of Reference	Frame of Reference	C.7.4.1	M
Equipment	General Equipment	C.7.5.1	M
Image	General Image	C.7.6.1	M
	Image Plane	C.7.6.2	M
	Image Pixel	C.7.6.3	M
	Contrast/bolus	C.7.6.4	C - Required if contrast media was used in this image
	Device	C.7.6.12	U
	Specimen	C.7.6.22	U
	MR Image	C.8.3.1	M
	Overlay Plane	C.9.2	U
	VOI LUT	C.11.2	U
	SOP Common	C.12.1	M

As you can see, the MR Image IOD is composite and composed of Patient, Study, Series, Frame of Reference, Equipment and Image IEs.

The *module* heading defines which modules make up the information relevant to the IE.

A module is a named and defined grouping of attributes (data elements) with related meaning. PS 3.3:

> 3.8.8 Module: A set of Attributes within an Information Entity or Normalized IOD which are logically related to each other.

Grouping attributes into modules simplifies the definition of multiple composite IODs. For example, the composite IODs for a CT image and an MR Image both have modules for Patient, Clinical Trial Subject, etc.

Annex C of PS 3.3 defines all the modules used for the IOD definitions. For example, from the table above, we see that the "Patient" module is at section C.7.1.1 of PS 3.3. This section gives a table of all the attributes (data elements) in this module.

The last column in the table above records whether the particular module is Mandatory, Conditional or User Option (defined in section A 1.3 of PS 3.3)

Lastly module definitions may make use of *Attribute macros*. Attribute macros are very much like modules, in that they are a named group of attributes that often occur together in module definitions, or definitions of other macros. From PS 3.3:

> 3.11.1 Attribute Macro: a set of Attributes that are described in a single table that is referenced by multiple Modules or other tables.

For example, here is the Patient Orientation Macro definition table from section 10.12 in PS 3.3:

Attribute Name	Tag	Type	Attribute Description
Patient Orientation Code Sequence	(0054,0410)		Sequence that describes the orientation of the patient with respect to gravity. See C.8.11.5.1.2 for further explanation. Only a single Item shall be included in this Sequence.
>Include 'Code Sequence Macro' Table 8.8-1.			Baseline Context ID 19
>Patient Orientation Modifier Code Sequence	(0054,0412)		Patient orientation modifier. Required if needed to fully specify the orientation of the patient with respect to gravity. Only a single Item shall be included in this Sequence.
>>Include 'Code Sequence Macro' Table 8.8-1.			Baseline Context ID 20
Patient Gantry Relationship Code Sequence	(0054,0414)		Sequence that describes the orientation of the patient with respect to the head of the table. See Section C.8.4.6.1.3 for further explanation. Only a single Item is permitted in this Sequence.
>Include 'Code Sequence Macro' Table 8.8-1.			Baseline Context ID 21

As you can see, this macro specifies some tags that should appear when this macro is "Included" - and also includes other macros.

DICOM services (DIMSE)

We now go back to messages.

The DICOM application sending the message is called the Service Class User (SCU). We might also call this the client.

The DICOM application receiving the message is called the Service Class Provider (SCP). We might also call this the server - for this particular message.

Quoting from PS 3.7 section 6.3:

> A Message is composed of a Command Set followed by a conditional Data Set (see PS 3.5 for the definition of a Data Set). The Command Set is used to indicate the operations/notifications to be performed on or with the Data Set.

The command set consists of command elements (elements with group number 0000).

Valid sequences of command elements in the command set form valid DICOM Message Service Elements (DIMSEs). Sections 9 and 10 of PS 3.7 define the valid DIMSEs.

For example, there is a DIMSE service called "C-ECHO" that requests confirmation from the responding application that the echo message arrived.

The definition of the DIMSE services specifies, for a particular DIMSE service, whether the DIMSE commend set should be followed by a data set.

In particular, the data set will be a full Information Object Definition's worth of data.

Of most interest to us, the "C-STORE" service command set should always be followed by a data set conforming to an image data IOD.

DICOM service object pairs (SOPs)

As we've seen, some DIMSE services should be followed by particular types of data.

For example, the "C-STORE" DIMSE command set should be followed by an IOD of data to store, but the "C-ECHO" has no data object following.

The association of a particular type of DIMSE (command set) with the associated IOD's-worth of data is a Service Object Pair. The DIMSE is the "Service" and the data IOD is the "Object". Thus the combination of a "C-STORE" DIMSE and an "MR Image" IOD would be a SOP. Services that do not have data following are a particular type of SOP where the Object is null. For example, the "C-ECHO" service is the entire contents of a Verification SOP (PS 3.4, section A.4).

DICOM defines which pairings are possible, by listing them all as Service Object Pair classes (SOP classes).

Usually a SOP class describes the pairing of exactly one DIMSE service with one defined IOD. For example, the "MR Image storage" SOP class pairs the "C-STORE" DIMSE with the "MR Image" IOD.

Sometimes a SOP class describes the pairings of one of several possible DIMSEs with a particular IOP. For example, the "Modality Performed Procedure Step" SOP class describes the pairing of *either* ("N-CREATE", Modality Performed Procedure Step IOD) *or* ("N-SET", Modality Performed Procedure Step IOD) (see PS 3.4 F.7.1). For this reason a SOP class is best described as the pairing of a *DIMSE service group* with an IOD, where the DIMSE service group usually contains just one DIMSE service, but sometimes has more. For example, the "MR Image Storage" SOP class has a DIMSE service group of one element ["C-STORE"]. The "Modality Performed Procedure Step" SOP class has a DIMSE service group with two elements: ["N-CREATE", "N-SET"].

From PS 3.4:

> 6.4 DIMSE SERVICE GROUP
>
> DIMSE Service Group specifies one or more operations/notifications defined in PS 3.7 which are applicable to an IOD.
>
> DIMSE Service Groups are defined in this Part of the DICOM Standard, in the specification of a Service - Object Pair Class.
>
> 6.5 SERVICE-OBJECT PAIR (SOP) CLASS
>
> A Service-Object Pair (SOP) Class is defined by the union of an IOD and a DIMSE Service Group. The SOP Class definition contains the rules and semantics which may restrict the use of the services in the DIMSE Service Group and/or the Attributes of the IOD.

The Annexes of PS 3.4 define the SOP classes.

A pairing of actual data of form (DIMSE group, IOD) that conforms to the SOP class definition, is a SOP class instance. That is, the instance comprises the actual values of the service and data elements being transmitted.

For example, there is a SOP class called "MR Image Storage". This is the association of the "C-STORE" DIMSE command with the "MR Image" IOD. A particular "C-STORE" request command set along with the particular "MR Image" IOD data set would be an *instance* of the MR Image SOP class.

DICOM files

Now let us return to the confusing definition of the DICOM file format from section 7 of PS 3.10:

> 7 DICOM File Format
>
> The DICOM File Format provides a means to encapsulate in a file the Data Set representing a SOP Instance related to a DICOM IOD. As shown in Figure 7-1, the byte stream of the Data Set is placed into the file after the DICOM File Meta Information. Each file contains a single SOP Instance.

The DICOM file Meta Information is:

- File preamble - 128 bytes, content unspecified
- DICOM prefix - 4 bytes "DICM" character string

- 5 meta information elements (group 0002) as defined in table 7.1 of PS 3.10

There follows the IOD dataset part of the SOP instance. In the case of a file storing an MR Image, this dataset will be of IOD type "MR Image"

9.3 Developer documentation page

9.3.1 NiBabel Developer Guidelines

NiBabel source code

Working with *nibabel* source code

Contents:

Introduction These pages describe a git and github workflow for the nibabel project.

There are several different workflows here, for different ways of working with *nibabel*.

This is not a comprehensive git reference, it's just a workflow for our own project. It's tailored to the github hosting service. You may well find better or quicker ways of getting stuff done with git, but these should get you started.

For general resources for learning git, see *git resources*.

Install git

Overview

Debian / Ubuntu	`sudo apt-get install git-core`
Fedora	`sudo yum install git-core`
Windows	Download and install msysGit
OS X	Use the git-osx-installer

In detail See the git page for the most recent information.

Have a look at the github install help pages available from github help

There are good instructions here: https://git-scm.com/book/en/v2/Getting-Started-Installing-Git

Following the latest source These are the instructions if you just want to follow the latest *nibabel* source, but you don't need to do any development for now.

The steps are:

- *Install git*
- get local copy of the git repository from github
- update local copy from time to time

Get the local copy of the code From the command line:

```
git clone git://github.com/nipy/nibabel.git
```

You now have a copy of the code tree in the new `nibabel` directory.

Updating the code From time to time you may want to pull down the latest code. Do this with:

```
cd nibabel
git pull
```

The tree in `nibabel` will now have the latest changes from the initial repository.

Making a patch You've discovered a bug or something else you want to change in nibabel .. — excellent!

You've worked out a way to fix it — even better!

You want to tell us about it — best of all!

The easiest way is to make a *patch* or set of patches. Here we explain how. Making a patch is the simplest and quickest, but if you're going to be doing anything more than simple quick things, please consider following the *Git for development* model instead.

Making patches

Overview

```
# tell git who you are
git config --global user.email you@yourdomain.example.com
git config --global user.name "Your Name Comes Here"
# get the repository if you don't have it
git clone git://github.com/nipy/nibabel.git
# make a branch for your patching
cd nibabel
git branch the-fix-im-thinking-of
git checkout the-fix-im-thinking-of
# hack, hack, hack
# Tell git about any new files you've made
git add somewhere/tests/test_my_bug.py
# commit work in progress as you go
git commit -am 'BF - added tests for Funny bug'
# hack hack, hack
git commit -am 'BF - added fix for Funny bug'
# make the patch files
git format-patch -M -C master
```

Then, send the generated patch files to the nibabel mailing list — where we will thank you warmly.

In detail

1. Tell git who you are so it can label the commits you've made:

```
   git config --global user.email you@yourdomain.example.com
   git config --global user.name "Your Name Comes Here"
```

2. If you don't already have one, clone a copy of the nibabel repository:

```
   git clone git://github.com/nipy/nibabel.git
   cd nibabel
```

3. Make a 'feature branch'. This will be where you work on your bug fix. It's nice and safe and leaves you with access to an unmodified copy of the code in the main branch:

```
git branch the-fix-im-thinking-of
git checkout the-fix-im-thinking-of
```

4. Do some edits, and commit them as you go:

```
# hack, hack, hack
# Tell git about any new files you've made
git add somewhere/tests/test_my_bug.py
# commit work in progress as you go
git commit -am 'BF - added tests for Funny bug'
# hack hack, hack
git commit -am 'BF - added fix for Funny bug'
```

   Note the `-am` options to `commit`. The `m` flag just signals that you're going to type a message on the command line. The `a` flag — you can just take on faith — or see why the -a flag?.

5. When you have finished, check you have committed all your changes:

```
git status
```

6. Finally, make your commits into patches. You want all the commits since you branched from the `master` branch:

```
git format-patch -M -C master
```

   You will now have several files named for the commits:

```
0001-BF-added-tests-for-Funny-bug.patch
0002-BF-added-fix-for-Funny-bug.patch
```

   Send these files to the nibabel mailing list.

When you are done, to switch back to the main copy of the code, just return to the `master` branch:

```
git checkout master
```

Moving from patching to development If you find you have done some patches, and you have one or more feature branches, you will probably want to switch to development mode. You can do this with the repository you have.

Fork the nibabel repository on github — *Making your own copy (fork) of nibabel*. Then:

```
# checkout and refresh master branch from main repo
git checkout master
git pull origin master
# rename pointer to main repository to 'upstream'
git remote rename origin upstream
# point your repo to default read / write to your fork on github
git remote add origin git@github.com:your-user-name/nibabel.git
# push up any branches you've made and want to keep
git push origin the-fix-im-thinking-of
```

Then you can, if you want, follow the *Development workflow*.

Git for development Contents:

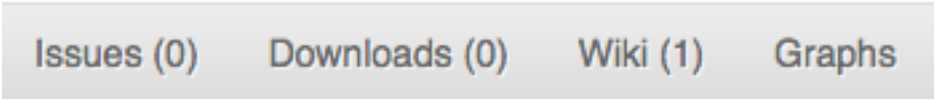
Making your own copy (fork) of nibabel You need to do this only once. The instructions here are very similar to the instructions at https://help.github.com/articles/fork-a-repo/ — please see that page for more detail. We're repeating some of it here just to give the specifics for the nibabel project, and to suggest some default names.

Set up and configure a github account If you don't have a github account, go to the github page, and make one.

You then need to configure your account to allow write access — see the `Generating SSH keys` help on github help.

Create your own forked copy of nibabel

1. Log into your github account.
2. Go to the nibabel github home at nibabel github.
3. Click on the *fork* button:



Now, after a short pause and some 'Hardcore forking action', you should find yourself at the home page for your own forked copy of nibabel.

Set up your fork First you follow the instructions for *Making your own copy (fork) of nibabel*.

Overview

```
git clone git@github.com:your-user-name/nibabel.git
cd nibabel
git remote add upstream git://github.com/nipy/nibabel.git
```

In detail

Clone your fork

1. Clone your fork to the local computer with `git clone git@github.com:your-user-name/nibabel.git`
2. Investigate. Change directory to your new repo: `cd nibabel`. Then `git branch -a` to show you all branches. You'll get something like:

```
* master
remotes/origin/master
```

This tells you that you are currently on the `master` branch, and that you also have a `remote` connection to `origin/master`. What remote repository is `remote/origin`? Try `git remote -v` to see the URLs for the remote. They will point to your github fork.

Now you want to connect to the upstream nibabel github repository, so you can merge in changes from trunk.

Linking your repository to the upstream repo

```
cd nibabel
git remote add upstream git://github.com/nipy/nibabel.git
```

`upstream` here is just the arbitrary name we're using to refer to the main nibabel repository at nibabel github.

Note that we've used `git://` for the URL rather than `git@`. The `git://` URL is read only. This means we that we can't accidentally (or deliberately) write to the upstream repo, and we are only going to use it to merge into our own code.

Just for your own satisfaction, show yourself that you now have a new 'remote', with `git remote -v show`, giving you something like:

```
upstream     git://github.com/nipy/nibabel.git (fetch)
upstream     git://github.com/nipy/nibabel.git (push)
origin       git@github.com:your-user-name/nibabel.git (fetch)
origin       git@github.com:your-user-name/nibabel.git (push)
```

Configure git

Overview Your personal git configurations are saved in the `.gitconfig` file in your home directory.

Here is an example `.gitconfig` file:

```
[user]
        name = Your Name
        email = you@yourdomain.example.com

[alias]
        ci = commit -a
        co = checkout
        st = status
        stat = status
        br = branch
        wdiff = diff --color-words

[core]
        editor = vim

[merge]
        summary = true
```

You can edit this file directly or you can use the `git config --global` command:

```
git config --global user.name "Your Name"
git config --global user.email you@yourdomain.example.com
git config --global alias.ci "commit -a"
git config --global alias.co checkout
git config --global alias.st "status -a"
git config --global alias.stat "status -a"
git config --global alias.br branch
git config --global alias.wdiff "diff --color-words"
git config --global core.editor vim
git config --global merge.summary true
```

To set up on another computer, you can copy your `~/.gitconfig` file, or run the commands above.

In detail

user.name and user.email It is good practice to tell git who you are, for labeling any changes you make to the code. The simplest way to do this is from the command line:

```
git config --global user.name "Your Name"
git config --global user.email you@yourdomain.example.com
```

This will write the settings into your git configuration file, which should now contain a user section with your name and email:

```
[user]
      name = Your Name
      email = you@yourdomain.example.com
```

Of course you'll need to replace `Your Name` and `you@yourdomain.example.com` with your actual name and email address.

Aliases You might well benefit from some aliases to common commands.

For example, you might well want to be able to shorten `git checkout` to `git co`. Or you may want to alias `git diff --color-words` (which gives a nicely formatted output of the diff) to `git wdiff`

The following `git config --global` commands:

```
git config --global alias.ci "commit -a"
git config --global alias.co checkout
git config --global alias.st "status -a"
git config --global alias.stat "status -a"
git config --global alias.br branch
git config --global alias.wdiff "diff --color-words"
```

will create an `alias` section in your `.gitconfig` file with contents like this:

```
[alias]
        ci = commit -a
        co = checkout
        st = status -a
        stat = status -a
        br = branch
        wdiff = diff --color-words
```

Editor You may also want to make sure that your editor of choice is used

```
git config --global core.editor vim
```

Merging To enforce summaries when doing merges (`~/.gitconfig` file again):

```
[merge]
   log = true
```

Or from the command line:

```
git config --global merge.log true
```

Fancy log output This is a very nice alias to get a fancy log output; it should go in the `alias` section of your `.gitconfig` file:

```
lg = log --graph --pretty=format:'%Cred%h%Creset -%C(yellow)%d%Creset %s %Cgreen(%cr) %C(bold blue)[%
```

You use the alias with:

```
git lg
```

and it gives graph / text output something like this (but with color!):

```
* 6d8e1ee - (HEAD, origin/my-fancy-feature, my-fancy-feature) NF - a fancy file (45 minutes ago) [Mat
*   d304a73 - (origin/placeholder, placeholder) Merge pull request #48 from hhuuggoo/master (2 weeks
|\
| * 4aff2a8 - fixed bug 35, and added a test in test_bugfixes (2 weeks ago) [Hugo]
|/
* a7ff2e5 - Added notes on discussion/proposal made during Data Array Summit. (2 weeks ago) [Corran W
* 68f6752 - Initial implimentation of AxisIndexer - uses 'index_by' which needs to be changed to a ca
*   376adbd - Merge pull request #46 from terhorst/master (2 weeks ago) [Jonathan Terhorst]
|\
| * b605216 - updated joshu example to current api (3 weeks ago) [Jonathan Terhorst]
| * 2e991e8 - add testing for outer ufunc (3 weeks ago) [Jonathan Terhorst]
| * 7beda5a - prevent axis from throwing an exception if testing equality with non-axis object (3 wee
| * 65af65e - convert unit testing code to assertions (3 weeks ago) [Jonathan Terhorst]
| *   956fbab - Merge remote-tracking branch 'upstream/master' (3 weeks ago) [Jonathan Terhorst]
| |\
| |/
```

Thanks to Yury V. Zaytsev for posting it.

Development workflow You already have your own forked copy of the nibabel repository, by following *Making your own copy (fork) of nibabel*. You have *Set up your fork*. You have configured git by following *Configure git*. Now you are ready for some real work.

Workflow summary In what follows we'll refer to the upstream nibabel `master` branch, as "trunk".

- Don't use your `master` branch for anything. Consider deleting it.
- When you are starting a new set of changes, fetch any changes from trunk, and start a new *feature branch* from that.
- Make a new branch for each separable set of changes — "one task, one branch" (ipython git workflow).
- Name your branch for the purpose of the changes - e.g. `bugfix-for-issue-14` or `refactor-database-code`.
- If you can possibly avoid it, avoid merging trunk or any other branches into your feature branch while you are working.
- If you do find yourself merging from trunk, consider *Rebasing on trunk*
- Ask on the nibabel mailing list if you get stuck.
- Ask for code review!

This way of working helps to keep work well organized, with readable history. This in turn makes it easier for project maintainers (that might be you) to see what you've done, and why you did it.

See linux git workflow and ipython git workflow for some explanation.

Consider deleting your master branch It may sound strange, but deleting your own `master` branch can help reduce confusion about which branch you are on. See deleting master on github for details.

Update the mirror of trunk First make sure you have done *Linking your repository to the upstream repo*.

From time to time you should fetch the upstream (trunk) changes from github:

```
git fetch upstream
```

This will pull down any commits you don't have, and set the remote branches to point to the right commit. For example, 'trunk' is the branch referred to by (remote/branchname) `upstream/master` - and if there have been commits since you last checked, `upstream/master` will change after you do the fetch.

Make a new feature branch When you are ready to make some changes to the code, you should start a new branch. Branches that are for a collection of related edits are often called 'feature branches'.

Making an new branch for each set of related changes will make it easier for someone reviewing your branch to see what you are doing.

Choose an informative name for the branch to remind yourself and the rest of us what the changes in the branch are for. For example `add-ability-to-fly`, or `buxfix-for-issue-42`.

```
# Update the mirror of trunk
git fetch upstream
# Make new feature branch starting at current trunk
git branch my-new-feature upstream/master
git checkout my-new-feature
```

Generally, you will want to keep your feature branches on your public github fork of nibabel. To do this, you git push this new branch up to your github repo. Generally (if you followed the instructions in these pages, and by default), git will have a link to your github repo, called `origin`. You push up to your own repo on github with:

```
git push origin my-new-feature
```

In git >= 1.7 you can ensure that the link is correctly set by using the `--set-upstream` option:

```
git push --set-upstream origin my-new-feature
```

From now on git will know that `my-new-feature` is related to the `my-new-feature` branch in the github repo.

The editing workflow

Overview

```
# hack hack
git add my_new_file
git commit -am 'NF - some message'
git push
```

In more detail

1. Make some changes
2. See which files have changed with `git status` (see git status). You'll see a listing like this one:

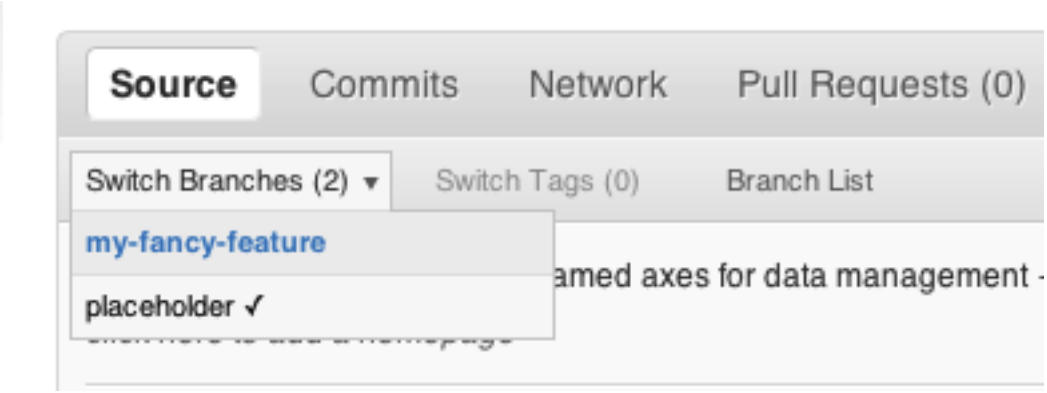
```
    # On branch ny-new-feature
    # Changed but not updated:
    #   (use "git add <file>..." to update what will be committed)
    #   (use "git checkout -- <file>..." to discard changes in working directory)
    #
    #  modified:   README
```

```
#
# Untracked files:
#   (use "git add <file>..." to include in what will be committed)
#
#  INSTALL
no changes added to commit (use "git add" and/or "git commit -a")
```

3. Check what the actual changes are with `git diff` (git diff).
4. Add any new files to version control `git add new_file_name` (see git add).
5. To commit all modified files into the local copy of your repo,, do `git commit -am 'A commit message'`. Note the `-am` options to `commit`. The `m` flag just signals that you're going to type a message on the command line. The `a` flag — you can just take on faith — or see why the -a flag? — and the helpful use-case description in the tangled working copy problem. The git commit manual page might also be useful.
6. To push the changes up to your forked repo on github, do a `git push` (see git push).

Ask for your changes to be reviewed or merged When you are ready to ask for someone to review your code and consider a merge:

1. Go to the URL of your forked repo, say `https://github.com/your-user-name/nibabel`.
2. Use the 'Switch Branches' dropdown menu near the top left of the page to select the branch with your changes:



3. Click on the 'Pull request' button:

Enter a title for the set of changes, and some explanation of what you've done. Say if there is anything you'd like particular attention for - like a complicated change or some code you are not happy with.

If you don't think your request is ready to be merged, just say so in your pull request message. This is still a good way of getting some preliminary code review.

Some other things you might want to do

Delete a branch on github

```
git checkout master
# delete branch locally
git branch -D my-unwanted-branch
# delete branch on github
git push origin :my-unwanted-branch
```

(Note the colon `:` before `test-branch`. See also: https://github.com/guides/remove-a-remote-branch

Several people sharing a single repository If you want to work on some stuff with other people, where you are all committing into the same repository, or even the same branch, then just share it via github.

First fork nibabel into your account, as from *Making your own copy (fork) of nibabel*.

Then, go to your forked repository github page, say `https://github.com/your-user-name/nibabel`

Click on the 'Admin' button, and add anyone else to the repo as a collaborator:

Now all those people can do:

```
git clone git@githhub.com:your-user-name/nibabel.git
```

Remember that links starting with `git@` use the ssh protocol and are read-write; links starting with `git://` are read-only.

Your collaborators can then commit directly into that repo with the usual:

```
git commit -am 'ENH - much better code'
git push origin master # pushes directly into your repo
```

Explore your repository To see a graphical representation of the repository branches and commits:

```
gitk --all
```

To see a linear list of commits for this branch:

```
git log
```

You can also look at the network graph visualizer for your github repo.

Finally the *Fancy log output* `lg` alias will give you a reasonable text-based graph of the repository.

Rebasing on trunk Let's say you thought of some work you'd like to do. You *Update the mirror of trunk* and *Make a new feature branch* called `cool-feature`. At this stage trunk is at some commit, let's call it E. Now you make some new commits on your `cool-feature` branch, let's call them A, B, C. Maybe your changes take a while, or you come back to them after a while. In the meantime, trunk has progressed from commit E to commit (say) G:

```
      A---B---C cool-feature
     /
D---E---F---G trunk
```

At this stage you consider merging trunk into your feature branch, and you remember that this here page sternly advises you not to do that, because the history will get messy. Most of the time you can just ask for a review, and not worry that trunk has got a little ahead. But sometimes, the changes in trunk might affect your changes, and you need to harmonize them. In this situation you may prefer to do a rebase.

rebase takes your changes (A, B, C) and replays them as if they had been made to the current state of `trunk`. In other words, in this case, it takes the changes represented by A, B, C and replays them on top of G. After the rebase, your history will look like this:

```
              A'--B'--C' cool-feature
             /
D---E---F---G trunk
```

See rebase without tears for more detail.

To do a rebase on trunk:

```
# Update the mirror of trunk
git fetch upstream
# go to the feature branch
git checkout cool-feature
# make a backup in case you mess up
git branch tmp cool-feature
# rebase cool-feature onto trunk
git rebase --onto upstream/master upstream/master cool-feature
```

In this situation, where you are already on branch `cool-feature`, the last command can be written more succinctly as:

```
git rebase upstream/master
```

When all looks good you can delete your backup branch:

```
git branch -D tmp
```

If it doesn't look good you may need to have a look at *Recovering from mess-ups*.

If you have made changes to files that have also changed in trunk, this may generate merge conflicts that you need to resolve - see the git rebase man page for some instructions at the end of the "Description" section. There is some related help on merging in the git user manual - see resolving a merge.

Recovering from mess-ups Sometimes, you mess up merges or rebases. Luckily, in git it is relatively straightforward to recover from such mistakes.

If you mess up during a rebase:

```
git rebase --abort
```

If you notice you messed up after the rebase:

```
# reset branch back to the saved point
git reset --hard tmp
```

If you forgot to make a backup branch:

```
# look at the reflog of the branch
git reflog show cool-feature

8630830 cool-feature@{0}: commit: BUG: io: close file handles immediately
278dd2a cool-feature@{1}: rebase finished: refs/heads/my-feature-branch onto 11ee694744f2552d
26aa21a cool-feature@{2}: commit: BUG: lib: make seek_gzip_factory not leak gzip obj
...

# reset the branch to where it was before the botched rebase
git reset --hard cool-feature@{2}
```

Rewriting commit history

Note: Do this only for your own feature branches.

There's an embarassing typo in a commit you made? Or perhaps the you made several false starts you would like the posterity not to see.

This can be done via *interactive rebasing*.

Suppose that the commit history looks like this:

```
git log --oneline
eadc391 Fix some remaining bugs
a815645 Modify it so that it works
2dec1ac Fix a few bugs + disable
13d7934 First implementation
6ad92e5 * masked is now an instance of a new object, MaskedConstant
29001ed Add pre-nep for a copule of structured_array_extensions.
...
```

and `6ad92e5` is the last commit in the `cool-feature` branch. Suppose we want to make the following changes:

- Rewrite the commit message for `13d7934` to something more sensible.
- Combine the commits `2dec1ac`, `a815645`, `eadc391` into a single one.

We do as follows:

```
# make a backup of the current state
git branch tmp HEAD
# interactive rebase
git rebase -i 6ad92e5
```

This will open an editor with the following text in it:

```
pick 13d7934 First implementation
pick 2dec1ac Fix a few bugs + disable
pick a815645 Modify it so that it works
pick eadc391 Fix some remaining bugs

# Rebase 6ad92e5..eadc391 onto 6ad92e5
#
# Commands:
#  p, pick = use commit
#  r, reword = use commit, but edit the commit message
#  e, edit = use commit, but stop for amending
#  s, squash = use commit, but meld into previous commit
#  f, fixup = like "squash", but discard this commit's log message
#
```

```
# If you remove a line here THAT COMMIT WILL BE LOST.
# However, if you remove everything, the rebase will be aborted.
#
```

To achieve what we want, we will make the following changes to it:

```
r 13d7934 First implementation
pick 2dec1ac Fix a few bugs + disable
f a815645 Modify it so that it works
f eadc391 Fix some remaining bugs
```

This means that (i) we want to edit the commit message for `13d7934`, and (ii) collapse the last three commits into one. Now we save and quit the editor.

Git will then immediately bring up an editor for editing the commit message. After revising it, we get the output:

```
[detached HEAD 721fc64] FOO: First implementation
 2 files changed, 199 insertions(+), 66 deletions(-)
[detached HEAD 0f22701] Fix a few bugs + disable
 1 files changed, 79 insertions(+), 61 deletions(-)
Successfully rebased and updated refs/heads/my-feature-branch.
```

and the history looks now like this:

```
0f22701 Fix a few bugs + disable
721fc64 ENH: Sophisticated feature
6ad92e5 * masked is now an instance of a new object, MaskedConstant
```

If it went wrong, recovery is again possible as explained *above*.

Maintainer workflow This page is for maintainers — those of us who merge our own or other peoples' changes into the upstream repository.

Being as how you're a maintainer, you are completely on top of the basic stuff in *Development workflow*.

The instructions in *Linking your repository to the upstream repo* add a remote that has read-only access to the upstream repo. Being a maintainer, you've got read-write access.

It's good to have your upstream remote have a scary name, to remind you that it's a read-write remote:

```
git remote add upstream-rw git@github.com:nipy/nibabel.git
git fetch upstream-rw
```

Integrating changes Let's say you have some changes that need to go into trunk (`upstream-rw/master`).

The changes are in some branch that you are currently on. For example, you are looking at someone's changes like this:

```
git remote add someone git://github.com/someone/nibabel.git
git fetch someone
git branch cool-feature --track someone/cool-feature
git checkout cool-feature
```

So now you are on the branch with the changes to be incorporated upstream. The rest of this section assumes you are on this branch.

A few commits If there are only a few commits, consider rebasing to upstream:

```
# Fetch upstream changes
git fetch upstream-rw
# rebase
git rebase upstream-rw/master
```

Remember that, if you do a rebase, and push that, you'll have to close any github pull requests manually, because github will not be able to detect the changes have already been merged.

A long series of commits If there are a longer series of related commits, consider a merge instead:

```
git fetch upstream-rw
git merge --no-ff upstream-rw/master
```

The merge will be detected by github, and should close any related pull requests automatically.

Note the `--no-ff` above. This forces git to make a merge commit, rather than doing a fast-forward, so that these set of commits branch off trunk then rejoin the main history with a merge, rather than appearing to have been made directly on top of trunk.

Check the history Now, in either case, you should check that the history is sensible and you have the right commits:

```
git log --oneline --graph
git log -p upstream-rw/master..
```

The first line above just shows the history in a compact way, with a text representation of the history graph. The second line shows the log of commits excluding those that can be reached from trunk (`upstream-rw/master`), and including those that can be reached from current HEAD (implied with the `..` at the end). So, it shows the commits unique to this branch compared to trunk. The `-p` option shows the diff for these commits in patch form.

Push to trunk

```
git push upstream-rw my-new-feature:master
```

This pushes the `my-new-feature` branch in this repository to the `master` branch in the `upstream-rw` repository.

git resources

Tutorials and summaries

- github help has an excellent series of how-to guides.
- learn.github has an excellent series of tutorials
- The pro git book is a good in-depth book on git.
- A git cheat sheet is a page giving summaries of common commands.
- The git user manual
- The git tutorial
- The git community book
- git ready — a nice series of tutorials
- git casts — video snippets giving git how-tos.

- git magic — extended introduction with intermediate detail
- The git parable is an easy read explaining the concepts behind git.
- git foundation expands on the git parable.
- Fernando Perez' git page — Fernando's git page — many links and tips
- A good but technical page on git concepts
- git svn crash course: git for those of us used to subversion

Advanced git workflow There are many ways of working with git; here are some posts on the rules of thumb that other projects have come up with:

- Linus Torvalds on git management
- Linus Torvalds on linux git workflow . Summary; use the git tools to make the history of your edits as clean as possible; merge from upstream edits as little as possible in branches where you are doing active development.

Manual pages online You can get these on your own machine with (e.g) `git help push` or (same thing) `git push --help`, but, for convenience, here are the online manual pages for some common commands:

- git add
- git branch
- git checkout
- git clone
- git commit
- git config
- git diff
- git log
- git pull
- git push
- git remote
- git status

Documentation

Code Documentation

All documentation should be written using Numpy documentation conventions:

http://projects.scipy.org/numpy/wiki/CodingStyleGuidelines#docstring-standard

Git Repository

Layout

The main release branch is called `master`. This is a merge-only branch. Features finished or updated by some developer are merged from the corresponding branch into `master`. At a certain point the current state of `master` is tagged – a release is done.

Only usable feature should end-up in `master`. Ideally `master` should be releasable at all times.

Additionally, there are distribution branches. They are prefixed `dist/` and labeled after the packaging target (e.g. *debian* for a Debian package). If necessary, there can be multiple branches for each distribution target.

`dist/debian/proper` Official Debian packaging

`dist/debian/dev` Debian packaging of unofficial development snapshots. They do not go into the main Debian archive, but might be distributed through other channels (e.g. NeuroDebian).

Releases are merged into the packaging branches, packaging is updated if necessary and the branch gets tagged when a package version is released. Maintenance (as well as backport) releases or branches off from the respective packaging tag.

There might be additonal branches for each developer, prefixed with intials. Alternatively, several GitHub (or elsewhere) clones might be used.

Commits

Please prefix all commit summaries with one (or more) of the following labels. This should help others to easily classify the commits into meaningful categories:

- *BF* : bug fix
- *RF* : refactoring
- *NF* : new feature
- *BW* : addresses backward-compatibility
- *OPT* : optimization
- *BK* : breaks something and/or tests fail
- *PL* : making pylint happier
- *DOC*: for all kinds of documentation related commits
- *TEST*: for adding or changing tests

Merges

For easy tracking of what changes were absorbed during merge, we advise that you enable merge summaries within git:

```
git-config merge.summary true
```

See *Configure git* for more detail.

Changelog

The changelog is located in the toplevel directory of the source tree in the *Changelog* file. The content of this file should be formated as restructured text to make it easy to put it into manual appendix and on the website.

This changelog should neither replicate the VCS commit log nor the distribution packaging changelogs (e.g. debian/changelog). It should be focused on the user perspective and is intended to list rather macroscopic and/or important changes to the module, like feature additions or bugfixes in the algorithms with implications to the performance or validity of results.

It may list references to 3rd party bugtrackers, in case the reported bugs match the criteria listed above.

9.3.2 Adding test data

1. We really, really like test images, but
2. We are rather conservative about the size of our code repository.

So, we have two different ways of adding test data.

1. Small, open licensed files can go in the `nibabel/tests/data` directory (see below);
2. Larger files or files with extra licensing terms can go in their own git repositories and be added as submodules to the `nibabel-data` directory.

Small files

Small files are around 50K or less when compressed. By "compressed", we mean, compressed with zlib, which is what git uses when storing the file in the repository. You can check the exact length directly with Python and a script like:

```
import sys
import zlib

for fname in sys.argv[1:]:
    with open(fname, 'rb') as fobj:
        contents = fobj.read()
    compressed = zlib.compress(contents)
    print(fname, len(compressed) / 1024.)
```

One way of making files smaller when compressed is to set uninteresting values to zero or some other number so that the compression algorithm can be more effective.

Please don't compress the file yourself before committing to a git repo unless there's a really good reason; git will do this for you when adding to the repository, and it's a shame to make git compress a compressed file.

Files with open licenses

We very much prefer files with completely open licenses such as the PDDL 1.0 or the CC0 license.

The files in the `nibabel/tests/data` will get distributed with the nibabel source code, and this can easily get installed without the user having an opportunity to review the full license. We don't think this is compatible with extra license terms like agreeing to cite the people who provided the data or agreeing not to try and work out the identity of the person who has been scanned, because it would be too easy to miss these requirements when using nibabel. It is fine to use files with these kind of licenses, but they should go in their own repository to be used as a submodule, so they do not need to be distributed with nibabel.

Adding the file to `nibabel/tests/data`

If the file is less then about 50K compressed, and the license is open, then you might want to commit the file under `nibabel/tests/data`.

Put the license for any new files in the COPYING file at the top level of the nibabel repo. You'll see some examples in that file already.

Adding as a submodule to `nibabel-data`

Make a new git repository with the data.

There are example repos at

- https://github.com/yarikoptic/nitest-balls1
- https://github.com/matthew-brett/nitest-minc2

Despite the fact that both the examples are on github, Bitbucket is good for repos like this because they don't enforce repository size limits.

Don't forget to include a LICENSE and README file in the repo.

When all is done, and the repository is safely on the internet and accessible, add the repo as a submodule to the `nitests-data` directory, with something like this:

```
git submodule add https://bitbucket.org/nipy/rosetta-samples.git nitests-data/rosetta-samples
```

You should now have a checked out copy of the `rosetta-samples` repository in the `nibabel-data/rosetta-samples` directory. Commit the submodule that is now in your git staging area.

If you are writing tests using files from this repository, you should use the `needs_nibabel_data` decorator to skip the tests if the data has not been checked out into the submodules. See `nibabel/tests/test_parrec_data.py` for an example. For our example repository above it might look something like:

```
from .nibabel_data import get_nibabel_data, needs_nibabel_data

ROSETTA_DATA = pjoin(get_nibabel_data(), 'rosetta-samples')

@needs_nibabel_data('rosetta-samples')
def test_something():
    # Some test using the data
```

Using submodules for tests

Tests run via nibabel on travis start with an automatic checkout of all submodules in the project, so all test data submodules get checked out by default.

If you are running the tests locally, you may well want to do:

```
git submodule update --init
```

from the root nibabel directory. This will checkout all the test data repositories.

How much data should go in a single submodule?

The limiting factor is how long it takes travis-ci to checkout the data for the tests. Up to a hundred megabytes in one repository should be OK. The joy of submodules is we can always drop a submodule, split the repository into two and add only one back, so you aren't committing us to anything awful if you accidentally put some very large files into your own data repository.

If in doubt

If you are not sure, try us with a pull request to nibabel github, or on the nipy mailing list, we will try to help.

9.3.3 How to add a new image format to nibabel

These are some work-in-progress notes in the hope that they will help adding a new image format to NiBabel.

Philosophy

As usual, the general idea is to make your image as explicit and transparent as possible.

From the Zen of Python (`import this`), these guys spring to mind:

- Explicit is better than implicit.
- Errors should never pass silently.
- In the face of ambiguity, refuse the temptation to guess.
- Now is better than never.
- If the implementation is hard to explain, it's a bad idea.

So far we have tried to make the nibabel version of the image as close as possible to the way the user of the particular format is expecting to see it.

For example, the NIfTI format documents describe the image with the first dimension of the image data array being the fastest varying in memory (and on disk). Numpy defaults to having the last dimension of the array being the fastest varying in memory. We chose to have the first dimension vary fastest in memory to match the conventions in the NIfTI specification.

Helping us to review your code

You are likely to know the image format much much better than the rest of us do, but to help you with the code, we will need to learn. The following will really help us get up to speed:

1. Links in the code or in the docs to the information on the file format. For example, you'll see the canonical links for the NIfTI 2 format at the top of the *nifti2* file, in the module docstring;
2. Example files in the format; see Adding test data;
3. Good test coverage. The tests help us see how you are expecting the code and the format to be used. We recommend writing the tests first; the tests do an excellent job in helping us and you see how the API is going to work.

The format can be read-only

Read-only access to a format is better than no access to a format, and often much better. For example, we can read but not write PAR / REC and MINC files. Having the code to read the files makes it easier to work with these files in Python, and easier for someone else to add the ability to write the format later.

The image API

An image should conform to the image API. See the module docstring for *spatialimages* for a description of the API.

You should test whether your image does conform to the API by adding a test class for your image in `nibabel.tests.test_image_api`. For example, the API test for the PAR / REC image format looks like:

```
class TestPARRECAPI(LoadImageAPI):
    def loader(self, fname):
        return parrec.load(fname)

    example_images = PARREC_EXAMPLE_IMAGES
```

where your work is to define the `EXAMPLE_IMAGES` list — see the `nibabel.tests.test_parrec` file for the PAR / REC example images definition.

Where to start with the code

There is no API requirement that a new image format inherit from the general *SpatialImage* class, but in fact all our image formats do inherit from this class. We strongly suggest you do the same, to get many simple methods implemented for free. You can always override the ones you don't want.

There is also a generic header class you might consider building on to contain your image metadata — *Header*. See that class for the header API.

The API does not require it, but if it is possible, it may be good to implement the image data as loaded from disk as an array proxy. See the docstring of *arrayproxy* for a description of the API, and see the module code for an implementation of the API. You may be able to use the unmodified *ArrayProxy* class for your image type.

If you write a new array proxy class, add tests for the API of the class in `nibabel.tests.test_proxy_api`. See `TestPARRECAPI` for an example.

A nibabel image is the association of:

1. The image array data (as implemented by an array proxy or a numpy array);
2. An affine relating the image array coordinates to an RAS+ world (see Coordinate systems and affines);
3. Image metadata in the form of a header.

Your new image constructor may well be the default from *SpatialImage*, which looks like this:

```
def __init__(self, dataobj, affine, header=None,
             extra=None, file_map=None):
```

Your job when loading a file is to create:

1. `dataobj` - an array or array proxy;
2. `affine` - 4 by 4 array relating array coordinates to world coordinates;
3. `header` - a metadata container implementing at least `get_data_dtype`, `get_data_shape`.

You will likely implement this logic in the `from_file_map` method of the image class. See *PARRECImage* for an example.

A recipe for writing a new image format

1. Find one or more examples images;
2. Put them in `nibabel/tests/data` or a data submodule (see Adding test data);
3. Create a file `nibabel/tests/test_my_format_name_here.py`;
4. Use some program that can read the format correctly to fill out the needed fields for an `EXAMPLE_IMAGES` list (see `nibabel.tests.test_parrec.py` for example);
5. Add a test class using your `EXAMPLE_IMAGES` to `nibabel.tests.test_image_api`, using the PARREC image test class as an example. Now you have some failing tests — good job!;
6. If you can, extract the metadata information from the test file, so it is small enough to fit as a small test file into `nibabel/tests/data` (don't forget the license);
7. Write small maybe private functions to extract the header metadata from your new test file, testing these functions in `test_my_format_name_here.py`. See *parrec* for examples;
8. When that is working, try sub-classing *Header*, and working out how to make the `__init__` and `from_fileboj` methods for that class. Test in `test_my_format_name_here.py`;
9. When that is working, try sub-classing *SpatialImage* and working out how to load the file with the `from_file_map` class;
10. Now try seeing if you can get your `test_image_api.py` tests to pass;
11. Consider adding more test data files, maybe to a test data repository submodule (Adding test data). Check you can read these files correctly (see `nibabel.tests.test_parrec_data` for an example).
12. Ask for advice as early and as often as you can, either with a work-in-progress pull request (the easiest way for us to review) or on the mailing list or via github issues.

9.3.4 Developer discussions

Some miscellaneous documents on background, future development and work in progress.

Image use-cases in SPM

SPM uses a *vol struct* as a structure characterizing an object. This is a Matlab `struct`. A `struct` is like a Python dictionary, where field names (strings) are associated with values. There are various functions operating on vol structs, so the vol struct is rather like an object, where the methods are implemented as functions. Actually, the distinction between methods and functions in Matlab is fairly subtle - their call syntax is the same for example.

```
>> fname = 'some_image.nii';
>> vol = spm_vol(fname) % the vol struct

vol =

      fname: 'some_image.nii'
        mat: [4x4 double]
        dim: [91 109 91]
         dt: [2 0]
      pinfo: [3x1 double]
```

```
          n: [1 1]
    descrip: 'NIFTI-1 Image'
    private: [1x1 nifti]

>> vol.mat % the 'affine'

ans =

    -2     0     0    92
     0     2     0  -128
     0     0     2   -74
     0     0     0     1

>> help spm_vol
  Get header information etc for images.
  FORMAT V = spm_vol(P)
  P - a matrix of filenames.
  V - a vector of structures containing image volume information.
  The elements of the structures are:
        V.fname - the filename of the image.
        V.dim   - the x, y and z dimensions of the volume
        V.dt    - A 1x2 array.  First element is datatype (see spm_type).
                  The second is 1 or 0 depending on the endian-ness.
        V.mat   - a 4x4 affine transformation matrix mapping from
                  voxel coordinates to real world coordinates.
        V.pinfo - plane info for each plane of the volume.
               V.pinfo(1,:) - scale for each plane
               V.pinfo(2,:) - offset for each plane
                  The true voxel intensities of the jth image are given
                  by: val*V.pinfo(1,j) + V.pinfo(2,j)
               V.pinfo(3,:) - offset into image (in bytes).
                  If the size of pinfo is 3x1, then the volume is assumed
                  to be contiguous and each plane has the same scalefactor
                  and offset.
 _____________________________________________________________________

  The fields listed above are essential for the mex routines, but other
  fields can also be incorporated into the structure.

  The images are not memory mapped at this step, but are mapped when
  the mex routines using the volume information are called.

  Note that spm_vol can also be applied to the filename(s) of 4-dim
  volumes. In that case, the elements of V will point to a series of 3-dim
  images.

  This is a replacement for the spm_map_vol and spm_unmap_vol stuff of
  MatLab4 SPMs (SPM94-97), which is now obsolete.
 _____________________________________________________________________
  Copyright (C) 2005 Wellcome Department of Imaging Neuroscience


>> spm_type(vol.dt(1))

ans =

uint8
```

```
>> vol.private

ans =

NIFTI object: 1-by-1
            dat: [91x109x91 file_array]
            mat: [4x4 double]
     mat_intent: 'MNI152'
           mat0: [4x4 double]
    mat0_intent: 'MNI152'
        descrip: 'NIFTI-1 Image'
```

So, in our (provisional) terms:

- `vol.mat` == `img.affine`
- `vol.dim` == `img.shape`
- `vol.dt(1)` (`vol.dt[0]` in Python) is equivalent to `img.get_data_dtype()`
- `vol.fname` == `img.get_filename()`

SPM abstracts the implementation of the image to the `vol.private` member, that is not in fact required by the image interface.

Images in SPM are always 3D. Note this behavior:

```
>> fname = 'functional_01.nii';
>> vol = spm_vol(fname)

vol =

191x1 struct array with fields:
    fname
    mat
    dim
    dt
    pinfo
    n
    descrip
    private
```

That is, one vol struct per 3D volume in a 4D dataset.

SPM image methods / functions

Some simple ones:

```
>> fname = 'some_image.nii';
>> vol = spm_vol(fname);
>> img_arr = spm_read_vols(vol);
>> size(img_arr) % just loads in scaled data array

ans =

    91   109    91

>> spm_type(vol.dt(1)) % the disk-level (IO) type is uint8
```

```
ans =

uint8

>> class(img_arr) % always double regardless of IO type

ans =

double

>> new_fname = 'another_image.nii';
>> new_vol = vol;  % matlab always copies
>> new_vol.fname = new_fname;
>> spm_write_vol(new_vol, img_arr)

ans =

      fname: 'another_image.nii'
        mat: [4x4 double]
        dim: [91 109 91]
         dt: [2 0]
      pinfo: [3x1 double]
          n: [1 1]
    descrip: 'NIFTI-1 Image'
    private: [1x1 nifti]
```

Creating an image from scratch, and writing plane by plane (slice by slice):

```
>> new_vol = struct();
>> new_vol.fname = 'yet_another_image.nii';
>> new_vol.dim = [91 109 91];
>> new_vol.dt = [spm_type('float32') 0]; % little endian (0)
>> new_vol.mat = vol.mat;
>> new_vol.pinfo = [1 0 0]';
>> new_vol = spm_create_vol(new_vol);
>> for vox_z = 1:new_vol.dim(3)
new_vol = spm_write_plane(new_vol, img_arr(:,:,vox_z), vox_z);
end
```

I think it's true that writing the plane does not change the image scalefactors, so it's only practical to use `spm_write_plane` for data for which you already know the dynamic range across the volume.

Simple resampling from an image:

```
>> fname = 'some_image.nii';
>> vol = spm_vol(fname);
>> % for voxel coordinate 10,15,20 (1-based)
>> hold_val = 3; % third order spline resampling
>> val = spm_sample_vol(vol, 10, 15, 20, hold_val)

val =

    0.0510

>> img_arr = spm_read_vols(vol);
>> img_arr(10, 15, 20)  % same as simple indexing for integer coordinates

ans =
```

```
    0.0510

>> % more than one point
>> x = [10, 10.5]; y = [15, 15.5]; z = [20, 20.5];
>> vals = spm_sample_vol(vol, x, y, z, hold_val)

vals =

    0.0510    0.0531

>> % you can also get the derivatives, by asking for more output args
>> [vals, dx, dy, dz] = spm_sample_vol(vol, x, y, z, hold_val)

vals =

    0.0510    0.0531


dx =

    0.0033    0.0012


dy =

    0.0033    0.0012


dz =

    0.0020   -0.0017
```

This is to speed up optimization in registration - where the optimizer needs the derivatives.

`spm_sample_vol` always works in voxel coordinates. If you want some other coordinates, you would transform them yourself. For example, world coordinates according to the affine looks like:

```
>> wc = [-5, -12, 32];
>> vc = inv(vol.mat) * [wc 1]'

vc =

   48.5000
   58.0000
   53.0000
    1.0000

>> vals = spm_sample_vol(vol, vc(1), vc(2), vc(3), hold_val)

vals =

    0.6792
```

Odder sampling, often used, can be difficult to understand:

```
>> slice_mat = eye(4);
>> out_size = vol.dim(1:2);
>> slice_no = 4; % slice we want to fetch
>> slice_mat(3,4) = slice_no;
```

```
>> arr_slice = spm_slice_vol(vol, slice_mat, out_size, hold_val);
>> img_slice_4 = img_arr(:,:,slice_no);
>> all(arr_slice(:) == img_slice_4(:))

ans =

     1
```

This is the simplest use - but in general any affine transform can go in `slice_mat` above, giving optimized (for speed) sampling of slices from volumes, as long as the transform is an affine.

Miscellaneous functions operating on vol structs:

- `spm_conv_vol` - convolves volume with seperable functions in x, y, z
- `spm_render_vol` - does a projection of a volume onto a surface
- `spm_vol_check` - takes array of vol structs and checks for sameness of image dimensions and `mat` (affines) across the list.

And then, many SPM functions accept vol structs as arguments.

Keeping track of whether images have been modified since load

Summary

This is a discussion of a missing feature in nibabel: the ability to keep track of whether an image object in memory still corresponds to an image file (or files) on disk.

Motivation

We may need to know whether the image in memory corresponds to the image file on disk.

For example, we often need to get filenames for images when passing images to external programs. Imagine a realignment, in this case, in nipy (the package):

```
import nipy
img1 = nibabel.load('meanfunctional.nii')
img2 = nibabel.load('anatomical.nii')
realigner = nipy.interfaces.fsl.flirt()
params = realigner.run(source=img1, target=img2)
```

In `nipy.interfaces.fsl.flirt.run` there may at some point be calls like:

```
source_filename = nipy.as_filename(source_img)
target_filename = nipy.as_filename(target_img)
```

As the authors of the `flirt.run` method, we need to make sure that the `source_filename` corresponds to the `source_img`.

Of course, in the general case, if `source_img` has no corresponding filename (from `source_img.get_filename()`, then we will have to save a copy to disk, maybe with a temporary filename, and return that temporary name as `source_filename`.

In our particular case, `source_img` does have a filename (`meanfunctional.nii`). We would like to return that as `source_filename`. The question is, how can we be sure that the user has done nothing to `source_img` to make it diverge from its original state? Could `source_img` have diverged, in memory, from the state recorded in `meantunctional.nii`?

If the image and file have not diverged, we return `meanfunctional.nii` as the `source_filename`, otherwise we will have to do something like:

```
import tempfile
fname = tempfile.mkstemp('.nii')
img = source_img.to_filename(fname)
```

and return `fname` as `source_filename`.

Another situation where we might like to pass around image objects that are known to correspond to images on disk is when working in parallel. A set of nodes may have fast common access to a filesystem on which the images are stored. If a master is farming out images to nodes, a master node distribution jobs to workers might want to check if the image was identical to something on file and pass around a lightweight (proxied) image (with the data not loaded into memory), relying on the node pulling the image from disk when it uses it.

Possible implementation

One implementation is to have `dirty` flag, which, if set, would tell you that the image might not correspond to the disk file. We set this flag when anyone asks for the data, on the basis that the user may then do something to the data and you can't know if they have:

```
img = nibabel.load('some_image.nii')
data = img.get_data()
data[:] = 0
img2 = nibabel.load('some_image.nii')
assert not np.all(img2.get_data() == img.get_data())
```

The image consists of the data, the affine and a header. In order to keep track of the header and affine, we could cache them when loading the image:

```
img = nibabel.load('some_image.nii')
hdr = img.header
assert img._cache['header'] == img.header
hdr.set_data_dtype(np.complex64)
assert img._cache['header'] != img.header
```

When we need to know whether the image object and image file correspond, we could check the current header and current affine (the header may be separate from the affine for an SPM Analyze image) against their cached copies, if they are the same and the 'dirty' flag has not been set by a previous call to `get_data()`, we know that the image file does correspond to the image object.

This may be OK for small bits of memory like the affine and the header, but would quickly become prohibitive for larger image metadata such as large nifti header extensions. We could just always assume that images with large header extensions are *not* the same as for on disk.

The user might be able to override the result of these checks directly:

```
img = nibabel.load('some_image.nii')
assert img.is_dirty == False
hdr = img.header
hdr.set_data_dtype(np.complex64)
assert img.is_dirty == True
img.is_dirty == False
```

The checks are magic behind the scenes stuff that do some safe optimization (in the sense that we are not re-saving the data if that is not necessary), but drops back to the default (re-saving the data) if there is any uncertainty, or the cost is too high to be able to check.

Design of data packages for the nibabel and the nipy suite

See data-package-discuss for a more general discussion of design issues.

When developing or using nipy, many data files can be useful. We divide the data files nipy uses into at least 3 categories

1. *test data* - data files required for routine code testing
2. *template data* - data files required for algorithms to function, such as templates or atlases
3. *example data* - data files for running examples, or optional tests

Files used for routine testing are typically very small data files. They are shipped with the software, and live in the code repository. For example, in the case of `nipy` itself, there are some test files that live in the module path `nipy.testing.data`. Nibabel ships data files in `nibabel.tests.data`. See Adding test data for discussion.

template data and *example data* are example of *data packages*. What follows is a discussion of the design and use of data packages.

Use cases for data packages

Using the data package The programmer can use the data like this:

```
from nibabel.data import make_datasource

templates = make_datasource(dict(relpath='nipy/templates'))
fname = templates.get_filename('ICBM152', '2mm', 'T1.nii.gz')
```

where `fname` will be the absolute path to the template image `ICBM152/2mm/T1.nii.gz`.

The programmer can insist on a particular version of a `datasource`:

```
>>> if templates.version < '0.4':
...     raise ValueError('Need datasource version at least 0.4')
Traceback (most recent call last):
...
ValueError: Need datasource version at least 0.4
```

If the repository cannot find the data, then:

```
>>> make_datasource(dict(relpath='nipy/implausible'))
Traceback (most recent call last):
 ...
nibabel.data.DataError: ...
```

where `DataError` gives a helpful warning about why the data was not found, and how it should be installed.

Warnings during installation The example data and template data may be important, and so we want to warn the user if NIPY cannot find either of the two sets of data when installing the package. Thus:

```
python setup.py install
```

will import nipy after installation to check whether these raise an error:

```
>>> from nibabel.data import make_datasource
>>> templates = make_datasource(dict(relpath='nipy/templates'))
>>> example_data = make_datasource(dict(relpath='nipy/data'))
```

and warn the user accordingly, with some basic instructions for how to install the data.

Finding the data The routine `make_datasource` will look for data packages that have been installed. For the following call:

```
>>> templates = make_datasource(dict(relpath='nipy/templates'))
```

the code will:

1. Get a list of paths where data is known to be stored with `nibabel.data.get_data_path()`
2. For each of these paths, search for directory `nipy/templates`. If found, and of the correct format (see below), return a datasource, otherwise raise an Exception

The paths collected by `nibabel.data.get_data_paths()` are constructed from ':' (Unix) or ';' separated strings. The source of the strings (in the order in which they will be used in the search above) are:

1. The value of the `NIPY_DATA_PATH` environment variable, if set
2. A section = `DATA`, parameter = `path` entry in a `config.ini` file in `nipy_dir` where `nipy_dir` is `$HOME/.nipy` or equivalent.
3. Section = `DATA`, parameter = `path` entries in configuration `.ini` files, where the `.ini` files are found by `glob.glob(os.path.join(etc_dir, '*.ini')` and `etc_dir` is `/etc/nipy` on Unix, and some suitable equivalent on Windows.
4. The result of `os.path.join(sys.prefix, 'share', 'nipy')`
5. If `sys.prefix` is `/usr`, we add `/usr/local/share/nipy`. We need this because Python >= 2.6 in Debian / Ubuntu does default installs to `/usr/local`.
6. The result of `get_nipy_user_dir()`

Requirements for a data package To be a valid NIPY project data package, you need to satisfy:

1. The installer installs the data in some place that can be found using the method defined in *Finding the data*.

We recommend that:

1. By default, you install data in a standard location such as `<prefix>/share/nipy` where `<prefix>` is the standard Python prefix obtained by `>>> import sys; print sys.prefix`

Remember that there is a distinction between the NIPY project - the umbrella of neuroimaging in python - and the NIPY package - the main code package in the NIPY project. Thus, if you want to install data under the NIPY *package* umbrella, your data might go to `/usr/share/nipy/nipy/packagename` (on Unix). Note `nipy` twice - once for the project, once for the package. If you want to install data under - say - the `pbrain` package umbrella, that would go in `/usr/share/nipy/pbrain/packagename`.

Data package format The following tree is an example of the kind of pattern we would expect in a data directory, where the `nipy-data` and `nipy-templates` packages have been installed:

```
<ROOT>
`-- nipy
    |-- data
    |   |-- config.ini
    |   `-- placeholder.txt
    `-- templates
        |-- ICBM152
        |   `-- 2mm
        |       `-- T1.nii.gz
        |-- colin27
        |   `-- 2mm
```

```
        |       `-- T1.nii.gz
        `-- config.ini
```

The <ROOT> directory is the directory that will appear somewhere in the list from `nibabel.data.get_data_path()`. The `nipy` subdirectory signifies data for the `nipy` package (as opposed to other NIPY-related packages such as `pbrain`). The `data` subdirectory of `nipy` contains files from the `nipy-data` package. In the `nipy/data` or `nipy/templates` directories, there is a `config.ini` file, that has at least an entry like this:

```
[DEFAULT]
version = 0.2
```

giving the version of the data package.

Installing the data We use python distutils to install data packages, and the `data_files` mechanism to install the data. On Unix, with the following command:

```
python setup.py install --prefix=/my/prefix
```

data will go to:

```
/my/prefix/share/nipy
```

For the example above this will result in these subdirectories:

```
/my/prefix/share/nipy/nipy/data
/my/prefix/share/nipy/nipy/templates
```

because `nipy` is both the project, and the package to which the data relates.

If you install to a particular location, you will need to add that location to the output of `nibabel.data.get_data_path()` using one of the mechanisms above, for example, in your system configuration:

```
export NIPY_DATA_PATH=/my/prefix/share/nipy
```

Packaging for distributions For a particular data package - say `nipy-templates` - distributions will want to:

1. Install the data in set location. The default from `python setup.py install` for the data packages will be `/usr/share/nipy` on Unix.
2. Point a system installation of NIPY to these data.

For the latter, the most obvious route is to copy an `.ini` file named for the data package into the NIPY `etc_dir`. In this case, on Unix, we will want a file called `/etc/nipy/nipy_templates.ini` with contents:

```
[DATA]
path = /usr/share/nipy
```

Current implementation This section describes how we (the nipy community) implement data packages at the moment.

The data in the data packages will not usually be under source control. This is because images don't compress very well, and any change in the data will result in a large extra storage cost in the repository. If you're pretty clear that the data files aren't going to change, then a repository could work OK.

The data packages will be available at a central release location. For now this will be: http://nipy.org/data-packages/ .

A package, such as `nipy-templates-0.2.tar.gz` will have the following sort of structure:

```
<ROOT>
  |-- setup.py
  |-- README.txt
  |-- MANIFEST.in
  `-- templates
      |-- ICBM152
      |   |-- 1mm
      |   |   `-- T1_brain.nii.gz
      |   `-- 2mm
      |       `-- T1.nii.gz
      |-- colin27
      |   `-- 2mm
      |       `-- T1.nii.gz
      `-- config.ini
```

There should be only one `nipy/packagename` directory delivered by a particular package. For example, this package installs `nipy/templates`, but does not contain `nipy/data`.

Making a new package tarball is simply:

1. Downloading and unpacking e.g. `nipy-templates-0.1.tar.gz` to form the directory structure above;
2. Making any changes to the directory;
3. Running `setup.py sdist` to recreate the package.

The process of making a release should be:

1. Increment the major or minor version number in the `config.ini` file;
2. Make a package tarball as above;
3. Upload to distribution site.

There is an example nipy data package `nipy-examplepkg` in the `examples` directory of the NIPY repository.

The machinery for creating and maintaining data packages is available at https://github.com/nipy/data-packaging.

See the `README.txt` file there for more information.

9.3.5 A guide to making a nibabel release

This is a guide for developers who are doing a nibabel release.

Release tools

There are some release utilities that come with nibabel. nibabel should install these as the `nisext` package, and the testing stuff is understandably in the `testers` module of that package. nibabel has Makefile targets for their use. The relevant targets are:

```
make check-version-info
make check-files
make sdist-tests
```

The first installs the code from a git archive, from the repository, and for in-place use, and runs the `get_info()` function to confirm that installation is working and information parameters are set correctly.

The second (`sdist-tests`) makes an sdist source distribution archive, installs it to a temporary directory, and runs the tests of that install.

Release checklist

- Review the open list of nibabel issues. Check whether there are outstanding issues that can be closed, and whether there are any issues that should delay the release. Label them !
- Review and update the release notes. Review and update the `Changelog` file. Get a partial list of contributors with something like:

```
git log 2.0.0.. | grep '^Author' | cut -d' ' -f 2- | sort | uniq
```

  where `2.0.0` was the last release tag name.

  Then manually go over `git shortlog 2.0.0..` to make sure the release notes are as complete as possible and that every contributor was recognized.
- Look at `doc/source/index.rst` and add any authors not yet acknowledged.
- Update new authors and add thansk in `doc/source/index.rst` and consider any updates to the `AUTHOR` file.
- Use the opportunity to update the `.mailmap` file if there are any duplicate authors listed from `git shortlog -nse`.
- Check the copyright year in `doc/source/conf.py`
- Refresh the `README.rst` text from the `LONG_DESCRIPTION` in `info.py` by running `make refresh-readme`.

  Check the output of:

```
rst2html.py README.rst > ~/tmp/readme.html
```

  because this will be the output used by pypi
- Check the dependencies listed in `nibabel/info.py` (e.g. `NUMPY_MIN_VERSION`) and in `doc/source/installation.rst`. They should at least match. Do they still hold? Make sure nibabel on travis is testing the minimum dependencies specifically.
- Do a final check on the nipy buildbot. Use the `try_branch.py` scheduler available in nibotmi to test particular schedulers.
- If you have travis-ci building set up for your own repo you might want to push the code in it's current state to a branch that will build, e.g:

```
git branch -D pre-release-test # in case branch already exists
git co -b pre-release-test
git push your-github-user pre-release-test -u
```

- Clean:

```
make distclean
```

- Make sure all tests pass (from the nibabel root directory):

```
nosetests --with-doctest nibabel
```

- Make sure all tests pass from sdist:

```
make sdist-tests
```

  and the three ways of installing (from tarball, repo, local in repo):

```
make check-version-info
```

The last may not raise any errors, but you should detect in the output lines of this form:

```
{'sys_version': '2.6.6 (r266:84374, Aug 31 2010, 11:00:51) \n[GCC 4.0.1 (Apple Inc. build 5493)]
/var/folders/jg/jgfZ12ZXHwGSFKD85xLpLk+++TI/-Tmp-/tmpGPiD3E/pylib/nibabel/__init__.pyc
{'sys_version': '2.6.6 (r266:84374, Aug 31 2010, 11:00:51) \n[GCC 4.0.1 (Apple Inc. build 5493)]
/Users/mb312/dev_trees/nibabel/nibabel/__init__.pyc
{'sys_version': '2.6.6 (r266:84374, Aug 31 2010, 11:00:51) \n[GCC 4.0.1 (Apple Inc. build 5493)]
```

- Check the `setup.py` file is picking up all the library code and scripts, with:

```
make check-files
```

Look for output at the end about missed files, such as:

```
Missed script files:  /Users/mb312/dev_trees/nibabel/bin/nib-dicomfs, /Users/mb312/dev_trees/nib
```

Fix `setup.py` to carry across any files that should be in the distribution.

- You probably have virtualenvs for different Python versions. Check the tests pass for different configurations. The long-hand way looks like this:

```
workon python26
make distclean
make sdist-tests
deactivate
```

etc for the different virtualenvs.

- Check on different platforms, particularly windows and PPC. Look at the nipy buildbot automated test runs for this.
- Check the documentation doctests (forcing Python 2):

```
make -C doc doctest SPHINXBUILD="python :math:`(which sphinx-build)"
```

This should also be tested by nibabel on travis.

- Check everything compiles without syntax errors:

```
python -m compileall .
```

- The release should now be ready.
- Edit `nibabel/info.py` to set `_version_extra` to `''`; commit. Then:

```
make source-release
```

- Once everything looks good, you are ready to upload the source release to PyPi. See setuptools intro. Make sure you have a file \`HOME/.pypirc, of form:

```
[distutils]
index-servers =
    pypi

[pypi]
username:your.pypi.username
password:your-password

[server-login]
username:your.pypi.username
password:your-password
```

- When ready:

```
python setup.py register
python setup.py sdist --formats=gztar,zip upload
```

- Tag the release with tag of form `2.0.0`:

```
git tag -am "Something about this release' 2.0.0
```

- Push the tag and any other changes to trunk with:

```
git push --tags
```

- Force builds of the win32 and amd64 binaries from the buildbot. Go to pages:
  - https://nipy.bic.berkeley.edu/builders/nibabel-bdist32-27
  - https://nipy.bic.berkeley.edu/builders/nibabel-bdist32-34
  - https://nipy.bic.berkeley.edu/builders/nibabel-bdist64-27

  For each of these, enter the revision number (e.g. "2.0.0") in the field "Revision to build". Then get the built binaries in:
  - https://nipy.bic.berkeley.edu/nibabel-dist

  and upload them to pypi with the admin files interface.

  If you are already on a Windows machine, you could have done the manual command to upload instead: `python setup.py bdist_wininst upload`.
- Now the version number is OK, push the docs to github pages with:

```
make upload-html
```

- Set up maintenance / development branches

  If this is this is a full release you need to set up two branches, one for further substantial development (often called 'trunk') and another for maintenance releases.
  - Branch to maintenance:

```
git co -b maint/2.0.x
```

    Set `_version_extra` back to `.dev` and bump `_version_micro` by 1. Thus the maintenance series will have version numbers like - say - '2.0.1.dev' until the next maintenance release - say '2.0.1'. Commit. Don't forget to push upstream with something like:

```
git push upstream-remote maint/2.0.x --set-upstream
```

  - Start next development series:

```
git co main-master
```

    then restore `.dev` to `_version_extra`, and bump `_version_minor` by 1. Thus the development series ('trunk') will have a version number here of '2.1.0.dev' and the next full release will be '2.1.0'.

    Next merge the maintenace branch with the "ours" strategy. This just labels the maintenance *info.py* edits as seen but discarded, so we can merge from maintenance in future without getting spurious merge conflicts:

```
git merge -s ours maint/2.0.x
```

  If this is just a maintenance release from `maint/2.0.x` or similar, just tag and set the version number to - say - `2.0.2.dev`.

- Push the main branch:

```
git push upstream-remote main-master
```

- Make next development release tag

  After each release the master branch should be tagged with an annotated (or/and signed) tag, naming the intended next version, plus an 'upstream/' prefix and 'dev' suffix. For example 'upstream/1.0.0.dev' means "development start for upcoming version 1.0.0.

  This tag is used in the Makefile rules to create development snapshot releases to create proper versions for those. The version derives its name from the last available annotated tag, the number of commits since that, and an abbreviated SHA1. See the docs of `git describe` for more info.

  Please take a look at the Makefile rules `devel-src`, `devel-dsc` and `orig-src`.

- Announce to the mailing lists.

9.3.6 Advanced Testing

Setup

Before running advanced tests, please update all submodules of nibabel, by running `git submodule update --init`

Long-running tests

Long-running tests are not enabled by default, and can be resource-intensive. To run these tests:

- Set environment variable `NIPY_EXTRA_TESTS=slow`
- Run `nosetests`.

Note that some tests may require a machine with >4GB of RAM.

9.4 DICOM concepts and implementations

Contents:

9.4.1 DICOM information

DICOM is a large and sometimes confusing imaging data format.

In the other pages in this series we try and document our understanding of various aspects of DICOM relevant to converting to formats such as NIfTI .

There are a large number of DICOM image conversion programs already, partly because it is a complicated format with features that vary from manufacturer to manufacturer.

We use the excellent PyDICOM as our back-end for reading DICOM.

Here is a selected list of other tools and relevant resources:

- Grassroots DICOM : GDCM . It is C++ code wrapped with swig and so callable from Python. ITK apparently uses it for DICOM conversion. BSD license.

- dcm2nii - a BSD licensed converter by Chris Rorden. As usual, Chris has done an excellent job of documentation, and it is well battle-tested. There's a nice set of example data to test against and a list of other DICOM software. The MRIcron install page points to the source code. Chris has also put effort into extracting diffusion parameters from the DICOM images.
- SPM8 - SPM has a stable and robust general DICOM conversion tool implemented in the `spm_dicom_convert.m` and `spm_dicom_headers.m` scripts. The conversions don't try to get the diffusion parameters. The code is particularly useful because it has been well-tested and is written in Matlab - and so is relatively easy to read. GPL license. We've described some of the algorithms that SPM uses for DICOM conversion in *SPM DICOM conversion*.
- DICOM2Nrrd: a command line converter to convert DICOM images to Nrrd format. You can call the command from within the Slicer GUI. It does have algorithms for getting diffusion information from the DICOM headers, and has been tested with Philips, GE and Siemens data. It's not clear whether it yet supports the *Siemens mosaic format*. BSD style license.
- The famous Philips cookbook: https://www.archive.org/details/DicomCookbook
- http://dicom.online.fr/fr/dicomlinks.htm

9.4.2 Sample images

- http://www.barre.nom.fr/medical/samples/
- http://pubimage.hcuge.ch:8080/
- Via links from the dcm2nii page.

9.4.3 Defining the DICOM orientation

DICOM patient coordinate system

First we define the standard DICOM patient-based coordinate system. This is what DICOM means by x, y and z axes in its orientation specification. From section C.7.6.2.1.1 of the DICOM object definitions (2009):

> If Anatomical Orientation Type (0010,2210) is absent or has a value of BIPED, the x-axis is increasing to the left hand side of the patient. The y-axis is increasing to the posterior side of the patient. The z-axis is increasing toward the head of the patient.

(we'll ignore the quadupeds for now).

In a way it's funny to call this the 'patient-based' coordinate system. 'Doctor-based coordinate system' is a better name. Think of a doctor looking at the patient from the foot of the scanner bed. Imagine the doctor's right hand held in front of her like Spiderman about to shoot a web, with her palm towards the patient, defining a right-handed coordinate system. Her thumb points to her right (the patient's left), her index finger points down, and the middle finger points at the patient.

DICOM pixel data

C.7.6.3.1.4 - Pixel Data Pixel Data (7FE0,0010) for this image. The order of pixels sent for each image plane is left to right, top to bottom, i.e., the upper left pixel (labeled 1,1) is sent first followed by the remainder of row 1, followed by the first pixel of row 2 (labeled 2,1) then the remainder of row 2 and so on.

The resulting pixel array then has size ('Rows', 'Columns'), with row-major storage (rows first, then columns). We'll call this the DICOM *pixel array*.

Pixel spacing

Section 10.7.1.3: Pixel Spacing The first value is the row spacing in mm, that is the spacing between the centers of adjacent rows, or vertical spacing. The second value is the column spacing in mm, that is the spacing between the centers of adjacent columns, or horizontal spacing.

DICOM voxel to patient coordinate system mapping

See:

- http://www.dclunie.com/medical-image-faq/html/part2.html
- http://fixunix.com/dicom/50449-image-position-patient-image-orientation-patient.html

See wikipedia direction cosine for a definition of direction cosines.

From section C.7.6.2.1.1 of the DICOM object definitions (2009):

> The Image Position (0020,0032) specifies the x, y, and z coordinates of the upper left hand corner of the image; it is the center of the first voxel transmitted. Image Orientation (0020,0037) specifies the direction cosines of the first row and the first column with respect to the patient. These Attributes shall be provide as a pair. Row value for the x, y, and z axes respectively followed by the Column value for the x, y, and z axes respectively.

From Section C.7.6.1.1.1 we see that the 'positive row axis' is left to right, and is the direction of the rows, given by the direction of last pixel in the first row from the first pixel in that row. Similarly the 'positive column axis' is top to bottom and is the direction of the columns, given by the direction of the last pixel in the first column from the first pixel in that column.

Let's rephrase: the first three values of 'Image Orientation Patient' are the direction cosine for the 'positive row axis'. That is, they express the direction change in (x, y, z), in the DICOM patient coordinate system (DPCS), as you move along the row. That is, as you move from one column to the next. That is, as the *column* array index changes. Similarly, the second triplet of values of 'Image Orientation Patient' (`img_ornt_pat[3:]` in Python), are the direction cosine for the 'positive column axis', and express the direction you move, in the DPCS, as you move from row to row, and therefore as the *row* index changes.

Further down section C.7.6.2.1.1 (RCS below is the *reference coordinate system* - see DICOM object definitions section 3.17.1):

> The Image Plane Attributes, in conjunction with the Pixel Spacing Attribute, describe the position and orientation of the image slices relative to the patient-based coordinate system. In each image frame the Image Position (Patient) (0020,0032) specifies the origin of the image with respect to the patient-based coordinate system. RCS and the Image Orientation (Patient) (0020,0037) attribute values specify the orientation of the image frame rows and columns. The mapping of pixel location (i, j) to the RCS is calculated as follows:
>
> $$\begin{bmatrix} P_x \\ P_y \\ P_z \\ 1 \end{bmatrix} = \begin{bmatrix} X_x\Delta i & Y_x\Delta j & 0 & S_x \\ X_y\Delta i & Y_y\Delta j & 0 & S_y \\ X_z\Delta i & Y_z\Delta j & 0 & S_z \\ 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} i \\ j \\ 0 \\ 1 \end{bmatrix} = M \begin{bmatrix} i \\ j \\ 0 \\ 1 \end{bmatrix}$$
>
> Where:
>
> 1. P_{xyz} : The coordinates of the voxel (i,j) in the frame's image plane in units of mm.
> 2. S_{xyz} : The three values of the Image Position (Patient) (0020,0032) attributes. It is the location in mm from the origin of the RCS.
> 3. X_{xyz} : The values from the row (X) direction cosine of the Image Orientation (Patient) (0020,0037) attribute.

4. Y_{xyz} : The values from the column (Y) direction cosine of the Image Orientation (Patient) (0020,0037) attribute.
5. i : Column index to the image plane. The first column is index zero.
6. Δi: Column pixel resolution of the Pixel Spacing (0028,0030) attribute in units of mm.
7. j : Row index to the image plane. The first row index is zero.
8. Δj - Row pixel resolution of the Pixel Spacing (0028,0030) attribute in units of mm.

(i, j), columns, rows in DICOM

We stop to ask ourselves, what does DICOM mean by voxel (i, j)?

Isn't that obvious? Oh dear, no it isn't. See the *DICOM voxel to patient coordinate system mapping* formula above. In particular, you'll see:

- i : Column index to the image plane. The first column is index zero.
- j : Row index to the image plane. The first row index is zero.

That is, if we have the *DICOM pixel data* as defined above, and we call that `pixel_array`, then voxel (i, j) in the notation above is given by `pixel_array[j, i]`.

What does this mean? It means that, if we want to apply the formula above to array indices in `pixel_array`, we first have to apply a column / row flip to the indices. Say M_{pixar} (sorry) is the affine to go from array indices in `pixel_array` to mm in the DPCS. Then, given M above:

$$M_{pixar} = M \begin{pmatrix} 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

DICOM affines again

The *(i, j), columns, rows in DICOM* is rather confusing, so we're going to rephrase the affine mapping; we'll use r for the row index (instead of j above), and c for the column index (instead of i).

Next we define a flipped version of 'ImageOrientationPatient', F, that has flipped columns. Thus if the vector of 6 values in 'ImageOrientationPatient' are $(i_1..i_6)$, then:

$$F = \begin{bmatrix} i_4 & i_1 \\ i_5 & i_2 \\ i_6 & i_3 \end{bmatrix}$$

Now the first column of F contains what the DICOM docs call the 'column (Y) direction cosine', and second column contains the 'row (X) direction cosine'. We prefer to think of these as (respectively) the row index direction cosine and the column index direction cosine.

Now we can rephrase the DICOM affine mapping with:

DICOM affine formula

$$\begin{bmatrix} P_x \\ P_y \\ P_z \\ 1 \end{bmatrix} = \begin{bmatrix} F_{11}\Delta r & F_{12}\Delta c & 0 & S_x \\ F_{21}\Delta r & F_{22}\Delta c & 0 & S_y \\ F_{31}\Delta r & F_{32}\Delta c & 0 & S_z \\ 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} r \\ c \\ 0 \\ 1 \end{bmatrix} = A \begin{bmatrix} r \\ c \\ 0 \\ 1 \end{bmatrix}$$

Where:

- P_{xyz} : The coordinates of the voxel (c, r) in the frame's image plane in units of mm.
- S_{xyz} : The three values of the Image Position (Patient) (0020,0032) attributes. It is the location in mm from the origin of the RCS.
- $F_{:,1}$: The values from the column (Y) direction cosine of the Image Orientation (Patient) (0020,0037) attribute - see above.
- $F_{:,2}$: The values from the row (X) direction cosine of the Image Orientation (Patient) (0020,0037) attribute - see above.
- r : Row index to the image plane. The first row index is zero.
- Δr - Row pixel resolution of the Pixel Spacing (0028,0030) attribute in units of mm.
- c : Column index to the image plane. The first column is index zero.
- Δc: Column pixel resolution of the Pixel Spacing (0028,0030) attribute in units of mm.

For later convenience we also define values useful for 3D volumes:

- s : slice index to the slice plane. The first slice index is zero.
- Δs - spacing in mm between slices.

Getting a 3D affine from a DICOM slice or list of slices

Let us say, we have a single DICOM file, or a list of DICOM files that we believe to be a set of slices from the same volume. We'll call the first the *single slice* case, and the second, *multi slice*.

In the *multi slice* case, we can assume that the 'ImageOrientationPatient' field is the same for all the slices.

We want to get the affine transformation matrix A that maps from voxel coordinates in the DICOM file(s), to mm in the *DICOM patient coordinate system*.

By voxel coordinates, we mean coordinates of form (r, c, s) - the row, column and slice indices - as for the *DICOM affine formula*.

In the single slice case, the voxel coordinates are just the indices into the pixel array, with the third (slice) coordinate always being 0.

In the multi-slice case, we have arranged the slices in ascending or descending order, where slice numbers range from 0 to $N - 1$ - where N is the number of slices - and the slice coordinate is a number on this scale.

We know, from *DICOM affine formula*, that the first, second and fourth columns in A are given directly by the (flipped) 'ImageOrientationPatient', 'PixelSpacing' and 'ImagePositionPatient' field of the first (or only) slice.

Our job then is to fill the first three rows of the third column of A. Let's call this the vector $\mathbf{k}$ with values k_1, k_2, k_3.

DICOM affine Definitions

See also the definitions in *DICOM affine formula*. In addition

- T^1 is the 3 element vector of the 'ImagePositionPatient' field of the first header in the list of headers for this volume.
- T^N is the 'ImagePositionPatient' vector for the last header in the list for this volume, if there is more than one header in the volume.
- vector $\mathbf{n} = (n_1, n_2, n_3)$ is the result of taking the cross product of the two columns of F from *DICOM affine formula*.

Derivations

For the single slice case we just fill $\mathbf{k}$ with $\mathbf{n} \cdot \Delta s$ - on the basis that the Z dimension should be right-handed orthogonal to the X and Y directions.

For the multi-slice case, we can fill in $\mathbf{k}$ by using the information from T^N, because T^N is the translation needed to take the first voxel in the last (slice index = $N - 1$) slice to mm space. So:

$$\begin{pmatrix} T^N \\ 1 \end{pmatrix} = A \begin{pmatrix} 0 \\ 0 \\ -1+N \\ 1 \end{pmatrix}$$

From this it follows that:

$$\left\{ k_1 : \frac{T^1_1 - T^N_1}{1-N}, \quad k_2 : \frac{T^1_2 - T^N_2}{1-N}, \quad k_3 : \frac{T^1_3 - T^N_3}{1-N} \right\}$$

and therefore:

3D affine formulae

$$A_{multi} = \begin{pmatrix} F_{11}\Delta r & F_{12}\Delta c & \frac{T^1_1 - T^N_1}{1-N} & T^1_1 \\ F_{21}\Delta r & F_{22}\Delta c & \frac{T^1_2 - T^N_2}{1-N} & T^1_2 \\ F_{31}\Delta r & F_{32}\Delta c & \frac{T^1_3 - T^N_3}{1-N} & T^1_3 \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

$$A_{single} = \begin{pmatrix} F_{11}\Delta r & F_{12}\Delta c & \Delta sn_1 & T^1_1 \\ F_{21}\Delta r & F_{22}\Delta c & \Delta sn_2 & T^1_2 \\ F_{31}\Delta r & F_{32}\Delta c & \Delta sn_3 & T^1_3 \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

See `derivations/spm_dicom_orient.py` for the derivations and some explanations.

Working out the Z coordinates for a set of slices

We may have the problem (see e.g. *Sorting files into volumes*) of trying to sort a set of slices into anatomical order. For this we want to use the orientation information to tell us where the slices are in space, and therefore, what order they should have.

To do this sorting, we need something that is proportional, plus a constant, to the voxel coordinate for the slice (the value for the slice index).

Our DICOM might have the 'SliceLocation' field (0020,1041). 'SliceLocation' seems to be proportianal to slice location, at least for some GE and Philips DICOMs I was looking at. But, there is a more reliable way (that doesn't depend on this field), and uses only the very standard 'ImageOrientationPatient' and 'ImagePositionPatient' fields.

Consider the case where we have a set of slices, of unknown order, from the same volume.

Now let us say we have one of these slices - slice i. We have the affine for this slice from the calculations above, for a single slice (A_{single}).

Now let's say we have another slice j from the same volume. It will have the same affine, except that the 'ImagePositionPatient' field will change to reflect the different position of this slice in space. Let us say that there a translation of d slices between i and j. If A_i (A for slice i) is A_{single} then A_j for j is given by:

$$A_j = A_{single} \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & d \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

and 'ImagePositionPatient' for j is:

$$T^j = \begin{pmatrix} T^1_1 + \Delta s d n_1 \\ T^1_2 + \Delta s d n_2 \\ T^1_3 + \Delta s d n_3 \end{pmatrix}$$

Remember that the third column of A gives the vector resulting from a unit change in the slice voxel coordinate. So, the 'ImagePositionPatient' of slice - say slice j - can be thought of the addition of two vectors $T^j = \mathbf{a} + \mathbf{b}$, where $\mathbf{a}$ is the position of the first voxel in some slice (here slice 1, therefore $\mathbf{a} = T^1$) and $\mathbf{b}$ is d times the third colum of A. Obviously d can be negative or positive. This leads to various ways of recovering something that is proportional to d plus a constant. The algorithm suggested in this ITK post on ordering slices - and the one used by SPM - is to take the inner product of T^j with the unit vector component of third column of A_j - in the descriptions here, this is the vector $\mathbf{n}$:

$$T^j \cdot \mathbf{c} = \left(T^1_1 n_1 + T^1_2 n_2 + T^1_3 n_3 + \Delta s d n^2_1 + \Delta s d n^2_2 + \Delta s d n^2_3 \right)$$

This is the distance of 'ImagePositionPatient' along the slice direction cosine.

The unknown T^1 terms pool into a constant, and the operation has the neat feature that, because the n^2_{123} terms, by definition, sum to 1, the whole can be expressed as $\lambda + \Delta s d$ - i.e. it is equal to the slice voxel size (Δs) multiplied by d, plus a constant.

Again, see `derivations/spm_dicom_orient.py` for the derivations.

9.4.4 DICOM fields

In which we pick out some interesting fields in the DICOM header.

We're getting the information mainly from the standard DICOM object definitions

We won't talk about the orientation, patient position-type fields here because we've covered those somewhat in *DICOM voxel to patient coordinate system mapping*.

Fields for ordering DICOM files into images

You'll see some discussion of this in *SPM DICOM conversion*.

Section 7.3.1: general series module

- Modality (0008,0060) - Type of equipment that originally acquired the data used to create the images in this Series. See C.7.3.1.1.1 for Defined Terms.
- Series Instance UID (0020,000E) - Unique identifier of the Series.
- Series Number (0020,0011) - A number that identifies this Series.
- Series Time (0008,0031) - Time the Series started.

Section C.7.6.1:

- Instance Number (0020,0013) - A number that identifies this image.
- Acquisition Number (0020,0012) - A number identifying the single continuous gathering of data over a period of time that resulted in this image.
- Acquisition Time (0008,0032) - The time the acquisition of data that resulted in this image started

Section C.7.6.2.1.2:

Slice Location (0020,1041) is defined as the relative position of the image plane expressed in mm. This information is relative to an unspecified implementation specific reference point.

Section C.8.3.1 MR Image Module

- Slice Thickness (0018,0050) - Nominal reconstructed slice thickness, in mm.

Section C.8.3.1 MR Image Module

- Spacing Between Slices (0018,0088) - Spacing between slices, in mm. The spacing is measured from the center-tocenter of each slice.
- Temporal Position Identifier (0020,0100) - Temporal order of a dynamic or functional set of Images.
- Number of Temporal Positions (0020,0105) - Total number of temporal positions prescribed.
- Temporal Resolution (0020,0110) - Time delta between Images in a dynamic or functional set of images

Multi-frame images

An image for which the pixel data is a continuous stream of sequential frames.

Section C.7.6.6: Multi-Frame Module

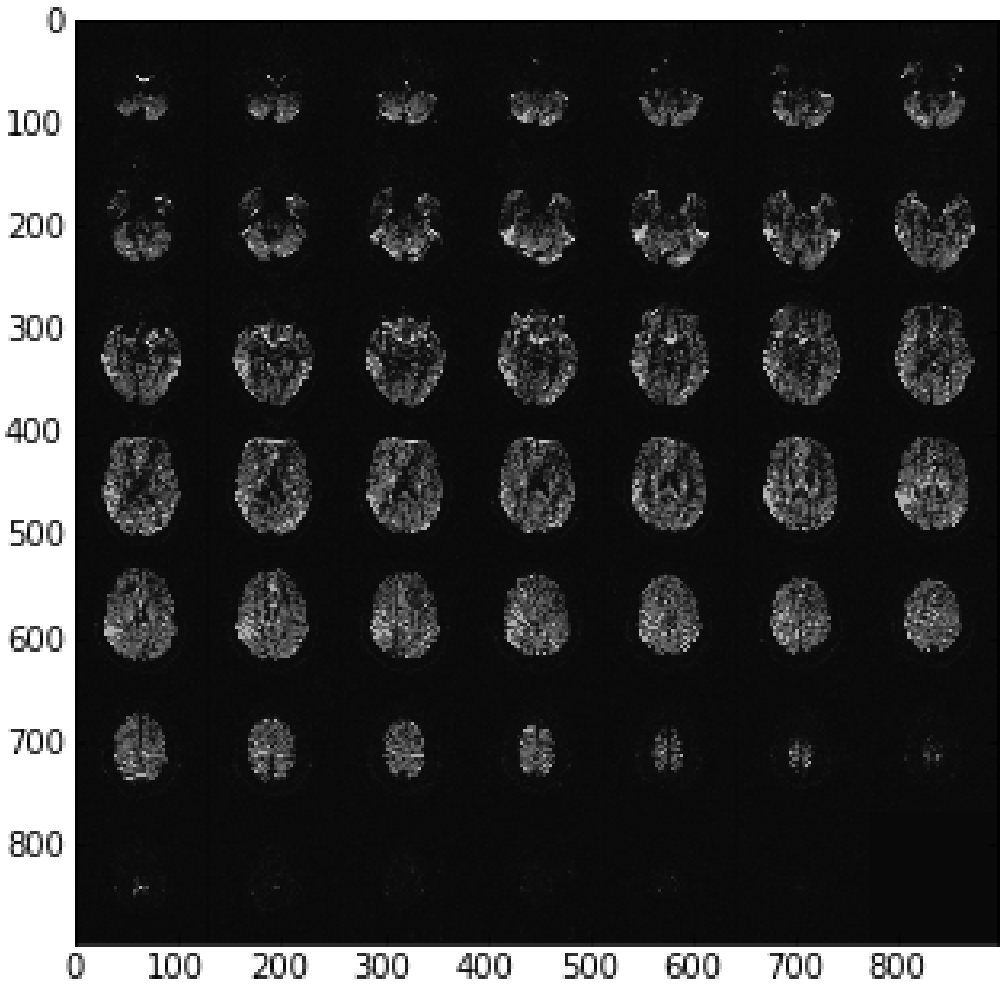
- Number of Frames (0028,0008) - Number of frames in a Multi-frame Image.
- Frame Increment Pointer (0028,0009) - Contains the Data Element Tag of the attribute that is used as the frame increment in Multi-frame pixel data.

9.4.5 Siemens mosaic format

Siemens mosaic format is a way of storing a 3D image in a DICOM image file. The simplest DICOM images only knows how to store 2D files. For example, a 3D image in DICOM is usually stored as a series of 2D slices, each slices as a separate DICOM image. . Mosaic format stores the 3D image slices as a 2D grid - or mosaic.

For example here are the pixel data as loaded directly from a DICOM image with something like:

```
import matplotlib.pylab as plt
import dicom
dcm_data = dicom.read_file('my_file.dcm')
plt.imshow(dcm_data.pixel_array)
```



Getting the slices from the mosaic

The apparent image in the DICOM file is a 2D array that consists of blocks, that are the output 2D slices. Let's call the original array the *slab*, and the contained slices *slices*. The slices are of pixel dimension `n_slice_rows` x `n_slice_cols`. The slab is of pixel dimension `n_slab_rows` x `n_slab_cols`. Because the arrangement of blocks in the slab is defined as being square, the number of blocks per slab row and slab column is the same. Let `n_blocks` be the number of blocks contained in the slab. There is also `n_slices` - the number of slices actually collected, some number <= `n_blocks`. We have the value `n_slices` from the 'NumberOfImagesInMosaic' field of the Siemens private (CSA) header. `n_row_blocks` and `n_col_blocks` are therefore given by `ceil(sqrt(n_slices))`, and `n_blocks` is `n_row_blocks ** 2`. Also `n_slice_rows == n_slab_rows / n_row_blocks`, etc. Using these numbers we can therefore reconstruct the slices from the 2D DICOM pixel array.

DICOM orientation for mosaic

See *DICOM patient coordinate system* and *DICOM voxel to patient coordinate system mapping*. We want a 4 x 4 affine A that will take us from (transposed) voxel coordinates in the DICOM image to mm in the *DICOM patient coordinate system*. See *(i, j), columns, rows in DICOM* for what we mean by transposed voxel coordinates.

We can think of the affine A as the (3,3) component, RS, and a (3,1) translation vector $\mathbf{t}$. RS can in turn be thought of

as the dot product of a (3,3) rotation matrix R and a scaling matrix S, where `S = diag(s)` and $\mathbf{s}$ is a (3,) vector of voxel sizes. $\mathbf{t}$ is a (3,1) translation vector, defining the coordinate in millimeters of the first voxel in the voxel volume (the voxel given by `voxel_array[0,0,0]`).

In the case of the mosaic, we have the first two columns of R from the F - the left/right flipped version of the `ImageOrientationPatient` DICOM field described in *DICOM affines again*. To make a full rotation matrix, we can generate the last column from the cross product of the first two. However, Siemens defines, in its private *CSA header*, a `SliceNormalVector` which gives the third column, but possibly with a z flip, so that R is orthogonal, but not a rotation matrix (it has a determinant of < 0).

The first two values of $\mathbf{s}$ (s_1, s_2) are given by the `PixelSpacing` field. We get s_3 (the slice scaling value) from `SpacingBetweenSlices`.

The *SPM DICOM conversion* code has a comment saying that mosaic DICOM imagqes have an incorrect `ImagePositionPatient` field. The `ImagePositionPatient` field usually gives the $\mathbf{t}$ vector. The comments imply that Siemens has derived `ImagePositionPatient` from the (correct) position of the center of the first slice (once the mosaic has been unpacked), but has then adjusted the vector to point to the top left voxel, where the slice size used for this adjustment is the size of the mosaic, before it has been unpacked. Let's call the correct position in millimeters of the center of the first slice $\mathbf{c} = [c_x, c_y, c_z]$. We have the derived RS matrix from the calculations above. The unpacked (eventual, real) slice dimensions are (rd_{rows}, rd_{cols}) and the mosaic dimensions are (md_{rows}, md_{cols}). The `ImagePositionPatient` vector $\mathbf{i}$ resulted from:

$$\mathbf{i} = \mathbf{c} + RS \begin{bmatrix} -(md_{rows} - 1)/2 \\ -(md_{cols} - 1)/2 \\ 0 \end{bmatrix}$$

To correct the faulty translation, we reverse it, and add the correct translation for the unpacked slice size (rd_{rows}, rd_{cols}), giving the true image position $\mathbf{t}$:

$$\mathbf{t} = \mathbf{i} - (RS \begin{bmatrix} -(md_{rows} - 1)/2 \\ -(md_{cols} - 1)/2 \\ 0 \end{bmatrix}) + (RS \begin{bmatrix} -(rd_{rows} - 1)/2 \\ -(rd_{cols} - 1)/2 \\ 0 \end{bmatrix})$$

Because of the final zero in the voxel translations, this simplifies to:

$$\mathbf{t} = \mathbf{i} + Q \begin{bmatrix} (md_{rows} - rd_{rowss})/2 \\ (md_{cols} - rd_{cols})/2 \end{bmatrix}$$

where:

$$Q = \begin{bmatrix} rs_{11} & rs_{12} \\ rs_{21} & rs_{22} \\ rs_{31} & rs_{32} \end{bmatrix}$$

Data scaling

SPM gets the DICOM scaling, offset for the image ('RescaleSlope', 'RescaleIntercept'). It writes these scalings into the nifti header. Then it writes the raw image data (unscaled) to disk. Obviously these will have the corrent scalings applied when the nifti image is read again.

A comment in the code here says that the data are not scaled by the maximum amount. I assume by this they mean that the DICOM scaling may not be the maximum scaling, whereas the standard SPM image write is, hence the difference, because they are using the DICOM scaling rather then their own. The comment continues by saying that the scaling as applied (the DICOM - not maximum - scaling) can lead to rounding errors but that it will get around some unspecified problems.

9.4.6 Siemens format DICOM with CSA header

Recent Siemens DICOM images have useful information stored in a private header. We'll call this the *CSA header*.

CSA header

See this Siemens Syngo DICOM conformance statement, and a GDCM Siemens header dump.

The CSA header is stored in DICOM private tags. In the images we are looking at, there are several relevant tags:

```
(0029, 1008) [CSA Image Header Type]              OB: 'IMAGE NUM 4 '
(0029, 1009) [CSA Image Header Version]           OB: '20100114'
(0029, 1010) [CSA Image Header Info]              OB: Array of 11560 bytes
(0029, 1018) [CSA Series Header Type]             OB: 'MR'
(0029, 1019) [CSA Series Header Version]          OB: '20100114'
(0029, 1020) [CSA Series Header Info]             OB: Array of 80248 bytes
```

In our case we want to read the 'CSAImageHeaderInfo'.

From the SPM (SPM8) code `spm_dicom_headers.m`

The CSAImageHeaderInfo and the CSA Series Header Info fields are of the same format. The fields can be of two types, CSA1 and CSA2.

Both are always little-endian, whatever the machine endian is.

The CSA2 format begins with the string 'SV10', the CSA1 format does not.

The code below keeps track of the position *within the CSA header stream*. We'll call this `csa_position`. At this point (after reading the 8 bytes of the header), `csa_position == 8`. There's a variable that sets the last byte position in the file that is sensibly still CSA header, and we'll call that `csa_max_pos`.

CSA1

Start header

1. n_tags, uint32, number of tags. Number of tags should apparently be between 1 and 128. If this is not true we just abort and move to `csa_max_pos`.
2. unused, uint32, apparently has value 77

Each tag

1. name : S64, null terminated string 64 bytes
2. vm : int32
3. vr : S4, first 3 characters only
4. syngodt : int32
5. nitems : int32
6. xx : int32 - apparently either 77 or 205

`nitems` gives the number of items in the tag. The items follow directly after the tag.

Each item

1. xx : int32 * 4 . The first of these seems to be the length of the item in bytes, modified as below.

At this point SPM does a check, by calculating the length of this item `item_len` with `xx[0]` - the `nitems` of the *first* read tag. If `item_len` is less than 0 or greater than `csa_max_pos-csa_position` (the remaining number of bytes to read in the whole header) then we break from the item reading loop, setting the value below to ''.

Then we calculate `item_len` rounded up to the nearest 4 byte boundary tp get `next_item_pos`.

2. value : uint8, `item_len`.

We set the stream position to `next_item_pos`.

CSA2

Start header

1. hdr_id : S4 == 'SV10'
2. unused1 : uint8, 4
3. n_tags, uint32, number of tags. Number of tags should apparently be between 1 and 128. If this is not true we just abort and move to `csa_max_pos`.
4. unused2, uint32, apparently has value 77

Each tag

1. name : S64, null terminated string 64 bytes
2. vm : int32
3. vr : S4, first 3 characters only
4. syngodt : int32
5. nitems : int32
6. xx : int32 - apparently either 77 or 205

`nitems` gives the number of items in the tag. The items follow directly after the tag.

Each item

1. xx : int32 * 4 . The first of these seems to be the length of the item in bytes, modified as below.

Now there's a different length check from CSA1. `item_len` is given just by `xx[1]`. If `item_len` > `csa_max_pos - csa_position` (the remaining bytes in the header), then we just read the remaning bytes in the header (as above) into `value` below, as uint8, move the filepointer to the next 4 byte boundary, and give up reading.

2. value : uint8, `item_len`.

We set the stream position to the next 4 byte boundary.

9.4.7 SPM DICOM conversion

These are some notes on the algorithms that SPM uses to convert from DICOM to nifti. There are other notes in *Siemens mosaic format*.

The relevant SPM files are `spm_dicom_headers.m`, `spm_dicom_dict.mat` and `spm_dicom_convert.m`. These notes refer the version in SPM8, as of around January 2010.

`spm_dicom_dict.mat`

This is obviously a Matlab `.mat` file. It contains variables `group` and `element`, and `values`, where `values` is a struct array, one element per (group, element) pair, with fields `name` and `vr` (the last a cell array).

`spm_dicom_headers.m`

Reads the given DICOM files into a struct. It looks like this was written by John Ahsburner (JA). Relevant fixes are:

File opening

When opening the DICOM file, SPM (subfunction `readdicomfile`)

1. opens as little endian
2. reads 4 characters starting at pos 128
3. checks if these are `DICM`; if so then continues file read; otherwise, tests to see if this is what SPM calls *truncated DICOM file format* - lacking 128 byte lead in and `DICM` string:
   (a) Seeks to beginning of file
   (b) Reads two unsigned short values into `group` and `tag`
   (c) If the (`group`, `element`) pair exist in `spm_dicom_dict.mat`, then set file pointer to 0 and continue read with `read_dicom` subfunction..
   (d) If `group` == 8 and `element` == 0, this is apparently the signature for a 'GE Twin+excite' for which JA notes there is no documentation; set file pointer to 0 and continue read with `read_dicom` subfunction.
   (e) Otherwise - crash out with error saying that this is not DICOM file.

tag read for Philips Integra

The `read_dicom` subfunction reads a tag, then has a loop during which the tag is processed (by setting values into the return structure). At the end of the loop, it reads the next tag. The loop breaks when the current tag is empty, or is the item delimitation tag (group=FFFE, element=E00D).

After it has broken out of the loop, if the last tag was (FFFE, E00D) (item delimitation tag), and the tag length was not 0, then SPM sets the file pointer back by 4 bytes from the current position. JA comments that he didn't find that in the standard, but that it seemed to be needed for the Philips Integra.

Tag length

Tag lengths as read in `read_tag` subfunction. If current format is explicit (as in 'explicit little endian'):

1. For VR of x00x00, then group, element must be (FFFE, E00D) (item delimitation tag). JA comments that GE 'ImageDelimitationItem' has no VR, just 4 0 bytes. In this case the tag length is zero, and we read another two bytes ahead.

There's a check for not-even tag length. If not even:

1. 4294967295 appears to be OK - and decoded as Inf for tag length.
2. 13 appears to mean 10 and is reset to be 10
3. Any other odd number is not valid and gives a tag length of 0

SQ VR type (Sequnce of items type)

tag length of 13 set to tag length 10.

spm_dicom_convert.m

Written by John Ashburner and Jesper Andersson.

File categorization

SPM makes a special case of Siemens 'spectroscopy images'. These are images that have 'SOPClassUID' == '1.3.12.2.1107.5.9.1' and the private tag of (29, 1210); for these it pulls out the affine, and writes a volume of ones corresponding to the acquisition planes.

For images that are not spectroscopy:

- Discards images that do not have any of ('MR', 'PT', 'CT') in 'Modality' field.
- Discards images lacking any of 'StartOfPixelData', 'SamplesperPixel', 'Rows', 'Columns', 'BitsAllocated', 'BitsStored', 'HighBit', 'PixelRespresentation'
- Discards images lacking any of 'PixelSpacing', 'ImagePositionPatient', 'ImageOrientationPatient' - presumably on the basis that SPM cannot reconstruct the affine.
- Fields 'SeriesNumber', 'AcquisitionNumber' and 'InstanceNumber' are set to 1 if absent.

Next SPM distinguishes between *Siemens mosaic format* and standard DICOM.

Mosaic images are those with the Siemens private tag:

```
(0029, 1009) [CSA Image Header Version]          OB: '20100114'
```

and a readable CSA header (see *Siemens mosaic format*), and with non-empty fields from that header of 'AcquisitionMatrixText', 'NumberOfImagesInMosaic', and with non-zero 'NumberOfImagesInMosaic'. The rest are standard DICOM.

For converting mosaic format, see *Siemens mosaic format*. The rest of this page refers to standard (slice by slice) DICOMs.

Sorting files into volumes

First pass Take first header, put as start of first volume. For each subsequent header:

1. Get `ICE_Dims` if present. Look for Siemens 'CSAImageHeaderInfo', check it has a 'name' field, then pull dimensions out of 'ICE_Dims' field in form of 9 integers separated by '_', where 'X' in this string replaced by '-1' - giving 'ICE1'

Then, for each currently identified volume:

1. If we have ICE1 above, and we do have 'CSAIMageHeaderInfo', with a 'name', in the first header in this volume, then extract ICE dims in the same way as above, for the first header in this volume, and check whether all but ICE1[6:8] are the same as ICE2. Set flag that all ICE dims are identical for this volume. Set this flag to True if we did not have ICE1 or CSA information.
2. Match the current header to the current volume iff the following match:
   (a) SeriesNumber
   (b) Rows
   (c) Columns
   (d) ImageOrientationPatient (to tolerance of sum squared difference 1e-4)
   (e) PixelSpacing (to tolerance of sum squared difference 1e-4)
   (f) ICE dims as defined above
   (g) ImageType (iff imagetype exists in both)zv
   (h) SequenceName (iff sequencename exists in both)
   (i) SeriesInstanceUID (iff exists in both)
   (j) EchoNumbers (iff exists in both)
3. If the current header matches the current volume, insert it there, otherwise make a new volume for this header

Second pass We now have a list of volumes, where each volume is a list of headers that may match.

For each volume:

1. Estimate the z direction cosine by (effectively) finding the cross product of the x and y direction cosines contained in 'ImageOrientationPatient' - call this `z_dir_cos`
2. For each header in this volume, get the z coordinate by taking the dot product of the 'ImagePositionPatient' vector and `z_dir_cos` (see *Working out the Z coordinates for a set of slices*).
3. Sort the headers according to this estimated z coordinate.
4. If this volume is more than one slice, and there are any slices with the same z coordinate (as defined above), run the *Possible volume resort* on this volume - on the basis that it may have caught more than one volume-worth of slices. Return one or more volume's worth of lists.

Final check For each volume, recalculate z coordinate as above. Calculate the z gaps. Subtract the mean of the z gaps from all z gaps. If the average of the (gap-mean(gap)) is greater than 1e-4, then print a warning that there are missing DICOM files.

Possible volume resort This step happens if there were volumes with slices having the same z coordinate in the *Second pass* step above. The resort is on the set of DICOM headers that were in the volume, for which there were slices with identical z coordinates. We'll call the list of headers that the routine is still working on - `work_list`.

1. If there is no 'InstanceNumber' field for the first header in `work_list`, bail out.
2. Print a message about the 'AcquisitionNumber' not changing from volume to volume. This may be a relic from previous code, because this version of SPM does not use the 'AcquisitionNumber' field except for making filenames.
3. Calculate the z coordinate as for *Second pass*, for each DICOM header.

4. Sort the headers by 'InstanceNumber'
5. If any headers have the same 'InstanceNumber', then discard all but the first header with the same number. At this point the remaining headers in `work_list` will have different 'InstanceNumber's, but may have the same z coordinate.
6. Now sort by z coordinate
7. If there are `N` headers, make a `N` length vector of flags `is_processed`, for which all values == False
8. Make an output list of header lists, call it `hdr_vol_out`, set to empty.
9. While there are still any False elements in `is_processed`:
   (a) Find first header for which corresponding `is_processed` is False - call this `hdr_to_check`
   (b) Collect indices (in `work_list`) of headers which have the same z coordinate as `hdr_to_check`, call this list `z_same_indices`.
   (c) Sort `work_list[z_same_indices]` by 'InstanceNumber'
   (d) For each index in `z_same_indices` such that `i` indexes the indices, and `zsind` is `z_same_indices[i]`: append header corresponding to `zsind` to `hdr_vol_out[i]`. This assumes that the original `work_list` contained two or more volumes, each with an identical set of z coordinates.
   (e) Set corresponding `is_processed` flag to True for all `z_same_indices`.
10. Finally, if the headers in `work_list` have 'InstanceNumber's that cannot be sorted to a sequence ascending in units of 1, or if any of the lists in `hdr_vol_out` have different lengths, emit a warning about missing DICOM files.

Writing DICOM volumes

This means - writing DICOM volumes from standard (slice by slice) DICOM datasets rather than *Siemens mosaic format*.

Making the affine We need the (4,4) affine A going from voxel (array) coordinates in the DICOM pixel data, to mm coordinates in the *DICOM patient coordinate system*.

This section tries to explain how SPM achieves this, but I don't completely understand their method. See *Getting a 3D affine from a DICOM slice or list of slices* for what I believe to be a simpler explanation.

First define the constants, matrices and vectors as in *DICOM affine Definitions*.

N is the number of slices in the volume.

Then define the following matrices:

$$R = \begin{pmatrix} 1 & a & 1 & 0 \\ 1 & b & 0 & 1 \\ 1 & c & 0 & 0 \\ 1 & d & 0 & 0 \end{pmatrix}$$

$$L = \begin{pmatrix} T_1^1 & e & F_{11}\Delta r & F_{12}\Delta c \\ T_2^1 & f & F_{21}\Delta r & F_{22}\Delta c \\ T_3^1 & g & F_{31}\Delta r & F_{32}\Delta c \\ 1 & h & 0 & 0 \end{pmatrix}$$

For a volume with more than one slice (header), then $a = 1; b = 1, c = N, d = 1$. e, f, g are the values from T^N, and $h == 1$.

For a volume with only one slice (header) $a = 0, b = 0, c = 1, d = 0$ and e, f, g, h are $n_1\Delta s, n_2\Delta s, n_3\Delta s, 0$.

The full transform appears to be $A_{spm} = RL^{-1}$.

Now, SPM, don't forget, is working in terms of Matlab array indexing, which starts at (1,1,1) for a three dimensional array, whereas DICOM expects a (0,0,0) start (see *DICOM affine formula*). In this particular part of the SPM DICOM code, somewhat confusingly, the (0,0,0) to (1,1,1) indexing is dealt with in the A transform, rather than the `analyze_to_dicom` transformation used by SPM in other places. So, the transform A_{spm} goes from (1,1,1) based voxel indices to mm. To get the (0, 0, 0)-based transform we want, we need to pre-apply the transform to take 0-based voxel indices to 1-based voxel indices:

$$A = RL^{-1} \begin{pmatrix} 1 & 0 & 0 & 1 \\ 0 & 1 & 0 & 1 \\ 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

This formula with the definitions above result in the single and multi slice formulae in *3D affine formulae*.

See `derivations/spm_dicom_orient.py` for the derivations and some explanations.

Writing the voxel data Just apply scaling and offset from 'RescaleSlope' and 'RescaleIntercept' for each slice and write volume.

9.4.8 dcm2nii algorithms

dcm2nii is an open source DICOM to nifti conversion program, written by Chris Rorden, in Delphi (object orientated pascal). It's part of Chris' popular mricron collection of programs. The source appears to be best found on the mricron NITRC site. It's BSD licensed.

These are working notes looking at Chris' algorithms for working with DICOM.

Compiling dcm2nii

Follow the download / install instructions at the http://www.lazarus.freepascal.org/ site. I was on a Mac, and folowed the instructions here: http://wiki.lazarus.freepascal.org/Installing_Lazarus_on_MacOS_X . Default build with version 0.9.28.2 gave an error linking against Carbon, so I needed to download a snapshot of fixed Lazarus 0.9.28.3 from http://www.hu.freepascal.org/lazarus . Open `<mricron>/dcm2nii/dcm2nii.lpi` using the Lazarus GUI. Follow instructions for compiler setup in the mricron `Readme.txt`; in particular I set other compiler options to:

```
-k-macosx_version_min -k10.5
-XR/Developer/SDKs/MacOSX10.5.sdk/
```

Further inspiration for building also came from the `debian/rules` file in Michael Hanke's mricron debian package: http://neuro.debian.net/debian/pool/main/m/mricron/

Some tag modifications

Note - Chris tells me that `dicomfastread.pas` was an attempt to do a fast dicom read that is not yet fully compatible, and that the algorithm used is in fact `dicomcompat.pas`.

Looking in the source file `<mricron>/dcm2nii/dicomfastread.pas`.

Named fields here are as from *DICOM fields*

- If 'MOSAIC' is the last string in 'ImageType', this is a mosaic
- 'DateTime' field is combination of 'StudyDate' and 'StudyTime'; fixes in file `dicomtypes.pas` for different scanner date / time formats.
- AcquisitionNumber read as normal, but then set to 1, if this a mosaic image, as set above.
- If 'EchoNumbers' > 0 and < 16, add 'EchoNumber' * 100 to the 'AcquisitionNumber' - presumably to identify different echos from the same series as being different series.

- If 'ScanningSequence' sequence contains 'RM', add 100 to the 'SeriesNumber' - maybe to differentiate research and not-research scans with the same acquisition number.
- is_4D flag labeling DICOM file as a 4D file:
  - There's a Philips private tag (2001, 1018) - labeled 'Number of Slices MR' by pydicom call this `NS`
  - If `NS>0` and 'NumberofTemporalPositions' > 0, and 'NumberOfFrames' is > 1

Sorting slices into volumes

Looking in the source file `<mricron>/dcm2nii/sortdicom.pas`.

In function `ShellSortDCM`:

Sort compares two dicom images, call them `dcm1` and `dcm2`. Tests are:

1. Are the two images 'repeats' - defined by same 'InstanceNumber' (0020, 0013), and 'AcquisitionNumber' (0020, 0012) and 'SeriesNumber' (0020, 0011) and a combination of 'StudyDate' and 'StudyTime')? Then report an error about files having the same index, flag repeated values.
2. Is `dcm1` less than `dcm2`, defined with comparisons in the following order:
   (a) StudyDate/Time
   (b) SeriesNumber
   (c) AcquisitionNumber
   (d) InstanceNumber

   This should obviously only ever be > or <, not ==, because of the first check.

Next remove repeated values as found in the first step above.

There's a function ''

9.5 API Documentation

nibabel	Read / write access to some common neuroimaging file formats

9.5.1 nibabel

Read / write access to some common neuroimaging file formats

This package provides read +/- write access to some common medical and neuroimaging file formats, including: ANALYZE (plain, SPM99, SPM2 and later), GIFTI, NIfTI1, NIfTI2, MINC1, MINC2, MGH and ECAT as well as Philips PAR/REC. We can read and write Freesurfer geometry, and read Freesurfer morphometry and annotation files. There is some very limited support for DICOM. NiBabel is the successor of PyNIfTI.

The various image format classes give full or selective access to header (meta) information and access to the image data is made available via NumPy arrays.

Website

Current documentation on nibabel can always be found at the NIPY nibabel website.

Mailing Lists

Please see the nipy devel list. The nipy devel list is fine for user and developer questions about nibabel.

Code

You can find our sources and single-click downloads:

- Main repository on Github;
- Documentation for all releases and current development tree;
- Download the current release from pypi;
- Download current development version as a zip file;
- Downloads of all available releases.

License

Nibabel is licensed under the terms of the MIT license. Some code included with nibabel is licensed under the BSD license. Please see the COPYING file in the nibabel distribution.

Quickstart

```
import nibabel as nib

img1 = nib.load('my_file.nii')
img2 = nib.load('other_file.nii.gz')
img3 = nib.load('spm_file.img')

data = img1.get_data()
affine = img1.affine

print(img1)

nib.save(img1, 'my_file_copy.nii.gz')

new_image = nib.Nifti1Image(data, affine)
nib.save(new_image, 'new_image.nii.gz')
```

For more detailed information see the *NiBabel Manual*.

get_info()

get_info

nibabel.**get_info**()

9.5.2 File Formats

analyze	Read / write access to the basic Mayo Analyze format

Continued on next page

Table 9.3 – continued from previous page

spm2analyze	Read / write access to SPM2 version of analyze image format
spm99analyze	Read / write access to SPM99 version of analyze image format
gifti	GIfTI format IO
freesurfer	Reading functions for freesurfer files
minc1	Read MINC1 format images
minc2	Preliminary MINC2 support
nicom	DICOM reader
nifti1	Read / write access to NIfTI1 image format
nifti2	Read / write access to NIfTI2 image format
ecat	Read ECAT format images
parrec	Read images in PAR/REC format.
trackvis	Read and write trackvis files

analyze

Read / write access to the basic Mayo Analyze format

The Analyze header format

This is a binary header format and inherits from `WrapStruct`

Apart from the attributes and methods of WrapStruct:

Class attributes are:

```
.default_x_flip
```

with methods:

```
.get/set_data_shape
.get/set_data_dtype
.get/set_zooms
.get/set_data_offset
.get_base_affine()
.get_best_affine()
.data_to_fileobj
.data_from_fileobj
```

and class methods:

```
.from_header(hdr)
```

More sophisticated headers can add more methods and attributes.

Notes This - basic - analyze header cannot encode full affines (only diagonal affines), and cannot do integer scaling.

The inability to store affines means that we have to guess what orientation the image has. Most Analyze images are stored on disk in (fastest-changing to slowest-changing) R->L, P->A and I->S order. That is, the first voxel is the rightmost, most posterior and most inferior voxel location in the image, and the next voxel is one voxel towards the left of the image.

Most people refer to this disk storage format as 'radiological', on the basis that, if you load up the data as an array `img_arr` where the first axis is the fastest changing, then take a slice in the I->S axis - `img_arr[:,:,10]` - then the right part of the brain will be on the left of your displayed slice. Radiologists like looking at images where the left of the brain is on the right side of the image.

Conversely, if the image has the voxels stored with the left voxels first - L->R, P->A, I->S, then this would be 'neurological' format. Neurologists like looking at images where the left side of the brain is on the left of the image.

When we are guessing at an affine for Analyze, this translates to the problem of whether the affine should consider proceeding within the data down an X line as being from left to right, or right to left.

By default we assume that the image is stored in R->L format. We encode this choice in the `default_x_flip` flag that can be True or False. True means assume radiological.

If the image is 3D, and the X, Y and Z zooms are x, y, and z, then:

```
if default_x_flip is True::
    affine = np.diag((-x,y,z,1))
else:
    affine = np.diag((x,y,z,1))
```

In our implementation, there is no way of saving this assumed flip into the header. One way of doing this, that we have not used, is to allow negative zooms, in particular, negative X zooms. We did not do this because the image can be loaded with and without a default flip, so the saved zoom will not constrain the affine.

AnalyzeHeader([binaryblock, endianness, check])	Class for basic analyze header
AnalyzeImage(dataobj, affine[, header, ...])	Class for basic Analyze format image
load	class method to create image from filename *filename*

AnalyzeHeader

class nibabel.analyze.**AnalyzeHeader**(*binaryblock=None*, *endianness=None*, *check=True*)

Bases: *nibabel.wrapstruct.LabeledWrapStruct*

Class for basic analyze header

Implements zoom-only setting of affine transform, and no image scaling

Initialize header from binary data block

Parametersbinaryblock : {None, string} optional

binary block to set into header. By default, None, in which case we insert the default empty header block

endianness : {None, '<','>', other endian code} string, optional

endianness of the binaryblock. If None, guess endianness from the data.

check : bool, optional

Whether to check content of header in initialization. Default is True.

Examples

```
>>> hdr1 = AnalyzeHeader() # an empty header
>>> hdr1.endianness == native_code
True
>>> hdr1.get_data_shape()
(0,)
>>> hdr1.set_data_shape((1,2,3)) # now with some content
>>> hdr1.get_data_shape()
(1, 2, 3)
```

We can set the binary block directly via this initialization. Here we get it from the header we have just made

```
>>> binblock2 = hdr1.binaryblock
>>> hdr2 = AnalyzeHeader(binblock2)
>>> hdr2.get_data_shape()
(1, 2, 3)
```

Empty headers are native endian by default

```
>>> hdr2.endianness == native_code
True
```

You can pass valid opposite endian headers with the `endianness` parameter. Even empty headers can have endianness

```
>>> hdr3 = AnalyzeHeader(endianness=swapped_code)
>>> hdr3.endianness == swapped_code
True
```

If you do not pass an endianness, and you pass some data, we will try to guess from the passed data.

```
>>> binblock3 = hdr3.binaryblock
>>> hdr4 = AnalyzeHeader(binblock3)
>>> hdr4.endianness == swapped_code
True
```

__init__(*binaryblock=None*, *endianness=None*, *check=True*)

Initialize header from binary data block

Parametersbinaryblock : {None, string} optional

binary block to set into header. By default, None, in which case we insert the default empty header block

endianness : {None, '<','>', other endian code} string, optional

endianness of the binaryblock. If None, guess endianness from the data.

check : bool, optional

Whether to check content of header in initialization. Default is True.

Examples

```
>>> hdr1 = AnalyzeHeader() # an empty header
>>> hdr1.endianness == native_code
True
>>> hdr1.get_data_shape()
(0,)
>>> hdr1.set_data_shape((1,2,3)) # now with some content
>>> hdr1.get_data_shape()
(1, 2, 3)
```

We can set the binary block directly via this initialization. Here we get it from the header we have just made

```
>>> binblock2 = hdr1.binaryblock
>>> hdr2 = AnalyzeHeader(binblock2)
>>> hdr2.get_data_shape()
(1, 2, 3)
```

Empty headers are native endian by default

```
>>> hdr2.endianness == native_code
True
```

You can pass valid opposite endian headers with the `endianness` parameter. Even empty headers can have endianness

```
>>> hdr3 = AnalyzeHeader(endianness=swapped_code)
>>> hdr3.endianness == swapped_code
True
```

If you do not pass an endianness, and you pass some data, we will try to guess from the passed data.

```
>>> binblock3 = hdr3.binaryblock
>>> hdr4 = AnalyzeHeader(binblock3)
>>> hdr4.endianness == swapped_code
True
```

as_analyze_map()
Return header as mapping for conversion to Analyze types

Collect data from custom header type to fill in fields for Analyze and derived header types (such as Nifti1 and Nifti2).

When Analyze types convert another header type to their own type, they call this this method to check if there are other Analyze / Nifti fields that the source header would like to set.

Returnsanalyze_map : mapping

Object that can be used as a mapping thus:

```
for key in analyze_map:
    value = analyze_map[key]
```

where `key` is the name of a field that can be set in an Analyze header type, such as Nifti1, and `value` is a value for the field. For example, *analyze_map* might be a something like `dict(regular='y', slice_duration=0.3)` where `regular` is a field present in both Analyze and Nifti1, and `slice_duration` is a field restricted to Nifti1 and Nifti2. If a particular Analyze header type does not recognize the field name, it will throw away the value without error. See `Analyze.from_header()`.

Notes

You can also return a Nifti header with the relevant fields set.

Your header still needs methods `get_data_dtype`, `get_data_shape` and `get_zooms`, for the conversion, and these get called *after* using the analyze map, so the methods will override values set in the map.

data_from_fileobj(*fileobj*)
Read scaled data array from *fileobj*

Use this routine to get the scaled image data from an image file *fileobj*, given a header *self*. "Scaled" means, with any header scaling factors applied to the raw data in the file. Use *raw_data_from_fileobj* to get the raw data.

Parametersfileobj : file-like
Must be open, and implement `read` and `seek` methods

Returnsarr : ndarray

scaled data array

Notes

We use the header to get any scale or intercept values to apply to the data. Raw Analyze files don't have scale factors or intercepts, but this routine also works with formats based on Analyze, that do have scaling, such as SPM analyze formats and NIfTI.

data_to_fileobj(*data*, *fileobj*, *rescale=True*)
Write *data* to *fileobj*, maybe rescaling data, modifying *self*

In writing the data, we match the header to the written data, by setting the header scaling factors, iff *rescale* is True. Thus we modify *self* in the process of writing the data.

Parametersdata : array-like
data to write; should match header defined shape
fileobj : file-like object
Object with file interface, implementing `write` and `seek`
rescale : {True, False}, optional
Whether to try and rescale data to match output dtype specified by header. If True and scaling needed and header cannot scale, then raise `HeaderTypeError`.

Examples

```
>>> from nibabel.analyze import AnalyzeHeader
>>> hdr = AnalyzeHeader()
>>> hdr.set_data_shape((1, 2, 3))
>>> hdr.set_data_dtype(np.float64)
>>> from io import BytesIO
>>> str_io = BytesIO()
>>> data = np.arange(6).reshape(1,2,3)
>>> hdr.data_to_fileobj(data, str_io)
>>> data.astype(np.float64).tostring('F') == str_io.getvalue()
True
```

classmethod default_structarr(*klass*, *endianness=None*)
Return header data for empty header with given endianness

default_x_flip = True

classmethod from_header(*klass*, *header=None*, *check=True*)
Class method to create header from another header

Parametersheader : `Header` instance or mapping
a header of this class, or another class of header for conversion to this type
check : {True, False}
whether to check header for integrity
Returnshdr : header instance
fresh header instance of our own class

get_base_affine()
Get affine from basic (shared) header fields

Note that we get the translations from the center of the image.

Examples

```
>>> hdr = AnalyzeHeader()
>>> hdr.set_data_shape((3, 5, 7))
>>> hdr.set_zooms((3, 2, 1))
>>> hdr.default_x_flip
True
>>> hdr.get_base_affine() # from center of image
array([[-3.,  0.,  0.,  3.],
       [ 0.,  2.,  0., -4.],
       [ 0.,  0.,  1., -3.],
       [ 0.,  0.,  0.,  1.]])
```

get_best_affine()
Get affine from basic (shared) header fields

Note that we get the translations from the center of the image.

Examples

```
>>> hdr = AnalyzeHeader()
>>> hdr.set_data_shape((3, 5, 7))
>>> hdr.set_zooms((3, 2, 1))
>>> hdr.default_x_flip
True
>>> hdr.get_base_affine() # from center of image
array([[-3.,  0.,  0.,  3.],
       [ 0.,  2.,  0., -4.],
       [ 0.,  0.,  1., -3.],
       [ 0.,  0.,  0.,  1.]])
```

get_data_dtype()
Get numpy dtype for data

For examples see `set_data_dtype`

get_data_offset()
Return offset into data file to read data

Examples

```
>>> hdr = AnalyzeHeader()
>>> hdr.get_data_offset()
0
>>> hdr['vox_offset'] = 12
>>> hdr.get_data_offset()
12
```

get_data_shape()
Get shape of data

Examples

```
>>> hdr = AnalyzeHeader()
>>> hdr.get_data_shape()
(0,)
>>> hdr.set_data_shape((1,2,3))
>>> hdr.get_data_shape()
(1, 2, 3)
```

Expanding number of dimensions gets default zooms

```
>>> hdr.get_zooms()
(1.0, 1.0, 1.0)
```

get_slope_inter()
Get scalefactor and intercept

These are not implemented for basic Analyze

get_zooms()
Get zooms from header

Returnsz : tuple
tuple of header zoom values

Examples

```
>>> hdr = AnalyzeHeader()
>>> hdr.get_zooms()
(1.0,)
>>> hdr.set_data_shape((1,2))
>>> hdr.get_zooms()
(1.0, 1.0)
>>> hdr.set_zooms((3, 4))
>>> hdr.get_zooms()
(3.0, 4.0)
```

classmethod guessed_endian(*klass*, *hdr*)
Guess intended endianness from mapping-like `hdr`

Parametershdr : mapping-like
hdr for which to guess endianness

Returnsendianness : {'<', '>'}
Guessed endianness of header

Examples

Zeros header, no information, guess native

```
>>> hdr = AnalyzeHeader()
>>> hdr_data = np.zeros((), dtype=header_dtype)
>>> AnalyzeHeader.guessed_endian(hdr_data) == native_code
True
```

A valid native header is guessed native

```
>>> hdr_data = hdr.structarr.copy()
>>> AnalyzeHeader.guessed_endian(hdr_data) == native_code
True
```

And, when swapped, is guessed as swapped

```
>>> sw_hdr_data = hdr_data.byteswap(swapped_code)
>>> AnalyzeHeader.guessed_endian(sw_hdr_data) == swapped_code
True
```

The algorithm is as follows:

First, look at the first value in the `dim` field; this should be between 0 and 7. If it is between 1 and 7, then this must be a native endian header.

```
>>> hdr_data = np.zeros((), dtype=header_dtype) # blank binary data
>>> hdr_data['dim'][0] = 1
>>> AnalyzeHeader.guessed_endian(hdr_data) == native_code
True
>>> hdr_data['dim'][0] = 6
>>> AnalyzeHeader.guessed_endian(hdr_data) == native_code
True
>>> hdr_data['dim'][0] = -1
>>> AnalyzeHeader.guessed_endian(hdr_data) == swapped_code
True
```

If the first `dim` value is zeros, we need a tie breaker. In that case we check the `sizeof_hdr` field. This should be 348. If it looks like the byteswapped value of 348, assumed swapped. Otherwise assume native.

```
>>> hdr_data = np.zeros((), dtype=header_dtype) # blank binary data
>>> AnalyzeHeader.guessed_endian(hdr_data) == native_code
True
>>> hdr_data['sizeof_hdr'] = 1543569408
>>> AnalyzeHeader.guessed_endian(hdr_data) == swapped_code
True
>>> hdr_data['sizeof_hdr'] = -1
>>> AnalyzeHeader.guessed_endian(hdr_data) == native_code
True
```

This is overridden by the `dim[0]` value though:

```
>>> hdr_data['sizeof_hdr'] = 1543569408
>>> hdr_data['dim'][0] = 1
>>> AnalyzeHeader.guessed_endian(hdr_data) == native_code
True
```

has_data_intercept = False

has_data_slope = False

raw_data_from_fileobj (*fileobj*)

Read unscaled data array from *fileobj*

Parametersfileobj : file-like

Must be open, and implement `read` and `seek` methods

Returnsarr : ndarray

unscaled data array

set_data_dtype(*datatype*)
Set numpy dtype for data from code or dtype or type

Examples

```
>>> hdr = AnalyzeHeader()
>>> hdr.set_data_dtype(np.uint8)
>>> hdr.get_data_dtype()
dtype('uint8')
>>> hdr.set_data_dtype(np.dtype(np.uint8))
>>> hdr.get_data_dtype()
dtype('uint8')
>>> hdr.set_data_dtype('implausible')
Traceback (most recent call last):
   ...
HeaderDataError: data dtype "implausible" not recognized
>>> hdr.set_data_dtype('none')
Traceback (most recent call last):
   ...
HeaderDataError: data dtype "none" known but not supported
>>> hdr.set_data_dtype(np.void)
Traceback (most recent call last):
   ...
HeaderDataError: data dtype "<type 'numpy.void'>" known but not supported
```

set_data_offset(*offset*)
Set offset into data file to read data

set_data_shape(*shape*)
Set shape of data

If `ndims == len(shape)` then we set zooms for dimensions higher than `ndims` to 1.0

Parametersshape : sequence
sequence of integers specifying data array shape

set_slope_inter(*slope*, *inter=None*)
Set slope and / or intercept into header

Set slope and intercept for image data, such that, if the image data is `arr`, then the scaled image data will be `(arr * slope) + inter`

In this case, for Analyze images, we can't store the slope or the intercept, so this method only checks that *slope* is None or NaN or 1.0, and that *inter* is None or NaN or 0.

Parametersslope : None or float
If float, value must be NaN or 1.0 or we raise a `HeaderTypeError`
inter : None or float, optional
If float, value must be 0.0 or we raise a `HeaderTypeError`

set_zooms(*zooms*)
Set zooms into header fields

See docstring for `get_zooms` for examples

sizeof_hdr = 348

template_dtype = dtype([('sizeof_hdr', '<i4'), ('data_type', 'S10'), ('db_name', 'S18'), ('extents', '<i4'), ('session_erro

AnalyzeImage

class nibabel.analyze.**AnalyzeImage**(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)
Bases: *nibabel.spatialimages.SpatialImage*

Class for basic Analyze format image

Initialize image

The image is a combination of (array, affine matrix, header), with optional metadata in *extra*, and filename / file-like objects contained in the *file_map* mapping.

Parametersdataobj : object

Object containg image data. It should be some object that retuns an array from `np.asanyarray`. It should have a `shape` attribute or property

affine : None or (4,4) array-like

homogenous affine giving relationship between voxel coordinates and world coordinates. Affine can also be None. In this case, `obj.affine` also returns None, and the affine as written to disk will depend on the file format.

header : None or mapping or header instance, optional

metadata for this image format

extra : None or mapping, optional

metadata to associate with image that cannot be stored in the metadata of this image type

file_map : mapping, optional

mapping giving file information for this image format

__init__(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)
Initialize image

The image is a combination of (array, affine matrix, header), with optional metadata in *extra*, and filename / file-like objects contained in the *file_map* mapping.

Parametersdataobj : object
Object containg image data. It should be some object that retuns an array from `np.asanyarray`. It should have a `shape` attribute or property

affine : None or (4,4) array-like
homogenous affine giving relationship between voxel coordinates and world coordinates. Affine can also be None. In this case, `obj.affine` also returns None, and the affine as written to disk will depend on the file format.

header : None or mapping or header instance, optional
metadata for this image format

extra : None or mapping, optional
metadata to associate with image that cannot be stored in the metadata of this image type

file_map : mapping, optional
mapping giving file information for this image format

ImageArrayProxy
alias of `ArrayProxy`

files_types = (('image', '.img'), ('header', '.hdr'))

classmethod from_file_map(**args*, ***kwargs*)
class method to create image from mapping in *file_map* '

Parametersfile_map : dict

Mapping with (kay, value) pairs of (`file_type`, FileHolder instance giving file-likes for each file needed for this image type.

mmap : {True, False, 'c', 'r'}, optional, keyword only

mmap controls the use of numpy memory mapping for reading image array data. If False, do not try numpy `memmap` for data array. If one of {'c', 'r'}, try numpy memmap with `mode=mmap`. A *mmap* value of True gives the same behavior as `mmap='c'`. If image data file cannot be memory-mapped, ignore *mmap* value and read array from file.

Returnsimg : AnalyzeImage instance

classmethod from_filename(**args*, ***kwargs*)

class method to create image from filename *filename*

Parametersfilename : str

Filename of image to load

mmap : {True, False, 'c', 'r'}, optional, keyword only

mmap controls the use of numpy memory mapping for reading image array data. If False, do not try numpy `memmap` for data array. If one of {'c', 'r'}, try numpy memmap with `mode=mmap`. A *mmap* value of True gives the same behavior as `mmap='c'`. If image data file cannot be memory-mapped, ignore *mmap* value and read array from file.

Returnsimg : Analyze Image instance

get_data_dtype()

header_class

alias of *AnalyzeHeader*

classmethod load(**args*, ***kwargs*)

class method to create image from filename *filename*

Parametersfilename : str

Filename of image to load

mmap : {True, False, 'c', 'r'}, optional, keyword only

mmap controls the use of numpy memory mapping for reading image array data. If False, do not try numpy `memmap` for data array. If one of {'c', 'r'}, try numpy memmap with `mode=mmap`. A *mmap* value of True gives the same behavior as `mmap='c'`. If image data file cannot be memory-mapped, ignore *mmap* value and read array from file.

Returnsimg : Analyze Image instance

set_data_dtype(*dtype*)

to_file_map(*file_map=None*)

Write image to *file_map* or contained `self.file_map`

Parametersfile_map : None or mapping, optional

files mapping. If None (default) use object's `file_map` attribute instead

load

`nibabel.analyze.`**load**(**args*, ***kwargs*)

class method to create image from filename *filename*

Parametersfilename : str

Filename of image to load

mmap : {True, False, 'c', 'r'}, optional, keyword only

mmap controls the use of numpy memory mapping for reading image array data. If False, do not try numpy `memmap` for data array. If one of {'c', 'r'}, try numpy memmap with `mode=mmap`. A *mmap* value of True gives the same behavior as `mmap='c'`. If image data file cannot be memory-mapped, ignore *mmap* value and read array from file.

Returnsimg : Analyze Image instance

spm2analyze

Read / write access to SPM2 version of analyze image format

Spm2AnalyzeHeader([binaryblock, endianness, ...])	Class for SPM2 variant of basic Analyze header
Spm2AnalyzeImage(dataobj, affine[, header, ...])	Class for SPM2 variant of basic Analyze image

Spm2AnalyzeHeader

class nibabel.spm2analyze.**Spm2AnalyzeHeader**(*binaryblock=None*, *endianness=None*, *check=True*)

Bases: *nibabel.spm99analyze.Spm99AnalyzeHeader*

Class for SPM2 variant of basic Analyze header

SPM2 variant adds the following to basic Analyze format:

- voxel origin;
- slope scaling of data;
- reading - but not writing - intercept of data.

Initialize header from binary data block

Parametersbinaryblock : {None, string} optional

binary block to set into header. By default, None, in which case we insert the default empty header block

endianness : {None, '<','>', other endian code} string, optional

endianness of the binaryblock. If None, guess endianness from the data.

check : bool, optional

Whether to check content of header in initialization. Default is True.

Examples

```
>>> hdr1 = AnalyzeHeader() # an empty header
>>> hdr1.endianness == native_code
True
>>> hdr1.get_data_shape()
(0,)
>>> hdr1.set_data_shape((1,2,3)) # now with some content
>>> hdr1.get_data_shape()
(1, 2, 3)
```

We can set the binary block directly via this initialization. Here we get it from the header we have just made

```
>>> binblock2 = hdr1.binaryblock
>>> hdr2 = AnalyzeHeader(binblock2)
>>> hdr2.get_data_shape()
(1, 2, 3)
```

Empty headers are native endian by default

```
>>> hdr2.endianness == native_code
True
```

You can pass valid opposite endian headers with the `endianness` parameter. Even empty headers can have endianness

```
>>> hdr3 = AnalyzeHeader(endianness=swapped_code)
>>> hdr3.endianness == swapped_code
True
```

If you do not pass an endianness, and you pass some data, we will try to guess from the passed data.

```
>>> binblock3 = hdr3.binaryblock
>>> hdr4 = AnalyzeHeader(binblock3)
>>> hdr4.endianness == swapped_code
True
```

__init__(*binaryblock=None*, *endianness=None*, *check=True*)

Initialize header from binary data block

Parametersbinaryblock : {None, string} optional
binary block to set into header. By default, None, in which case we insert the default empty header block

endianness : {None, '<','>', other endian code} string, optional
endianness of the binaryblock. If None, guess endianness from the data.

check : bool, optional
Whether to check content of header in initialization. Default is True.

Examples

```
>>> hdr1 = AnalyzeHeader() # an empty header
>>> hdr1.endianness == native_code
True
>>> hdr1.get_data_shape()
(0,)
>>> hdr1.set_data_shape((1,2,3)) # now with some content
>>> hdr1.get_data_shape()
(1, 2, 3)
```

We can set the binary block directly via this initialization. Here we get it from the header we have just made

```
>>> binblock2 = hdr1.binaryblock
>>> hdr2 = AnalyzeHeader(binblock2)
>>> hdr2.get_data_shape()
(1, 2, 3)
```

Empty headers are native endian by default

```
>>> hdr2.endianness == native_code
True
```

You can pass valid opposite endian headers with the `endianness` parameter. Even empty headers can have endianness

```
>>> hdr3 = AnalyzeHeader(endianness=swapped_code)
>>> hdr3.endianness == swapped_code
True
```

If you do not pass an endianness, and you pass some data, we will try to guess from the passed data.

```
>>> binblock3 = hdr3.binaryblock
>>> hdr4 = AnalyzeHeader(binblock3)
>>> hdr4.endianness == swapped_code
True
```

get_slope_inter()

Get data scaling (slope) and intercept from header data

Uses the algorithm from SPM2 spm_vol_ana.m by John Ashburner

Parametersself : header

Mapping with fields: * scl_slope - slope * scl_inter - possible intercept (SPM2 use - shared by nifti) * glmax - the (recorded) maximum value in the data (unscaled) * glmin - recorded minimum unscaled value * cal_max - the calibrated (scaled) maximum value in the dataset * cal_min - ditto minimum value

Returnsscl_slope : None or float

slope. None if there is no valid scaling from these fields

scl_inter : None or float

intercept. Also None if there is no valid slope, intercept

Examples

```
>>> fields = {'scl_slope':1,'scl_inter':0,'glmax':0,'glmin':0,'cal_max':0, 'cal_min':0}
>>> hdr = Spm2AnalyzeHeader()
>>> for key, value in fields.items():
...     hdr[key] = value
>>> hdr.get_slope_inter()
(1.0, 0.0)
>>> hdr['scl_inter'] = 0.5
>>> hdr.get_slope_inter()
(1.0, 0.5)
>>> hdr['scl_inter'] = np.nan
>>> hdr.get_slope_inter()
(1.0, 0.0)
```

If 'scl_slope' is 0, nan or inf, cannot use 'scl_slope'. Without valid information in the gl / cal fields, we cannot get scaling, and return None

```
>>> hdr['scl_slope'] = 0
>>> hdr.get_slope_inter()
(None, None)
>>> hdr['scl_slope'] = np.nan
>>> hdr.get_slope_inter()
(None, None)
```

Valid information in the gl AND cal fields are needed

```
>>> hdr['cal_max'] = 0.8
>>> hdr['cal_min'] = 0.2
>>> hdr.get_slope_inter()
(None, None)
>>> hdr['glmax'] = 110
>>> hdr['glmin'] = 10
>>> np.allclose(hdr.get_slope_inter(), [0.6/100, 0.2-0.6/100*10])
True
```

template_dtype = dtype([('sizeof_hdr', '<i4'), ('data_type', 'S10'), ('db_name', 'S18'), ('extents', '<i4'), ('session_erro

Spm2AnalyzeImage

class nibabel.spm2analyze.**Spm2AnalyzeImage**(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)

Bases: *nibabel.spm99analyze.Spm99AnalyzeImage*

Class for SPM2 variant of basic Analyze image

Initialize image

The image is a combination of (array, affine matrix, header), with optional metadata in *extra*, and filename / file-like objects contained in the *file_map* mapping.

Parametersdataobj : object

Object containg image data. It should be some object that retuns an array from `np.asanyarray`. It should have a `shape` attribute or property

affine : None or (4,4) array-like

homogenous affine giving relationship between voxel coordinates and world coordinates. Affine can also be None. In this case, `obj.affine` also returns None, and the affine as written to disk will depend on the file format.

header : None or mapping or header instance, optional

metadata for this image format

extra : None or mapping, optional

metadata to associate with image that cannot be stored in the metadata of this image type

file_map : mapping, optional

mapping giving file information for this image format

__init__(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)

Initialize image

The image is a combination of (array, affine matrix, header), with optional metadata in *extra*, and filename / file-like objects contained in the *file_map* mapping.

Parametersdataobj : object

Object containg image data. It should be some object that retuns an array from `np.asanyarray`. It should have a `shape` attribute or property

affine : None or (4,4) array-like

homogenous affine giving relationship between voxel coordinates and world coordinates. Affine can also be None. In this case, `obj.affine` also returns None, and the affine as written to disk will depend on the file format.

header : None or mapping or header instance, optional

metadata for this image format

extra : None or mapping, optional

metadata to associate with image that cannot be stored in the metadata of this image type

file_map : mapping, optional

mapping giving file information for this image format

header_class

alias of *Spm2AnalyzeHeader*

spm99analyze

Read / write access to SPM99 version of analyze image format

Spm99AnalyzeHeader([binaryblock, ...])	Class for SPM99 variant of basic Analyze header
Spm99AnalyzeImage(dataobj, affine[, header, ...])	Class for SPM99 variant of basic Analyze image
SpmAnalyzeHeader([binaryblock, endianness, ...])	Basic scaling Spm Analyze header

Spm99AnalyzeHeader

class nibabel.spm99analyze.**Spm99AnalyzeHeader**(*binaryblock=None*, *endianness=None*, *check=True*)

Bases: *nibabel.spm99analyze.SpmAnalyzeHeader*

Class for SPM99 variant of basic Analyze header

SPM99 variant adds the following to basic Analyze format:

- voxel origin;
- slope scaling of data.

Initialize header from binary data block

Parametersbinaryblock : {None, string} optional

binary block to set into header. By default, None, in which case we insert the default empty header block

endianness : {None, '<','>', other endian code} string, optional

endianness of the binaryblock. If None, guess endianness from the data.

check : bool, optional

Whether to check content of header in initialization. Default is True.

Examples

```
>>> hdr1 = AnalyzeHeader() # an empty header
>>> hdr1.endianness == native_code
True
>>> hdr1.get_data_shape()
(0,)
>>> hdr1.set_data_shape((1,2,3)) # now with some content
>>> hdr1.get_data_shape()
(1, 2, 3)
```

We can set the binary block directly via this initialization. Here we get it from the header we have just made

```
>>> binblock2 = hdr1.binaryblock
>>> hdr2 = AnalyzeHeader(binblock2)
>>> hdr2.get_data_shape()
(1, 2, 3)
```

Empty headers are native endian by default

```
>>> hdr2.endianness == native_code
True
```

You can pass valid opposite endian headers with the `endianness` parameter. Even empty headers can have endianness

```
>>> hdr3 = AnalyzeHeader(endianness=swapped_code)
>>> hdr3.endianness == swapped_code
True
```

If you do not pass an endianness, and you pass some data, we will try to guess from the passed data.

```
>>> binblock3 = hdr3.binaryblock
>>> hdr4 = AnalyzeHeader(binblock3)
>>> hdr4.endianness == swapped_code
True
```

__init__(*binaryblock=None*, *endianness=None*, *check=True*)

Initialize header from binary data block

Parametersbinaryblock : {None, string} optional
binary block to set into header. By default, None, in which case we insert the default empty header block

endianness : {None, '<','>', other endian code} string, optional
endianness of the binaryblock. If None, guess endianness from the data.

check : bool, optional
Whether to check content of header in initialization. Default is True.

Examples

```
>>> hdr1 = AnalyzeHeader() # an empty header
>>> hdr1.endianness == native_code
True
>>> hdr1.get_data_shape()
(0,)
>>> hdr1.set_data_shape((1,2,3)) # now with some content
>>> hdr1.get_data_shape()
(1, 2, 3)
```

We can set the binary block directly via this initialization. Here we get it from the header we have just made

```
>>> binblock2 = hdr1.binaryblock
>>> hdr2 = AnalyzeHeader(binblock2)
>>> hdr2.get_data_shape()
(1, 2, 3)
```

Empty headers are native endian by default

```
>>> hdr2.endianness == native_code
True
```

You can pass valid opposite endian headers with the `endianness` parameter. Even empty headers can have endianness

```
>>> hdr3 = AnalyzeHeader(endianness=swapped_code)
>>> hdr3.endianness == swapped_code
True
```

If you do not pass an endianness, and you pass some data, we will try to guess from the passed data.

```
>>> binblock3 = hdr3.binaryblock
>>> hdr4 = AnalyzeHeader(binblock3)
>>> hdr4.endianness == swapped_code
True
```

get_best_affine()

Get affine from header, using SPM origin field if sensible

The default translations are got from the `origin` field, if set, or from the center of the image otherwise.

Examples

```
>>> hdr = Spm99AnalyzeHeader()
>>> hdr.set_data_shape((3, 5, 7))
>>> hdr.set_zooms((3, 2, 1))
>>> hdr.default_x_flip
True
>>> hdr.get_origin_affine() # from center of image
array([[-3.,  0.,  0.,  3.],
       [ 0.,  2.,  0., -4.],
       [ 0.,  0.,  1., -3.],
       [ 0.,  0.,  0.,  1.]])
>>> hdr['origin'][:3] = [3,4,5]
>>> hdr.get_origin_affine() # using origin
array([[-3.,  0.,  0.,  6.],
       [ 0.,  2.,  0., -6.],
       [ 0.,  0.,  1., -4.],
       [ 0.,  0.,  0.,  1.]])
>>> hdr['origin'] = 0 # unset origin
>>> hdr.set_data_shape((3, 5, 7))
>>> hdr.get_origin_affine() # from center of image
array([[-3.,  0.,  0.,  3.],
       [ 0.,  2.,  0., -4.],
       [ 0.,  0.,  1., -3.],
       [ 0.,  0.,  0.,  1.]])
```

get_origin_affine()

Get affine from header, using SPM origin field if sensible

The default translations are got from the `origin` field, if set, or from the center of the image otherwise.

Examples

```
>>> hdr = Spm99AnalyzeHeader()
>>> hdr.set_data_shape((3, 5, 7))
>>> hdr.set_zooms((3, 2, 1))
>>> hdr.default_x_flip
True
>>> hdr.get_origin_affine() # from center of image
array([[-3.,  0.,  0.,  3.],
       [ 0.,  2.,  0., -4.],
       [ 0.,  0.,  1., -3.],
       [ 0.,  0.,  0.,  1.]])
>>> hdr['origin'][:3] = [3,4,5]
```

```
>>> hdr.get_origin_affine() # using origin
array([[-3.,  0.,  0.,  6.],
       [ 0.,  2.,  0., -6.],
       [ 0.,  0.,  1., -4.],
       [ 0.,  0.,  0.,  1.]])
>>> hdr['origin'] = 0 # unset origin
>>> hdr.set_data_shape((3, 5, 7))
>>> hdr.get_origin_affine() # from center of image
array([[-3.,  0.,  0.,  3.],
       [ 0.,  2.,  0., -4.],
       [ 0.,  0.,  1., -3.],
       [ 0.,  0.,  0.,  1.]])
```

set_origin_from_affine(*affine*)

Set SPM origin to header from affine matrix.

The `origin` field was read but not written by SPM99 and 2. It was used for storing a central voxel coordinate, that could be used in aligning the image to some standard position - a proxy for a full translation vector that was usually stored in a separate matlab .mat file.

Nifti uses the space occupied by the SPM `origin` field for important other information (the transform codes), so writing the origin will make the header a confusing Nifti file. If you work with both Analyze and Nifti, you should probably avoid doing this.

Parametersaffine : array-like, shape (4,4)

Affine matrix to set

ReturnsNone :

Examples

```
>>> hdr = Spm99AnalyzeHeader()
>>> hdr.set_data_shape((3, 5, 7))
>>> hdr.set_zooms((3,2,1))
>>> hdr.get_origin_affine()
array([[-3.,  0.,  0.,  3.],
       [ 0.,  2.,  0., -4.],
       [ 0.,  0.,  1., -3.],
       [ 0.,  0.,  0.,  1.]])
>>> affine = np.diag([3,2,1,1])
>>> affine[:3,3] = [-6, -6, -4]
>>> hdr.set_origin_from_affine(affine)
>>> np.all(hdr['origin'][:3] == [3,4,5])
True
>>> hdr.get_origin_affine()
array([[-3.,  0.,  0.,  6.],
       [ 0.,  2.,  0., -6.],
       [ 0.,  0.,  1., -4.],
       [ 0.,  0.,  0.,  1.]])
```

Spm99AnalyzeImage

class nibabel.spm99analyze.**Spm99AnalyzeImage**(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)

Bases: *nibabel.analyze.AnalyzeImage*

Class for SPM99 variant of basic Analyze image

Initialize image

The image is a combination of (array, affine matrix, header), with optional metadata in *extra*, and filename / file-like objects contained in the *file_map* mapping.

Parametersdataobj : object

Object containg image data. It should be some object that retuns an array from `np.asanyarray`. It should have a `shape` attribute or property

affine : None or (4,4) array-like

homogenous affine giving relationship between voxel coordinates and world coordinates. Affine can also be None. In this case, `obj.affine` also returns None, and the affine as written to disk will depend on the file format.

header : None or mapping or header instance, optional

metadata for this image format

extra : None or mapping, optional

metadata to associate with image that cannot be stored in the metadata of this image type

file_map : mapping, optional

mapping giving file information for this image format

__init__(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)

Initialize image

The image is a combination of (array, affine matrix, header), with optional metadata in *extra*, and filename / file-like objects contained in the *file_map* mapping.

Parametersdataobj : object

Object containg image data. It should be some object that retuns an array from `np.asanyarray`. It should have a `shape` attribute or property

affine : None or (4,4) array-like

homogenous affine giving relationship between voxel coordinates and world coordinates. Affine can also be None. In this case, `obj.affine` also returns None, and the affine as written to disk will depend on the file format.

header : None or mapping or header instance, optional

metadata for this image format

extra : None or mapping, optional

metadata to associate with image that cannot be stored in the metadata of this image type

file_map : mapping, optional

mapping giving file information for this image format

files_types = (('image', '.img'), ('header', '.hdr'), ('mat', '.mat'))

classmethod from_file_map(**args*, ***kwargs*)

class method to create image from mapping in *file_map* '

Parametersfile_map : dict

Mapping with (kay, value) pairs of (`file_type`, FileHolder instance giving file-likes for each file needed for this image type.

mmap : {True, False, 'c', 'r'}, optional, keyword only

mmap controls the use of numpy memory mapping for reading image array data. If False, do not try numpy `memmap` for data array. If one of {'c', 'r'}, try numpy memmap with `mode=mmap`. A *mmap* value of True gives the same behavior as `mmap='c'`. If image data file cannot be memory-mapped, ignore *mmap* value and read array from file.

Returnsimg : Spm99AnalyzeImage instance

header_class
alias of *Spm99AnalyzeHeader*

to_file_map (*file_map=None*)
Write image to *file_map* or contained `self.file_map`

Extends Analyze `to_file_map` method by writing `mat` file
Parametersfile_map : None or mapping, optional
files mapping. If None (default) use object's `file_map` attribute instead

SpmAnalyzeHeader

class `nibabel.spm99analyze.`**SpmAnalyzeHeader**(*binaryblock=None*, *endianness=None*, *check=True*)

Bases: *nibabel.analyze.AnalyzeHeader*

Basic scaling Spm Analyze header

Initialize header from binary data block

Parametersbinaryblock : {None, string} optional

binary block to set into header. By default, None, in which case we insert the default empty header block

endianness : {None, '<','>', other endian code} string, optional

endianness of the binaryblock. If None, guess endianness from the data.

check : bool, optional

Whether to check content of header in initialization. Default is True.

Examples

```
>>> hdr1 = AnalyzeHeader() # an empty header
>>> hdr1.endianness == native_code
True
>>> hdr1.get_data_shape()
(0,)
>>> hdr1.set_data_shape((1,2,3)) # now with some content
>>> hdr1.get_data_shape()
(1, 2, 3)
```

We can set the binary block directly via this initialization. Here we get it from the header we have just made

```
>>> binblock2 = hdr1.binaryblock
>>> hdr2 = AnalyzeHeader(binblock2)
>>> hdr2.get_data_shape()
(1, 2, 3)
```

Empty headers are native endian by default

```
>>> hdr2.endianness == native_code
True
```

You can pass valid opposite endian headers with the `endianness` parameter. Even empty headers can have endianness

```
>>> hdr3 = AnalyzeHeader(endianness=swapped_code)
>>> hdr3.endianness == swapped_code
True
```

If you do not pass an endianness, and you pass some data, we will try to guess from the passed data.

```
>>> binblock3 = hdr3.binaryblock
>>> hdr4 = AnalyzeHeader(binblock3)
>>> hdr4.endianness == swapped_code
True
```

__init__(*binaryblock=None*, *endianness=None*, *check=True*)

Initialize header from binary data block

Parametersbinaryblock : {None, string} optional
binary block to set into header. By default, None, in which case we insert the default empty header block

endianness : {None, '<','>', other endian code} string, optional
endianness of the binaryblock. If None, guess endianness from the data.

check : bool, optional
Whether to check content of header in initialization. Default is True.

Examples

```
>>> hdr1 = AnalyzeHeader() # an empty header
>>> hdr1.endianness == native_code
True
>>> hdr1.get_data_shape()
(0,)
>>> hdr1.set_data_shape((1,2,3)) # now with some content
>>> hdr1.get_data_shape()
(1, 2, 3)
```

We can set the binary block directly via this initialization. Here we get it from the header we have just made

```
>>> binblock2 = hdr1.binaryblock
>>> hdr2 = AnalyzeHeader(binblock2)
>>> hdr2.get_data_shape()
(1, 2, 3)
```

Empty headers are native endian by default

```
>>> hdr2.endianness == native_code
True
```

You can pass valid opposite endian headers with the `endianness` parameter. Even empty headers can have endianness

```
>>> hdr3 = AnalyzeHeader(endianness=swapped_code)
>>> hdr3.endianness == swapped_code
True
```

If you do not pass an endianness, and you pass some data, we will try to guess from the passed data.

```
>>> binblock3 = hdr3.binaryblock
>>> hdr4 = AnalyzeHeader(binblock3)
>>> hdr4.endianness == swapped_code
True
```

classmethod default_structarr(*klass*, *endianness=None*)
Create empty header binary block with given endianness

get_slope_inter()
Get scalefactor and intercept

If scalefactor is 0.0 return None to indicate no scalefactor. Intercept is always None because SPM99 analyze cannot store intercepts.

has_data_intercept = False

has_data_slope = True

set_slope_inter(*slope*, *inter=None*)
Set slope and / or intercept into header

Set slope and intercept for image data, such that, if the image data is `arr`, then the scaled image data will be `(arr * slope) + inter`

The SPM Analyze header can't save an intercept value, and we raise an error unless *inter* is None, NaN or 0

Parametersslope : None or float
If None, implies *slope* of NaN. NaN is a signal to the image writing routines to rescale on save. 0, Inf, -Inf are invalid and cause a HeaderDataError

inter : None or float, optional
intercept. Must be None, NaN or 0, because SPM99 cannot store intercepts.

template_dtype = dtype([('sizeof_hdr', '<i4'), ('data_type', 'S10'), ('db_name', 'S18'), ('extents', '<i4'), ('session_error

gifti

GIfTI format IO

giftiio
gifti

Module: gifti.gifti

GiftiCoordSystem([dataspace, xformspace, xform])	
GiftiDataArray([data])	
GiftiImage([meta, labeltable, darrays, version])	
GiftiLabel([key, label, red, green, blue, alpha])	
GiftiLabelTable()	
GiftiMetaData([nvpair])	A list of GiftiNVPairs in stored in
GiftiNVPairs([name, value])	
data_tag(dataarray, encoding, datatype, ordering)	Creates the data tag depending on the required encoding

Module: gifti.giftiio

read(filename)	Load a Gifti image from a file
write(image, filename)	Save the current image to a new file

Module: gifti.parse_gifti_fast

Outputter()	
parse_gifti_file(fname[, buffer_size])	Parse gifti file named *fname*, return image
read_data_block(encoding, endian, ordering, ...)	Tries to unzip, decode, parse the funny string data

Module: gifti.util

GiftiCoordSystem

class nibabel.gifti.gifti.**GiftiCoordSystem**(*dataspace=0*, *xformspace=0*, *xform=None*)

Bases: object

__init__(*dataspace=0*, *xformspace=0*, *xform=None*)

dataspace
alias of int

print_summary()

to_xml()

xform
alias of ndarray

xformspace
alias of int

GiftiDataArray

class nibabel.gifti.gifti.**GiftiDataArray**(*data=None*)

Bases: object

__init__(*data=None*)

coordsys
alias of *GiftiCoordSystem*

data
alias of ndarray

datatype
alias of int

dims
alias of list

encoding
alias of int

endian
alias of int

ext_fname
alias of str

ext_offset
alias of str

classmethod from_array(*klass*, *darray*, *intent*, *datatype=None*, *encoding='GIFTI_ENCODING_B64GZ'*, *endian='little'*, *coordsys=None*, *ordering='C'*, *meta=None*)
Creates a new Gifti data array

Parametersdarray : ndarray
NumPy data array

intent : string
NIFTI intent code, see nifti1.intent_codes

datatype : None or string, optional
NIFTI data type codes, see nifti1.data_type_codes If None, the datatype of the NumPy array is taken.

encoding : string, optionaal
Encoding of the data, see util.gifti_encoding_codes; default: GIFTI_ENCODING_B64GZ

endian : string, optional
The Endianness to store the data array. Should correspond to the machine endianness. default: system byteorder

coordsys : GiftiCoordSystem, optional
If None, a identity transformation is taken.

ordering : string, optional
The ordering of the array. see util.array_index_order_codes; default: RowMajorOrder - C ordering

meta : None or dict, optional
A dictionary for metadata information. If None, gives empty dict.

Returnsda : instance of our own class

get_metadata()
Returns metadata as dictionary

ind_ord
alias of int

intent
alias of int

meta
alias of *GiftiMetaData*

num_dim
alias of int

print_summary()

to_xml()

to_xml_close()

to_xml_open()

GiftiImage

class nibabel.gifti.gifti.**GiftiImage**(*meta=None*, *labeltable=None*, *darrays=None*, *version='1.0'*)
Bases: object

__init__(*meta=None*, *labeltable=None*, *darrays=None*, *version='1.0'*)

add_gifti_data_array(*dataarr*)
Adds a data array to the GiftiImage
Parametersdataarr : GiftiDataArray

filename
alias of `str`

getArraysFromIntent(*intent*)
Returns a a list of GiftiDataArray elements matching the given intent

get_labeltable()

get_metadata()

numDA
alias of `int`

print_summary()

remove_gifti_data_array(*ith*)
Removes the ith data array element from the GiftiImage

remove_gifti_data_array_by_intent(*intent*)
Removes all the data arrays with the given intent type

set_labeltable(*labeltable*)
Set the labeltable for this GiftiImage
Parameterslabeltable : GiftiLabelTable

set_metadata(*meta*)
Set the metadata for this GiftiImage
Parametersmeta : GiftiMetaData
ReturnsNone :

to_xml()
Return XML corresponding to image content

version
alias of `str`

GiftiLabel
class nibabel.gifti.gifti.**GiftiLabel**(*key=0*, *label=''*, *red=None*, *green=None*, *blue=None*, *alpha=None*)
Bases: `object`

__init__(*key=0*, *label=''*, *red=None*, *green=None*, *blue=None*, *alpha=None*)

alpha
alias of `float`

blue
alias of `float`

get_rgba()
Returns RGBA as tuple

green
alias of `float`

key
alias of `int`

label
alias of str

red
alias of float

GiftiLabelTable

class nibabel.gifti.gifti.**GiftiLabelTable**
Bases: object

__init__()

get_labels_as_dict()

print_summary()

to_xml()

GiftiMetaData

class nibabel.gifti.gifti.**GiftiMetaData**(*nvpair=None*)
Bases: object

A list of GiftiNVPairs in stored in the list self.data

__init__(*nvpair=None*)

classmethod from_dict(*klass*, *data_dict*)

get_metadata()
Returns metadata as dictionary

print_summary()

to_xml()

GiftiNVPairs

class nibabel.gifti.gifti.**GiftiNVPairs**(*name=''*, *value=''*)
Bases: object

__init__(*name=''*, *value=''*)

name
alias of str

value
alias of str

data_tag

nibabel.gifti.gifti.**data_tag**(*dataarray*, *encoding*, *datatype*, *ordering*)
Creates the data tag depending on the required encoding

read

nibabel.gifti.giftiio.**read**(*filename*)
Load a Gifti image from a file

Parametersfilename : string

The Gifti file to open, it has usually ending .gii

Returnsimg : GiftiImage

Returns a GiftiImage

write
nibabel.gifti.giftiio.**write**(*image*, *filename*)
Save the current image to a new file

Parametersimage : GiftiImage

A GiftiImage instance to store

filename : string

Filename to store the Gifti file to

ReturnsNone :

Notes

We write all files with utf-8 encoding, and specify this at the top of the XML file with the `encoding` attribute.

The Gifti spec suggests using the following suffixes to your filename when saving each specific type of data:

.gii Generic GIFTI File

.coord.gii Coordinates

.func.gii Functional

.label.gii Labels

.rgba.giiRGB or RGBA

.shape.gii Shape

.surf.gii Surface

.tensor.gii Tensors

.time.gii Time Series

.topo.gii Topology

The Gifti file is stored in endian convention of the current machine.

Outputter
class nibabel.gifti.parse_gifti_fast.**Outputter**
Bases: object

__init__()

CharacterDataHandler(*data*)
Collect character data chunks pending collation

The parser breaks the data up into chunks of size depending on the buffer_size of the parser. A large bit of character data, with standard parser buffer_size (such as 8K) can easily span many calls to this function. We thus collect the chunks and process them when we hit start or end tags.

EndElementHandler(*name*)

StartElementHandler(*name*, *attrs*)

flush_chardata()
Collate and process collected character data

initialize()
Initialize outputter

pending_data
True if there is character data pending for processing

parse_gifti_file
nibabel.gifti.parse_gifti_fast.**parse_gifti_file**(*fname*, *buffer_size=None*)
Parse gifti file named *fname*, return image

Parametersfname : str

filename of gifti file

buffer_size: None or int, optional :

size of read buffer. None gives default of 35000000 unless on python < 2.6, in which case it is read only in the parser. In that case values other than None cause a ValueError on execution

Returnsimg : gifti image

read_data_block
nibabel.gifti.parse_gifti_fast.**read_data_block**(*encoding*, *endian*, *ordering*, *datatype*, *shape*, *data*)
Tries to unzip, decode, parse the funny string data

freesurfer

Reading functions for freesurfer files

Module: freesurfer.io

read_annot(filepath[, orig_ids])	Read in a Freesurfer annotation from a .annot file.
read_geometry(filepath)	Read a triangular format Freesurfer surface mesh.
read_label(filepath[, read_scalars])	Load in a Freesurfer .label file.
read_morph_data(filepath)	Read a Freesurfer morphometry data file.
write_annot(filepath, labels, ctab, names)	Write out a Freesurfer annotation file.
write_geometry(filepath, coords, faces[, ...])	Write a triangular format Freesurfer surface mesh.

Module: freesurfer.mghformat

Header and image reading / writing functions for MGH image format

Author: Krish Subramaniam

MGHError	Exception for MGH format related problems.
MGHHeader([binaryblock, check])	Class for MGH format header
MGHImage(dataobj, affine[, header, extra, ...])	Class for MGH format image
load	class method to create image from filename *filename*

read_annot
nibabel.freesurfer.io.**read_annot**(*filepath*, *orig_ids=False*)
Read in a Freesurfer annotation from a .annot file.

Parametersfilepath : str

Path to annotation file.

orig_ids : bool

Whether to return the vertex ids as stored in the annotation file or the positional colortable ids. With orig_ids=False vertices with no id have an id set to -1.

Returnslabels : ndarray, shape (n_vertices,)

Annotation id at each vertex. If a vertex does not belong to any label and orig_ids=False, its id will be set to -1.

ctab : ndarray, shape (n_labels, 5)

RGBA + label id colortable array.

names : list of str

The names of the labels. The length of the list is n_labels.

read_geometry
nibabel.freesurfer.io.**read_geometry**(*filepath*)
Read a triangular format Freesurfer surface mesh.

Parametersfilepath : str

Path to surface file

Returnscoords : numpy array

nvtx x 3 array of vertex (x, y, z) coordinates

faces : numpy array

nfaces x 3 array of defining mesh triangles

read_label
nibabel.freesurfer.io.**read_label**(*filepath*, *read_scalars=False*)
Load in a Freesurfer .label file.

Parametersfilepath : str

Path to label file

read_scalars : bool

If true, read and return scalars associated with each vertex

Returnslabel_array : numpy array

Array with indices of vertices included in label

scalar_array : numpy array (floats)

If read_scalars is True, array of scalar data for each vertex

read_morph_data
nibabel.freesurfer.io.**read_morph_data**(*filepath*)
Read a Freesurfer morphometry data file.

This function reads in what Freesurfer internally calls "curv" file types, (e.g. ?h. curv, ?h.thickness), but as that has the potential to cause confusion where "curv" also refers to the surface curvature values, we refer to these files as "morphometry" files with PySurfer.

Parametersfilepath : str

Path to morphometry file

Returnscurv : numpy array

Vector representation of surface morpometry values

write_annot
nibabel.freesurfer.io.**write_annot**(*filepath*, *labels*, *ctab*, *names*)
Write out a Freesurfer annotation file.

See: https://surfer.nmr.mgh.harvard.edu/fswiki/LabelsClutsAnnotationFiles#Annotation

Parametersfilepath : str

Path to annotation file to be written

labels : ndarray, shape (n_vertices,)

Annotation id at each vertex.

ctab : ndarray, shape (n_labels, 5)

RGBA + label id colortable array.

names : list of str

The names of the labels. The length of the list is n_labels.

write_geometry
nibabel.freesurfer.io.**write_geometry**(*filepath*, *coords*, *faces*, *create_stamp=None*)
Write a triangular format Freesurfer surface mesh.

Parametersfilepath : str

Path to surface file

coords : numpy array

nvtx x 3 array of vertex (x, y, z) coordinates

faces : numpy array

nfaces x 3 array of defining mesh triangles

create_stamp : str

User/time stamp (default: "created by <user> on <ctime>")

MGHError
class nibabel.freesurfer.mghformat.**MGHError**
Bases: exceptions.Exception

Exception for MGH format related problems.

To be raised whenever MGH is not happy, or we are not happy with MGH.

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

MGHHeader

class nibabel.freesurfer.mghformat.**MGHHeader**(*binaryblock=None*, *check=True*)
Bases: object

Class for MGH format header

The header also consists of the footer data which MGH places after the data chunk.

Initialize header from binary data block

Parametersbinaryblock : {None, string} optional

binary block to set into header. By default, None, in which case we insert the default empty header block

check : bool, optional

Whether to check content of header in initialization. Default is True.

__init__(*binaryblock=None*, *check=True*)
Initialize header from binary data block
Parametersbinaryblock : {None, string} optional
binary block to set into header. By default, None, in which case we insert the default empty header block
check : bool, optional
Whether to check content of header in initialization. Default is True.

binaryblock
binary block of data as string
Returnsbinaryblock : string
string giving binary data block

check_fix()
Pass. maybe for now

copy()
Return copy of header

data_from_fileobj(*fileobj*)
Read data array from *fileobj*
Parametersfileobj : file-like
Must be open, and implement read and seek methods
Returnsarr : ndarray
data array

classmethod from_fileobj(*klass*, *fileobj*, *check=True*)
classmethod for loading a MGH fileobject

classmethod from_header(*klass*, *header=None*, *check=True*)
Class method to create MGH header from another MGH header

get_affine()
Get the affine transform from the header information. MGH format doesn't store the transform directly. Instead it's gleaned from the zooms (delta), direction cosines (Mdc), RAS centers (Pxyz_c) and the dimensions.

get_best_affine()
Get the affine transform from the header information. MGH format doesn't store the transform directly. Instead it's gleaned from the zooms (delta), direction cosines (Mdc), RAS centers (Pxyz_c) and the dimensions.

get_data_bytespervox()
Get the number of bytes per voxel of the data

get_data_dtype()
Get numpy dtype for MGH data

For examples see `set_data_dtype`

get_data_offset()
Return offset into data file to read data

get_data_shape()
Get shape of data

get_data_size()
Get the number of bytes the data chunk occupies.

get_footer_offset()
Return offset where the footer resides. Occurs immediately after the data chunk.

get_ras2vox()
return the inverse get_affine()

get_slope_inter()
MGH format does not do scaling?

get_vox2ras()
return the get_affine()

get_vox2ras_tkr()
Get the vox2ras-tkr transform. See "Torig" here: https://surfer.nmr.mgh.harvard.edu/fswiki/CoordinateSystems

get_zooms()
Get zooms from header
Returnsz : tuple
tuple of header zoom values

items()
Return items from header data

keys()
Return keys from header data

set_data_dtype(*datatype*)
Set numpy dtype for data from code or dtype or type

set_data_shape(*shape*)
Set shape of data
Parametersshape : sequence
sequence of integers specifying data array shape

set_zooms(*zooms*)
Set zooms into header fields

See docstring for `get_zooms` for examples

template_dtype = dtype([('version', '>i4'), ('dims', '>i4', (4,)), ('type', '>i4'), ('dof', '>i4'), ('goodRASFlag', '>i2'), ('de

values()
Return values from header data

writeftr_to(*fileobj*)
Write footer to fileobj

Footer data is located after the data chunk. So move there and write.
Parametersfileobj : file-like object
Should implement `write` and `seek` method
ReturnsNone :

writehdr_to(*fileobj*)
Write header to fileobj

Write starts at the beginning.
Parametersfileobj : file-like object
Should implement `write` and `seek` method
ReturnsNone :

MGHImage
class `nibabel.freesurfer.mghformat.`**MGHImage**(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)
Bases: *nibabel.spatialimages.SpatialImage*

Class for MGH format image

Initialize image

The image is a combination of (array, affine matrix, header), with optional metadata in *extra*, and filename / file-like objects contained in the *file_map* mapping.

Parametersdataobj : object

Object containg image data. It should be some object that retuns an array from `np.asanyarray`. It should have a `shape` attribute or property

affine : None or (4,4) array-like

homogenous affine giving relationship between voxel coordinates and world coordinates. Affine can also be None. In this case, `obj.affine` also returns None, and the affine as written to disk will depend on the file format.

header : None or mapping or header instance, optional

metadata for this image format

extra : None or mapping, optional

metadata to associate with image that cannot be stored in the metadata of this image type

file_map : mapping, optional

mapping giving file information for this image format

__init__(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)
Initialize image

The image is a combination of (array, affine matrix, header), with optional metadata in *extra*, and filename / file-like objects contained in the *file_map* mapping.
Parametersdataobj : object
Object containg image data. It should be some object that retuns an array from `np.asanyarray`. It should have a `shape` attribute or property
affine : None or (4,4) array-like

homogenous affine giving relationship between voxel coordinates and world coordinates. Affine can also be None. In this case, `obj.affine` also returns None, and the affine as written to disk will depend on the file format.

header : None or mapping or header instance, optional
metadata for this image format

extra : None or mapping, optional
metadata to associate with image that cannot be stored in the metadata of this image type

file_map : mapping, optional
mapping giving file information for this image format

ImageArrayProxy
alias of `ArrayProxy`

files_types = (('image', '.mgh'),)

classmethod filespec_to_file_map(*klass*, *filespec*)
Check for compressed .mgz format, then .mgh format

classmethod from_file_map(**args*, ***kwargs*)
Load image from *file_map*

Parametersfile_map : None or mapping, optional
files mapping. If None (default) use object's `file_map` attribute instead

mmap : {True, False, 'c', 'r'}, optional, keyword only
mmap controls the use of numpy memory mapping for reading image array data. If False, do not try numpy `memmap` for data array. If one of {'c', 'r'}, try numpy memmap with `mode=mmap`. A *mmap* value of True gives the same behavior as `mmap='c'`. If image data file cannot be memory-mapped, ignore *mmap* value and read array from file.

classmethod from_filename(**args*, ***kwargs*)
class method to create image from filename *filename*

Parametersfilename : str
Filename of image to load

mmap : {True, False, 'c', 'r'}, optional, keyword only
mmap controls the use of numpy memory mapping for reading image array data. If False, do not try numpy `memmap` for data array. If one of {'c', 'r'}, try numpy memmap with `mode=mmap`. A *mmap* value of True gives the same behavior as `mmap='c'`. If image data file cannot be memory-mapped, ignore *mmap* value and read array from file.

Returnsimg : MGHImage instance

header_class
alias of *MGHHeader*

classmethod load(**args*, ***kwargs*)
class method to create image from filename *filename*

Parametersfilename : str
Filename of image to load

mmap : {True, False, 'c', 'r'}, optional, keyword only
mmap controls the use of numpy memory mapping for reading image array data. If False, do not try numpy `memmap` for data array. If one of {'c', 'r'}, try numpy memmap with `mode=mmap`. A *mmap* value of True gives the same behavior as `mmap='c'`. If image data file cannot be memory-mapped, ignore *mmap* value and read array from file.

Returnsimg : MGHImage instance

to_file_map(*file_map=None*)
Write image to *file_map* or contained `self.file_map`

Parametersfile_map : None or mapping, optional
files mapping. If None (default) use object's `file_map` attribute instead

load
nibabel.freesurfer.mghformat.**load**(**args*, ***kwargs*)
class method to create image from filename *filename*

Parametersfilename : str

Filename of image to load

mmap : {True, False, 'c', 'r'}, optional, keyword only

mmap controls the use of numpy memory mapping for reading image array data. If False, do not try numpy `memmap` for data array. If one of {'c', 'r'}, try numpy memmap with `mode=mmap`. A *mmap* value of True gives the same behavior as `mmap='c'`. If image data file cannot be memory-mapped, ignore *mmap* value and read array from file.

Returnsimg : MGHImage instance

minc1

Read MINC1 format images

Minc1File(mincfile)	Class to wrap MINC1 format opened netcdf object
Minc1Image(dataobj, affine[, header, extra, ...])	Class for MINC1 format images
MincError	Error when reading MINC files
MincFile(*args, **kwargs)	Deprecated alternative name for Minc1File
MincHeader([data_dtype, shape, zooms])	Class to contain header for MINC formats
MincImage(*args, **kwargs)	Deprecated alternative name for Minc1Image
MincImageArrayProxy(minc_file)	MINC implementation of array proxy protocol

Minc1File

class nibabel.minc1.**Minc1File**(*mincfile*)
Bases: `object`

Class to wrap MINC1 format opened netcdf object

Although it has some of the same methods as a `Header`, we use this only when reading a MINC file, to pull out useful header information, and for the method of reading the data out

__init__(*mincfile*)

get_affine()

get_data_dtype()

get_data_shape()

get_scaled_data(*sliceobj=()*)
Return scaled data for slice definition *sliceobj*
Parametersslicesobj : tuple, optional
slice definition. If not specified, return whole array
Returnsscaled_arr : array
array from minc file with scaling applied

get_zooms()
Get real-world sizes of voxels

Minc1Image

class nibabel.minc1.**Minc1Image**(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)
Bases: *nibabel.spatialimages.SpatialImage*

Class for MINC1 format images

The MINC1 image class uses the default header type, rather than a specific MINC header type - and reads the relevant information from the MINC file on load.

Initialize image

The image is a combination of (array, affine matrix, header), with optional metadata in *extra*, and filename / file-like objects contained in the *file_map* mapping.

Parametersdataobj : object

Object containg image data. It should be some object that retuns an array from `np.asanyarray`. It should have a `shape` attribute or property

affine : None or (4,4) array-like

homogenous affine giving relationship between voxel coordinates and world coordinates. Affine can also be None. In this case, `obj.affine` also returns None, and the affine as written to disk will depend on the file format.

header : None or mapping or header instance, optional

metadata for this image format

extra : None or mapping, optional

metadata to associate with image that cannot be stored in the metadata of this image type

file_map : mapping, optional

mapping giving file information for this image format

__init__(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)
Initialize image

The image is a combination of (array, affine matrix, header), with optional metadata in *extra*, and filename / file-like objects contained in the *file_map* mapping.

Parametersdataobj : object
Object containg image data. It should be some object that retuns an array from `np.asanyarray`. It should have a `shape` attribute or property
affine : None or (4,4) array-like
homogenous affine giving relationship between voxel coordinates and world coordinates. Affine can also be None. In this case, `obj.affine` also returns None, and the affine as written to disk will depend on the file format.
header : None or mapping or header instance, optional
metadata for this image format
extra : None or mapping, optional
metadata to associate with image that cannot be stored in the metadata of this image type
file_map : mapping, optional
mapping giving file information for this image format

ImageArrayProxy
alias of *MincImageArrayProxy*

files_types = (('image', '.mnc'),)

classmethod from_file_map(*klass*, *file_map*)

header_class
alias of *MincHeader*

MincError

class nibabel.minc1.**MincError**
Bases: exceptions.Exception

Error when reading MINC files

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

MincFile

class nibabel.minc1.**MincFile**(**args*, ***kwargs*)
Bases: *nibabel.deprecated.FutureWarningMixin*, *nibabel.minc1.Minc1File*

Deprecated alternative name for Minc1File

__init__(**args*, ***kwargs*)

warn_message = 'MincFile is deprecated; please use Minc1File instead'

MincHeader

class nibabel.minc1.**MincHeader**(*data_dtype=<type 'numpy.float32'>*, *shape=(0,)*, *zooms=None*)
Bases: *nibabel.spatialimages.Header*

Class to contain header for MINC formats

__init__(*data_dtype=<type 'numpy.float32'>*, *shape=(0,)*, *zooms=None*)

data_from_fileobj(*fileobj*)
See Header class for an implementation we can't use

data_layout = 'C'

data_to_fileobj(*data*, *fileobj*, *rescale=True*)
See Header class for an implementation we can't use

MincImage

class nibabel.minc1.**MincImage**(**args*, ***kwargs*)
Bases: *nibabel.deprecated.FutureWarningMixin*, *nibabel.minc1.Minc1Image*

Deprecated alternative name for Minc1Image

__init__(**args*, ***kwargs*)

warn_message = 'MincImage is deprecated; please use Minc1Image instead'

MincImageArrayProxy

class nibabel.minc1.**MincImageArrayProxy**(*minc_file*)
Bases: object

MINC implementation of array proxy protocol

The array proxy allows us to freeze the passed fileobj and header such that it returns the expected data array.

__init__(*minc_file*)

is_proxy

shape

minc2

Preliminary MINC2 support

Use with care; I haven't tested this against a wide range of MINC files.

If you have a file that isn't read correctly, please send an example.

Test reading with something like:

```
import nibabel as nib
img = nib.load('my_funny.mnc')
data = img.get_data()
print(data.mean())
print(data.max())
print(data.min())
```

and compare against command line output of:

```
mincstats my_funny.mnc
```

Hdf5Bunch(var)	Make object for accessing attributes of variable
Minc2File(mincfile)	Class to wrap MINC2 format file
Minc2Image(dataobj, affine[, header, extra, ...])	Class for MINC2 images

Hdf5Bunch

class nibabel.minc2.**Hdf5Bunch**(*var*)
Bases: object

Make object for accessing attributes of variable

__init__(*var*)

Minc2File

class nibabel.minc2.**Minc2File**(*mincfile*)
Bases: *nibabel.minc1.Minc1File*

Class to wrap MINC2 format file

Although it has some of the same methods as a Header, we use this only when reading a MINC2 file, to pull out useful header information, and for the method of reading the data out

__init__(*mincfile*)

get_data_dtype()

get_data_shape()

get_scaled_data(*sliceobj=()*)
Return scaled data for slice definition *sliceobj*
Parameterssliceobj : tuple, optional
slice definition. If not specified, return whole array
Returnsscaled_arr : array
array from minc file with scaling applied

Minc2Image

class nibabel.minc2.**Minc2Image**(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)
Bases: *nibabel.minc1.Minc1Image*

Class for MINC2 images

The MINC2 image class uses the default header type, rather than a specific MINC header type - and reads the relevant information from the MINC file on load.

Initialize image

The image is a combination of (array, affine matrix, header), with optional metadata in *extra*, and filename / file-like objects contained in the *file_map* mapping.

Parametersdataobj : object

Object containg image data. It should be some object that retuns an array from `np.asanyarray`. It should have a `shape` attribute or property

affine : None or (4,4) array-like

homogenous affine giving relationship between voxel coordinates and world coordinates. Affine can also be None. In this case, `obj.affine` also returns None, and the affine as written to disk will depend on the file format.

header : None or mapping or header instance, optional

metadata for this image format

extra : None or mapping, optional

metadata to associate with image that cannot be stored in the metadata of this image type

file_map : mapping, optional

mapping giving file information for this image format

__init__(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)
Initialize image

The image is a combination of (array, affine matrix, header), with optional metadata in *extra*, and filename / file-like objects contained in the *file_map* mapping.
Parametersdataobj : object
Object containg image data. It should be some object that retuns an array from `np.asanyarray`. It should have a `shape` attribute or property
affine : None or (4,4) array-like
homogenous affine giving relationship between voxel coordinates and world coordinates. Affine can also be None. In this case, `obj.affine` also returns None, and the affine as written to disk will depend on the file format.

header : None or mapping or header instance, optional
metadata for this image format
extra : None or mapping, optional
metadata to associate with image that cannot be stored in the metadata of this image type
file_map : mapping, optional
mapping giving file information for this image format

classmethod **from_file_map**(*klass*, *file_map*)

nicom

DICOM reader

csareader	CSA header reader from SPM spec
dicomreaders	
dicomwrappers	Classes to wrap DICOM objects and files
dwiparams	Process diffusion imaging parameters
structreader	Stream-like reader for packed data

Module: nicom.csareader

CSA header reader from SPM spec

CSAError	
CSAReadError	
get_acq_mat_txt(csa_dict)	
get_b_matrix(csa_dict)	
get_b_value(csa_dict)	
get_csa_header(dcm_data[, csa_type])	Get CSA header information from DICOM header
get_g_vector(csa_dict)	
get_ice_dims(csa_dict)	
get_n_mosaic(csa_dict)	
get_scalar(csa_dict, tag_name)	
get_slice_normal(csa_dict)	
get_vector(csa_dict, tag_name, n)	
is_mosaic(csa_dict)	Return True if the data is of Mosaic type
nt_str(s)	Strip string to first null
read(csa_str)	Read CSA header from string *csa_str*

Module: nicom.dicomreaders

DicomReadError	
mosaic_to_nii(dcm_data)	Get Nifti file from Siemens
read_mosaic_dir(dicom_path[, globber, ...])	Read all Siemens mosaic DICOMs in directory, return arrays, params
read_mosaic_dwi_dir(dicom_path[, globber, ...])	
slices_to_series(wrappers)	Sort sequence of slice wrappers into series

Module: nicom.dicomwrappers

Classes to wrap DICOM objects and files

The wrappers encapsulate the capabilities of the different DICOM formats.

They also allow dictionary-like access to named fields.

For calculated attributes, we return None where needed data is missing. It seemed strange to raise an error during attribute processing, other than an AttributeError - breaking the 'properties manifesto'. So, any processing that needs to raise an error, should be in a method, rather than in a property, or property-like thing.

MosaicWrapper(dcm_data[, csa_header, n_mosaic])	Class for Siemens mosaic format data
MultiframeWrapper(dcm_data)	Wrapper for Enhanced MR Storage SOP Class
SiemensWrapper(dcm_data[, csa_header])	Wrapper for Siemens format DICOMs
Wrapper(dcm_data)	Class to wrap general DICOM files
WrapperError	
WrapperPrecisionError	
none_or_close(val1, val2[, rtol, atol])	Match if *val1* and *val2* are both None, or are close
wrapper_from_data(dcm_data)	Create DICOM wrapper from DICOM data object
wrapper_from_file(file_like, *args, **kwargs)	Create DICOM wrapper from *file_like* object

Module: nicom.dwiparams

Process diffusion imaging parameters

- `q` is a vector in Q space
- `b` is a b value
- `g` is the unit vector along the direction of q (the gradient direction)

Thus:

b = norm(q)

g = q / norm(q)

(`norm(q)` is the Euclidean norm of `q`)

The B matrix `B` is a symmetric positive semi-definite matrix. If `q_est` is the closest q vector equivalent to the B matrix, then:

B ~ (q_est . q_est.T) / norm(q_est)

B2q(B[, tol])	Estimate q vector from input B matrix *B*
nearest_pos_semi_def(B)	Least squares positive semi-definite tensor estimation
q2bg(q_vector[, tol])	Return b value and q unit vector from q vector *q_vector*

Module: nicom.structreader

Stream-like reader for packed data

Unpacker(buf[, ptr, endian])	Class to unpack values from buffer object

Module: nicom.utils

Utilities for working with DICOM datasets

find_private_section(dcm_data, group_no, creator)	Return start element in group *group_no* given creator name *creator*

CSAError
class nibabel.nicom.csareader.**CSAError**
Bases: exceptions.Exception

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

CSAReadError
class nibabel.nicom.csareader.**CSAReadError**
Bases: *nibabel.nicom.csareader.CSAError*

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

get_acq_mat_txt
nibabel.nicom.csareader.**get_acq_mat_txt**(*csa_dict*)

get_b_matrix
nibabel.nicom.csareader.**get_b_matrix**(*csa_dict*)

get_b_value
nibabel.nicom.csareader.**get_b_value**(*csa_dict*)

get_csa_header
nibabel.nicom.csareader.**get_csa_header**(*dcm_data*, *csa_type='image'*)
Get CSA header information from DICOM header

Return None if the header does not contain CSA information of the specified *csa_type*

Parametersdcm_data : dicom.Dataset

DICOM dataset. Should implement `__getitem__` and, if initial check for presence of `dcm_data[(0x29, 0x10)]` passes, should satisfy interface for `find_private_section`.

csa_type : {'image', 'series'}, optional

Type of CSA field to read; default is 'image'

Returnscsa_info : None or dict

Parsed CSA field of *csa_type* or None, if we cannot find the CSA information.

get_g_vector
nibabel.nicom.csareader.**get_g_vector**(*csa_dict*)

get_ice_dims
nibabel.nicom.csareader.**get_ice_dims**(*csa_dict*)

get_n_mosaic
nibabel.nicom.csareader.**get_n_mosaic**(*csa_dict*)

get_scalar
nibabel.nicom.csareader.**get_scalar**(*csa_dict*, *tag_name*)

get_slice_normal
nibabel.nicom.csareader.**get_slice_normal**(*csa_dict*)

get_vector
nibabel.nicom.csareader.**get_vector**(*csa_dict*, *tag_name*, *n*)

is_mosaic
nibabel.nicom.csareader.**is_mosaic**(*csa_dict*)
Return True if the data is of Mosaic type

Parameterscsa_dict : dict

dict containing read CSA data

Returnstf : bool

True if the *dcm_data* appears to be of Siemens mosaic type, False otherwise

nt_str
nibabel.nicom.csareader.**nt_str**(*s*)
Strip string to first null

Parameterss : bytes

Returnssdash : str

s stripped to first occurence of null (0)

read
nibabel.nicom.csareader.**read**(*csa_str*)
Read CSA header from string *csa_str*

Parameterscsa_str : str

byte string containing CSA header information

Returnsheader : dict

header information as dict, where *header* has fields (at least) `type, n_tags, tags`. `header['tags']` is also a dictionary with one key, value pair for each tag in the header.

DicomReadError
class nibabel.nicom.dicomreaders.**DicomReadError**
Bases: exceptions.Exception

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

mosaic_to_nii
nibabel.nicom.dicomreaders.**mosaic_to_nii**(*dcm_data*)
Get Nifti file from Siemens

Parametersdcm_data : dicom.DataSet

DICOM header / image as read by dicom package

Returnsimg : Nifti1Image

Nifti image object

read_mosaic_dir
nibabel.nicom.dicomreaders.**read_mosaic_dir**(*dicom_path*, *globber='*.dcm'*, *check_is_dwi=False*, *dicom_kwargs=None*)
Read all Siemens mosaic DICOMs in directory, return arrays, params

Parametersdicom_path : str

path containing mosaic DICOM images

globber : str, optional

glob to apply within *dicom_path* to select DICOM files. Default is *.dcm

check_is_dwi : bool, optional

If True, raises an error if we don't find DWI information in the DICOM headers.

dicom_kwargs : None or dict

Extra keyword arguments to pass to the pydicom read_file function.

Returnsdata : 4D array

data array with last dimension being acquisition. If there were N acquisitions, each of shape (X, Y, Z), *data* will be shape (X, Y, Z, N)

affine : (4,4) array

affine relating 3D voxel space in data to RAS world space

b_values : (N,) array

b values for each acquisition. nan if we did not find diffusion information for these images.

unit_gradients : (N, 3) array

gradient directions of unit length for each acquisition. (nan, nan, nan) if we did not find diffusion information.

read_mosaic_dwi_dir
nibabel.nicom.dicomreaders.**read_mosaic_dwi_dir**(*dicom_path*, *globber='*.dcm'*, *dicom_kwargs=None*)

slices_to_series
nibabel.nicom.dicomreaders.**slices_to_series**(*wrappers*)
Sort sequence of slice wrappers into series

This follows the SPM model fairly closely

Parameterswrappers : sequence

sequence of `Wrapper` objects for sorting into volumes

Returnsseries : sequence

sequence of sequences of wrapper objects, where each sequence is wrapper objects comprising a series, sorted into slice order

MosaicWrapper
class nibabel.nicom.dicomwrappers.**MosaicWrapper**(*dcm_data*, *csa_header=None*, *n_mosaic=None*)
Bases: *nibabel.nicom.dicomwrappers.SiemensWrapper*

Class for Siemens mosaic format data

Mosaic format is a way of storing a 3D image in a 2D slice - and it's as simple as you'd imagine it would be - just storing the slices in a mosaic similar to a light-box print.

We need to allow for this when getting the data and (because of an idiosyncrasy in the way Siemens stores the images) calculating the position of the first voxel.

Adds attributes:

•n_mosaic : int

•mosaic_size : float

Initialize Siemens Mosaic wrapper

The Siemens-specific information is in the *csa_header*, either passed in here, or read from the input *dcm_data*.

Parametersdcm_data : object

object should allow 'get' and '__getitem__' access. If *csa_header* is None, it should also be possible for to extract a CSA header from *dcm_data*. Usually this will be a `dicom.dataset.Dataset` object resulting from reading a DICOM file. A dict should also work.

csa_header : None or mapping, optional

mapping giving values for Siemens CSA image sub-header.

n_mosaic : None or int, optional

number of images in mosaic. If None, try to get this number from *csa_header*. If this fails, raise an error

__init__(*dcm_data*, *csa_header=None*, *n_mosaic=None*)
Initialize Siemens Mosaic wrapper

The Siemens-specific information is in the *csa_header*, either passed in here, or read from the input *dcm_data*.

Parametersdcm_data : object

object should allow 'get' and '__getitem__' access. If *csa_header* is None, it should also be possible for to extract a CSA header from *dcm_data*. Usually this will be a `dicom.dataset.Dataset` object resulting from reading a DICOM file. A dict should also work.

csa_header : None or mapping, optional
mapping giving values for Siemens CSA image sub-header.
n_mosaic : None or int, optional
number of images in mosaic. If None, try to get this number from *csa_header*. If this fails, raise an error

get_data()
Get scaled image data from DICOMs

Resorts data block from mosaic to 3D
Returnsdata : array
array with data as scaled from any scaling in the DICOM fields.

Notes

The apparent image in the DICOM file is a 2D array that consists of blocks, that are the output 2D slices. Let's call the original array the *slab*, and the contained slices *slices*. The slices are of pixel dimension `n_slice_rows` x `n_slice_cols`. The slab is of pixel dimension `n_slab_rows` x `n_slab_cols`. Because the arrangement of blocks in the slab is defined as being square, the number of blocks per slab row and slab column is the same. Let `n_blocks` be the number of blocks contained in the slab. There is also `n_slices` - the number of slices actually collected, some number <= `n_blocks`. We have the value `n_slices` from the 'NumberOfImagesInMosaic' field of the Siemens private (CSA) header. `n_row_blocks` and `n_col_blocks` are therefore given by `ceil(sqrt(n_slices))`, and `n_blocks` is `n_row_blocks ** 2`. Also `n_slice_rows == n_slab_rows / n_row_blocks`, etc. Using these numbers we can therefore reconstruct the slices from the 2D DICOM pixel array.

image_position()
Return position of first voxel in data block

Adjusts Siemens mosaic position vector for bug in mosaic format position. See `dicom_mosaic` in doc/theory for details.
ParametersNone :
Returnsimg_pos : (3,) array
position in mm of voxel (0,0,0) in Mosaic array

image_shape()
Return image shape as returned by `get_data()`

is_mosaic = True

MultiframeWrapper
class nibabel.nicom.dicomwrappers.**MultiframeWrapper**(*dcm_data*)
Bases: *nibabel.nicom.dicomwrappers.Wrapper*

Wrapper for Enhanced MR Storage SOP Class

tested with Philips' Enhanced DICOM implementation

Attributesis_multiframe : boolean

Identifies *dcmdata* as multi-frame

frames : sequence

A sequence of `dicom.dataset.Dataset` objects populated by the `dicom.dataset.Dataset.PerFrameFunctionalGroupsSequence` attribute

shared : object

The first (and only) `dicom.dataset.Dataset` object from a `dicom.dataset.Dataset.SharedFunctionalgroupSequence`.

Methodsimage_shape(self) :

image_orient_patient(self) :

voxel_sizes(self) :

image_position(self) :

series_signature(self) :

get_data(self) :

Initializes MultiframeWrapper

Parametersdcm_data : object

object should allow 'get' and '__getitem__' access. Usually this will be a `dicom.dataset.Dataset` object resulting from reading a DICOM file, but a dictionary should also work.

__init__(*dcm_data*)

Initializes MultiframeWrapper

Parametersdcm_data : object

object should allow 'get' and '__getitem__' access. Usually this will be a `dicom.dataset.Dataset` object resulting from reading a DICOM file, but a dictionary should also work.

get_data()

image_orient_patient()

Note that this is _not_ LR flipped

image_position()

image_shape()

The array shape as it will be returned by `get_data()`

is_multiframe = True

series_signature()

voxel_sizes()

Get i, j, k voxel sizes

SiemensWrapper

class `nibabel.nicom.dicomwrappers.`**SiemensWrapper**(*dcm_data*, *csa_header=None*)

Bases: *nibabel.nicom.dicomwrappers.Wrapper*

Wrapper for Siemens format DICOMs

Adds attributes:

- csa_header : mapping
- b_matrix : (3,3) array
- q_vector : (3,) array

Initialize Siemens wrapper

The Siemens-specific information is in the *csa_header*, either passed in here, or read from the input *dcm_data*.

Parametersdcm_data : object

object should allow 'get' and '__getitem__' access. If *csa_header* is None, it should also be possible to extract a CSA header from *dcm_data*. Usually this will be a `dicom.dataset.Dataset` object resulting from reading a DICOM file. A dict should also work.

csa_header : None or mapping, optional

mapping giving values for Siemens CSA image sub-header. If None, we try and read the CSA information from *dcm_data*. If this fails, we fall back to an empty dict.

__init__(*dcm_data*, *csa_header=None*)

Initialize Siemens wrapper

The Siemens-specific information is in the *csa_header*, either passed in here, or read from the input *dcm_data*.

Parametersdcm_data : object

object should allow 'get' and '__getitem__' access. If *csa_header* is None, it should also be possible to extract a CSA header from *dcm_data*. Usually this will be a `dicom.dataset.Dataset` object resulting from reading a DICOM file. A dict should also work.

csa_header : None or mapping, optional

mapping giving values for Siemens CSA image sub-header. If None, we try and read the CSA information from *dcm_data*. If this fails, we fall back to an empty dict.

b_matrix()

Get DWI B matrix referring to voxel space

ParametersNone :

ReturnsB : (3,3) array or None

B matrix in *voxel* orientation space. Returns None if this is not a Siemens header with the required information. We return None if this is a b0 acquisition

is_csa = True

q_vector()

Get DWI q vector referring to voxel space

ParametersNone :

Returnsq: (3,) array :

Estimated DWI q vector in *voxel* orientation space. Returns None if this is not (detectably) a DWI

series_signature()

Add ICE dims from CSA header to signature

slice_normal()

Wrapper

class `nibabel.nicom.dicomwrappers.`**Wrapper**(*dcm_data*)

Bases: `object`

Class to wrap general DICOM files

Methods:

- get_affine()
- get_data()
- get_pixel_array()
- is_same_series(other)

•__getitem__ : return attributes from *dcm_data*

•get(key[, default]) - as usual given __getitem__ above

Attributes and things that look like attributes:

•dcm_data : object

•image_shape : tuple

•image_orient_patient : (3,2) array

•slice_normal : (3,) array

•rotation_matrix : (3,3) array

•voxel_sizes : tuple length 3

•image_position : sequence length 3

•slice_indicator : float

•series_signature : tuple

Initialize wrapper

Parametersdcm_data : object

object should allow 'get' and '__getitem__' access. Usually this will be a `dicom.dataset.Dataset` object resulting from reading a DICOM file, but a dictionary should also work.

__init__(*dcm_data*)

Initialize wrapper

Parametersdcm_data : object

object should allow 'get' and '__getitem__' access. Usually this will be a `dicom.dataset.Dataset` object resulting from reading a DICOM file, but a dictionary should also work.

b_matrix = None

b_value()

Return b value for diffusion or None if not available

b_vector()

Return b vector for diffusion or None if not available

get(*key*, *default=None*)

Get values from underlying dicom data

get_affine()

Return mapping between voxel and DICOM coordinate system

ParametersNone :

Returnsaff : (4,4) affine

Affine giving transformation between voxels in data array and mm in the DICOM patient coordinate system.

get_data()

Get scaled image data from DICOMs

We return the data as DICOM understands it, first dimension is rows, second dimension is columns

Returnsdata : array

array with data as scaled from any scaling in the DICOM fields.

get_pixel_array()
Return unscaled pixel array from DICOM

image_orient_patient()
Note that this is _not_ LR flipped

image_position()
Return position of first voxel in data block
ParametersNone :
Returnsimg_pos : (3,) array
position in mm of voxel (0,0) in image array

image_shape()
The array shape as it will be returned by `get_data()`

instance_number()
Just because we use this a lot for sorting

is_csa = False

is_mosaic = False

is_multiframe = False

is_same_series(*other*)
Return True if *other* appears to be in same series
Parametersother : object
object with `series_signature` attribute that is a mapping. Usually it's a `Wrapper` or sub-class instance.
Returnstf : bool
True if *other* might be in the same series as *self*, False otherwise.

q_vector = None

rotation_matrix()
Return rotation matrix between array indices and mm

Note that we swap the two columns of the 'ImageOrientPatient' when we create the rotation matrix. This is takes into account the slightly odd ij transpose construction of the DICOM orientation fields - see doc/theory/dicom_orientaiton.rst.

series_signature()
Signature for matching slices into series

We use *signature* in `self.is_same_series(other)`.
Returnssignature : dict
with values of 2-element sequences, where first element is value, and second element is function to compare this value with another. This allows us to pass things like arrays, that might need to be `allclose` instead of equal

slice_indicator()
A number that is higher for higher slices in Z

Comparing this number between two adjacent slices should give a difference equal to the voxel size in Z.

See doc/theory/dicom_orientation for description

slice_normal()

voxel_sizes()
voxel sizes for array as returned by `get_data()`

WrapperError
class nibabel.nicom.dicomwrappers.**WrapperError**
Bases: exceptions.Exception

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

WrapperPrecisionError
class nibabel.nicom.dicomwrappers.**WrapperPrecisionError**
Bases: *nibabel.nicom.dicomwrappers.WrapperError*

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

none_or_close
nibabel.nicom.dicomwrappers.**none_or_close**(*val1*, *val2*, *rtol=1e-05*, *atol=1e-06*)
Match if *val1* and *val2* are both None, or are close

Parametersval1 : None or array-like

val2 : None or array-like

rtol : float, optional

Relative tolerance; see np.allclose

atol : float, optional

Absolute tolerance; see np.allclose

Returnstf : bool

True iff (both *val1* and *val2* are None) or (*val1* and *val2* are close arrays, as detected by np.allclose with parameters *rtol* and *atal*).

Examples

```
>>> none_or_close(None, None)
True
>>> none_or_close(1, None)
False
>>> none_or_close(None, 1)
False
>>> none_or_close([1,2], [1,2])
True
>>> none_or_close([0,1], [0,2])
False
```

wrapper_from_data
nibabel.nicom.dicomwrappers.**wrapper_from_data**(*dcm_data*)
Create DICOM wrapper from DICOM data object

Parametersdcm_data : dicom.dataset.Dataset instance or similar

Object allowing attribute access, with DICOM attributes. Probably a dataset as read by pydicom.

Returnsdcm_w : dicomwrappers.Wrapper or subclass

DICOM wrapper corresponding to DICOM data type

wrapper_from_file
nibabel.nicom.dicomwrappers.**wrapper_from_file**(*file_like*, **args*, ***kwargs*)
Create DICOM wrapper from *file_like* object

Parametersfile_like : object

filename string or file-like object, pointing to a valid DICOM file readable by `pydicom`

***args** : positional

args to `dicom.read_file` command.

****kwargs** : keyword

args to `dicom.read_file` command. `force=True` might be a likely keyword argument.

Returnsdcm_w : `dicomwrappers.Wrapper` or subclass

DICOM wrapper corresponding to DICOM data type

B2q
nibabel.nicom.dwiparams.**B2q**(*B*, *tol=None*)
Estimate q vector from input B matrix *B*

We require that the input *B* is symmetric positive definite.

Because the solution is a square root, the sign of the returned vector is arbitrary. We set the vector to have a positive x component by convention.

ParametersB : (3,3) array-like

B matrix - symmetric. We do not check the symmetry.

tol : None or float

absolute tolerance below which to consider eigenvalues of the B matrix to be small enough not to worry about them being negative, in check for positive semi-definite-ness. None (default) results in a fairly tight numerical threshold proportional to the maximum eigenvalue

Returnsq : (3,) vector

Estimated q vector from B matrix *B*

nearest_pos_semi_def
nibabel.nicom.dwiparams.**nearest_pos_semi_def**(*B*)
Least squares positive semi-definite tensor estimation

Reference: Niethammer M, San Jose Estepar R, Bouix S, Shenton M, Westin CF. On diffusion tensor estimation. Conf Proc IEEE Eng Med Biol Soc. 2006;1:2622-5. PubMed PMID: 17946125; PubMed Central PMCID: PMC2791793.

ParametersB : (3,3) array-like

B matrix - symmetric. We do not check the symmetry.

Returnsnpds : (3,3) array

Estimated nearest positive semi-definite array to matrix *B*.

Examples

```
>>> B = np.diag([1, 1, -1])
>>> nearest_pos_semi_def(B)
array([[ 0.75,  0.  ,  0.  ],
       [ 0.  ,  0.75,  0.  ],
       [ 0.  ,  0.  ,  0.  ]])
```

q2bg

nibabel.nicom.dwiparams.**q2bg**(*q_vector*, *tol=1e-05*)

Return b value and q unit vector from q vector *q_vector*

Parametersq_vector : (3,) array-like

q vector

tol : float, optional

q vector L2 norm below which *q_vector* considered to be *b_value* of zero, and therefore *g_vector* also considered to zero.

Returnsb_value : float

L2 Norm of *q_vector* or 0 if L2 norm < *tol*

g_vector : shape (3,) ndarray

q_vector / *b_value* or 0 if L2 norma < *tol*

Examples

```
>>> q2bg([1, 0, 0])
(1.0, array([ 1.,  0.,  0.]))
>>> q2bg([0, 10, 0])
(10.0, array([ 0.,  1.,  0.]))
>>> q2bg([0, 0, 0])
(0.0, array([ 0.,  0.,  0.]))
```

Unpacker

class nibabel.nicom.structreader.**Unpacker**(*buf*, *ptr=0*, *endian=None*)

Bases: object

Class to unpack values from buffer object

The buffer object is usually a string. Caches compiled `struct` format strings so that repeated unpacking with the same format string should be faster than using `struct.unpack` directly.

Examples

```
>>> a = b'1234567890'
>>> upk = Unpacker(a)
>>> upk.unpack('2s') == (b'12',)
True
>>> upk.unpack('2s') == (b'34',)
True
>>> upk.ptr
```

```
4
>>> upk.read(3) == b'567'
True
>>> upk.ptr
7
```

Initialize unpacker

Parametersbuf : buffer

object implementing buffer protocol (e.g. str)

ptr : int, optional

offset at which to begin reads from *buf*

endian : None or str, optional

endian code to prepend to format, as for `unpack` endian codes. None (the default) corresponds to the default behavior of `struct` - assuming system endian unless you specify the byte order specifically in the format string passed to `unpack`

__init__(*buf*, *ptr=0*, *endian=None*)

Initialize unpacker

Parametersbuf : buffer
object implementing buffer protocol (e.g. str)
ptr : int, optional
offset at which to begin reads from *buf*
endian : None or str, optional
endian code to prepend to format, as for `unpack` endian codes. None (the default) corresponds to the default behavior of `struct` - assuming system endian unless you specify the byte order specifically in the format string passed to `unpack`

read(*n_bytes=-1*)

Return byte string of length *n_bytes* at current position

Returns sub-string from `self.buf` and updates `self.ptr` to the position after the read data.
Parametersn_bytes : int, optional
number of bytes to read. Can be -1 (the default) in which case we return all the remaining bytes in `self.buf`
Returnss : byte string

unpack(*fmt*)

Unpack values from contained buffer

Unpacks values from `self.buf` and updates `self.ptr` to the position after the read data.
Parametersfmt : str
format string as for `unpack`
Returnsvalues : tuple
values as unpacked from `self.buf` according to *fmt*

find_private_section

nibabel.nicom.utils.**find_private_section**(*dcm_data*, *group_no*, *creator*)

Return start element in group *group_no* given creator name *creator*

Private attribute tags need to announce where they will go by putting a tag in the private group (here *group_no*) between elements 1 and 0xFF. The element number of these tags give the start of matching information, in the higher tag numbers.

Parametersdcm_data : dicom `dataset`

Iterating over *dcm_data* produces `elements` with attributes `tag`, `VR`, `value`

group_no : int

Group number in which to search

creator : str or bytes or regex

Name of section - e.g. 'SIEMENS CSA HEADER' - or regex to search for section name. Regex used via `creator.search(element_value)` where `element_value` is the value of the data element.

Returnselement_start : int

Element number at which named section starts

nifti1

Read / write access to NIfTI1 image format

NIfTI1 format defined at http://nifti.nimh.nih.gov/nifti-1/

Nifti1Extension(code, content)	Baseclass for NIfTI1 header extensions.
Nifti1Extensions	Simple extension collection, implemented as a list-subclass.
Nifti1Header([binaryblock, endianness, ...])	Class for NIfTI1 header
Nifti1Image(dataobj, affine[, header, ...])	Class for single file NIfTI1 format image
Nifti1Pair(dataobj, affine[, header, extra, ...])	Class for NIfTI1 format image, header pair
Nifti1PairHeader([binaryblock, endianness, ...])	Class for NIfTI1 pair header
load(filename)	Load NIfTI1 single or pair from *filename*
save(img, filename)	Save NIfTI1 single or pair to *filename*

Nifti1Extension

class `nibabel.nifti1.`**`Nifti1Extension`**(*code*, *content*)

Bases: `object`

Baseclass for NIfTI1 header extensions.

This class is sufficient to handle very simple text-based extensions, such as *comment*. More sophisticated extensions should/will be supported by dedicated subclasses.

Parameterscode : int|str

Canonical extension code as defined in the NIfTI standard, given either as integer or corresponding label (see `extension_codes`)

content : str

Extension content as read from the NIfTI file header. This content is converted into a runtime representation.

`__init__`(*code*, *content*)

Parameterscode : int|str

Canonical extension code as defined in the NIfTI standard, given either as integer or corresponding label (see `extension_codes`)

content : str

Extension content as read from the NIfTI file header. This content is converted into a runtime representation.

get_code()
Return the canonical extension type code.

get_content()
Return the extension content in its runtime representation.

get_sizeondisk()
Return the size of the extension in the NIfTI file.

write_to(*fileobj*, *byteswap*)
Write header extensions to fileobj

Write starts at fileobj current file position.
Parametersfileobj : file-like object
Should implement `write` method
byteswap : boolean
Flag if byteswapping the data is required.
ReturnsNone :

Nifti1Extensions

class nibabel.nifti1.**Nifti1Extensions**
Bases: `list`

Simple extension collection, implemented as a list-subclass.

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

count(*ecode*)
Returns the number of extensions matching a given *ecode*.
Parameterscode : int | str
The ecode can be specified either literal or as numerical value.

classmethod from_fileobj(*klass*, *fileobj*, *size*, *byteswap*)
Read header extensions from a fileobj
Parametersfileobj : file-like object
We begin reading the extensions at the current file position
size : int
Number of bytes to read. If negative, fileobj will be read till its end.
byteswap : boolean
Flag if byteswapping the read data is required.
ReturnsAn extension list. This list might be empty in case not extensions :

were present in fileobj. :

get_codes()
Return a list of the extension code of all available extensions

get_sizeondisk()
Return the size of the complete header extensions in the NIfTI file.

write_to(*fileobj*, *byteswap*)
Write header extensions to fileobj

Write starts at fileobj current file position.
Parametersfileobj : file-like object
Should implement `write` method
byteswap : boolean

Flag if byteswapping the data is required.

ReturnsNone :

Nifti1Header

class nibabel.nifti1.**Nifti1Header**(*binaryblock=None*, *endianness=None*, *check=True*, *extensions=()*)

Bases: *nibabel.spm99analyze.SpmAnalyzeHeader*

Class for NIfTI1 header

The NIfTI1 header has many more coded fields than the simpler Analyze variants. NIfTI1 headers also have extensions.

Nifti allows the header to be a separate file, as part of a nifti image / header pair, or to precede the data in a single file. The object needs to know which type it is, in order to manage the voxel offset pointing to the data, extension reading, and writing the correct magic string.

This class handles the header-preceding-data case.

Initialize header from binary data block and extensions

__init__(*binaryblock=None*, *endianness=None*, *check=True*, *extensions=()*)

Initialize header from binary data block and extensions

copy()

Return copy of header

Take reference to extensions as well as copy of header contents

classmethod default_structarr(*klass*, *endianness=None*)

Create empty header binary block with given endianness

exts_klass

alias of *Nifti1Extensions*

classmethod from_fileobj(*klass*, *fileobj*, *endianness=None*, *check=True*)

classmethod from_header(*klass*, *header=None*, *check=True*)

Class method to create header from another header

Extend Analyze header copy by copying extensions from other Nifti types.

Parametersheader : Header instance or mapping

a header of this class, or another class of header for conversion to this type

check : {True, False}

whether to check header for integrity

Returnshdr : header instance

fresh header instance of our own class

get_best_affine()

Select best of available transforms

get_data_shape()

Get shape of data

Notes

Applies freesurfer hack for large vectors described in issue 100 and save_nifti.m.

Allows for freesurfer hack for 7th order icosahedron surface described in issue 309, load_nifti.m, and save_nifti.m.

Examples

```
>>> hdr = Nifti1Header()
>>> hdr.get_data_shape()
(0,)
>>> hdr.set_data_shape((1,2,3))
>>> hdr.get_data_shape()
(1, 2, 3)
```

Expanding number of dimensions gets default zooms

```
>>> hdr.get_zooms()
(1.0, 1.0, 1.0)
```

get_dim_info()

Gets NIfTI MRI slice etc dimension information

Returnsfreq : {None,0,1,2}
Which data array axis is frequency encode direction
phase : {None,0,1,2}
Which data array axis is phase encode direction
slice : {None,0,1,2}
Which data array axis is slice encode direction
where ‘‘data array‘‘ is the array returned by ‘‘get_data‘‘ :

Because NIfTI1 files are natively Fortran indexed: :
0 is fastest changing in file 1 is medium changing in file 2 is slowest changing in file
‘‘None‘‘ means the axis appears not to be specified. :

Examples

See set_dim_info function

get_intent(*code_repr='label'*)

Get intent code, parameters and name

Parameterscode_repr : string
string giving output form of intent code representation. Default is ‘label’; use ‘code’ for integer representation.
Returnscode : string or integer
intent code, or string describing code
parameters : tuple
parameters for the intent
name : string
intent name

Examples

```
>>> hdr = Nifti1Header()
>>> hdr.set_intent('t test', (10,), name='some score')
>>> hdr.get_intent()
```

```
('t test', (10.0,), 'some score')
>>> hdr.get_intent('code')
(3, (10.0,), 'some score')
```

get_n_slices()
Return the number of slices

get_qform(*coded=False*)
Return 4x4 affine matrix from qform parameters in header
Parameterscoded : bool, optional
If True, return {affine or None}, and qform code. If False, just return affine. {affine or None} means, return None if qform code == 0, and affine otherwise.
Returnsaffine : None or (4,4) ndarray
If *coded* is False, always return affine reconstructed from qform quaternion. If *coded* is True, return None if qform code is 0, else return the affine.
code : int
Qform code. Only returned if *coded* is True.

get_qform_quaternion()
Compute quaternion from b, c, d of quaternion

Fills a value by assuming this is a unit quaternion

get_sform(*coded=False*)
Return 4x4 affine matrix from sform parameters in header
Parameterscoded : bool, optional
If True, return {affine or None}, and sform code. If False, just return affine. {affine or None} means, return None if sform code == 0, and affine otherwise.
Returnsaffine : None or (4,4) ndarray
If *coded* is False, always return affine from sform fields. If *coded* is True, return None if sform code is 0, else return the affine.
code : int
Sform code. Only returned if *coded* is True.

get_slice_duration()
Get slice duration
Returnsslice_duration : float
time to acquire one slice

Notes

The NIfTI1 spec appears to require the slice dimension to be defined for slice_duration to have meaning.

Examples

```
>>> hdr = Nifti1Header()
>>> hdr.set_dim_info(slice=2)
>>> hdr.set_slice_duration(0.3)
>>> print("%0.1f" % hdr.get_slice_duration())
0.3
```

get_slice_times()
Get slice times from slice timing information
Returnsslice_times : tuple

Times of acquisition of slices, where 0 is the beginning of the acquisition, ordered by position in file. nifti allows slices at the top and bottom of the volume to be excluded from the standard slice timing specification, and calls these "padding slices". We give padding slices `None` as a time of acquisition

Examples

```
>>> hdr = Nifti1Header()
>>> hdr.set_dim_info(slice=2)
>>> hdr.set_data_shape((1, 1, 7))
>>> hdr.set_slice_duration(0.1)
>>> hdr['slice_code'] = slice_order_codes['sequential increasing']
>>> slice_times = hdr.get_slice_times()
>>> np.allclose(slice_times, [0, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6])
True
```

get_slope_inter()

Get data scaling (slope) and DC offset (intercept) from header data

Returnsslope : None or float
scaling (slope). None if there is no valid scaling from these fields

inter : None or float
offset (intercept). None if there is no valid scaling or if offset is not finite.

Examples

```
>>> hdr = Nifti1Header()
>>> hdr.get_slope_inter()
(1.0, 0.0)
>>> hdr['scl_slope'] = 0
>>> hdr.get_slope_inter()
(None, None)
>>> hdr['scl_slope'] = np.nan
>>> hdr.get_slope_inter()
(None, None)
>>> hdr['scl_slope'] = 1
>>> hdr['scl_inter'] = 1
>>> hdr.get_slope_inter()
(1.0, 1.0)
>>> hdr['scl_inter'] = np.inf
>>> hdr.get_slope_inter()
Traceback (most recent call last):
    ...
HeaderDataError: Valid slope but invalid intercept inf
```

get_xyzt_units()

has_data_intercept = True

has_data_slope = True

is_single = True

pair_magic = 'ni1'

pair_vox_offset = 0

quaternion_threshold = -3.5762786865234375e-07

set_data_shape(*shape*)
Set shape of data

If `ndims == len(shape)` then we set zooms for dimensions higher than `ndims` to 1.0

Nifti1 images can have up to seven dimensions. For FreeSurfer-variant Nifti surface files, the first dimension is assumed to correspond to vertices/nodes on a surface, and dimensions two and three are constrained to have depth of 1. Dimensions 4-7 are constrained only by type bounds.

Parametersshape : sequence
sequence of integers specifying data array shape

Notes

Applies freesurfer hack for large vectors described in issue 100 and save_nifti.m.

Allows for freesurfer hack for 7th order icosahedron surface described in issue 309, load_nifti.m, and save_nifti.m.

The Nifti1 standard header allows for the following "point set" definition of a surface, not currently implemented in nibabel.

```
To signify that the vector value at each voxel is really a
spatial coordinate (e.g., the vertices or nodes of a surface mesh):
  - dataset must have a 5th dimension
  - intent_code must be NIFTI_INTENT_POINTSET
  - dim[0] = 5
  - dim[1] = number of points
  - dim[2] = dim[3] = dim[4] = 1
  - dim[5] must be the dimensionality of space (e.g., 3 => 3D space).
  - intent_name may describe the object these points come from
    (e.g., "pial", "gray/white" , "EEG", "MEG").
```

set_dim_info(*freq=None*, *phase=None*, *slice=None*)
Sets nifti MRI slice etc dimension information

Parametersfreq : {None, 0, 1, 2}
axis of data array referring to frequency encoding
phase : {None, 0, 1, 2}
axis of data array referring to phase encoding
slice : {None, 0, 1, 2}
axis of data array referring to slice encoding
''None'' means the axis is not specified. :

Notes

This is stored in one byte in the header

Examples

```
>>> hdr = Nifti1Header()
>>> hdr.set_dim_info(1, 2, 0)
>>> hdr.get_dim_info()
(1, 2, 0)
```

```
>>> hdr.set_dim_info(freq=1, phase=2, slice=0)
>>> hdr.get_dim_info()
(1, 2, 0)
>>> hdr.set_dim_info()
>>> hdr.get_dim_info()
(None, None, None)
>>> hdr.set_dim_info(freq=1, phase=None, slice=0)
>>> hdr.get_dim_info()
(1, None, 0)
```

set_intent(*code*, *params=()*, *name=''*)

Set the intent code, parameters and name

If parameters are not specified, assumed to be all zero. Each intent code has a set number of parameters associated. If you specify any parameters, then it will need to be the correct number (e.g the "f test" intent requires 2). However, parameters can also be set in the file data, so we also allow not setting any parameters (empty parameter tuple).

Parameterscode : integer or string
code specifying nifti intent

params : list, tuple of scalars
parameters relating to intent (see intent_codes) defaults to (). Unspecified parameters are set to 0.0

name : string
intent name (description). Defaults to ''

ReturnsNone :

Examples

```
>>> hdr = Nifti1Header()
>>> hdr.set_intent(0) # unknown code
>>> hdr.set_intent('z score')
>>> hdr.get_intent()
('z score', (), '')
>>> hdr.get_intent('code')
(5, (), '')
>>> hdr.set_intent('t test', (10,), name='some score')
>>> hdr.get_intent()
('t test', (10.0,), 'some score')
>>> hdr.set_intent('f test', (2, 10), name='another score')
>>> hdr.get_intent()
('f test', (2.0, 10.0), 'another score')
>>> hdr.set_intent('f test')
>>> hdr.get_intent()
('f test', (0.0, 0.0), '')
```

set_qform(*affine*, *code=None*, *strip_shears=True*)

Set qform header values from 4x4 affine

Parametersaffine : None or 4x4 array
affine transform to write into sform. If None, only set code.

code : None, string or integer, optional
String or integer giving meaning of transform in *affine*. The default is None. If code is None, then:
•If affine is None, *code*-> 0
•If affine not None and existing qform code in header == 0, *code*-> 2 (aligned)

•If affine not None and existing qform code in header != 0, *code*-> existing qform code in header

strip_shears : bool, optional
Whether to strip shears in *affine*. If True, shears will be silently stripped. If False, the presence of shears will raise a `HeaderDataError`

Notes

The qform transform only encodes translations, rotations and zooms. If there are shear components to the *affine* transform, and *strip_shears* is True (the default), the written qform gives the closest approximation where the rotation matrix is orthogonal. This is to allow quaternion representation. The orthogonal representation enforces orthogonal axes.

Examples

```
>>> hdr = Nifti1Header()
>>> int(hdr['qform_code']) # gives 0 - unknown
0
>>> affine = np.diag([1,2,3,1])
>>> np.all(hdr.get_qform() == affine)
False
>>> hdr.set_qform(affine)
>>> np.all(hdr.get_qform() == affine)
True
>>> int(hdr['qform_code']) # gives 2 - aligned
2
>>> hdr.set_qform(affine, code='talairach')
>>> int(hdr['qform_code'])
3
>>> hdr.set_qform(affine, code=None)
>>> int(hdr['qform_code'])
3
>>> hdr.set_qform(affine, code='scanner')
>>> int(hdr['qform_code'])
1
>>> hdr.set_qform(None)
>>> int(hdr['qform_code'])
0
```

set_sform(*affine*, *code=None*)
Set sform transform from 4x4 affine

Parametersaffine : None or 4x4 array
affine transform to write into sform. If None, only set *code*

code : None, string or integer, optional
String or integer giving meaning of transform in *affine*. The default is None. If code is None, then:
•If affine is None, *code*-> 0
•If affine not None and existing sform code in header == 0, *code*-> 2 (aligned)
•If affine not None and existing sform code in header != 0, *code*-> existing sform code in header

Examples

```
>>> hdr = Nifti1Header()
>>> int(hdr['sform_code']) # gives 0 - unknown
0
>>> affine = np.diag([1,2,3,1])
>>> np.all(hdr.get_sform() == affine)
False
>>> hdr.set_sform(affine)
>>> np.all(hdr.get_sform() == affine)
True
>>> int(hdr['sform_code']) # gives 2 - aligned
2
>>> hdr.set_sform(affine, code='talairach')
>>> int(hdr['sform_code'])
3
>>> hdr.set_sform(affine, code=None)
>>> int(hdr['sform_code'])
3
>>> hdr.set_sform(affine, code='scanner')
>>> int(hdr['sform_code'])
1
>>> hdr.set_sform(None)
>>> int(hdr['sform_code'])
0
```

set_slice_duration(*duration*)
Set slice duration

Parametersduration : scalar
time to acquire one slice

Examples

See `get_slice_duration`

set_slice_times(*slice_times*)
Set slice times into *hdr*

Parametersslice_times : tuple
tuple of slice times, one value per slice tuple can include None to indicate no slice time for that slice

Examples

```
>>> hdr = Nifti1Header()
>>> hdr.set_dim_info(slice=2)
>>> hdr.set_data_shape([1, 1, 7])
>>> hdr.set_slice_duration(0.1)
>>> times = [None, 0.2, 0.4, 0.1, 0.3, 0.0, None]
>>> hdr.set_slice_times(times)
>>> hdr.get_value_label('slice_code')
'alternating decreasing'
>>> int(hdr['slice_start'])
1
```

```
>>> int(hdr['slice_end'])
5
```

set_slope_inter(*slope*, *inter=None*)
Set slope and / or intercept into header

Set slope and intercept for image data, such that, if the image data is `arr`, then the scaled image data will be `(arr * slope) + inter`

(*slope*, *inter*) of (NaN, NaN) is a signal to a containing image to set *slope*, *inter* automatically on write.

Parametersslope : None or float
If None, implies *slope* of NaN. If *slope* is None or NaN then *inter* should be None or NaN. Values of 0, Inf or -Inf raise HeaderDataError

inter : None or float, optional
Intercept. If None, implies *inter* of NaN. If *slope* is None or NaN then *inter* should be None or NaN. Values of Inf or -Inf raise HeaderDataError

set_xyzt_units(*xyz=None*, *t=None*)

single_magic = 'n+1'

single_vox_offset = 352

template_dtype = dtype([('sizeof_hdr', '<i4'), ('data_type', 'S10'), ('db_name', 'S18'), ('extents', '<i4'), ('session_error

write_to(*fileobj*)

Nifti1Image

class nibabel.nifti1.**Nifti1Image**(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)
Bases: *nibabel.nifti1.Nifti1Pair*

Class for single file NIfTI1 format image

__init__(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)

files_types = (('image', '.nii'),)

header_class
alias of *Nifti1Header*

update_header()
Harmonize header with image data and affine

Nifti1Pair

class nibabel.nifti1.**Nifti1Pair**(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)
Bases: *nibabel.analyze.AnalyzeImage*

Class for NIfTI1 format image, header pair

__init__(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)

get_qform(*coded=False*)
Return 4x4 affine matrix from qform parameters in header

Parameterscoded : bool, optional
If True, return {affine or None}, and qform code. If False, just return affine. {affine or None} means, return None if qform code == 0, and affine otherwise.

Returnsaffine : None or (4,4) ndarray

If *coded* is False, always return affine reconstructed from qform quaternion. If *coded* is True, return None if qform code is 0, else return the affine.

code : int
Qform code. Only returned if *coded* is True.

See also:

set_qform, *get_sform*

get_sform(*coded=False*)
Return 4x4 affine matrix from sform parameters in header

Parameterscoded : bool, optional
If True, return {affine or None}, and sform code. If False, just return affine. {affine or None} means, return None if sform code == 0, and affine otherwise.

Returnsaffine : None or (4,4) ndarray
If *coded* is False, always return affine from sform fields. If *coded* is True, return None if sform code is 0, else return the affine.

code : int
Sform code. Only returned if *coded* is True.

See also:

set_sform, *get_qform*

header_class
alias of *Nifti1PairHeader*

set_qform(*affine*, *code=None*, *strip_shears=True*, ***kwargs*)
Set qform header values from 4x4 affine

Parametersaffine : None or 4x4 array
affine transform to write into sform. If None, only set code.

code : None, string or integer
String or integer giving meaning of transform in *affine*. The default is None. If code is None, then:
- If affine is None, *code*-> 0
- If affine not None and existing qform code in header == 0, *code*-> 2 (aligned)
- If affine not None and existing qform code in header != 0, *code*-> existing qform code in header

strip_shears : bool, optional
Whether to strip shears in *affine*. If True, shears will be silently stripped. If False, the presence of shears will raise a `HeaderDataError`

update_affine : bool, optional
Whether to update the image affine from the header best affine after setting the qform. Must be keyword argument (because of different position in *set_qform*). Default is True

See also:

get_qform, *set_sform*

Examples

```
>>> data = np.arange(24).reshape((2,3,4))
>>> aff = np.diag([2, 3, 4, 1])
>>> img = Nifti1Pair(data, aff)
>>> img.get_qform()
array([[ 2.,  0.,  0.,  0.],
       [ 0.,  3.,  0.,  0.],
       [ 0.,  0.,  4.,  0.],
       [ 0.,  0.,  0.,  1.]])
```

```
>>> img.get_qform(coded=True)
(None, 0)
>>> aff2 = np.diag([3, 4, 5, 1])
>>> img.set_qform(aff2, 'talairach')
>>> qaff, code = img.get_qform(coded=True)
>>> np.all(qaff == aff2)
True
>>> int(code)
3
```

set_sform(*affine*, *code=None*, ***kwargs*)

Set sform transform from 4x4 affine

Parametersaffine : None or 4x4 array

affine transform to write into sform. If None, only set *code*

code : None, string or integer

String or integer giving meaning of transform in *affine*. The default is None. If code is None, then:

- If affine is None, *code*-> 0
- If affine not None and existing sform code in header == 0, *code*-> 2 (aligned)
- If affine not None and existing sform code in header != 0, *code*-> existing sform code in header

update_affine : bool, optional

Whether to update the image affine from the header best affine after setting the qform. Must be keyword argument (because of different position in *set_qform*). Default is True

See also:

get_sform, *set_qform*

Examples

```
>>> data = np.arange(24).reshape((2,3,4))
>>> aff = np.diag([2, 3, 4, 1])
>>> img = Nifti1Pair(data, aff)
>>> img.get_sform()
array([[ 2.,  0.,  0.,  0.],
       [ 0.,  3.,  0.,  0.],
       [ 0.,  0.,  4.,  0.],
       [ 0.,  0.,  0.,  1.]])
>>> saff, code = img.get_sform(coded=True)
>>> saff
array([[ 2.,  0.,  0.,  0.],
       [ 0.,  3.,  0.,  0.],
       [ 0.,  0.,  4.,  0.],
       [ 0.,  0.,  0.,  1.]])
>>> int(code)
2
>>> aff2 = np.diag([3, 4, 5, 1])
>>> img.set_sform(aff2, 'talairach')
>>> saff, code = img.get_sform(coded=True)
>>> np.all(saff == aff2)
True
>>> int(code)
3
```

update_header()

Harmonize header with image data and affine

See AnalyzeImage.update_header for more examples

Examples

```
>>> data = np.zeros((2,3,4))
>>> affine = np.diag([1.0,2.0,3.0,1.0])
>>> img = Nifti1Image(data, affine)
>>> hdr = img.header
>>> np.all(hdr.get_qform() == affine)
True
>>> np.all(hdr.get_sform() == affine)
True
```

Nifti1PairHeader

class nibabel.nifti1.**Nifti1PairHeader**(*binaryblock=None*, *endianness=None*, *check=True*, *extensions=()*)

Bases: *nibabel.nifti1.Nifti1Header*

Class for NIfTI1 pair header

Initialize header from binary data block and extensions

__init__(*binaryblock=None*, *endianness=None*, *check=True*, *extensions=()*)

Initialize header from binary data block and extensions

is_single = False

load

nibabel.nifti1.**load**(*filename*)

Load NIfTI1 single or pair from *filename*

Parametersfilename : str

filename of image to be loaded

Returnsimg : Nifti1Image or Nifti1Pair

NIfTI1 single or pair image instance

RaisesImageFileError :

if *filename* doesn't look like NIfTI1;

IOError :

if *filename* does not exist.

save

nibabel.nifti1.**save**(*img*, *filename*)

Save NIfTI1 single or pair to *filename*

Parametersfilename : str

filename to which to save image

nifti2

Read / write access to NIfTI2 image format

Format described here:

https://www.nitrc.org/forum/message.php?msg_id=3738

Stuff about the CIFTI file format here:

https://www.nitrc.org/plugins/mwiki/index.php/cifti:ConnectivityMatrixFileFormats

Nifti2Header([binaryblock, endianness, ...])	Class for NIfTI2 header
Nifti2Image(dataobj, affine[, header, ...])	Class for single file NIfTI2 format image
Nifti2Pair(dataobj, affine[, header, extra, ...])	Class for NIfTI2 format image, header pair
Nifti2PairHeader([binaryblock, endianness, ...])	Class for NIfTI2 pair header
load(filename)	Load NIfTI2 single or pair image from *filename*
save(img, filename)	Save NIfTI2 single or pair to *filename*

Nifti2Header

class nibabel.nifti2.**Nifti2Header**(*binaryblock=None*, *endianness=None*, *check=True*, *extensions=()*)

Bases: *nibabel.nifti1.Nifti1Header*

Class for NIfTI2 header

NIfTI2 is a slightly simplified variant of NIfTI1 which replaces 32-bit floats with 64-bit floats, and increases some integer widths to 32 or 64 bits.

Initialize header from binary data block and extensions

__init__(*binaryblock=None*, *endianness=None*, *check=True*, *extensions=()*)
Initialize header from binary data block and extensions

classmethod default_structarr(*klass*, *endianness=None*)
Create empty header binary block with given endianness

get_data_shape()
Get shape of data

Notes

Does not use Nifti1 freesurfer hack for large vectors described in `Nifti1Header.set_data_shape()`

Examples

```
>>> hdr = Nifti2Header()
>>> hdr.get_data_shape()
(0,)
>>> hdr.set_data_shape((1,2,3))
>>> hdr.get_data_shape()
(1, 2, 3)
```

Expanding number of dimensions gets default zooms

```
>>> hdr.get_zooms()
(1.0, 1.0, 1.0)
```

pair_magic = 'ni2'

pair_vox_offset = 0

quaternion_threshold = -6.6613381477509392e-16

set_data_shape(*shape*)
Set shape of data

If `ndims == len(shape)` then we set zooms for dimensions higher than `ndims` to 1.0

Parametersshape : sequence
sequence of integers specifying data array shape

Notes

Does not apply nifti1 Freesurfer hack for long vectors (see `Nifti1Header.set_data_shape()`)

single_magic = 'n+2'

single_vox_offset = 544

sizeof_hdr = 540

template_dtype = dtype([('sizeof_hdr', '<i4'), ('magic', 'S4'), ('eol_check', 'i1', (4,)), ('datatype', '<i2'), ('bitpix', '<i2')

Nifti2Image

class nibabel.nifti2.**Nifti2Image**(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)
Bases: *nibabel.nifti1.Nifti1Image*

Class for single file NIfTI2 format image

__init__(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)

header_class
alias of *Nifti2Header*

Nifti2Pair

class nibabel.nifti2.**Nifti2Pair**(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)
Bases: *nibabel.nifti1.Nifti1Pair*

Class for NIfTI2 format image, header pair

__init__(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)

header_class
alias of *Nifti2PairHeader*

Nifti2PairHeader

class nibabel.nifti2.**Nifti2PairHeader**(*binaryblock=None*, *endianness=None*, *check=True*, *extensions=()*)
Bases: *nibabel.nifti2.Nifti2Header*

Class for NIfTI2 pair header

Initialize header from binary data block and extensions

__init__(*binaryblock=None*, *endianness=None*, *check=True*, *extensions=()*)
Initialize header from binary data block and extensions

is_single = False

load

nibabel.nifti2.**load**(*filename*)
Load NIfTI2 single or pair image from *filename*

Parametersfilename : str

filename of image to be loaded

Returnsimg : Nifti2Image or Nifti2Pair

nifti2 single or pair image instance

RaisesImageFileError :

if *filename* doesn't look like nifti2;

IOError :

if *filename* does not exist.

save

nibabel.nifti2.**save**(*img*, *filename*)
Save NIfTI2 single or pair to *filename*

Parametersfilename : str

filename to which to save image

ecat

Read ECAT format images

An ECAT format image consists of:

- a *main header*;
- at least one *matrix list* (mlist);

ECAT thinks of memory locations in terms of *blocks*. One block is 512 bytes. Thus block 1 starts at 0 bytes, block 2 at 512 bytes, and so on.

The matrix list is an array with one row per frame in the data.

Columns in the matrix list are:

- 0 - Matrix identifier (frame number)
- 1 - matrix data start block number (subheader followed by image data)
- 2 - Last block number of matrix (image) data
- **3 - Matrix status:**

- 1 - exists - rw
- 2 - exists - ro
- 3 - matrix deleted

There is one sub-header for each image frame (or matrix in the terminology above). A sub-header can also be called an *image header*. The sub-header is one block (512 bytes), and the frame (image) data follows.

There is very little documentation of the ECAT format, and many of the comments in this code come from a combination of trial and error and wild speculation.

XMedcon can read and write ECAT 6 format, and read ECAT 7 format: see http://xmedcon.sourceforge.net and the ECAT files in the source of XMedCon, currently `libs/tpc/*ecat*` and `source/m-ecat*`. Unfortunately XMedCon is GPL and some of the header files are adapted from CTI files (called CTI code below). It's not clear what the licenses are for these files.

EcatHeader([binaryblock, endianness, check])	Class for basic Ecat PET header
EcatImage(dataobj, affine, header, ...[, ...])	Class returns a list of Ecat images, with one image(hdr/data) per frame
EcatImageArrayProxy(subheader)	Ecat implemention of array proxy protocol
EcatSubHeader(hdr, mlist, fileobj)	parses the subheaders in the ecat (.v) file
get_frame_order(mlist)	Returns the order of the frames stored in the file
get_series_framenumbers(mlist)	Returns framenumber of data as it was collected,
load	
read_mlist(fileobj, endianness)	read (nframes, 4) matrix list array from *fileobj*
read_subheaders(fileobj, mlist, endianness)	Retrieve all subheaders and return list of subheader recarrays

EcatHeader

class nibabel.ecat.**EcatHeader**(*binaryblock=None*, *endianness=None*, *check=True*)

Bases: *nibabel.wrapstruct.WrapStruct*

Class for basic Ecat PET header

Sub-parts of standard Ecat File

- •main header
- •matrix list which lists the information for each frame collected (can have 1 to many frames)
- •subheaders specific to each frame with possibly-variable sized data blocks

This just reads the main Ecat Header, it does not load the data or read the mlist or any sub headers

Initialize Ecat header from bytes object

Parametersbinaryblock : {None, bytes} optional

binary block to set into header, By default, None in which case we insert default empty header block

endianness : {None, '<', '>', other endian code}, optional

endian code of binary block, If None, guess endianness from the data

check : {True, False}, optional

Whether to check and fix header for errors. No checks currently implemented, so value has no effect.

__init__(*binaryblock=None*, *endianness=None*, *check=True*)

Initialize Ecat header from bytes object

Parametersbinaryblock : {None, bytes} optional
binary block to set into header, By default, None in which case we insert default empty header block
endianness : {None, '<', '>', other endian code}, optional
endian code of binary block, If None, guess endianness from the data
check : {True, False}, optional
Whether to check and fix header for errors. No checks currently implemented, so value has no effect.

classmethod **default_structarr**(*klass*, *endianness=None*)
Return header data for empty header with given endianness

get_data_dtype()
Get numpy dtype for data from header

get_filetype()
Type of ECAT Matrix File from code stored in header

get_patient_orient()
gets orientation of patient based on code stored in header, not always reliable

classmethod **guessed_endian**(*klass*, *hdr*)
Guess endian from MAGIC NUMBER value of header data

template_dtype = dtype([('magic_number', 'S14'), ('original_filename', 'S32'), ('sw_version', '<u2'), ('system_type', '

EcatImage

class nibabel.ecat.**EcatImage**(*dataobj*, *affine*, *header*, *subheader*, *mlist*, *extra=None*, *file_map=None*)
Bases: *nibabel.spatialimages.SpatialImage*

Class returns a list of Ecat images, with one image(hdr/data) per frame

Initialize Image

The image is a combination of (array, affine matrix, header, subheader, mlist) with optional meta data in *extra*, and filename / file-like objects contained in the *file_map*.

Parametersdataabj : array-like

image data

affine : None or (4,4) array-like

homogeneous affine giving relationship between voxel coords and world coords.

header : None or header instance

meta data for this image format

subheader : None or subheader instance

meta data for each sub-image for frame in the image

mlist : None or array

Matrix list array giving offset and order of data in file

extra : None or mapping, optional

metadata associated with this image that cannot be stored in header or subheader

file_map : mapping, optional

mapping giving file information for this image format

Examples

```
>>> import os
>>> import nibabel as nib
>>> nibabel_dir = os.path.dirname(nib.__file__)
>>> from nibabel import ecat
>>> ecat_file = os.path.join(nibabel_dir,'tests','data','tinypet.v')
>>> img = ecat.load(ecat_file)
>>> frame0 = img.get_frame(0)
>>> frame0.shape == (10, 10, 3)
True
>>> data4d = img.get_data()
>>> data4d.shape == (10, 10, 3, 1)
True
```

__init__(*dataobj*, *affine*, *header*, *subheader*, *mlist*, *extra=None*, *file_map=None*)

Initialize Image

The image is a combination of (array, affine matrix, header, subheader, mlist) with optional meta data in *extra*, and filename / file-like objects contained in the *file_map*.

Parametersdataabj : array-like
image data

affine : None or (4,4) array-like
homogeneous affine giving relationship between voxel coords and world coords.

header : None or header instance
meta data for this image format

subheader : None or subheader instance
meta data for each sub-image for frame in the image

mlist : None or array
Matrix list array giving offset and order of data in file

extra : None or mapping, optional
metadata associated with this image that cannot be stored in header or subheader

file_map : mapping, optional
mapping giving file information for this image format

Examples

```
>>> import os
>>> import nibabel as nib
>>> nibabel_dir = os.path.dirname(nib.__file__)
>>> from nibabel import ecat
>>> ecat_file = os.path.join(nibabel_dir,'tests','data','tinypet.v')
>>> img = ecat.load(ecat_file)
>>> frame0 = img.get_frame(0)
>>> frame0.shape == (10, 10, 3)
True
>>> data4d = img.get_data()
>>> data4d.shape == (10, 10, 3, 1)
True
```

ImageArrayProxy

alias of *EcatImageArrayProxy*

affine

files_types = (('image', '.v'), ('header', '.v'))

classmethod from_file_map(*klass*, *file_map*)
class method to create image from mapping specified in file_map

classmethod from_filespec(*klass*, *filespec*)

classmethod from_image(*klass*, *img*)

get_data_dtype(*frame*)

get_frame(*frame*, *orientation=None*)
Get full volume for a time frame
Parameters
•**frame** – Time frame index from where to fetch data
•**orientation** – None (default), 'neurological' or 'radiological'
Return type Numpy array containing (possibly oriented) raw data

get_frame_affine(*frame*)
returns 4X4 affine

get_mlist()
get access to the mlist

get_subheaders()
get access to subheaders

header_class
alias of *EcatHeader*

classmethod load(*klass*, *filespec*)

shape

to_file_map(*file_map=None*)
Write ECAT7 image to *file_map* or contained `self.file_map`

The format consist of:
•**A main header (512L) with dictionary entries in the form**[numAvail, nextDir, previousDir, numUsed]
•For every frame (3D volume in 4D data) - A subheader (size = frame_offset) - Frame data (3D volume)

EcatImageArrayProxy

class nibabel.ecat.**EcatImageArrayProxy**(*subheader*)
Bases: `object`

Ecat implemention of array proxy protocol

The array proxy allows us to freeze the passed fileobj and header such that it returns the expected data array.

__init__(*subheader*)

is_proxy

shape

EcatSubHeader

class nibabel.ecat.**EcatSubHeader**(*hdr*, *mlist*, *fileobj*)
Bases: object

parses the subheaders in the ecat (.v) file there is one subheader for each frame in the ecat file

Parametershdr : EcatHeader

ECAT main header

mlist : array shape (N, 4)

Matrix list

fileobj : ECAT file <filename>.v fileholder or file object

with read, seek methods

__init__(*hdr*, *mlist*, *fileobj*)
parses the subheaders in the ecat (.v) file there is one subheader for each frame in the ecat file
Parametershdr : EcatHeader
ECAT main header
mlist : array shape (N, 4)
Matrix list
fileobj : ECAT file <filename>.v fileholder or file object
with read, seek methods

data_from_fileobj(*frame=0*, *orientation=None*)
Read scaled data from file for a given frame
Parameters
•**frame** – Time frame index from where to fetch data
•**orientation** – None (default), 'neurological' or 'radiological'
Return type Numpy array containing (possibly oriented) raw data
See also:

raw_data_from_fileobj

get_frame_affine(*frame=0*)
returns best affine for given frame of data

get_nframes()
returns number of frames

get_shape(*frame=0*)
returns shape of given frame

get_zooms(*frame=0*)
returns zooms ...pixdims

raw_data_from_fileobj(*frame=0*, *orientation=None*)
Get raw data from file object.
Parameters
•**frame** – Time frame index from where to fetch data
•**orientation** – None (default), 'neurological' or 'radiological'
Return type Numpy array containing (possibly oriented) raw data
See also:

data_from_fileobj

get_frame_order

nibabel.ecat.**get_frame_order**(*mlist*)

Returns the order of the frames stored in the file Sometimes Frames are not stored in the file in chronological order, this can be used to extract frames in correct order

Returnsid_dict: dict mapping frame number -> [mlist_row, mlist_id] :

(where mlist id is value in the first column of the mlist matrix) :

Examples

```
>>> import os
>>> import nibabel as nib
>>> nibabel_dir = os.path.dirname(nib.__file__)
>>> from nibabel import ecat
>>> ecat_file = os.path.join(nibabel_dir,'tests','data','tinypet.v')
>>> img = ecat.load(ecat_file)
>>> mlist = img.get_mlist()
>>> get_frame_order(mlist)
{0: [0, 16842758]}
```

get_series_framenumbers

nibabel.ecat.**get_series_framenumbers**(*mlist*)

Returns framenumber of data as it was collected, as part of a series; not just the order of how it was stored in this or across other files

For example, if the data is split between multiple files this should give you the true location of this frame as collected in the series (Frames are numbered starting at ONE (1) not Zero)

Returnsframe_dict: dict mapping order_stored -> frame in series :

where frame in series counts from 1; [1,2,3,4...]

Examples

```
>>> import os
>>> import nibabel as nib
>>> nibabel_dir = os.path.dirname(nib.__file__)
>>> from nibabel import ecat
>>> ecat_file = os.path.join(nibabel_dir,'tests','data','tinypet.v')
>>> img = ecat.load(ecat_file)
>>> mlist = img.get_mlist()
>>> get_series_framenumbers(mlist)
{0: 1}
```

load

nibabel.ecat.**load**(*klass*, *filespec*)

read_mlist

nibabel.ecat.**read_mlist**(*fileobj*, *endianness*)
read (nframes, 4) matrix list array from *fileobj*

Parametersfileobj : file-like

an open file-like object implementing `seek` and `read`

Returnsmlist : (nframes, 4) ndarray

matrix list is an array with `nframes` rows and columns:

- 0 - Matrix identifier (frame number)
- 1 - matrix data start block number (subheader followed by image data)
- 2 - Last block number of matrix (image) data
- **3 - Matrix status:**
  - 1 - exists - rw
  - 2 - exists - ro
  - 3 - matrix deleted

Notes

A block is 512 bytes.

`block_no` in the code below is 1-based. block 1 is the main header, and the mlist blocks start at block number 2.

The 512 bytes in an mlist block contain 32 rows of the int32 (nframes, 4) mlist matrix.

The first row of these 32 looks like a special row. The 4 values appear to be (respectively):

- not sure - maybe negative number of mlist rows (out of 31) that are blank and not used in this block. Called *nfree* but unused in CTI code;
- block_no - of next set of mlist entries or 2 if no more entries. We also allow 1 or 0 to signal no more entries;
- <no idea>. Called *prvblk* in CTI code, so maybe previous block no;
- n_rows - number of mlist rows in this block (between ?0 and 31) (called *nused* in CTI code).

read_subheaders

nibabel.ecat.**read_subheaders**(*fileobj*, *mlist*, *endianness*)
Retrieve all subheaders and return list of subheader recarrays

Parametersfileobj : file-like

implementing `read` and `seek`

mlist : (nframes, 4) ndarray

Columns are: * 0 - Matrix identifier. * 1 - subheader block number * 2 - Last block number of matrix data block. * 3 - Matrix status:

endianness : {'<', '>'}

little / big endian code

Returnssubheaders : list

List of subheader structured arrays

parrec

Read images in PAR/REC format.

This is yet another MRI image format generated by Philips scanners. It is an ASCII header (PAR) plus a binary blob (REC).

This implementation aims to read version 4 and 4.2 of this format. Other versions could probably be supported, but we need example images to test against. If you want us to support another version, and have an image we can add to the test suite, let us know. You would make us very happy by submitting a pull request.

PAR file format

The PAR format appears to have two sections:

General information This is a set of lines each giving one key : value pair, examples:

```
.    EPI factor        <0,1=no EPI>     :   39
.    Dynamic scan      <0=no 1=yes> ?   :   1
.    Diffusion         <0=no 1=yes> ?   :   0
```

(from nibabe/tests/data/phantom_EPI_asc_CLEAR_2_1.PAR)

Image information There is a # prefixed list of fields under the heading "IMAGE INFORMATION DEFINITION". From the same file, here is the start of this list:

```
# === IMAGE INFORMATION DEFINITION =============================================
#  The rest of this file contains ONE line per image, this line contains the following information:
#
#  slice number                             (integer)
#  echo number                              (integer)
#  dynamic scan number                      (integer)
```

There follows a space separated table with values for these fields, each row containing all the named values. Here's the first few lines from the example file above:

```
# === IMAGE INFORMATION ==========================================================
#  sl ec  dyn ph ty    idx pix scan% rec size                (re)scale              window        ang

1   1    1  1 0 2     0  16    62   64   64     0.00000   1.29035 4.28404e-003  1070  1860 -13.26  -0
2   1    1  1 0 2     1  16    62   64   64     0.00000   1.29035 4.28404e-003  1122  1951 -13.26  -0
3   1    1  1 0 2     2  16    62   64   64     0.00000   1.29035 4.28404e-003  1137  1977 -13.26  -0
```

Orientation

PAR files refer to orientations "ap", "fh" and "rl".

Nibabel's required affine output axes are RAS (left to Right, posterior to Anterior, inferior to Superior). The correspondence of the PAR file's axes to RAS axes is:

- ap = anterior -> posterior = negative A in RAS

- fh = foot -> head = S in RAS
- rl = right -> left = negative R in RAS

The orientation of the PAR file axes corresponds to DICOM's LPS coordinate system (right to Left, anterior to Posterior, inferior to Superior), but in a different order.

We call the PAR file's axis system "PSL" (Posterior, Superior, Left)

Data type

It seems that everyone agrees that Philips stores REC data in little-endian format - see https://github.com/nipy/nibabel/issues/274

Philips XML header files, and some previous experience, suggest that the REC data is always stored as 8 or 16 bit unsigned integers - see https://github.com/nipy/nibabel/issues/275

PARRECArrayProxy(*args, **kwargs)	Initialize PARREC array proxy
PARRECError	Exception for PAR/REC format related problems.
PARRECHeader(info, image_defs[, ...])	PAR/REC header
PARRECImage(dataobj, affine[, header, ...])	PAR/REC image
load	Create PARREC image from filename *filename*
one_line(long_str)	Make maybe mutli-line *long_str* into one long line
parse_PAR_header(fobj)	Parse a PAR header and aggregate all information into useful containers.
vol_is_full(slice_nos, slice_max[, slice_min])	Vector with True for slices in complete volume, False otherwise
vol_numbers(slice_nos)	Calculate volume numbers inferred from slice numbers *slice_nos*

PARRECArrayProxy

class nibabel.parrec.**PARRECArrayProxy**(**args*, ***kwargs*)

Bases: object

Initialize PARREC array proxy

Parametersfile_like : file-like object

Filename or object implementing `read, seek, tell`

header : PARRECHeader instance

Implementing `get_data_shape, get_data_dtype, get_sorted_slice_indices, get_data_scaling, get_rec_shape`.

mmap : {True, False, 'c', 'r'}, optional, keyword only

mmap controls the use of numpy memory mapping for reading data. If False, do not try numpy `memmap` for data array. If one of {'c', 'r'}, try numpy memmap with `mode=mmap`. A *mmap* value of True gives the same behavior as `mmap='c'`. If *file_like* cannot be memory-mapped, ignore *mmap* value and read array from file.

scaling : {'fp', 'dv'}, optional, keyword only

Type of scaling to use - see header `get_data_scaling` method.

__init__(**args*, ***kwargs*)

Initialize PARREC array proxy

Parametersfile_like : file-like object

Filename or object implementing `read, seek, tell`

header : PARRECHeader instance

Implementing `get_data_shape`, `get_data_dtype`, `get_sorted_slice_indices`, `get_data_scaling`, `get_rec_shape`.

mmap : {True, False, 'c', 'r'}, optional, keyword only
mmap controls the use of numpy memory mapping for reading data. If False, do not try numpy `memmap` for data array. If one of {'c', 'r'}, try numpy memmap with `mode=mmap`. A *mmap* value of True gives the same behavior as `mmap='c'`. If *file_like* cannot be memory-mapped, ignore *mmap* value and read array from file.

scaling : {'fp', 'dv'}, optional, keyword only
Type of scaling to use - see header `get_data_scaling` method.

dtype

get_unscaled()

is_proxy

shape

PARRECError

class nibabel.parrec.**PARRECError**
Bases: exceptions.Exception

Exception for PAR/REC format related problems.

To be raised whenever PAR/REC is not happy, or we are not happy with PAR/REC.

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

PARRECHeader

class nibabel.parrec.**PARRECHeader**(*info*, *image_defs*, *permit_truncated=False*)
Bases: *nibabel.spatialimages.Header*

PAR/REC header

Parametersinfo : dict

"General information" from the PAR file (as returned by *parse_PAR_header()*).

image_defs : array

Structured array with image definitions from the PAR file (as returned by *parse_PAR_header()*).

permit_truncated : bool, optional

If True, a warning is emitted instead of an error when a truncated recording is detected.

__init__(*info*, *image_defs*, *permit_truncated=False*)
Parametersinfo : dict
"General information" from the PAR file (as returned by *parse_PAR_header()*).
image_defs : array
Structured array with image definitions from the PAR file (as returned by *parse_PAR_header()*).
permit_truncated : bool, optional
If True, a warning is emitted instead of an error when a truncated recording is detected.

as_analyze_map()
Convert PAR parameters to NIFTI1 format

copy()

classmethod from_fileobj(*klass*, *fileobj*, *permit_truncated=False*)

classmethod from_header(*klass*, *header=None*)

get_affine(*origin='scanner'*)
Compute affine transformation into scanner space.

The method only considers global rotation and offset settings in the header and ignores potentially deviating information in the image definitions.

Parametersorigin : {'scanner', 'fov'}
Transformation origin. By default the transformation is computed relative to the scanner's iso center. If 'fov' is requested the transformation origin will be the center of the field of view instead.

Returnsaff : (4, 4) array
4x4 array, with output axis order corresponding to RAS or (x,y,z) or (lr, pa, fh).

Notes

Transformations appear to be specified in (ap, fh, rl) axes. The orientation of data is recorded in the "slice orientation" field of the PAR header "General Information".

We need to:
•translate to coordinates in terms of the center of the FOV
•apply voxel size scaling
•reorder / flip the data to Philips' PSL axes
•apply the rotations
•apply any isocenter scaling offset if *origin* == "scanner"
•reorder and flip to RAS axes

get_bvals_bvecs()
Get bvals and bvecs from data

Returnsb_vals : None or array
Array of b values, shape (n_directions,), or None if not a diffusion acquisition.

b_vectors : None or array
Array of b vectors, shape (n_directions, 3), or None if not a diffusion acquisition.

get_data_offset()
PAR header always has 0 data offset (into REC file)

get_data_scaling(*method='dv'*)
Returns scaling slope and intercept.

Parametersmethod : {'fp', 'dv'}
Scaling settings to be reported – see notes below.

Returnsslope : array
scaling slope

intercept : array
scaling intercept

Notes

The PAR header contains two different scaling settings: 'dv' (value on console) and 'fp' (floating point value). Here is how they are defined:

PV: value in REC RS: rescale slope RI: rescale intercept SS: scale slope

DV = PV * RS + RI FP = DV / (RS * SS)

get_echo_train_length()
Echo train length of the recording

get_q_vectors()
Get Q vectors from the data
Returnsq_vectors : None or array
Array of q vectors (bvals * bvecs), or None if not a diffusion acquisition.

get_rec_shape()

get_slice_orientation()
Returns the slice orientation label.
Returnsorientation : {'transverse', 'sagittal', 'coronal'}

get_sorted_slice_indices()
Indices to sort (and maybe discard) slices in REC file

Returns list for indexing into the last (third) dimension of the REC data array, and (equivalently) the only dimension of `self.image_defs`.

If the recording is truncated, the returned indices take care of discarding any indices that are not meant to be used.

get_voxel_size()
Returns the spatial extent of a voxel.

Does not include the slice gap in the slice extent.

This function is deprecated and we will remove it in future versions of nibabel. Please use `get_zooms` instead. If you need the slice thickness not including the slice gap, use `self.image_defs['slice thickness']`.
Returnsvox_size: shape (3,) ndarray :

get_water_fat_shift()
Water fat shift, in pixels

set_data_offset(*offset*)
PAR header always has 0 data offset (into REC file)

PARRECImage

class nibabel.parrec.**PARRECImage**(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)
Bases: *nibabel.spatialimages.SpatialImage*

PAR/REC image

Initialize image

The image is a combination of (array, affine matrix, header), with optional metadata in *extra*, and filename / file-like objects contained in the *file_map* mapping.

Parametersdataobj : object

Object containg image data. It should be some object that retuns an array from `np.asanyarray`. It should have a `shape` attribute or property

affine : None or (4,4) array-like

homogenous affine giving relationship between voxel coordinates and world coordinates. Affine can also be None. In this case, `obj.affine` also returns None, and the affine as written to disk will depend on the file format.

header : None or mapping or header instance, optional

metadata for this image format

extra : None or mapping, optional

metadata to associate with image that cannot be stored in the metadata of this image type

file_map : mapping, optional

mapping giving file information for this image format

__init__(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)

Initialize image

The image is a combination of (array, affine matrix, header), with optional metadata in *extra*, and filename / file-like objects contained in the *file_map* mapping.

Parametersdataobj : object
Object containg image data. It should be some object that retuns an array from `np.asanyarray`. It should have a `shape` attribute or property

affine : None or (4,4) array-like
homogenous affine giving relationship between voxel coordinates and world coordinates. Affine can also be None. In this case, `obj.affine` also returns None, and the affine as written to disk will depend on the file format.

header : None or mapping or header instance, optional
metadata for this image format

extra : None or mapping, optional
metadata to associate with image that cannot be stored in the metadata of this image type

file_map : mapping, optional
mapping giving file information for this image format

ImageArrayProxy

alias of *PARRECArrayProxy*

files_types = (('image', '.rec'), ('header', '.par'))

classmethod **from_file_map**(**args*, ***kwargs*)

Create PARREC image from file map *file_map*

Parametersfile_map : dict
dict with keys `image, header` and values being fileholder objects for the respective REC and PAR files.

mmap : {True, False, 'c', 'r'}, optional, keyword only
mmap controls the use of numpy memory mapping for reading image array data. If False, do not try numpy `memmap` for data array. If one of {'c', 'r'}, try numpy memmap with `mode=mmap`. A *mmap* value of True gives the same behavior as `mmap='c'`. If image data file cannot be memory-mapped, ignore *mmap* value and read array from file.

permit_truncated : {False, True}, optional, keyword-only
If False, raise an error for an image where the header shows signs that fewer slices / volumes were recorded than were expected.

scaling : {'dv', 'fp'}, optional, keyword-only
Scaling method to apply to data (see *PARRECHeader.get_data_scaling()*).

classmethod **from_filename**(**args*, ***kwargs*)

Create PARREC image from filename *filename*

Parametersfilename : str
Filename of "PAR" or "REC" file

mmap : {True, False, 'c', 'r'}, optional, keyword only
mmap controls the use of numpy memory mapping for reading image array data. If False, do not try numpy `memmap` for data array. If one of {'c', 'r'}, try numpy memmap with `mode=mmap`. A *mmap* value of True gives the same behavior as `mmap='c'`. If image data file cannot be memory-mapped, ignore *mmap* value and read array from file.
permit_truncated : {False, True}, optional, keyword-only
If False, raise an error for an image where the header shows signs that fewer slices / volumes were recorded than were expected.
scaling : {'dv', 'fp'}, optional, keyword-only
Scaling method to apply to data (see *PARRECHeader.get_data_scaling()*).

header_class
alias of *PARRECHeader*

classmethod load(**args*, ***kwargs*)
Create PARREC image from filename *filename*
Parametersfilename : str
Filename of "PAR" or "REC" file
mmap : {True, False, 'c', 'r'}, optional, keyword only
mmap controls the use of numpy memory mapping for reading image array data. If False, do not try numpy `memmap` for data array. If one of {'c', 'r'}, try numpy memmap with `mode=mmap`. A *mmap* value of True gives the same behavior as `mmap='c'`. If image data file cannot be memory-mapped, ignore *mmap* value and read array from file.
permit_truncated : {False, True}, optional, keyword-only
If False, raise an error for an image where the header shows signs that fewer slices / volumes were recorded than were expected.
scaling : {'dv', 'fp'}, optional, keyword-only
Scaling method to apply to data (see *PARRECHeader.get_data_scaling()*).

load

nibabel.parrec.**load**(**args*, ***kwargs*)
Create PARREC image from filename *filename*

Parametersfilename : str

Filename of "PAR" or "REC" file

mmap : {True, False, 'c', 'r'}, optional, keyword only

mmap controls the use of numpy memory mapping for reading image array data. If False, do not try numpy `memmap` for data array. If one of {'c', 'r'}, try numpy memmap with `mode=mmap`. A *mmap* value of True gives the same behavior as `mmap='c'`. If image data file cannot be memory-mapped, ignore *mmap* value and read array from file.

permit_truncated : {False, True}, optional, keyword-only

If False, raise an error for an image where the header shows signs that fewer slices / volumes were recorded than were expected.

scaling : {'dv', 'fp'}, optional, keyword-only

Scaling method to apply to data (see *PARRECHeader.get_data_scaling()*).

one_line

nibabel.parrec.**one_line**(*long_str*)
Make maybe mutli-line *long_str* into one long line

parse_PAR_header

nibabel.parrec.**parse_PAR_header**(*fobj*)
Parse a PAR header and aggregate all information into useful containers.

Parametersfobj : file-object

The PAR header file object.

Returnsgeneral_info : dict

Contains all "General Information" from the header file

image_info : ndarray

Structured array with fields giving all "Image information" in the header

vol_is_full

nibabel.parrec.**vol_is_full**(*slice_nos*, *slice_max*, *slice_min=1*)
Vector with True for slices in complete volume, False otherwise

Parametersslice_nos : sequence

Sequence of slice numbers, e.g. `[1, 2, 3, 4, 1, 2, 3, 4]`.

slice_max : int

Highest slice number for a full slice set. Slice set will be `range(slice_min, slice_max+1)`.

slice_min : int

Lowest slice number for full slice set.

Returnsis_full : array

Bool vector with True for slices in full volumes, False for slices in partial volumes. A full volume is a volume with all slices in the `slice set` as defined above.

RaisesValueError :

if any *slice_nos* value is outside slice set.

vol_numbers

nibabel.parrec.**vol_numbers**(*slice_nos*)
Calculate volume numbers inferred from slice numbers *slice_nos*

The volume number for each slice is the number of times this slice has occurred previously in the *slice_nos* sequence

Parametersslice_nos : sequence

Sequence of slice numbers, e.g. `[1, 2, 3, 4, 1, 2, 3, 4]`.

Returnsvol_nos : list

A list, the same length of *slice_nos* giving the volume number for each corresponding slice number.

trackvis

Read and write trackvis files

DataError	Error in trackvis data
HeaderError	Error in trackvis header
TrackvisFile(streamlines[, mapping, ...])	Convenience class to encapsulate trackvis file information
TrackvisFileError	Error from TrackvisFile class
aff_from_hdr(trk_hdr[, atleast_v2])	Return voxel to mm affine from trackvis header
aff_to_hdr(affine, trk_hdr[, pos_vox, set_order])	Set affine *affine* into trackvis header *trk_hdr*
empty_header([endianness, version])	Empty trackvis header
read(fileobj[, as_generator, points_space])	Read trackvis file, return streamlines, header
write(fileobj, streamlines[, hdr_mapping, ...])	Write header and *streamlines* to trackvis file *fileobj*

DataError

class nibabel.trackvis.**DataError**
Bases: exceptions.Exception

Error in trackvis data

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

HeaderError

class nibabel.trackvis.**HeaderError**
Bases: exceptions.Exception

Error in trackvis header

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

TrackvisFile

class nibabel.trackvis.**TrackvisFile**(*streamlines*, *mapping=None*, *endianness=None*, *filename=None*, *points_space=None*, *affine=None*)
Bases: object

Convenience class to encapsulate trackvis file information

Parametersstreamlines : sequence

sequence of streamlines. This object does not accept generic iterables as input because these can be consumed and make the object unusable. Please use the function interface to work with generators / iterables

mapping : None or mapping

Mapping defining header attributes

endianness : {None, '<', '>'}

Set here explicit endianness if required. Endianness otherwise inferred from *streamlines*

filename : None or str, optional

filename

points_space : {None, 'voxel', 'rasmm'}, optional

Space in which streamline points are expressed in memory. Default (None) means streamlines contain points in trackvis *voxmm* space (voxel positions * voxel sizes). 'voxel' means points are in voxel space (and need to be multiplied by voxel size for saving in file). 'rasmm' mean the points are expressed in mm space according to the affine. See `read` and `write` function docstrings for more detail.

affine : None or (4,4) ndarray, optional

Affine expressing relationship of voxels in an image to mm in RAS mm space. If 'points_space' is not None, you can use this to give the relationship between voxels, rasmm and voxmm space (above).

__init__(*streamlines*, *mapping=None*, *endianness=None*, *filename=None*, *points_space=None*, *affine=None*)

classmethod from_file(*klass*, *file_like*, *points_space=None*)

get_affine(*atleast_v2=None*)

Get affine from header in object

Returnsaff : (4,4) ndarray

affine from header

atleast_v2 : None or bool, optional

See `aff_from_hdr` docstring for detail. If True, require valid affine in `vox_to_ras` field of header.

Notes

This method currently works for trackvis version 1 headers, but we consider it unsafe for version 1 headers, and in future versions of nibabel we will raise an error for trackvis headers < version 2.

set_affine(*affine*, *pos_vox=None*, *set_order=None*)

Set affine *affine* into trackvis header

Affine is mapping from voxel space to Nifti RAS) output coordinate system convention; x: Left -> Right, y: Posterior -> Anterior, z: Inferior -> Superior. Sets affine if possible, and voxel sizes, and voxel axis ordering.

Parametersaffine : (4,4) array-like

Affine voxel to mm transformation

pos_vos : None or bool, optional

If None, currently defaults to False - this will change in future versions of nibabel. If False, allow negative voxel sizes in header to record axis flips. Negative voxels cause problems for trackvis (the application). If True, enforce positive voxel sizes.

set_order : None or bool, optional

If None, currently defaults to False - this will change in future versions of nibabel. If False, do not set `voxel_order` field in *trk_hdr*. If True, calculcate `voxel_order` from *affine* and set into *trk_hdr*.

ReturnsNone :

to_file(*file_like*)

TrackvisFileError

class nibabel.trackvis.**TrackvisFileError**
Bases: exceptions.Exception

Error from TrackvisFile class

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

aff_from_hdr

nibabel.trackvis.**aff_from_hdr**(*trk_hdr*, *atleast_v2=None*)
Return voxel to mm affine from trackvis header

Affine is mapping from voxel space to Nifti (RAS) output coordinate system convention; x: Left -> Right, y: Posterior -> Anterior, z: Inferior -> Superior.

Parameterstrk_hdr : mapping

Mapping with trackvis header keys `version`. If `version == 2`, we also expect `vox_to_ras`.

atleast_v2 : None or bool

If None, currently defaults to False. This will change to True in future versions. If True, require that there is a valid 'vox_to_ras' affine, raise HeaderError otherwise. If False, look for valid 'vox_to_ras' affine, but fall back to best guess from version 1 fields otherwise.

Returnsaff : (4,4) array

affine giving mapping from voxel coordinates (affine applied on the left to points on the right) to millimeter coordinates in the RAS coordinate system

Notes

Our initial idea was to try and work round the deficiencies of the version 1 format by using the DICOM orientation fields to store the affine. This proved difficult in practice because trackvis (the application) doesn't allow negative voxel sizes (needed for recording axis flips) and sets the origin field to 0. In future, we'll raise an error rather than try and estimate the affine from version 1 fields

aff_to_hdr

nibabel.trackvis.**aff_to_hdr**(*affine*, *trk_hdr*, *pos_vox=None*, *set_order=None*)
Set affine *affine* into trackvis header *trk_hdr*

Affine is mapping from voxel space to Nifti RAS) output coordinate system convention; x: Left -> Right, y: Posterior -> Anterior, z: Inferior -> Superior. Sets affine if possible, and voxel sizes, and voxel axis ordering.

Parametersaffine : (4,4) array-like

Affine voxel to mm transformation

trk_hdr : mapping

Mapping implementing __setitem__

pos_vos : None or bool

If None, currently defaults to False - this will change in future versions of nibabel. If False, allow negative voxel sizes in header to record axis flips. Negative voxels cause problems for trackvis (the application). If True, enforce positive voxel sizes.

set_order : None or bool

If None, currently defaults to False - this will change in future versions of nibabel. If False, do not set `voxel_order` field in *trk_hdr*. If True, calculcate `voxel_order` from *affine* and set into *trk_hdr*.

ReturnsNone :

Notes

version 2 of the trackvis header has a dedicated field for the nifti RAS affine. In theory trackvis 1 has enough information to store an affine, with the fields 'origin', 'voxel_size' and 'image_orientation_patient'. Unfortunately, to be able to store any affine, we'd need to be able to set negative voxel sizes, to encode axis flips. This is because 'image_orientation_patient' is only two columns of the 3x3 rotation matrix, and we need to know the number of flips to reconstruct the third column reliably. It turns out that negative flips upset trackvis (the application). The application also ignores the origin field, and may not use the 'image_orientation_patient' field.

empty_header

nibabel.trackvis.**empty_header**(*endianness=None*, *version=2*)

Empty trackvis header

Parametersendianness : {'<','>'}, optional

Endianness of empty header to return. Default is native endian.

version : int, optional

Header version. 1 or 2. Default is 2

Returnshdr : structured array

structured array containing empty trackvis header

Notes

The trackvis header can store enough information to give an affine mapping between voxel and world space. Often this information is missing. We make no attempt to fill it with sensible defaults on the basis that, if the information is missing, it is better to be explicit.

Examples

```
>>> hdr = empty_header()
>>> print(hdr['version'])
2
>>> np.asscalar(hdr['id_string']) == b'TRACK'
True
>>> endian_codes[hdr['version'].dtype.byteorder] == native_code
```

```
    True
    >>> hdr = empty_header(swapped_code)
    >>> endian_codes[hdr['version'].dtype.byteorder] == swapped_code
    True
    >>> hdr = empty_header(version=1)
    >>> print(hdr['version'])
    1
```

read

nibabel.trackvis.**read**(*fileobj*, *as_generator=False*, *points_space=None*)

Read trackvis file, return streamlines, header

Parametersfileobj : string or file-like object

If string, a filename; otherwise an open file-like object pointing to trackvis file (and ready to read from the beginning of the trackvis header data)

as_generator : bool, optional

Whether to return tracks as sequence (False, default) or as a generator (True).

points_space : {None, 'voxel', 'rasmm'}, optional

The coordinates in which you want the points in the *output* streamlines expressed. If None, then return the points exactly as they are stored in the trackvis file. The points will probably be in trackviz voxmm space - see Notes for `write` function. If 'voxel', we convert the points to voxel space simply by dividing by the recorded voxel size. If 'rasmm' we'll convert the points to RAS mm space (real space). For 'rasmm' we check if the affine is set and matches the voxel sizes and voxel order.

Returnsstreamlines : sequence or generator

Returns sequence if *as_generator* is False, generator if True. Value is sequence or generator of 3 element sequences with elements:

1.points : ndarray shape (N,3) where N is the number of points

2.scalars : None or ndarray shape (N, M) where M is the number of scalars per point

3.properties : None or ndarray shape (P,) where P is the number of properties

hdr : structured array

structured array with trackvis header fields

Notes

The endianness of the input data can be deduced from the endianness of the returned *hdr* or *streamlines*

Points are in trackvis *voxel mm*. Each track has N points, each with 3 coordinates, `x, y, z`, where `x` is the floating point voxel coordinate along the first image axis, multiplied by the voxel size for that axis.

write

nibabel.trackvis.**write**(*fileobj*, *streamlines*, *hdr_mapping=None*, *endianness=None*, *points_space=None*)

Write header and *streamlines* to trackvis file *fileobj*

The parameters from the streamlines override conflicting parameters in the *hdr_mapping* information. In particular, the number of streamlines, the number of scalars, and the number of properties are written according to *streamlines* rather than *hdr_mapping*.

Parametersfileobj : filename or file-like

If filename, open file as 'wb', otherwise *fileobj* should be an open file-like object, with a `write` method.

streamlines : iterable

iterable returning 3 element sequences with elements:

1.points : ndarray shape (N,3) where N is the number of points

2.scalars : None or ndarray shape (N, M) where M is the number of scalars per point

3.properties : None or ndarray shape (P,) where P is the number of properties

If *streamlines* has a `len` (for example, it is a list or a tuple), then we can write the number of streamlines into the header. Otherwise we write 0 for the number of streamlines (a valid trackvis header) and write streamlines into the file until the iterable is exhausted. M - the number of scalars - has to be the same for each streamline in *streamlines*. Similarly for P. See *points_space* and Notes for more detail on the coordinate system for `points` above.

hdr_mapping : None, ndarray or mapping, optional

Information for filling header fields. Can be something dict-like (implementing `items`) or a structured numpy array

endianness : {None, '<', '>'}, optional

Endianness of file to be written. '<' is little-endian, '>' is big-endian. None (the default) is to use the endianness of the *streamlines* data.

points_space : {None, 'voxel', 'rasmm'}, optional

The coordinates in which the points in the input streamlines are expressed. If None, then assume the points are as you want them (probably trackviz voxmm space - see Notes). If 'voxel', the points are in voxel space, and we will transform them to trackviz voxmm space. If 'rasmm' the points are in RAS mm space (real space). We transform them to trackvis voxmm space. If 'voxel' or 'rasmm' we insist that the voxel sizes and ordering are set to non-default values. If 'rasmm' we also check if the affine is set and matches the voxel sizes

ReturnsNone :

Notes

Trackvis (the application) expects the `points` in the streamlines be in what we call *trackviz voxmm* coordinates. If we have a point (x, y, z) in voxmm coordinates, and `voxel_size` has the voxel sizes for each of the 3 dimensions, then x, y, z refer to mm in voxel space. Thus if i, j, k is a point in voxel coordinates, then `x = i * voxel_size[0]; y = j * voxel_size[1]; z = k * voxel_size[2]`. The spatial direction of x, y and z are defined with the "voxel_order" field. For example, if the original image had RAS voxel ordering then "voxel_order" would be "RAS". RAS here refers to the spatial direction of the voxel axes: "R" means that moving along first voxel axis moves from left to right in space, "A" -> second axis goes from posterior to anterior, "S" -> inferior to superior. If "voxel_order" is empty we assume "LPS".

This information comes from some helpful replies on the trackviz forum about interpreting point coordiantes

Examples

```
>>> from io import BytesIO
>>> file_obj = BytesIO()
>>> pts0 = np.random.uniform(size=(10,3))
>>> pts1 = np.random.uniform(size=(10,3))
>>> streamlines = ([(pts0, None, None), (pts1, None, None)])
>>> write(file_obj, streamlines)
>>> _ = file_obj.seek(0) # returns 0 in python 3
>>> streams, hdr = read(file_obj)
>>> len(streams)
2
```

If there are too many streamlines to fit in memory, you can pass an iterable thing instead of a list

```
>>> file_obj = BytesIO()
>>> def gen():
...     yield (pts0, None, None)
...     yield (pts0, None, None)
>>> write(file_obj, gen())
>>> _ = file_obj.seek(0)
>>> streams, hdr = read(file_obj)
>>> len(streams)
2
```

9.5.3 Image Utilities

eulerangles	Module implementing Euler angle rotations and their conversions
funcs	Processor functions for images
imageclasses	Define supported image classes and names
imageglobals	Defaults for images and headers
loadsave	Utilities to load and save image objects
orientations	Utilities for calculating and applying affine orientations
quaternions	Functions to operate on, or return, quaternions.
spatialimages	A simple spatial image class
volumeutils	Utility functions for analyze-like formats

eulerangles

Module implementing Euler angle rotations and their conversions

See:

- https://en.wikipedia.org/wiki/Rotation_matrix
- https://en.wikipedia.org/wiki/Euler_angles
- http://mathworld.wolfram.com/EulerAngles.html

See also: *Representing Attitude with Euler Angles and Quaternions: A Reference* (2006) by James Diebel. A cached PDF link last found here:

http://citeseerx.ist.psu.edu/viewdoc/summary?doi=10.1.1.110.5134

Euler's rotation theorem tells us that any rotation in 3D can be described by 3 angles. Let's call the 3 angles the *Euler angle vector* and call the angles in the vector $alpha$, $beta$ and $gamma$. The vector is [$alpha$, $beta$. $gamma$

] and, in this description, the order of the parameters specifies the order in which the rotations occur (so the rotation corresponding to $alpha$ is applied first).

In order to specify the meaning of an *Euler angle vector* we need to specify the axes around which each of the rotations corresponding to $alpha$, $beta$ and $gamma$ will occur.

There are therefore three axes for the rotations $alpha$, $beta$ and $gamma$; let's call them i j, k.

Let us express the rotation $alpha$ around axis *i* as a 3 by 3 rotation matrix *A*. Similarly $beta$ around *j* becomes 3 x 3 matrix *B* and $gamma$ around *k* becomes matrix *G*. Then the whole rotation expressed by the Euler angle vector [$alpha$, $beta$. $gamma$], *R* is given by:

```
R = np.dot(G, np.dot(B, A))
```

See http://mathworld.wolfram.com/EulerAngles.html

The order GBA expresses the fact that the rotations are performed in the order of the vector ($alpha$ around axis *i* = *A* first).

To convert a given Euler angle vector to a meaningful rotation, and a rotation matrix, we need to define:

- the axes *i*, *j*, *k*
- whether a rotation matrix should be applied on the left of a vector to be transformed (vectors are column vectors) or on the right (vectors are row vectors).
- whether the rotations move the axes as they are applied (intrinsic rotations) - compared the situation where the axes stay fixed and the vectors move within the axis frame (extrinsic)
- the handedness of the coordinate system

See: https://en.wikipedia.org/wiki/Rotation_matrix#Ambiguities

We are using the following conventions:

- axes *i*, *j*, *k* are the *z*, *y*, and *x* axes respectively. Thus an Euler angle vector [$alpha$, $beta$. $gamma$] in our convention implies a $alpha$ radian rotation around the z axis, followed by a $beta$ rotation around the y axis, followed by a $gamma$ rotation around the *x* axis.
- the rotation matrix applies on the left, to column vectors on the right, so if *R* is the rotation matrix, and *v* is a 3 x N matrix with N column vectors, the transformed vector set *vdash* is given by `vdash = np.dot(R, v)`.
- extrinsic rotations - the axes are fixed, and do not move with the rotations.
- a right-handed coordinate system

The convention of rotation around `z`, followed by rotation around `y`, followed by rotation around `x`, is known (confusingly) as "xyz", pitch-roll-yaw, Cardan angles, or Tait-Bryan angles.

angle_axis2euler(theta, vector[, is_normalized])	Convert angle, axis pair to Euler angles
euler2angle_axis([z, y, x])	Return angle, axis corresponding to these Euler angles
euler2mat([z, y, x])	Return matrix for rotations around z, y and x axes
euler2quat([z, y, x])	Return quaternion corresponding to these Euler angles
mat2euler(M[, cy_thresh])	Discover Euler angle vector from 3x3 matrix
quat2euler(q)	Return Euler angles corresponding to quaternion *q*

angle_axis2euler

nibabel.eulerangles.**angle_axis2euler**(*theta*, *vector*, *is_normalized=False*)

Convert angle, axis pair to Euler angles

Parameterstheta : scalar

angle of rotation

vector : 3 element sequence

vector specifying axis for rotation.

is_normalized : bool, optional

True if vector is already normalized (has norm of 1). Default False

Returnsz : scalar

y : scalar

x : scalar

Rotations in radians around z, y, x axes, respectively

Notes

It's possible to reduce the amount of calculation a little, by combining parts of the `angle_axis2mat` and `mat2euler` functions, but the reduction in computation is small, and the code repetition is large.

Examples

```
>>> z, y, x = angle_axis2euler(0, [1, 0, 0])
>>> np.allclose((z, y, x), 0)
True
```

euler2angle_axis

`nibabel.eulerangles.`**`euler2angle_axis`**(*z=0*, *y=0*, *x=0*)

Return angle, axis corresponding to these Euler angles

Uses the z, then y, then x convention above

Parametersz : scalar

Rotation angle in radians around z-axis (performed first)

y : scalar

Rotation angle in radians around y-axis

x : scalar

Rotation angle in radians around x-axis (performed last)

Returnstheta : scalar

angle of rotation

vector : array shape (3,)

axis around which rotation occurs

Examples

```
>>> theta, vec = euler2angle_axis(0, 1.5, 0)
>>> print(theta)
1.5
>>> np.allclose(vec, [0, 1, 0])
True
```

euler2mat

nibabel.eulerangles.**euler2mat**(*z=0*, *y=0*, *x=0*)

Return matrix for rotations around z, y and x axes

Uses the z, then y, then x convention above

Parametersz : scalar

Rotation angle in radians around z-axis (performed first)

y : scalar

Rotation angle in radians around y-axis

x : scalar

Rotation angle in radians around x-axis (performed last)

ReturnsM : array shape (3,3)

Rotation matrix giving same rotation as for given angles

Notes

The direction of rotation is given by the right-hand rule (orient the thumb of the right hand along the axis around which the rotation occurs, with the end of the thumb at the positive end of the axis; curl your fingers; the direction your fingers curl is the direction of rotation). Therefore, the rotations are counterclockwise if looking along the axis of rotation from positive to negative.

Examples

```
>>> zrot = 1.3 # radians
>>> yrot = -0.1
>>> xrot = 0.2
>>> M = euler2mat(zrot, yrot, xrot)
>>> M.shape == (3, 3)
True
```

The output rotation matrix is equal to the composition of the individual rotations

```
>>> M1 = euler2mat(zrot)
>>> M2 = euler2mat(0, yrot)
>>> M3 = euler2mat(0, 0, xrot)
>>> composed_M = np.dot(M3, np.dot(M2, M1))
>>> np.allclose(M, composed_M)
True
```

You can specify rotations by named arguments

```
>>> np.all(M3 == euler2mat(x=xrot))
True
```

When applying M to a vector, the vector should column vector to the right of M. If the right hand side is a 2D array rather than a vector, then each column of the 2D array represents a vector.

```
>>> vec = np.array([1, 0, 0]).reshape((3,1))
>>> v2 = np.dot(M, vec)
>>> vecs = np.array([[1, 0, 0],[0, 1, 0]]).T # giving 3x2 array
>>> vecs2 = np.dot(M, vecs)
```

Rotations are counter-clockwise.

```
>>> zred = np.dot(euler2mat(z=np.pi/2), np.eye(3))
>>> np.allclose(zred, [[0, -1, 0],[1, 0, 0], [0, 0, 1]])
True
>>> yred = np.dot(euler2mat(y=np.pi/2), np.eye(3))
>>> np.allclose(yred, [[0, 0, 1],[0, 1, 0], [-1, 0, 0]])
True
>>> xred = np.dot(euler2mat(x=np.pi/2), np.eye(3))
>>> np.allclose(xred, [[1, 0, 0],[0, 0, -1], [0, 1, 0]])
True
```

euler2quat

nibabel.eulerangles.**euler2quat**(*z=0*, *y=0*, *x=0*)

Return quaternion corresponding to these Euler angles

Uses the z, then y, then x convention above

Parametersz : scalar

Rotation angle in radians around z-axis (performed first)

y : scalar

Rotation angle in radians around y-axis

x : scalar

Rotation angle in radians around x-axis (performed last)

Returnsquat : array shape (4,)

Quaternion in w, x, y z (real, then vector) format

Notes

We can derive this formula in Sympy using:

1. Formula giving quaternion corresponding to rotation of theta radians about arbitrary axis: http://mathworld.wolfram.com/EulerParameters.html
2. Generated formulae from 1.) for quaternions corresponding to theta radians rotations about `x, y, z` axes
3. Apply quaternion multiplication formula - https://en.wikipedia.org/wiki/Quaternions#Hamilton_product - to formulae from 2.) to give formula for combined rotations.

mat2euler

nibabel.eulerangles.**mat2euler**(*M*, *cy_thresh=None*)

Discover Euler angle vector from 3x3 matrix

Uses the conventions above.

ParametersM : array-like, shape (3,3)

cy_thresh : None or scalar, optional

threshold below which to give up on straightforward arctan for estimating x rotation. If None (default), estimate from precision of input.

Returnsz : scalar

y : scalar

x : scalar

Rotations in radians around z, y, x axes, respectively

Notes

If there was no numerical error, the routine could be derived using Sympy expression for z then y then x rotation matrix, which is:

```
[                       cos(y)*cos(z),                       -cos(y)*sin(z),          sin(y)],
[cos(x)*sin(z) + cos(z)*sin(x)*sin(y), cos(x)*cos(z) - sin(x)*sin(y)*sin(z), -cos(y)*sin(x)],
[sin(x)*sin(z) - cos(x)*cos(z)*sin(y), cos(z)*sin(x) + cos(x)*sin(y)*sin(z),  cos(x)*cos(y)]
```

with the obvious derivations for z, y, and x

z = atan2(-r12, r11) y = asin(r13) x = atan2(-r23, r33)

Problems arise when cos(y) is close to zero, because both of:

```
z = atan2(cos(y)*sin(z), cos(y)*cos(z))
x = atan2(cos(y)*sin(x), cos(x)*cos(y))
```

will be close to atan2(0, 0), and highly unstable.

The `cy` fix for numerical instability below is from: *Graphics Gems IV*, Paul Heckbert (editor), Academic Press, 1994, ISBN: 0123361559. Specifically it comes from EulerAngles.c by Ken Shoemake, and deals with the case where cos(y) is close to zero:

See: http://www.graphicsgems.org/

The code appears to be licensed (from the website) as "can be used without restrictions".

quat2euler

nibabel.eulerangles.**quat2euler**(*q*)

Return Euler angles corresponding to quaternion *q*

Parametersq : 4 element sequence

w, x, y, z of quaternion

Returnsz : scalar

Rotation angle in radians around z-axis (performed first)

y : scalar

Rotation angle in radians around y-axis

x : scalar

Rotation angle in radians around x-axis (performed last)

Notes

It's possible to reduce the amount of calculation a little, by combining parts of the `quat2mat` and `mat2euler` functions, but the reduction in computation is small, and the code repetition is large.

funcs

Processor functions for images

as_closest_canonical(img[, enforce_diag])	Return *img* with data reordered to be closest to canonical
concat_images(images[, check_affines, axis])	Concatenate images in list to single image, along specified dimension
four_to_three(img)	Create 3D images from 4D image by slicing over last axis
squeeze_image(img)	Return image, remove axes length 1 at end of image shape

as_closest_canonical

nibabel.funcs.**as_closest_canonical**(*img*, *enforce_diag=False*)

Return *img* with data reordered to be closest to canonical

Canonical order is the ordering of the output axes.

Parametersimg : `spatialimage`

enforce_diag : {False, True}, optional

If True, before transforming image, check if the resulting image affine will be close to diagonal, and if not, raise an error

Returnscanonical_img : `spatialimage`

Version of *img* where the underlying array may have been reordered and / or flipped so that axes 0,1,2 are those axes in the input data that are, respectively, closest to the output axis orientation. We modify the affine accordingly. If *img* is already has the correct data ordering, we just return *img* unmodified.

concat_images

nibabel.funcs.**concat_images**(*images*, *check_affines=True*, *axis=None*)

Concatenate images in list to single image, along specified dimension

Parametersimages : sequence

sequence of `SpatialImage` or filenames of the same dimensionalitys

check_affines : {True, False}, optional

If True, then check that all the affines for *images* are nearly the same, raising a `ValueError` otherwise. Default is True

axis : None or int, optional

If None, concatenates on a new dimension. This requires all images to be the same shape. If not None, concatenates on the specified dimension. This requires all images to be the same shape, except on the specified dimension.

Returns :

———- :

concat_img : `SpatialImage`

New image resulting from concatenating *images* across last dimension

four_to_three

`nibabel.funcs.`**`four_to_three`**(*img*)

Create 3D images from 4D image by slicing over last axis

Parametersimg : image

4D image instance of some class with methods `get_data`, `header` and `affine`, and a class constructor allowing klass(data, affine, header)

Returnsimgs : list

list of 3D images

squeeze_image

`nibabel.funcs.`**`squeeze_image`**(*img*)

Return image, remove axes length 1 at end of image shape

For example, an image may have shape (10,20,30,1,1). In this case squeeze will result in an image with shape (10,20,30). See doctests for further description of behavior.

Parametersimg : `SpatialImage`

Returnssqueezed_img : `SpatialImage`

Copy of img, such that data, and data shape have been squeezed, for dimensions > 3rd, and at the end of the shape list

Examples

```
>>> import nibabel as nf
>>> shape = (10,20,30,1,1)
>>> data = np.arange(np.prod(shape)).reshape(shape)
>>> affine = np.eye(4)
>>> img = nf.Nifti1Image(data, affine)
>>> img.shape == (10, 20, 30, 1, 1)
True
>>> img2 = squeeze_image(img)
>>> img2.shape == (10, 20, 30)
True
```

If the data are 3D then last dimensions of 1 are ignored

```
>>> shape = (10,1,1)
>>> data = np.arange(np.prod(shape)).reshape(shape)
>>> img = nf.ni1.Nifti1Image(data, affine)
>>> img.shape == (10, 1, 1)
True
>>> img2 = squeeze_image(img)
>>> img2.shape == (10, 1, 1)
True
```

Only *final* dimensions of 1 are squeezed

```
>>> shape = (1, 1, 5, 1, 2, 1, 1)
>>> data = data.reshape(shape)
>>> img = nf.ni1.Nifti1Image(data, affine)
>>> img.shape == (1, 1, 5, 1, 2, 1, 1)
True
>>> img2 = squeeze_image(img)
>>> img2.shape == (1, 1, 5, 1, 2)
True
```

imageclasses

Define supported image classes and names

---

imageglobals

Defaults for images and headers

error_level is the problem level (see BatteryRunners) at which an error will be raised, by the batteryrunners `log_raise` method. Thus a level of 0 will result in an error for any problem at all, and a level of 50 will mean no errors will be raised (unless someone's put some strange problem_level > 50 code in).

`logger` is the default logger (python log instance)

To set the log level (log message appears for problem of level >= log level), use e.g. `logger.level = 40`.

As for most loggers, if `logger.level == 0` then a default log level is used - use `logger.getEffectiveLevel()` to see what that default is.

Use `logger.level = 1` to see all messages.

ErrorLevel(level)	Context manager to set log error level
LoggingOutputSuppressor	Context manager to prevent global logger from printing

ErrorLevel

class nibabel.imageglobals.**ErrorLevel**(*level*)

Bases: object

Context manager to set log error level

__init__(*level*)

LoggingOutputSuppressor

class nibabel.imageglobals.**LoggingOutputSuppressor**
Bases: object

Context manager to prevent global logger from printing

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

loadsave

Utilities to load and save image objects

guessed_image_type(filename)	Guess image type from file *filename*
load(filename, **kwargs)	Load file given filename, guessing at file type
save(img, filename)	Save an image to file adapting format to *filename*
which_analyze_type(binaryblock)	Is *binaryblock* from NIfTI1, NIfTI2 or Analyze header?

guessed_image_type

nibabel.loadsave.**guessed_image_type**(*filename*)
Guess image type from file *filename*

Parametersfilename : str

File name containing an image

Returnsimage_class : class

Class corresponding to guessed image type

load

nibabel.loadsave.**load**(*filename*, ***kwargs*)
Load file given filename, guessing at file type

Parametersfilename : string

specification of file to load

****kwargs** : keyword arguments

Keyword arguments to format-specific load

Returnsimg : SpatialImage

Image of guessed type

save

nibabel.loadsave.**save**(*img*, *filename*)
Save an image to file adapting format to *filename*

Parametersimg : SpatialImage

image to save

filename : str

filename (often implying filenames) to which to save *img*.

ReturnsNone :

which_analyze_type

nibabel.loadsave.**which_analyze_type**(*binaryblock*)

Is *binaryblock* from NIfTI1, NIfTI2 or Analyze header?

Parametersbinaryblock : bytes

The *binaryblock* is 348 bytes that might be NIfTI1, NIfTI2, Analyze, or None of the the above.

Returnshdr_type : str

- a nifti1 header (pair or single) -> return 'nifti1'
- a nifti2 header (pair or single) -> return 'nifti2'
- an Analyze header -> return 'analyze'
- None of the above -> return None

Notes

Algorithm:

- read in the first 4 bytes from the file as 32-bit int `sizeof_hdr`
- if `sizeof_hdr` is 540 or byteswapped 540 -> assume nifti2
- Check for 'ni1', 'n+1' magic -> assume nifti1
- if `sizeof_hdr` is 348 or byteswapped 348 assume Analyze
- Return None

orientations

Utilities for calculating and applying affine orientations

OrientationError	
aff2axcodes(aff[, labels, tol])	axis direction codes for affine *aff*
apply_orientation(arr, ornt)	Apply transformations implied by *ornt* to the first
axcodes2ornt(axcodes[, labels])	Convert axis codes *axcodes* to an orientation
flip_axis(arr[, axis])	Flip contents of *axis* in array *arr*
inv_ornt_aff(ornt, shape)	Affine transform reversing transforms implied in *ornt*
io_orientation(affine[, tol])	Orientation of input axes in terms of output axes for *affine*
ornt2axcodes(ornt[, labels])	Convert orientation *ornt* to labels for axis directions
ornt_transform(start_ornt, end_ornt)	Return the orientation that transforms from *start_ornt* to *end_ornt*.

OrientationError

class nibabel.orientations.**OrientationError**

Bases: exceptions.Exception

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

aff2axcodes

nibabel.orientations.**aff2axcodes**(*aff*, *labels=None*, *tol=None*)
axis direction codes for affine *aff*

Parametersaff : (N,M) array-like

affine transformation matrix

labels : optional, None or sequence of (2,) sequences

Labels for negative and positive ends of output axes of *aff*. See docstring for `ornt2axcodes` for more detail

tol : None or float

Tolerance for SVD of affine - see `io_orientation` for more detail.

Returnsaxcodes : (N,) tuple

labels for positive end of voxel axes. Dropped axes get a label of None.

Examples

```
>>> aff = [[0,1,0,10],[-1,0,0,20],[0,0,1,30],[0,0,0,1]]
>>> aff2axcodes(aff, (('L','R'),('B','F'),('D','U')))
('B', 'R', 'U')
```

apply_orientation

nibabel.orientations.**apply_orientation**(*arr*, *ornt*)
Apply transformations implied by *ornt* to the first n axes of the array *arr*

Parametersarr : array-like of data with ndim >= n

ornt : (n,2) orientation array

orientation transform. `ornt[N,1]` is flip of axis N of the array implied by `shape`, where 1 means no flip and -1 means flip. For example, if `N==0 and `ornt[0,1] == -1`, and there's an array `arr` of shape *shape*, the flip would correspond to the effect of `np.flipud(arr)`. `ornt[:,0]` is the transpose that needs to be done to the implied array, as in `arr.transpose(ornt[:,0])`

Returnst_arr : ndarray

data array *arr* transformed according to ornt

axcodes2ornt

nibabel.orientations.**axcodes2ornt**(*axcodes*, *labels=None*)
Convert axis codes *axcodes* to an orientation

Parametersaxcodes : (N,) tuple

axis codes - see ornt2axcodes docstring

labels : optional, None or sequence of (2,) sequences

(2,) sequences are labels for (beginning, end) of output axis. That is, if the first element in *axcodes* is `front`, and the second (2,) sequence in *labels* is ('back', 'front') then the first row of *ornt* will be `[1, 1]`. If None, equivalent to `(('L','R'),('P','A'),('I','S'))` - that is - RAS axes.

Returnsornt : (N,2) array-like

orientation array - see io_orientation docstring

Examples

```
>>> axcodes2ornt(('F', 'L', 'U'), (('L','R'),('B','F'),('D','U')))
array([[ 1.,  1.],
       [ 0., -1.],
       [ 2.,  1.]])
```

flip_axis

nibabel.orientations.**flip_axis**(*arr*, *axis=0*)

Flip contents of *axis* in array *arr*

`flip_axis` is the same transform as `np.flipud`, but for any axis. For example `flip_axis(arr, axis=0)` is the same transform as `np.flipud(arr)`, and `flip_axis(arr, axis=1)` is the same transform as `np.fliplr(arr)`

Parametersarr : array-like

axis : int, optional

axis to flip. Default *axis* == 0

Returnsfarr : array

Array with axis *axis* flipped

Examples

```
>>> a = np.arange(6).reshape((2,3))
>>> a
array([[0, 1, 2],
       [3, 4, 5]])
>>> flip_axis(a, axis=0)
array([[3, 4, 5],
       [0, 1, 2]])
>>> flip_axis(a, axis=1)
array([[2, 1, 0],
       [5, 4, 3]])
```

inv_ornt_aff

nibabel.orientations.**inv_ornt_aff**(*ornt*, *shape*)

Affine transform reversing transforms implied in *ornt*

Imagine you have an array `arr` of shape *shape*, and you apply the transforms implied by *ornt* (more below), to get `tarr`. `tarr` may have a different shape `shape_prime`. This routine returns the affine that will take a array coordinate for `tarr` and give you the corresponding array coordinate in `arr`.

Parametersornt : (p, 2) ndarray

orientation transform. `ornt[P, 1]` is flip of axis N of the array implied by `shape`, where 1 means no flip and -1 means flip. For example, if `P==0` and `ornt[0, 1] == -1`, and there's an array `arr` of shape *shape*, the flip would correspond to the effect of `np.flipud(arr)`. `ornt[:,0]` gives us the (reverse of the) transpose that has been done to `arr`. If there are any NaNs in *ornt*, we raise an `OrientationError` (see notes)

shape : length p sequence

shape of array you may transform with *ornt*

Returnstransform_affine : (p + 1, p + 1) ndarray

An array `arr` (shape *shape*) might be transformed according to *ornt*, resulting in a transformed array `tarr`. *transformed_affine* is the transform that takes you from array coordinates in `tarr` to array coordinates in `arr`.

Notes

If a row in *ornt* contains NaN, this means that the input row does not influence the output space, and is thus effectively dropped from the output space. In that case one `tarr` coordinate maps to many `arr` coordinates, we can't invert the transform, and we raise an error

io_orientation

`nibabel.orientations.`**`io_orientation`**(*affine*, *tol=None*)

Orientation of input axes in terms of output axes for *affine*

Valid for an affine transformation from `p` dimensions to `q` dimensions (`affine.shape == (q + 1, p + 1)`).

The calculated orientations can be used to transform associated arrays to best match the output orientations. If `p` > `q`, then some of the output axes should be considered dropped in this orientation.

Parametersaffine : (q+1, p+1) ndarray-like

Transformation affine from `p` inputs to `q` outputs. Usually this will be a shape (4,4) matrix, transforming 3 inputs to 3 outputs, but the code also handles the more general case

tol : {None, float}, optional

threshold below which SVD values of the affine are considered zero. If *tol* is None, and `S` is an array with singular values for *affine*, and `eps` is the epsilon value for datatype of `S`, then *tol* set to `S.max() * max((q, p)) * eps`

Returnsorientations : (p, 2) ndarray

one row per input axis, where the first value in each row is the closest corresponding output axis. The second value in each row is 1 if the input axis is in the same direction as the corresponding output axis and -1 if it is in the opposite direction. If a row is [np.nan, np.nan], which can happen when p > q, then this row should be considered dropped.

ornt2axcodes

nibabel.orientations.**ornt2axcodes**(*ornt*, *labels=None*)

Convert orientation *ornt* to labels for axis directions

Parametersornt : (N,2) array-like

orientation array - see io_orientation docstring

labels : optional, None or sequence of (2,) sequences

(2,) sequences are labels for (beginning, end) of output axis. That is, if the first row in *ornt* is `[1, 1]`, and the second (2,) sequence in *labels* is ('back', 'front') then the first returned axis code will be `'front'`. If the first row in *ornt* had been `[1, -1]` then the first returned value would have been `'back'`. If None, equivalent to `(('L','R'),('P','A'),('I','S'))` - that is - RAS axes.

Returnsaxcodes : (N,) tuple

labels for positive end of voxel axes. Dropped axes get a label of None.

Examples

```
>>> ornt2axcodes([[1, 1],[0,-1],[2,1]], (('L','R'),('B','F'),('D','U')))
('F', 'L', 'U')
```

ornt_transform

nibabel.orientations.**ornt_transform**(*start_ornt*, *end_ornt*)

Return the orientation that transforms from *start_ornt* to *end_ornt*.

Parametersstart_ornt : (n,2) orientation array

Initial orientation.

end_ornt : (n,2) orientation array

Final orientation.

Returnsorientations : (p, 2) ndarray

The orientation that will transform the *start_ornt* to the *end_ornt*.

quaternions

Functions to operate on, or return, quaternions.

The module also includes functions for the closely related angle, axis pair as a specification for rotation.

Quaternions here consist of 4 values `w, x, y, z`, where `w` is the real (scalar) part, and `x, y, z` are the complex (vector) part.

Note - rotation matrices here apply to column vectors, that is, they are applied on the left of the vector. For example:

```
>>> import numpy as np
>>> q = [0, 1, 0, 0] # 180 degree rotation around axis 0
>>> M = quat2mat(q) # from this module
>>> vec = np.array([1, 2, 3]).reshape((3,1)) # column vector
>>> tvec = np.dot(M, vec)
```

angle_axis2mat(theta, vector[, is_normalized])	Rotation matrix of angle *theta* around *vector*
angle_axis2quat(theta, vector[, is_normalized])	Quaternion for rotation of angle *theta* around *vector*
conjugate(q)	Conjugate of quaternion
eye()	Return identity quaternion
fillpositive(xyz[, w2_thresh])	Compute unit quaternion from last 3 values
inverse(q)	Return multiplicative inverse of quaternion *q*
isunit(q)	Return True is this is very nearly a unit quaternion
mat2quat(M)	Calculate quaternion corresponding to given rotation matrix
mult(q1, q2)	Multiply two quaternions
nearly_equivalent(q1, q2[, rtol, atol])	Returns True if *q1* and *q2* give near equivalent transforms
norm(q)	Return norm of quaternion
quat2angle_axis(quat[, identity_thresh])	Convert quaternion to rotation of angle around axis
quat2mat(q)	Calculate rotation matrix corresponding to quaternion
rotate_vector(v, q)	Apply transformation in quaternion *q* to vector *v*

angle_axis2mat

nibabel.quaternions.**angle_axis2mat**(*theta*, *vector*, *is_normalized=False*)

Rotation matrix of angle *theta* around *vector*

Parameterstheta : scalar

angle of rotation

vector : 3 element sequence

vector specifying axis for rotation.

is_normalized : bool, optional

True if vector is already normalized (has norm of 1). Default False

Returnsmat : array shape (3,3)

rotation matrix for specified rotation

Notes

From: https://en.wikipedia.org/wiki/Rotation_matrix#Axis_and_angle

angle_axis2quat

nibabel.quaternions.**angle_axis2quat**(*theta*, *vector*, *is_normalized=False*)

Quaternion for rotation of angle *theta* around *vector*

Parameterstheta : scalar

angle of rotation

vector : 3 element sequence

vector specifying axis for rotation.

is_normalized : bool, optional

True if vector is already normalized (has norm of 1). Default False

Returnsquat : 4 element sequence of symbols

quaternion giving specified rotation

Notes

Formula from http://mathworld.wolfram.com/EulerParameters.html

Examples

```
>>> q = angle_axis2quat(np.pi, [1, 0, 0])
>>> np.allclose(q, [0, 1, 0,  0])
True
```

conjugate

nibabel.quaternions.**conjugate**(*q*)

Conjugate of quaternion

Parametersq : 4 element sequence

w, i, j, k of quaternion

Returnsconjq : array shape (4,)

w, i, j, k of conjugate of *q*

eye

nibabel.quaternions.**eye**()

Return identity quaternion

fillpositive

nibabel.quaternions.**fillpositive**(*xyz*, *w2_thresh=None*)

Compute unit quaternion from last 3 values

Parametersxyz : iterable

iterable containing 3 values, corresponding to quaternion x, y, z

w2_thresh : None or float, optional

threshold to determine if w squared is really negative. If None (default) then w2_thresh set equal to `-np.finfo(xyz.dtype).eps`, if possible, otherwise `-np.finfo(np.float).eps`

Returnswxyz : array shape (4,)

Full 4 values of quaternion

Notes

If w, x, y, z are the values in the full quaternion, assumes w is positive.

Gives error if w*w is estimated to be negative

w = 0 corresponds to a 180 degree rotation

The unit quaternion specifies that np.dot(wxyz, wxyz) == 1.

If w is positive (assumed here), w is given by:

w = np.sqrt(1.0-(x*x+y*y+z*z))

w2 = 1.0-(x*x+y*y+z*z) can be near zero, which will lead to numerical instability in sqrt. Here we use the system maximum float type to reduce numerical instability

Examples

```
>>> import numpy as np
>>> wxyz = fillpositive([0,0,0])
>>> np.all(wxyz == [1, 0, 0, 0])
True
>>> wxyz = fillpositive([1,0,0]) # Corner case; w is 0
>>> np.all(wxyz == [0, 1, 0, 0])
True
>>> np.dot(wxyz, wxyz)
1.0
```

inverse

nibabel.quaternions.**inverse**(*q*)

Return multiplicative inverse of quaternion *q*

Parametersq : 4 element sequence

w, i, j, k of quaternion

Returnsinvq : array shape (4,)

w, i, j, k of quaternion inverse

isunit

nibabel.quaternions.**isunit**(*q*)

Return True is this is very nearly a unit quaternion

mat2quat

nibabel.quaternions.**mat2quat**(*M*)

Calculate quaternion corresponding to given rotation matrix

ParametersM : array-like

3x3 rotation matrix

Returnsq : (4,) array

closest quaternion to input matrix, having positive q[0]

Notes

Method claimed to be robust to numerical errors in M

Constructs quaternion by calculating maximum eigenvector for matrix K (constructed from input *M*). Although this is not tested, a maximum eigenvalue of 1 corresponds to a valid rotation.

A quaternion q*-1 corresponds to the same rotation as q; thus the sign of the reconstructed quaternion is arbitrary, and we return quaternions with positive w (q[0]).

References

- https://en.wikipedia.org/wiki/Rotation_matrix#Quaternion
- Bar-Itzhack, Itzhack Y. (2000), "New method for extracting the quaternion from a rotation matrix", AIAA Journal of Guidance, Control and Dynamics 23(6):1085-1087 (Engineering Note), ISSN 0731-5090

Examples

```
>>> import numpy as np
>>> q = mat2quat(np.eye(3)) # Identity rotation
>>> np.allclose(q, [1, 0, 0, 0])
True
>>> q = mat2quat(np.diag([1, -1, -1]))
>>> np.allclose(q, [0, 1, 0, 0]) # 180 degree rotn around axis 0
True
```

mult

nibabel.quaternions.**mult**(*q1*, *q2*)

Multiply two quaternions

Parametersq1 : 4 element sequence

q2 : 4 element sequence

Returnsq12 : shape (4,) array

Notes

See : https://en.wikipedia.org/wiki/Quaternions#Hamilton_product

nearly_equivalent

nibabel.quaternions.**nearly_equivalent**(*q1*, *q2*, *rtol=1e-05*, *atol=1e-08*)

Returns True if *q1* and *q2* give near equivalent transforms

q1 may be nearly numerically equal to *q2*, or nearly equal to *q2* * -1 (because a quaternion multiplied by -1 gives the same transform).

Parametersq1 : 4 element sequence

w, x, y, z of first quaternion

q2 : 4 element sequence

w, x, y, z of second quaternion

Returnsequiv : bool

True if *q1* and *q2* are nearly equivalent, False otherwise

Examples

```
>>> q1 = [1, 0, 0, 0]
>>> nearly_equivalent(q1, [0, 1, 0, 0])
False
>>> nearly_equivalent(q1, [1, 0, 0, 0])
True
>>> nearly_equivalent(q1, [-1, 0, 0, 0])
True
```

norm

nibabel.quaternions.**norm**(*q*)

Return norm of quaternion

Parametersq : 4 element sequence

w, i, j, k of quaternion

Returnsn : scalar

quaternion norm

quat2angle_axis

nibabel.quaternions.**quat2angle_axis**(*quat*, *identity_thresh=None*)

Convert quaternion to rotation of angle around axis

Parametersquat : 4 element sequence

w, x, y, z forming quaternion

identity_thresh : None or scalar, optional

threshold below which the norm of the vector part of the quaternion (x, y, z) is deemed to be 0, leading to the identity rotation. None (the default) leads to a threshold estimated based on the precision of the input.

Returnstheta : scalar

angle of rotation

vector : array shape (3,)

axis around which rotation occurs

Notes

A quaternion for which x, y, z are all equal to 0, is an identity rotation. In this case we return a 0 angle and an arbitrary vector, here [1, 0, 0]

Examples

```
>>> theta, vec = quat2angle_axis([0, 1, 0, 0])
>>> np.allclose(theta, np.pi)
True
>>> vec
array([ 1.,  0.,  0.])
```

If this is an identity rotation, we return a zero angle and an arbitrary vector

```
>>> quat2angle_axis([1, 0, 0, 0])
(0.0, array([ 1.,  0.,  0.]))
```

quat2mat

nibabel.quaternions.**quat2mat**(*q*)

Calculate rotation matrix corresponding to quaternion

Parametersq : 4 element array-like

ReturnsM : (3,3) array

Rotation matrix corresponding to input quaternion *q*

Notes

Rotation matrix applies to column vectors, and is applied to the left of coordinate vectors. The algorithm here allows non-unit quaternions.

References

Algorithm from https://en.wikipedia.org/wiki/Rotation_matrix#Quaternion

Examples

```
>>> import numpy as np
>>> M = quat2mat([1, 0, 0, 0]) # Identity quaternion
>>> np.allclose(M, np.eye(3))
True
>>> M = quat2mat([0, 1, 0, 0]) # 180 degree rotn around axis 0
>>> np.allclose(M, np.diag([1, -1, -1]))
True
```

rotate_vector

nibabel.quaternions.**rotate_vector**(*v*, *q*)

Apply transformation in quaternion *q* to vector *v*

Parametersv : 3 element sequence

3 dimensional vector

q : 4 element sequence

w, i, j, k of quaternion

Returnsvdash : array shape (3,)

v rotated by quaternion *q*

Notes

See: https://en.wikipedia.org/wiki/Quaternions_and_spatial_rotation#Describing_rotations_with_quaternions

spatialimages

A simple spatial image class

The image class maintains the association between a 3D (or greater) array, and an affine transform that maps voxel coordinates to some world space. It also has a `header` - some standard set of meta-data that is specific to the image format, and `extra` - a dictionary container for any other metadata.

It has attributes:

- extra

methods:

- .get_data()
- .get_affine() (deprecated, use affine property instead)
- .get_header() (deprecated, use header property instead)
- .to_filename(fname) - writes data to filename(s) derived from `fname`, where the derivation may differ between formats.
- to_file_map() - save image to files with which the image is already associated.
- .get_shape() (deprecated)

properties:

- shape
- affine
- header
- dataobj

classmethods:

- from_filename(fname) - make instance by loading from filename
- from_file_map(fmap) - make instance from file map

- instance_to_filename(img, fname) - save `img` instance to filename `fname`.

You cannot slice an image, and trying to slice an image generates an informative TypeError.

There are several ways of writing data.

There is the usual way, which is the default:

```
img.to_filename(fname)
```

and that is, to take the data encapsulated by the image and cast it to the datatype the header expects, setting any available header scaling into the header to help the data match.

You can load the data into an image from file with:

```
img.from_filename(fname)
```

The image stores its associated files in its `file_map` attribute. In order to just save an image, for which you know there is an associated filename, or other storage, you can do:

```
img.to_file_map()
```

You can get the data out again with:

```
img.get_data()
```

Less commonly, for some image types that support it, you might want to fetch out the unscaled array via the object containing the data:

```
unscaled_data = img.dataobj.get_unscaled()
```

Analyze-type images (including nifti) support this, but others may not (MINC, for example).

Sometimes you might to avoid any loss of precision by making the data type the same as the input:

```
hdr = img.header
hdr.set_data_dtype(data.dtype)
img.to_filename(fname)
```

Files interface

The image has an attribute `file_map`. This is a mapping, that has keys corresponding to the file types that an image needs for storage. For example, the Analyze data format needs an `image` and a `header` file type for storage:

```
>>> import nibabel as nib
>>> data = np.arange(24, dtype='f4').reshape((2,3,4))
>>> img = nib.AnalyzeImage(data, np.eye(4))
>>> sorted(img.file_map)
['header', 'image']
```

The values of `file_map` are not in fact files but objects with attributes `filename`, `fileobj` and `pos`.

The reason for this interface, is that the contents of files has to contain enough information so that an existing image instance can save itself back to the files pointed to in `file_map`. When a file holder holds active file-like objects, then these may be affected by the initial file read; in this case, the contains file-like objects need to carry the position at which a write (with `to_files`) should place the data. The `file_map` contents should therefore be such, that this will work:

```
>>> # write an image to files
>>> from io import BytesIO
>>> file_map = nib.AnalyzeImage.make_file_map()
>>> file_map['image'].fileobj = BytesIO()
>>> file_map['header'].fileobj = BytesIO()
>>> img = nib.AnalyzeImage(data, np.eye(4))
>>> img.file_map = file_map
>>> img.to_file_map()
>>> # read it back again from the written files
>>> img2 = nib.AnalyzeImage.from_file_map(file_map)
>>> np.all(img2.get_data() == data)
True
>>> # write, read it again
>>> img2.to_file_map()
>>> img3 = nib.AnalyzeImage.from_file_map(file_map)
>>> np.all(img3.get_data() == data)
True
```

Header([data_dtype, shape, zooms])	Template class to implement header protocol
HeaderDataError	Class to indicate error in getting or setting header data
HeaderTypeError	Class to indicate error in parameters into header functions
ImageDataError	
ImageFileError	
SpatialImage(dataobj, affine[, header, ...])	Initialize image
supported_np_types(obj)	Numpy data types that instance *obj* supports

Header

class nibabel.spatialimages.**Header**(*data_dtype=<type 'numpy.float32'>*, *shape=(0,)*, *zooms=None*)

Bases: object

Template class to implement header protocol

__init__(*data_dtype=<type 'numpy.float32'>*, *shape=(0,)*, *zooms=None*)

copy()
Copy object to independent representation

The copy should not be affected by any changes to the original object.

data_from_fileobj(*fileobj*)
Read binary image data from *fileobj*

data_layout = 'F'

data_to_fileobj(*data*, *fileobj*, *rescale=True*)
Write array data *data* as binary to *fileobj*

Parametersdata : array-like
data to write
fileobj : file-like object
file-like object implementing 'write'
rescale : {True, False}, optional
Whether to try and rescale data to match output dtype specified by header. For this minimal header, *rescale* has no effect

default_x_flip = True

classmethod **from_fileobj**(*klass*, *fileobj*)

classmethod **from_header**(*klass*, *header=None*)

get_base_affine()

get_best_affine()

get_data_dtype()

get_data_shape()

get_zooms()

set_data_dtype(*dtype*)

set_data_shape(*shape*)

set_zooms(*zooms*)

write_to(*fileobj*)

HeaderDataError

class nibabel.spatialimages.**HeaderDataError**
Bases: exceptions.Exception

Class to indicate error in getting or setting header data

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

HeaderTypeError

class nibabel.spatialimages.**HeaderTypeError**
Bases: exceptions.Exception

Class to indicate error in parameters into header functions

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

ImageDataError

class nibabel.spatialimages.**ImageDataError**
Bases: exceptions.Exception

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

ImageFileError

class nibabel.spatialimages.**ImageFileError**
Bases: exceptions.Exception

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

SpatialImage

class nibabel.spatialimages.**SpatialImage**(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)

Bases: object

Initialize image

The image is a combination of (array, affine matrix, header), with optional metadata in *extra*, and filename / file-like objects contained in the *file_map* mapping.

Parametersdataobj : object

Object containg image data. It should be some object that retuns an array from `np.asanyarray`. It should have a `shape` attribute or property

affine : None or (4,4) array-like

homogenous affine giving relationship between voxel coordinates and world coordinates. Affine can also be None. In this case, `obj.affine` also returns None, and the affine as written to disk will depend on the file format.

header : None or mapping or header instance, optional

metadata for this image format

extra : None or mapping, optional

metadata to associate with image that cannot be stored in the metadata of this image type

file_map : mapping, optional

mapping giving file information for this image format

__init__(*dataobj*, *affine*, *header=None*, *extra=None*, *file_map=None*)

Initialize image

The image is a combination of (array, affine matrix, header), with optional metadata in *extra*, and filename / file-like objects contained in the *file_map* mapping.

Parametersdataobj : object
Object containg image data. It should be some object that retuns an array from `np.asanyarray`. It should have a `shape` attribute or property
affine : None or (4,4) array-like
homogenous affine giving relationship between voxel coordinates and world coordinates. Affine can also be None. In this case, `obj.affine` also returns None, and the affine as written to disk will depend on the file format.
header : None or mapping or header instance, optional
metadata for this image format
extra : None or mapping, optional
metadata to associate with image that cannot be stored in the metadata of this image type
file_map : mapping, optional
mapping giving file information for this image format

affine

dataobj

files_types = (('image', None),)

classmethod filespec_to_file_map(*klass*, *filespec*)

Make *file_map* for this class from filename *filespec*

Class method

Parametersfilespec : str
Filename that might be for this image file type.
Returnsfile_map : dict
file_map dict with (key, value) pairs of (`file_type`, FileHolder instance), where `file_type` is a string giving the type of the contained file.
RaisesImageFileError :
if *filespec* is not recognizable as being a filename for this image type.

classmethod `filespec_to_files`(*klass*, *filespec*)

classmethod `from_file_map`(*klass*, *file_map*)

classmethod `from_filename`(*klass*, *filename*)

classmethod `from_files`(*klass*, *file_map*)

classmethod `from_filespec`(*klass*, *filespec*)

classmethod `from_image`(*klass*, *img*)
Class method to create new instance of own class from *img*
Parametersimg : `spatialimage` instance
In fact, an object with the API of `spatialimage` - specifically `dataobj`, `affine`, `header` and `extra`.
Returnscimg : `spatialimage` instance
Image, of our own class

`get_affine`()
Get affine from image

Please use the *affine* property instead of *get_affine*; we will deprecate this method in future versions of nibabel.

`get_data`(*caching='fill'*)
Return image data from image with any necessary scalng applied

The image `dataobj` property can be an array proxy or an array. An array proxy is an object that knows how to load the image data from disk. An image with an array proxy `dataobj` is a *proxy image*; an image with an array in `dataobj` is an *array image*.

The default behavior for `get_data()` on a proxy image is to read the data from the proxy, and store in an internal cache. Future calls to `get_data` will return the cached array. This is the behavior selected with *caching* == "fill".

Once the data has been cached and returned from an array proxy, if you modify the returned array, you will also modify the cached array (because they are the same array). Regardless of the *caching* flag, this is always true of an array image.
Parameterscaching : {'fill', 'unchanged'}, optional
See the Notes section for a detailed explanation. This argument specifies whether the image object should fill in an internal cached reference to the returned image data array. "fill" specifies that the image should fill an internal cached reference if currently empty. Future calls to `get_data` will return this cached reference. You might prefer "fill" to save the image object from having to reload the array data from disk on each call to `get_data`. "unchanged" means that the image should not fill in the internal cached reference if the cache is currently empty. You might prefer "unchanged" to "fill" if you want to make sure that the call to `get_data` does not create an extra (cached) reference to the returned array. In this case it is easier for Python to free the memory from the returned array.
Returnsdata : array
array of image data
See also:

uncacheempty the array data cache

Notes

All images have a property `dataobj` that represents the image array data. Images that have been loaded from files usually do not load the array data from file immediately, in order to reduce image load time and memory use. For these images, `dataobj` is an *array proxy*; an object that knows how to load the image array data from file.

By default (*caching* == "fill"), when you call `get_data` on a proxy image, we load the array data from disk, store (cache) an internal reference to this array data, and return the array. The next time you call `get_data`, you will get the cached reference to the array, so we don't have to load the array data from disk again.

Array images have a `dataobj` property that already refers to an array in memory, so there is no benefit to caching, and the *caching* keywords have no effect.

For proxy images, you may not want to fill the cache after reading the data from disk because the cache will hold onto the array memory until the image object is deleted, or you use the image `uncache` method. If you don't want to fill the cache, then always use `get_data(caching='unchanged')`; in this case `get_data` will not fill the cache (store the reference to the array) if the cache is empty (no reference to the array). If the cache is full, "unchanged" leaves the cache full and returns the cached array reference.

The cache can effect the behavior of the image, because if the cache is full, or you have an array image, then modifying the returned array will modify the result of future calls to `get_data()`. For example you might do this:

```
>>> import os
>>> import nibabel as nib
>>> from nibabel.testing import data_path
>>> img_fname = os.path.join(data_path, 'example4d.nii.gz')
```

```
>>> img = nib.load(img_fname) # This is a proxy image
>>> nib.is_proxy(img.dataobj)
True
```

The array is not yet cached by a call to "get_data", so: >>> img.in_memory False

After we call `get_data` using the default *caching='fill', the cache contains a reference to the returned array ''data'*:

```
>>> data = img.get_data()
>>> img.in_memory
True
```

We modify an element in the returned data array:

```
>>> data[0, 0, 0, 0]
0
>>> data[0, 0, 0, 0] = 99
>>> data[0, 0, 0, 0]
99
```

The next time we call 'get_data', the method returns the cached reference to the (modified) array:

```
>>> data_again = img.get_data()
>>> data_again is data
True
>>> data_again[0, 0, 0, 0]
99
```

If you had *initially* used *caching* == 'unchanged' then the returned `data` array would have been loaded from file, but not cached, and:

```
>>> img = nib.load(img_fname)  # a proxy image again
>>> data = img.get_data(caching='unchanged')
>>> img.in_memory
False
>>> data[0, 0, 0] = 99
>>> data_again = img.get_data(caching='unchanged')
>>> data_again is data
False
>>> data_again[0, 0, 0, 0]
0
```

get_data_dtype()

get_filename()
Fetch the image filename

ParametersNone :

Returnsfname : None or str
Returns None if there is no filename, or a filename string. If an image may have several filenames associtated with it (e.g Analyze `.img, .hdr` pair) then we return the more characteristic filename (the `.img` filename in the case of Analyze')

get_header()
Get header from image

Please use the *header* property instead of *get_header*; we will deprecate this method in future versions of nibabel.

get_shape()
Return shape for image

This function deprecated; please use the `shape` property instead

header

header_class
alias of *Header*

in_memory
True when array data is in memory

classmethod instance_to_filename(*klass*, *img*, *filename*)
Save *img* in our own format, to name implied by *filename*

This is a class method

Parametersimg : `spatialimage` instance
In fact, an object with the API of `spatialimage` - specifically `dataobj`, `affine`, `header` and `extra`.

filename : str
Filename, implying name to which to save image.

classmethod load(*klass*, *filename*)

classmethod make_file_map (*klass*, *mapping=None*)
Class method to make files holder for this image type
Parametersmapping : None or mapping, optional
mapping with keys corresponding to image file types (such as 'image', 'header' etc, depending on image class) and values that are filenames or file-like. Default is None
Returnsfile_map : dict
dict with string keys given by first entry in tuples in sequence klass.files_types, and values of type FileHolder, where FileHolder objects have default values, other than those given by *mapping*

set_data_dtype (*dtype*)

set_filename (*filename*)
Sets the files in the object from a given filename

The different image formats may check whether the filename has an extension characteristic of the format, and raise an error if not.
Parametersfilename : str
If the image format only has one file associated with it, this will be the only filename set into the image `.file_map` attribute. Otherwise, the image instance will try and guess the other filenames from this given filename.

shape

to_file_map (*file_map=None*)

to_filename (*filename*)
Write image to files implied by filename string
Parametersfilename : str
filename to which to save image. We will parse *filename* with `filespec_to_file_map` to work out names for image, header etc.
ReturnsNone :

to_files (*file_map=None*)

to_filespec (*filename*)

uncache ()
Delete any cached read of data from proxied data

Remember there are two types of images:
•*array images* where the data `img.dataobj` is an array
•*proxy images* where the data `img.dataobj` is a proxy object
If you call `img.get_data()` on a proxy image, the result of reading from the proxy gets cached inside the image object, and this cache is what gets returned from the next call to `img.get_data()`. If you modify the returned data, as in:

```
data = img.get_data()
data[:] = 42
```

then the next call to `img.get_data()` returns the modified array, whether the image is an array image or a proxy image:

```
assert np.all(img.get_data() == 42)
```

When you uncache an array image, this has no effect on the return of `img.get_data()`, but when you uncache a proxy image, the result of `img.get_data()` returns to its original value.

update_header()
Harmonize header with image data and affine

```
>>> data = np.zeros((2,3,4))
>>> affine = np.diag([1.0,2.0,3.0,1.0])
>>> img = SpatialImage(data, affine)
>>> img.shape == (2, 3, 4)
True
>>> img.update_header()
>>> img.header.get_data_shape() == (2, 3, 4)
True
>>> img.header.get_zooms()
(1.0, 2.0, 3.0)
```

supported_np_types

nibabel.spatialimages.**supported_np_types**(*obj*)
Numpy data types that instance *obj* supports

Parametersobj : object

Object implementing *get_data_dtype* and *set_data_dtype*. The object should raise `HeaderDataError` for setting unsupported dtypes. The object will likely be a header or a *SpatialImage*

Returnsnp_types : set

set of numpy types that *obj* supports

volumeutils

Utility functions for analyze-like formats

BinOpener(fileish, *args, **kwargs)	Class to accept, maybe open, and context-manage file-likes / filenames
DtypeMapper()	Specialized mapper for numpy dtypes
Recoder(codes[, fields, map_maker])	class to return canonical code(s) from code or aliases
allopen(fileish, *args, **kwargs)	Compatibility wrapper for old `allopen` function
apply_read_scaling(arr[, slope, inter])	Apply scaling in *slope* and *inter* to array *arr*
array_from_file(shape, in_dtype, infile[, ...])	Get array from file with specified shape, dtype and file offset
array_to_file(data, fileobj[, out_dtype, ...])	Helper function for writing arrays to file objects
best_write_scale_ftype(arr[, slope, inter, ...])	Smallest float type to contain range of `arr` after scaling
better_float_of(first, second[, default])	Return more capable float type of *first* and *second*
finite_range(arr[, check_nan])	Return range (min, max) or range and flag (min, max, has_nan) from *arr*
fname_ext_ul_case(fname)	*fname* with ext changed to upper / lower case if file exists
int_scinter_ftype(ifmt[, slope, inter, default])	float type containing int type *ifmt* * *slope* + *inter*
make_dt_codes(codes_seqs)	Create full dt codes Recoder instance from datatype codes
pretty_mapping(mapping[, getterfunc])	Make pretty string from mapping
rec2dict(rec)	Convert recarray to dictionary
seek_tell(fileobj, offset[, write0])	Seek in *fileobj* or check we're in the right place already
shape_zoom_affine(shape, zooms[, x_flip])	Get affine implied by given shape and zooms
working_type(in_type[, slope, inter])	Return array type from applying *slope*, *inter* to array of *in_type*
write_zeros(fileobj, count[, block_size])	Write *count* zero bytes to *fileobj*

BinOpener

class nibabel.volumeutils.**BinOpener**(*fileish*, **args*, ***kwargs*)
Bases: *nibabel.openers.Opener*

Class to accept, maybe open, and context-manage file-likes / filenames

Provides context manager to close files that the constructor opened for you.

Parametersfileish : str or file-like

if str, then open with suitable opening method. If file-like, accept as is

***args** : positional arguments

passed to opening method when *fileish* is str. `mode`, if not specified, is *rb*. `compresslevel`, if relevant, and not specified, is set from class variable `default_compresslevel`

****kwargs** : keyword arguments

passed to opening method when *fileish* is str. Change of defaults as for *args

__init__(*fileish*, **args*, ***kwargs*)

compress_ext_map = {'.bz2': (<type 'bz2.BZ2File'>, ('mode', 'buffering', 'compresslevel')), None: (<built-in function o

DtypeMapper

class nibabel.volumeutils.**DtypeMapper**
Bases: `object`

Specialized mapper for numpy dtypes

We pass this mapper into the Recoder class to deal with numpy dtype hashing.

The hashing problem is that dtypes that compare equal may not have the same hash. This is true for numpys up to the current at time of writing (1.6.0). For numpy 1.2.1 at least, even dtypes that look exactly the same in terms of fields don't always have the same hash. This makes dtypes difficult to use as keys in a dictionary.

This class wraps a dictionary in order to implement a __getitem__ to deal with dtype hashing. If the key doesn't appear to be in the mapping, and it is a dtype, we compare (using ==) all known dtype keys to the input key, and return any matching values for the matching key.

__init__()

keys()

values()

Recoder

class nibabel.volumeutils.**Recoder**(*codes*, *fields=('code',)*, *map_maker=<type 'dict'>*)
Bases: `object`

class to return canonical code(s) from code or aliases

The concept is a lot easier to read in the implementation and tests than it is to explain, so...

```
>>> # If you have some codes, and several aliases, like this:
>>> code1 = 1; aliases1=['one', 'first']
>>> code2 = 2; aliases2=['two', 'second']
>>> # You might want to do this:
```

```
>>> codes = [[code1]+aliases1,[code2]+aliases2]
>>> recodes = Recoder(codes)
>>> recodes.code['one']
1
>>> recodes.code['second']
2
>>> recodes.code[2]
2
>>> # Or maybe you have a code, a label and some aliases
>>> codes=((1,'label1','one', 'first'),(2,'label2','two'))
>>> # you might want to get back the code or the label
>>> recodes = Recoder(codes, fields=('code','label'))
>>> recodes.code['first']
1
>>> recodes.code['label1']
1
>>> recodes.label[2]
'label2'
>>> # For convenience, you can get the first entered name by
>>> # indexing the object directly
>>> recodes[2]
2
```

Create recoder object

`codes` give a sequence of code, alias sequences `fields` are names by which the entries in these sequences can be accessed.

By default `fields` gives the first column the name "code". The first column is the vector of first entries in each of the sequences found in `codes`. Thence you can get the equivalent first column value with ob.code[value], where value can be a first column value, or a value in any of the other columns in that sequence.

You can give other columns names too, and access them in the same way - see the examples in the class docstring.

Parameterscodes : seqence of sequences

Each sequence defines values (codes) that are equivalent

fields : {('code',) string sequence}, optional

names by which elements in sequences can be accessed

map_maker: callable, optional :

constructor for dict-like objects used to store key value pairs. Default is `dict`. `map_maker()` generates an empty mapping. The mapping need only implement `__getitem__, __setitem__, keys, values`.

__init__(*codes*, *fields=('code',)*, *map_maker=<type 'dict'>*)

Create recoder object

`codes` give a sequence of code, alias sequences `fields` are names by which the entries in these sequences can be accessed.

By default `fields` gives the first column the name "code". The first column is the vector of first entries in each of the sequences found in `codes`. Thence you can get the equivalent first column value with ob.code[value], where value can be a first column value, or a value in any of the other columns in that sequence.

You can give other columns names too, and access them in the same way - see the examples in the class docstring.

Parameterscodes : seqence of sequences

Each sequence defines values (codes) that are equivalent

fields : {('code',) string sequence}, optional

names by which elements in sequences can be accessed

map_maker: callable, optional :

constructor for dict-like objects used to store key value pairs. Default is `dict`. `map_maker()` generates an empty mapping. The mapping need only implement `__getitem__`, `__setitem__`, `keys`, `values`.

add_codes(*code_syn_seqs*)

Add codes to object

Parameterscode_syn_seqs : sequence

sequence of sequences, where each sequence `S = code_syn_seqs[n]` for n in 0..len(code_syn_seqs), is a sequence giving values in the same order as `self.fields`. Each S should be at least of the same length as `self.fields`. After this call, if `self.fields == ['field1', 'field2'], then ``self.field1[S[n]] == S[0]` for all n in 0..len(S) and `self.field2[S[n]] == S[1]` for all n in 0..len(S).

Examples

```
>>> code_syn_seqs = ((1, 'one'), (2, 'two'))
>>> rc = Recoder(code_syn_seqs)
>>> rc.value_set() == set((1,2))
True
>>> rc.add_codes(((3, 'three'), (1, 'first')))
>>> rc.value_set() == set((1,2,3))
True
```

keys()

Return all available code and alias values

Returns same value as `obj.field1.keys()` and, with the default initializing `fields` argument of fields=('code',), this will return the same as `obj.code.keys()`

```
>>> codes = ((1, 'one'), (2, 'two'), (1, 'repeat value'))
>>> k = Recoder(codes).keys()
>>> set(k) == set([1, 2, 'one', 'repeat value', 'two'])
True
```

value_set(*name=None*)

Return set of possible returned values for column

By default, the column is the first column.

Returns same values as `set(obj.field1.values())` and, with the default initializing``fields`` argument of fields=('code',), this will return the same as `set(obj.code.values())`

Parametersname : {None, string}

Where default of none gives result for first column

>>> codes = ((1, 'one'), (2, 'two'), (1, 'repeat value')) :

>>> vs = Recoder(codes).value_set() :

>>> vs == set([1, 2]) # Sets are not ordered, hence this test :

True :

>>> rc = Recoder(codes, fields=('code', 'label')) :

>>> rc.value_set('label') == set(('one', 'two', 'repeat value')) :

True :

allopen

nibabel.volumeutils.**allopen**(*fileish*, **args*, ***kwargs*)

Compatibility wrapper for old `allopen` function

Wraps creation of `BinOpener` instance, while picking up module global `default_compresslevel`.

Please see docstring for `BinOpener` and `Opener` for details.

apply_read_scaling

nibabel.volumeutils.**apply_read_scaling**(*arr*, *slope=None*, *inter=None*)

Apply scaling in *slope* and *inter* to array *arr*

This is for loading the array from a file (as opposed to the reverse scaling when saving an array to file)

Return data will be `arr * slope + inter`. The trick is that we have to find a good precision to use for applying the scaling. The heuristic is that the data is always upcast to the higher of the types from *arr, 'slope*, *inter* if *slope* and / or *inter* are not default values. If the dtype of *arr* is an integer, then we assume the data more or less fills the integer range, and upcast to a type such that the min, max of `arr.dtype` * scale + inter, will be finite.

Parametersarr : array-like

slope : None or float, optional

slope value to apply to *arr* (`arr * slope + inter`). None corresponds to a value of 1.0

inter : None or float, optional

intercept value to apply to *arr* (`arr * slope + inter`). None corresponds to a value of 0.0

Returnsret : array

array with scaling applied. Maybe upcast in order to give room for the scaling. If scaling is default (1, 0), then *ret* may be *arr* `ret is arr`.

array_from_file

nibabel.volumeutils.**array_from_file**(*shape*, *in_dtype*, *infile*, *offset=0*, *order='F'*, *mmap=True*)

Get array from file with specified shape, dtype and file offset

Parametersshape : sequence

sequence specifying output array shape

in_dtype : numpy dtype

fully specified numpy dtype, including correct endianness

infile : file-like

open file-like object implementing at least read() and seek()

offset : int, optional

offset in bytes into *infile* to start reading array data. Default is 0

order : {'F', 'C'} string

order in which to write data. Default is 'F' (fortran order).

mmap : {True, False, 'c', 'r', 'r+'}

mmap controls the use of numpy memory mapping for reading data. If False, do not try numpy `memmap` for data array. If one of {'c', 'r', 'r+'}, try numpy memmap with `mode=mmap`. A *mmap* value of True gives the same behavior as `mmap='c'`. If *infile* cannot be memory-mapped, ignore *mmap* value and read array from file.

Returnsarr : array-like

array like object that can be sliced, containing data

Examples

```
>>> from io import BytesIO
>>> bio = BytesIO()
>>> arr = np.arange(6).reshape(1,2,3)
>>> _ = bio.write(arr.tostring('F')) # outputs int in python3
>>> arr2 = array_from_file((1,2,3), arr.dtype, bio)
>>> np.all(arr == arr2)
True
>>> bio = BytesIO()
>>> _ = bio.write(b' ' * 10)
>>> _ = bio.write(arr.tostring('F'))
>>> arr2 = array_from_file((1,2,3), arr.dtype, bio, 10)
>>> np.all(arr == arr2)
True
```

array_to_file

`nibabel.volumeutils.`**`array_to_file`**(*data*, *fileobj*, *out_dtype=None*, *offset=0*, *intercept=0.0*, *divslope=1.0*, *mn=None*, *mx=None*, *order='F'*, *nan2zero=True*)

Helper function for writing arrays to file objects

Writes arrays as scaled by *intercept* and *divslope*, and clipped at (prescaling) *mn* minimum, and *mx* maximum.

- Clip *data* array at min *mn*, max *max* where there are not None -> `clipped` (this is *pre scale clipping*)
- Scale `clipped` with `clipped_scaled = (clipped - intercept) / divslope`
- Clip `clipped_scaled` to fit into range of *out_dtype* (*post scale clipping*) -> `clipped_scaled_clipped`
- If converting to integer *out_dtype* and *nan2zero* is True, set NaN values in `clipped_scaled_clipped` to 0
- Write `clipped_scaled_clipped_n2z` to fileobj *fileobj* starting at offset *offset* in memory layout *order*

Parametersdata : array-like

array or array-like to write.

fileobj : file-like

file-like object implementing `write` method.

out_dtype : None or dtype, optional

dtype to write array as. Data array will be coerced to this dtype before writing. If None (default) then use input data type.

offset : None or int, optional

offset into fileobj at which to start writing data. Default is 0. None means start at current file position

intercept : scalar, optional

scalar to subtract from data, before dividing by `divslope`. Default is 0.0

divslope : None or scalar, optional

scalefactor to *divide* data by before writing. Default is 1.0. If None, there is no valid data, we write zeros.

mn : scalar, optional

minimum threshold in (unscaled) data, such that all data below this value are set to this value. Default is None (no threshold). The typical use is to set -np.inf in the data to have this value (which might be the minimum non-finite value in the data).

mx : scalar, optional

maximum threshold in (unscaled) data, such that all data above this value are set to this value. Default is None (no threshold). The typical use is to set np.inf in the data to have this value (which might be the maximum non-finite value in the data).

order : {'F', 'C'}, optional

memory order to write array. Default is 'F'

nan2zero : {True, False}, optional

Whether to set NaN values to 0 when writing integer output. Defaults to True. If False, NaNs will be represented as numpy does when casting; this depends on the underlying C library and is undefined. In practice *nan2zero* == False might be a good choice when you completely sure there will be no NaNs in the data. This value ignored for float ouptut types. NaNs are treated as zero *before* applying *intercept* and *divslope* - so an array `[np.nan]` with an *intercept* of 10 becomes `[-10]` after conversion to integer *out_dtype* with *nan2zero* set. That is because you will likely apply *divslope* and *intercept* in reverse order when reading the data back, returning the zero you probably expected from the input NaN.

Examples

```
>>> from io import BytesIO
>>> sio = BytesIO()
>>> data = np.arange(10, dtype=np.float)
>>> array_to_file(data, sio, np.float)
>>> sio.getvalue() == data.tostring('F')
True
>>> _ = sio.truncate(0); _ = sio.seek(0) # outputs 0 in python 3
>>> array_to_file(data, sio, np.int16)
>>> sio.getvalue() == data.astype(np.int16).tostring()
True
>>> _ = sio.truncate(0); _ = sio.seek(0)
>>> array_to_file(data.byteswap(), sio, np.float)
```

```
>>> sio.getvalue() == data.byteswap().tostring('F')
True
>>> _ = sio.truncate(0); _ = sio.seek(0)
>>> array_to_file(data, sio, np.float, order='C')
>>> sio.getvalue() == data.tostring('C')
True
```

best_write_scale_ftype

nibabel.volumeutils.**best_write_scale_ftype**(*arr*, *slope=1.0*, *inter=0.0*, *default=<type 'numpy.float32'>*)

Smallest float type to contain range of `arr` after scaling

Scaling that will be applied to `arr` is `(arr - inter) / slope`.

Note that `slope` and `inter` get promoted to 1D arrays for this purpose to avoid the numpy scalar casting rules, which prevent scalars upcasting the array.

Parametersarr : array-like

array that will be scaled

slope : array-like, optional

scalar such that output array will be `(arr - inter) / slope`.

inter : array-like, optional

scalar such that output array will be `(arr - inter) / slope`

default : numpy type, optional

minimum float type to return

Returnsftype : numpy type

Best floating point type for scaling. If no floating point type prevents overflow, return the top floating point type. If the input array `arr` already contains inf values, return the greater of the input type and the default type.

Examples

```
>>> arr = np.array([0, 1, 2], dtype=np.int16)
>>> best_write_scale_ftype(arr, 1, 0) is np.float32
True
```

Specify higher default return value

```
>>> best_write_scale_ftype(arr, 1, 0, default=np.float64) is np.float64
True
```

Even large values that don't overflow don't change output

```
>>> arr = np.array([0, np.finfo(np.float32).max], dtype=np.float32)
>>> best_write_scale_ftype(arr, 1, 0) is np.float32
True
```

Scaling > 1 reduces output values, so no upcast needed

```
    >>> best_write_scale_ftype(arr, np.float32(2), 0) is np.float32
    True
```

Scaling < 1 increases values, so upcast may be needed (and is here)

```
    >>> best_write_scale_ftype(arr, np.float32(0.5), 0) is np.float64
    True
```

better_float_of

nibabel.volumeutils.**better_float_of**(*first*, *second*, *default=<type 'numpy.float32'>*)

Return more capable float type of *first* and *second*

Return *default* if neither of *first* or *second* is a float

Parametersfirst : numpy type specifier

Any valid input to *np.dtype()*'

second : numpy type specifier

Any valid input to *np.dtype()*'

default : numpy type specifier, optional

Any valid input to *np.dtype()*'

Returnsbetter_type : numpy type

More capable of *first* or *second* if both are floats; if only one is a float return that, otherwise return *default*.

Examples

```
    >>> better_float_of(np.float32, np.float64) is np.float64
    True
    >>> better_float_of(np.float32, 'i4') is np.float32
    True
    >>> better_float_of('i2', 'u4') is np.float32
    True
    >>> better_float_of('i2', 'u4', np.float64) is np.float64
    True
```

finite_range

nibabel.volumeutils.**finite_range**(*arr*, *check_nan=False*)

Return range (min, max) or range and flag (min, max, has_nan) from *arr*

Parametersarr : array-like

check_nan : {False, True}, optional

Whether to return third output, a bool signaling whether there are NaN values in *arr*

Returnsmn : scalar

minimum of values in (flattened) array

mx : scalar

maximum of values in (flattened) array

has_nan : bool

Returned if *check_nan* is True. *has_nan* is True if there are one or more NaN values in *arr*

Examples

```
>>> a = np.array([[-1, 0, 1],[np.inf, np.nan, -np.inf]])
>>> finite_range(a)
(-1.0, 1.0)
>>> a = np.array([[-1, 0, 1],[np.inf, np.nan, -np.inf]])
>>> finite_range(a, check_nan=True)
(-1.0, 1.0, True)
>>> a = np.array([[np.nan],[np.nan]])
>>> finite_range(a) == (np.inf, -np.inf)
True
>>> a = np.array([[-3, 0, 1],[2,-1,4]], dtype=np.int)
>>> finite_range(a)
(-3, 4)
>>> a = np.array([[1, 0, 1],[2,3,4]], dtype=np.uint)
>>> finite_range(a)
(0, 4)
>>> a = a + 1j
>>> finite_range(a)
(1j, (4+1j))
>>> a = np.zeros((2,), dtype=[('f1', 'i2')])
>>> finite_range(a)
Traceback (most recent call last):
   ...
TypeError: Can only handle numeric types
```

fname_ext_ul_case

nibabel.volumeutils.**fname_ext_ul_case**(*fname*)

fname with ext changed to upper / lower case if file exists

Check for existence of *fname*. If it does exist, return unmodified. If it doesn't, check for existence of *fname* with case changed from lower to upper, or upper to lower. Return this modified *fname* if it exists. Otherwise return *fname* unmodified

Parametersfname : str

filename.

Returnsmod_fname : str

filename, maybe with extension of opposite case

int_scinter_ftype

nibabel.volumeutils.**int_scinter_ftype**(*ifmt*, *slope=1.0*, *inter=0.0*, *default=<type 'numpy.float32'>*)

float type containing int type *ifmt* * *slope* + *inter*

Return float type that can represent the max and the min of the *ifmt* type after multiplication with *slope* and addition of *inter* with something like `np.array([imin, imax], dtype=ifmt) * slope + inter`.

Note that `slope` and `inter` get promoted to 1D arrays for this purpose to avoid the numpy scalar casting rules, which prevent scalars upcasting the array.

Parametersifmt : object

numpy integer type (e.g. np.int32)

slope : float, optional

slope, default 1.0

inter : float, optional

intercept, default 0.0

default_out : object, optional

numpy floating point type, default is `np.float32`

Returnsftype : object

numpy floating point type

Notes

It is difficult to make floats overflow with just addition because the deltas are so large at the extremes of floating point. For example:

```
>>> arr = np.array([np.finfo(np.float32).max], dtype=np.float32)
>>> res = arr + np.iinfo(np.int16).max
>>> arr == res
array([ True], dtype=bool)
```

Examples

```
>>> int_scinter_ftype(np.int8, 1.0, 0.0) == np.float32
True
>>> int_scinter_ftype(np.int8, 1e38, 0.0) == np.float64
True
```

make_dt_codes

`nibabel.volumeutils.`**`make_dt_codes`**(*codes_seqs*)

Create full dt codes Recoder instance from datatype codes

Include created numpy dtype (from numpy type) and opposite endian numpy dtype

Parameterscodes_seqs : sequence of sequences

contained sequences make be length 3 or 4, but must all be the same length. Elements are data type code, data type name, and numpy type (such as `np.float32`). The fourth element is the nifti string representation of the code (e.g. "NIFTI_TYPE_FLOAT32")

Returnsrec : `Recoder` instance

Recoder that, by default, returns `code` when indexed with any of the corresponding code, name, type, dtype, or swapped dtype. You can also index with `niistring` values if codes_seqs had sequences of length 4 instead of 3.

pretty_mapping

nibabel.volumeutils.**pretty_mapping**(*mapping*, *getterfunc=None*)

Make pretty string from mapping

Adjusts text column to print values on basis of longest key. Probably only sensible if keys are mainly strings.

You can pass in a callable that does clever things to get the values out of the mapping, given the names. By default, we just use `__getitem__`

Parametersmapping : mapping

implementing iterator returning keys and .items()

getterfunc : None or callable

callable taking two arguments, `obj` and `key` where `obj` is the passed mapping. If None, just use `lambda obj, key: obj[key]`

Returnsstr : string

Examples

```
>>> d = {'a key': 'a value'}
>>> print(pretty_mapping(d))
a key  : a value
>>> class C(object): # to control ordering, show get_ method
...     def __iter__(self):
...         return iter(('short_field','longer_field'))
...     def __getitem__(self, key):
...         if key == 'short_field':
...             return 0
...         if key == 'longer_field':
...             return 'str'
...     def get_longer_field(self):
...         return 'method string'
>>> def getter(obj, key):
...     # Look for any 'get_<name>' methods
...     try:
...         return obj.__getattribute__('get_' + key)()
...     except AttributeError:
...         return obj[key]
>>> print(pretty_mapping(C(), getter))
short_field   : 0
longer_field  : method string
```

rec2dict

nibabel.volumeutils.**rec2dict**(*rec*)

Convert recarray to dictionary

Also converts scalar values to scalars

Parametersrec : ndarray

structured ndarray

Returnsdct : dict

dict with key, value pairs as for *rec*

Examples

```
>>> r = np.zeros((), dtype = [('x', 'i4'), ('s', 'S10')])
>>> d = rec2dict(r)
>>> d == {'x': 0, 's': b''}
True
```

seek_tell

nibabel.volumeutils.**seek_tell**(*fileobj*, *offset*, *write0=False*)

Seek in *fileobj* or check we're in the right place already

Parametersfileobj : file-like

object implementing `seek` and (if seek raises an IOError) `tell`

offset : int

position in file to which to seek

write0 : {False, True}, optional

If True, and standard seek fails, try to write zeros to the file to reach *offset*. This can be useful when writing bz2 files, that cannot do write seeks.

shape_zoom_affine

nibabel.volumeutils.**shape_zoom_affine**(*shape*, *zooms*, *x_flip=True*)

Get affine implied by given shape and zooms

We get the translations from the center of the image (implied by *shape*).

Parametersshape : (N,) array-like

shape of image data. `N` is the number of dimensions

zooms : (N,) array-like

zooms (voxel sizes) of the image

x_flip : {True, False}

whether to flip the X row of the affine. Corresponds to radiological storage on disk.

Returnsaff : (4,4) array

affine giving correspondance of voxel coordinates to mm coordinates, taking the center of the image as origin

Examples

```
>>> shape = (3, 5, 7)
>>> zooms = (3, 2, 1)
>>> shape_zoom_affine((3, 5, 7), (3, 2, 1))
array([[-3.,  0.,  0.,  3.],
       [ 0.,  2.,  0., -4.],
```

```
           [ 0.,  0.,  1., -3.],
           [ 0.,  0.,  0.,  1.]])
    >>> shape_zoom_affine((3, 5, 7), (3, 2, 1), False)
    array([[ 3.,  0.,  0., -3.],
           [ 0.,  2.,  0., -4.],
           [ 0.,  0.,  1., -3.],
           [ 0.,  0.,  0.,  1.]])
```

working_type

nibabel.volumeutils.**working_type**(*in_type*, *slope=1.0*, *inter=0.0*)

Return array type from applying *slope*, *inter* to array of *in_type*

Numpy type that results from an array of type *in_type* being combined with *slope* and *inter*. It returns something like the dtype type of `((np.zeros((2,), dtype=in_type) - inter) / slope)`, but ignoring the actual values of *slope* and *inter*.

Note that you would not necessarily get the same type by applying slope and inter the other way round. Also, you'll see that the order in which slope and inter are applied is the opposite of the order in which they are passed.

Parametersin_type : numpy type specifier

Numpy type of input array. Any valid input for `np.dtype()`

slope : scalar, optional

slope to apply to array. If 1.0 (default), ignore this value and its type.

inter : scalar, optional

intercept to apply to array. If 0.0 (default), ignore this value and its type.

Returnswtype: numpy type :

Numpy type resulting from applying *inter* and *slope* to array of type *in_type*.

write_zeros

nibabel.volumeutils.**write_zeros**(*fileobj*, *count*, *block_size=8194*)

Write *count* zero bytes to *fileobj*

Parametersfileobj : file-like object

with `write` method

count : int

number of bytes to write

block_size : int, optional

largest continuous block to write.

9.5.4 Float / integer conversion

arraywriters	Array writer objects
casting	Utilties for casting numpy values in various ways

arraywriters

Array writer objects

Array writers have init signature:

```
def __init__(self, array, out_dtype=None)
```

and methods

- scaling_needed() - returns True if array requires scaling for write
- finite_range() - returns min, max of self.array
- to_fileobj(fileobj, offset=None, order='F')

They must have attributes / properties of:

- array
- out_dtype
- has_nan

They may have attributes:

- slope
- inter

They are designed to write arrays to a fileobj with reasonable memory efficiency.

Array writers may be able to scale the array or apply an intercept, or do something else to make sense of conversions between float and int, or between larger ints and smaller.

ArrayWriter(array[, out_dtype])	Initialize array writer
ScalingError	
SlopeArrayWriter(array[, out_dtype, ...])	ArrayWriter that can use scalefactor for writing arrays
SlopeInterArrayWriter(array[, out_dtype, ...])	Array writer that can use slope and intercept to scale array
WriterError	
get_slope_inter(writer)	Return slope, intercept from array writer object
make_array_writer(data, out_type[, ...])	Make array writer instance for array *data* and output type *out_type*

ArrayWriter

class nibabel.arraywriters.**ArrayWriter**(*array*, *out_dtype=None*, ***kwargs*)

Bases: object

Initialize array writer

Parametersarray : array-like

array-like object

out_dtype : None or dtype

dtype with which *array* will be written. For this class, *out_dtype'* needs to be the same as the dtype of the input *array* or a swapped version of the same.

****kwargs** : keyword arguments

This class processes only:

- nan2zero : bool, optional Whether to set NaN values to 0 when writing integer output. Defaults to True. If False, NaNs get converted with numpy `astype`, and the behavior is undefined. Ignored for floating point output.
- check_scaling : bool, optional If True, check if scaling needed and raise error if so. Default is True

Examples

```
>>> arr = np.array([0, 255], np.uint8)
>>> aw = ArrayWriter(arr)
>>> aw = ArrayWriter(arr, np.int8)
Traceback (most recent call last):
    ...
WriterError: Scaling needed but cannot scale
>>> aw = ArrayWriter(arr, np.int8, check_scaling=False)
```

__init__(*array*, *out_dtype=None*, ***kwargs*)

Initialize array writer

Parametersarray : array-like
array-like object

out_dtype : None or dtype
dtype with which *array* will be written. For this class, *out_dtype'* needs to be the same as the dtype of the input *array* or a swapped version of the same.

****kwargs** : keyword arguments
This class processes only:
- nan2zero : bool, optional Whether to set NaN values to 0 when writing integer output. Defaults to True. If False, NaNs get converted with numpy `astype`, and the behavior is undefined. Ignored for floating point output.
- check_scaling : bool, optional If True, check if scaling needed and raise error if so. Default is True

Examples

```
>>> arr = np.array([0, 255], np.uint8)
>>> aw = ArrayWriter(arr)
>>> aw = ArrayWriter(arr, np.int8)
Traceback (most recent call last):
    ...
WriterError: Scaling needed but cannot scale
>>> aw = ArrayWriter(arr, np.int8, check_scaling=False)
```

array
Return array from arraywriter

finite_range()
Return (maybe cached) finite range of data array

has_nan
True if array has NaNs

out_dtype
Return *out_dtype* from arraywriter

scaling_needed()
Checks if scaling is needed for input array

Raises WriterError if no scaling possible.

The rules are in the code, but:
•If numpy will cast, return False (no scaling needed)
•If input or output is an object or structured type, raise
•If input is complex, raise
•If the output is float, return False
•If the input array is all zero, return False
•By now we are casting to (u)int. If the input type is a float, return True (we do need scaling)
•Now input and output types are (u)ints. If the min and max in the data are within range of the output type, return False
•Otherwise return True

to_fileobj(*fileobj*, *order='F'*, *nan2zero=None*)
Write array into *fileobj*
Parametersfileobj : file-like object

order : {'F', 'C'}
order (Fortran or C) to which to write array
nan2zero : {None, True, False}, optional, deprecated
Deprecated version of argument to __init__ with same name

ScalingError

class nibabel.arraywriters.**ScalingError**
Bases: *nibabel.arraywriters.WriterError*

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

SlopeArrayWriter

class nibabel.arraywriters.**SlopeArrayWriter**(*array*, *out_dtype=None*, *calc_scale=True*, *scaler_dtype=<type 'numpy.float32'>*, ***kwargs*)
Bases: *nibabel.arraywriters.ArrayWriter*

ArrayWriter that can use scalefactor for writing arrays

The scalefactor allows the array writer to write floats to int output types, and rescale larger ints to smaller. It can therefore lose precision.

It extends the ArrayWriter class with attribute:

•slope

and methods:

•reset() - reset slope to default (not adapted to self.array)

•calc_scale() - calculate slope to best write self.array

Initialize array writer

Parametersarray : array-like

array-like object

out_dtype : None or dtype

dtype with which *array* will be written. For this class, *out_dtype'* needs to be the same as the dtype of the input *array* or a swapped version of the same.

calc_scale : {True, False}, optional

Whether to calculate scaling for writing *array* on initialization. If False, then you can calculate this scaling with `obj.calc_scale()` - see examples

scaler_dtype : dtype-like, optional

specifier for numpy dtype for scaling

****kwargs** : keyword arguments

This class processes only:

- nan2zero : bool, optional Whether to set NaN values to 0 when writing integer output. Defaults to True. If False, NaNs get converted with numpy `astype`, and the behavior is undefined. Ignored for floating point output.

Examples

```
>>> arr = np.array([0, 254], np.uint8)
>>> aw = SlopeArrayWriter(arr)
>>> aw.slope
1.0
>>> aw = SlopeArrayWriter(arr, np.int8)
>>> aw.slope
2.0
>>> aw = SlopeArrayWriter(arr, np.int8, calc_scale=False)
>>> aw.slope
1.0
>>> aw.calc_scale()
>>> aw.slope
2.0
```

__init__(*array*, *out_dtype=None*, *calc_scale=True*, *scaler_dtype=<type 'numpy.float32'>*, ***kwargs*)

Initialize array writer

Parametersarray : array-like
array-like object

out_dtype : None or dtype
dtype with which *array* will be written. For this class, *out_dtype'* needs to be the same as the dtype of the input *array* or a swapped version of the same.

calc_scale : {True, False}, optional
Whether to calculate scaling for writing *array* on initialization. If False, then you can calculate this scaling with `obj.calc_scale()` - see examples

scaler_dtype : dtype-like, optional
specifier for numpy dtype for scaling

****kwargs** : keyword arguments
This class processes only:
- nan2zero : bool, optional Whether to set NaN values to 0 when writing integer output. Defaults to True. If False, NaNs get converted with numpy `astype`, and the behavior is undefined. Ignored for floating point output.

Examples

```
>>> arr = np.array([0, 254], np.uint8)
>>> aw = SlopeArrayWriter(arr)
>>> aw.slope
1.0
>>> aw = SlopeArrayWriter(arr, np.int8)
>>> aw.slope
2.0
>>> aw = SlopeArrayWriter(arr, np.int8, calc_scale=False)
>>> aw.slope
1.0
>>> aw.calc_scale()
>>> aw.slope
2.0
```

calc_scale(*force=False*)
Calculate / set scaling for floats/(u)ints to (u)ints

reset()
Set object to values before any scaling calculation

scaling_needed()
Checks if scaling is needed for input array

Raises WriterError if no scaling possible.

The rules are in the code, but:
- If numpy will cast, return False (no scaling needed)
- If input or output is an object or structured type, raise
- If input is complex, raise
- If the output is float, return False
- If the input array is all zero, return False
- If there is no finite value, return False (the writer will strip the non-finite values)
- By now we are casting to (u)int. If the input type is a float, return True (we do need scaling)
- Now input and output types are (u)ints. If the min and max in the data are within range of the output type, return False
- Otherwise return True

slope
get/set slope

to_fileobj(*fileobj*, *order='F'*, *nan2zero=None*)
Write array into *fileobj*

Parametersfileobj : file-like object

order : {'F', 'C'}
order (Fortran or C) to which to write array

nan2zero : {None, True, False}, optional, deprecated
Deprecated version of argument to __init__ with same name

SlopeInterArrayWriter

class nibabel.arraywriters.**SlopeInterArrayWriter**(*array*, *out_dtype=None*, *calc_scale=True*, *scaler_dtype=<type 'numpy.float32'>*, ***kwargs*)

Bases: *nibabel.arraywriters.SlopeArrayWriter*

Array writer that can use slope and intercept to scale array

The writer can subtract an intercept, and divided by a slope, in order to be able to convert floating point values into a (u)int range, or to convert larger (u)ints to smaller.

It extends the ArrayWriter class with attributes:

- inter
- slope

and methods:

- reset() - reset inter, slope to default (not adapted to self.array)
- calc_scale() - calculate inter, slope to best write self.array

Initialize array writer

Parametersarray : array-like

array-like object

out_dtype : None or dtype

dtype with which *array* will be written. For this class, *out_dtype'* needs to be the same as the dtype of the input *array* or a swapped version of the same.

calc_scale : {True, False}, optional

Whether to calculate scaling for writing *array* on initialization. If False, then you can calculate this scaling with `obj.calc_scale()` - see examples

scaler_dtype : dtype-like, optional

specifier for numpy dtype for slope, intercept

****kwargs** : keyword arguments

This class processes only:

- nan2zero : bool, optional Whether to set NaN values to 0 when writing integer output. Defaults to True. If False, NaNs get converted with numpy `astype`, and the behavior is undefined. Ignored for floating point output.

Examples

```
>>> arr = np.array([0, 255], np.uint8)
>>> aw = SlopeInterArrayWriter(arr)
>>> aw.slope, aw.inter
(1.0, 0.0)
>>> aw = SlopeInterArrayWriter(arr, np.int8)
>>> (aw.slope, aw.inter) == (1.0, 128)
True
>>> aw = SlopeInterArrayWriter(arr, np.int8, calc_scale=False)
>>> aw.slope, aw.inter
(1.0, 0.0)
>>> aw.calc_scale()
>>> (aw.slope, aw.inter) == (1.0, 128)
True
```

__init__(*array*, *out_dtype=None*, *calc_scale=True*, *scaler_dtype=<type 'numpy.float32'>*, ***kwargs*)

Initialize array writer

Parametersarray : array-like

array-like object

out_dtype : None or dtype
dtype with which *array* will be written. For this class, *out_dtype'* needs to be the same as the dtype of the input *array* or a swapped version of the same.

calc_scale : {True, False}, optional
Whether to calculate scaling for writing *array* on initialization. If False, then you can calculate this scaling with `obj.calc_scale()` - see examples

scaler_dtype : dtype-like, optional
specifier for numpy dtype for slope, intercept

****kwargs** : keyword arguments
This class processes only:

- nan2zero : bool, optional Whether to set NaN values to 0 when writing integer output. Defaults to True. If False, NaNs get converted with numpy `astype`, and the behavior is undefined. Ignored for floating point output.

Examples

```
>>> arr = np.array([0, 255], np.uint8)
>>> aw = SlopeInterArrayWriter(arr)
>>> aw.slope, aw.inter
(1.0, 0.0)
>>> aw = SlopeInterArrayWriter(arr, np.int8)
>>> (aw.slope, aw.inter) == (1.0, 128)
True
>>> aw = SlopeInterArrayWriter(arr, np.int8, calc_scale=False)
>>> aw.slope, aw.inter
(1.0, 0.0)
>>> aw.calc_scale()
>>> (aw.slope, aw.inter) == (1.0, 128)
True
```

inter
get/set inter

reset()
Set object to values before any scaling calculation

to_fileobj(*fileobj*, *order='F'*, *nan2zero=None*)
Write array into *fileobj*

Parametersfileobj : file-like object

order : {'F', 'C'}
order (Fortran or C) to which to write array

nan2zero : {None, True, False}, optional, deprecated
Deprecated version of argument to __init__ with same name

WriterError

class nibabel.arraywriters.**WriterError**
Bases: exceptions.Exception

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

get_slope_inter

nibabel.arraywriters.**get_slope_inter**(*writer*)

Return slope, intercept from array writer object

Parameterswriter : ArrayWriter instance

Returnsslope : scalar

slope in *writer* or 1.0 if not present

inter : scalar

intercept in *writer* or 0.0 if not present

Examples

```
>>> arr = np.arange(10)
>>> get_slope_inter(ArrayWriter(arr))
(1.0, 0.0)
>>> get_slope_inter(SlopeArrayWriter(arr))
(1.0, 0.0)
>>> get_slope_inter(SlopeInterArrayWriter(arr))
(1.0, 0.0)
```

make_array_writer

nibabel.arraywriters.**make_array_writer**(*data*, *out_type*, *has_slope=True*, *has_intercept=True*, ***kwargs*)

Make array writer instance for array *data* and output type *out_type*

Parametersdata : array-like

array for which to create array writer

out_type : dtype-like

input to numpy dtype to specify array writer output type

has_slope : {True, False}

If True, array write can use scaling to adapt the array to *out_type*

has_intercept : {True, False}

If True, array write can use intercept to adapt the array to *out_type*

****kwargs** : other keyword arguments

to pass to the arraywriter class

Returnswriter : arraywriter instance

Instance of array writer, with class adapted to *has_intercept* and *has_slope*.

Examples

```
>>> aw = make_array_writer(np.arange(10), np.uint8, True, True)
>>> type(aw) == SlopeInterArrayWriter
True
>>> aw = make_array_writer(np.arange(10), np.uint8, True, False)
>>> type(aw) == SlopeArrayWriter
True
>>> aw = make_array_writer(np.arange(10), np.uint8, False, False)
>>> type(aw) == ArrayWriter
True
```

casting

Utilties for casting numpy values in various ways

Most routines work round some numpy oddities in floating point precision and casting. Others work round numpy casting to and from python ints

CastingError	
FloatingError	
able_int_type(values)	Find the smallest integer numpy type to contain sequence *values*
as_int(x[, check])	Return python integer representation of number
best_float()	Floating point type with best precision
ceil_exact(val, flt_type)	Return nearest exact integer >= *val* in float type *flt_type*
float_to_int(arr, int_type[, nan2zero, infmax])	Convert floating point array *arr* to type *int_type*
floor_exact(val, flt_type)	Return nearest exact integer <= *val* in float type *flt_type*
floor_log2(x)	floor of log2 of abs(*x*)
have_binary128()	True if we have a binary128 IEEE longdouble
int_abs(arr)	Absolute values of array taking care of max negative int values
int_to_float(val, flt_type)	Convert integer *val* to floating point type *flt_type*
longdouble_lte_float64()	Return True if longdouble appears to have the same precision as float64
longdouble_precision_improved()	True if longdouble precision increased since initial import
ok_floats()	Return floating point types sorted by precision
on_powerpc()	True if we are running on a Power PC platform
shared_range(flt_type, int_type)	Min and max in float type that are >=min, <=max in integer type
type_info(np_type)	Return dict with min, max, nexp, nmant, width for numpy type *np_type*
ulp([val])	Return gap between *val* and nearest representable number of same type

CastingError

class nibabel.casting.**CastingError**
Bases: exceptions.Exception

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

FloatingError

class nibabel.casting.**FloatingError**
Bases: exceptions.Exception

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

able_int_type

nibabel.casting.**able_int_type**(*values*)

Find the smallest integer numpy type to contain sequence *values*

Prefers uint to int if minimum is >= 0

Parametersvalues : sequence

sequence of integer values

Returnsitype : None or numpy type

numpy integer type or None if no integer type holds all *values*

Examples

```
>>> able_int_type([0, 1]) == np.uint8
True
>>> able_int_type([-1, 1]) == np.int8
True
```

as_int

nibabel.casting.**as_int**(*x*, *check=True*)

Return python integer representation of number

This is useful because the numpy int(val) mechanism is broken for large values in np.longdouble.

It is also useful to work around a numpy 1.4.1 bug in conversion of uints to python ints.

This routine will still raise an OverflowError for values that are outside the range of float64.

Parametersx : object

integer, unsigned integer or floating point value

check : {True, False}

If True, raise error for values that are not integers

Returnsi : int

Python integer

Examples

```
>>> as_int(2.0)
2
>>> as_int(-2.0)
-2
>>> as_int(2.1)
Traceback (most recent call last):
    ...
FloatingError: Not an integer: 2.1
>>> as_int(2.1, check=False)
2
```

best_float

nibabel.casting.**best_float**()
Floating point type with best precision

This is nearly always np.longdouble, except on Windows, where np.longdouble is Intel80 storage, but with float64 precision for calculations. In that case we return float64 on the basis it's the fastest and smallest at the highest precision.

SPARC float128 also proved so slow that we prefer float64.

Returnsbest_type : numpy type

floating point type with highest precision

Notes

Needs to run without error for module import, because it is called in `ok_floats` below, and therefore in setting module global `OK_FLOATS`.

ceil_exact

nibabel.casting.**ceil_exact**(*val*, *flt_type*)
Return nearest exact integer >= *val* in float type *flt_type*

Parametersval : int

We have to pass val as an int rather than the floating point type because large integers cast as floating point may be rounded by the casting process.

flt_type : numpy type

numpy float type.

Returnsceil_val : object

value of same floating point type as *val*, that is the nearest exact integer in this type such that *floor_val* >= *val*. Thus if *val* is exact in *flt_type*, *ceil_val* == *val*.

Examples

Obviously 2 is within the range of representable integers for float32

```
>>> ceil_exact(2, np.float32)
2.0
```

As is 2**24-1 (the number of significand digits is 23 + 1 implicit)

```
>>> ceil_exact(2**24-1, np.float32) == 2**24-1
True
```

But 2**24+1 gives a number that float32 can't represent exactly

```
>>> ceil_exact(2**24+1, np.float32) == 2**24+2
True
```

As for the numpy ceil function, negatives ceil towards inf

```
    >>> ceil_exact(-2**24-1, np.float32) == -2**24
    True
```

float_to_int

nibabel.casting.**float_to_int**(*arr*, *int_type*, *nan2zero=True*, *infmax=False*)

Convert floating point array *arr* to type *int_type*

- Rounds numbers to nearest integer
- Clips values to prevent overflows when casting
- Converts NaN to 0 (for *nan2zero* == True)

Casting floats to integers is delicate because the result is undefined and platform specific for float values outside the range of *int_type*. Define `shared_min` to be the minimum value that can be exactly represented in both the float type of *arr* and *int_type*. Define *shared_max* to be the equivalent maximum value. To avoid undefined results we threshold *arr* at `shared_min` and `shared_max`.

Parametersarr : array-like

Array of floating point type

int_type : object

Numpy integer type

nan2zero : {True, False, None}

Whether to convert NaN value to zero. Default is True. If False, and NaNs are present, raise CastingError. If None, do not check for NaN values and pass through directly to the `astype` casting mechanism. In this last case, the resulting value is undefined.

infmax : {False, True}

If True, set np.inf values in *arr* to be *int_type* integer maximum value, -np.inf as *int_type* integer minimum. If False, set +/- infs to be `shared_min`, `shared_max` as defined above. Therefore False gives faster conversion at the expense of infs that are further from infinity.

Returnsiarr : ndarray

of type *int_type*

Notes

Numpy relies on the C library to cast from float to int using the standard `astype` method of the array.

Quoting from section F4 of the C99 standard:

> If the floating value is infinite or NaN or if the integral part of the floating value exceeds the range of the integer type, then the "invalid" floating-point exception is raised and the resulting value is unspecified.

Hence we threshold at `shared_min` and `shared_max` to avoid casting to values that are undefined.

See: https://en.wikipedia.org/wiki/C99 . There are links to the C99 standard from that page.

Examples

```
>>> float_to_int([np.nan, np.inf, -np.inf, 1.1, 6.6], np.int16)
array([     0,  32767, -32768,      1,      7], dtype=int16)
```

floor_exact

nibabel.casting.**floor_exact**(*val*, *flt_type*)

Return nearest exact integer <= *val* in float type *flt_type*

Parametersval : int

We have to pass val as an int rather than the floating point type because large integers cast as floating point may be rounded by the casting process.

flt_type : numpy type

numpy float type.

Returnsfloor_val : object

value of same floating point type as *val*, that is the nearest exact integer in this type such that *floor_val* <= *val*. Thus if *val* is exact in *flt_type*, *floor_val* == *val*.

Examples

Obviously 2 is within the range of representable integers for float32

```
>>> floor_exact(2, np.float32)
2.0
```

As is 2**24-1 (the number of significand digits is 23 + 1 implicit)

```
>>> floor_exact(2**24-1, np.float32) == 2**24-1
True
```

But 2**24+1 gives a number that float32 can't represent exactly

```
>>> floor_exact(2**24+1, np.float32) == 2**24
True
```

As for the numpy floor function, negatives floor towards -inf

```
>>> floor_exact(-2**24-1, np.float32) == -2**24-2
True
```

floor_log2

nibabel.casting.**floor_log2**(*x*)

floor of log2 of abs(*x*)

Embarrassingly, from https://en.wikipedia.org/wiki/Binary_logarithm

Parametersx : int

ReturnsL : None or int

floor of base 2 log of *x*. None if *x* == 0.

Examples

```
>>> floor_log2(2**9+1)
9
>>> floor_log2(-2**9+1)
8
>>> floor_log2(0.5)
-1
>>> floor_log2(0) is None
True
```

have_binary128

nibabel.casting.**have_binary128**()
True if we have a binary128 IEEE longdouble

int_abs

nibabel.casting.**int_abs**(*arr*)
Absolute values of array taking care of max negative int values

Parametersarr : array-like

Returnsabs_arr : array

array the same shape as *arr* in which all negative numbers have been changed to positive numbers with the magnitude.

Examples

This kind of thing is confusing in base numpy:

```
>>> import numpy as np
>>> np.abs(np.int8(-128))
-128
```

`int_abs` fixes that:

```
>>> int_abs(np.int8(-128))
128
>>> int_abs(np.array([-128, 127], dtype=np.int8))
array([128, 127], dtype=uint8)
>>> int_abs(np.array([-128, 127], dtype=np.float32))
array([ 128.,  127.], dtype=float32)
```

int_to_float

nibabel.casting.**int_to_float**(*val*, *flt_type*)
Convert integer *val* to floating point type *flt_type*

Why is this so complicated?

At least in numpy <= 1.6.1, numpy longdoubles do not correctly convert to ints, and ints do not correctly convert to longdoubles. Specifically, in both cases, the values seem to go through float64 conversion on the way, so to convert better, we need to split into float64s and sum up the result.

Parametersval : int

Integer value

flt_type : object

numpy floating point type

Returnsf : numpy scalar

of type *flt_type*

longdouble_lte_float64

nibabel.casting.**longdouble_lte_float64**()
Return True if longdouble appears to have the same precision as float64

longdouble_precision_improved

nibabel.casting.**longdouble_precision_improved**()
True if longdouble precision increased since initial import

This can happen on Windows compiled with MSVC. It may be because libraries compiled with mingw (longdouble is Intel80) get linked to numpy compiled with MSVC (longdouble is Float64)

ok_floats

nibabel.casting.**ok_floats**()
Return floating point types sorted by precision

Remove longdouble if it has no higher precision than float64

on_powerpc

nibabel.casting.**on_powerpc**()
True if we are running on a Power PC platform

Has to deal with older Macs and IBM POWER7 series among others

shared_range

nibabel.casting.**shared_range**(*flt_type*, *int_type*)
Min and max in float type that are >=min, <=max in integer type

This is not as easy as it sounds, because the float type may not be able to exactly represent the max or min integer values, so we have to find the next exactly representable floating point value to do the thresholding.

Parametersflt_type : dtype specifier

A dtype specifier referring to a numpy floating point type. For example, `f4`, `np.dtype('f4')`, `np.float32` are equivalent.

int_type : dtype specifier

A dtype specifier referring to a numpy integer type. For example, `i4`, `np.dtype('i4')`, `np.int32` are equivalent

Returnsmn : object

Number of type *flt_type* that is the minumum value in the range of *int_type*, such that `mn.astype(int_type)` >= min of *int_type*

mx : object

Number of type *flt_type* that is the maximum value in the range of *int_type*, such that `mx.astype(int_type)` <= max of *int_type*

Examples

```
>>> shared_range(np.float32, np.int32) == (-2147483648.0, 2147483520.0)
True
>>> shared_range('f4', 'i4') == (-2147483648.0, 2147483520.0)
True
```

type_info

`nibabel.casting.`**`type_info`**(*np_type*)

Return dict with min, max, nexp, nmant, width for numpy type *np_type*

Type can be integer in which case nexp and nmant are None.

Parametersnp_type : numpy type specifier

Any specifier for a numpy dtype

Returnsinfo : dict

with fields `min` (minimum value), `max` (maximum value), `nexp` (exponent width), `nmant` (significand precision not including implicit first digit), `minexp` (minimum exponent), `maxexp` (maximum exponent), `width` (width in bytes). (`nexp`, `nmant`, `minexp`, `maxexp`) are None for integer types. Both `min` and `max` are of type *np_type*.

RaisesFloatingError :

for floating point types we don't recognize

Notes

You might be thinking that `np.finfo` does this job, and it does, except for PPC long doubles (https://github.com/numpy/numpy/issues/2669) and float96 on Windows compiled with Mingw. This routine protects against such errors in `np.finfo` by only accepting values that we know are likely to be correct.

ulp

`nibabel.casting.`**`ulp`**(*val=1.0*)

Return gap between *val* and nearest representable number of same type

This is the value of a unit in the last place (ULP), and is similar in meaning to the MATLAB eps function.

Parametersval : scalar, optional

scalar value of any numpy type. Default is 1.0 (float64)

Returnsulp_val : scalar

gap between *val* and nearest representable number of same type

Notes

The wikipedia article on machine epsilon points out that the term *epsilon* can be used in the sense of a unit in the last place (ULP), or as the maximum relative rounding error. The MATLAB `eps` function uses the ULP meaning, but this function is `ulp` rather than `eps` to avoid confusion between different meanings of *eps*.

9.5.5 System utilities

data	Utilities to find files from NIPY data packages
environment	Settings from the system environment relevant to NIPY

data

Utilities to find files from NIPY data packages

Bomber(name, msg)	Class to raise an informative error when used
BomberError	Error when trying to access Bomber instance
DataError	
Datasource(base_path)	Simple class to add base path to relative path
VersionedDatasource(base_path[, config_filename])	Datasource with version information in config file
datasource_or_bomber(pkg_def, **options)	Return a viable datasource or a Bomber
find_data_dir(root_dirs, *names)	Find relative path given path prefixes to search
get_data_path()	Return specified or guessed locations of NIPY data files
make_datasource(pkg_def, **kwargs)	Return datasource defined by *pkg_def* as found in *data_path*

Bomber

class nibabel.data.**Bomber**(*name*, *msg*)

Bases: object

Class to raise an informative error when used

__init__(*name*, *msg*)

BomberError

class nibabel.data.**BomberError**

Bases: *nibabel.data.DataError*, exceptions.AttributeError

Error when trying to access Bomber instance

Should be instance of AttributeError to allow Python 3 inspect to do various `hasattr` checks without raising an error

__init__()

x.__init__(...) initializes x; see help(type(x)) for signature

DataError

class nibabel.data.**DataError**
Bases: exceptions.Exception

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

Datasource

class nibabel.data.**Datasource**(*base_path*)
Bases: object

Simple class to add base path to relative path

Initialize datasource

Parametersbase_path : str

path to prepend to all relative paths

Examples

```
>>> from os.path import join as pjoin
>>> repo = Datasource(pjoin('a', 'path'))
>>> fname = repo.get_filename('somedir', 'afile.txt')
>>> fname == pjoin('a', 'path', 'somedir', 'afile.txt')
True
```

__init__(*base_path*)
Initialize datasource
Parametersbase_path : str
path to prepend to all relative paths

Examples

```
>>> from os.path import join as pjoin
>>> repo = Datasource(pjoin('a', 'path'))
>>> fname = repo.get_filename('somedir', 'afile.txt')
>>> fname == pjoin('a', 'path', 'somedir', 'afile.txt')
True
```

get_filename(**path_parts*)
Prepend base path to **path_parts*

We make no check whether the returned path exists.
Parameters*path_parts : sequence of strings
Returnsfname : str
result of os.path.join(*path_parts), with ``self.base_path prepended

list_files(*relative=True*)
Recursively list the files in the data source directory.
Parametersrelative: bool, optional :
If True, path returned are relative to the base paht of the data source.

Returnsfile_list: list of strings :
List of the paths of all the files in the data source.

VersionedDatasource

class nibabel.data.**VersionedDatasource**(*base_path*, *config_filename=None*)
Bases: *nibabel.data.Datasource*

Datasource with version information in config file

Initialize versioned datasource

We assume that there is a configuration file with version information in datasource directory tree.

The configuration file contains an entry like:

```
[DEFAULT]
version = 0.3
```

The version should have at least a major and a minor version number in the form above.

Parametersbase_path : str

path to prepend to all relative paths

config_filaname : None or str

relative path to configuration file containing version

__init__(*base_path*, *config_filename=None*)
Initialize versioned datasource

We assume that there is a configuration file with version information in datasource directory tree.

The configuration file contains an entry like:

```
[DEFAULT]
version = 0.3
```

The version should have at least a major and a minor version number in the form above.
Parametersbase_path : str
path to prepend to all relative paths
config_filaname : None or str
relative path to configuration file containing version

datasource_or_bomber

nibabel.data.**datasource_or_bomber**(*pkg_def*, ***options*)
Return a viable datasource or a Bomber

This is to allow module level creation of datasource objects. We create the objects, so that, if the data exist, and are the correct version, the objects are valid datasources, otherwise, they raise an error on access, warning about the lack of data or the version numbers.

The parameters are as for `make_datasource` in this module.

Parameterspkg_def : dict

dict containing at least key 'relpath'. Can optioanlly have keys 'name' (package name), 'install hint' (for helpful error messages) and 'min version' giving the minimum necessary version string for the package.

data_path : sequence of strings or None, optional

Returnsds : datasource or `Bomber` instance

find_data_dir

`nibabel.data.`**`find_data_dir`**(*root_dirs*, **names*)

Find relative path given path prefixes to search

We raise a DataError if we can't find the relative path

Parametersroot_dirs : sequence of strings

sequence of paths in which to search for data directory

***names** : sequence of strings

sequence of strings naming directory to find. The name to search for is given by `os.path.join(*names)`

Returnsdata_dir : str

full path (root path added to **names* above)

get_data_path

`nibabel.data.`**`get_data_path`**()

Return specified or guessed locations of NIPY data files

The algorithm is to return paths, extracted from strings, where strings are found in the following order:

1. The contents of environment variable `NIPY_DATA_PATH`
2. Any section = `DATA`, key = `path` value in a `config.ini` file in your nipy user directory (found with `get_nipy_user_dir()`)
3. Any section = `DATA`, key = `path` value in any files found with a `sorted(glob.glob(os.path.join(sys_dir, '*.ini')))` search, where `sys_dir` is found with `get_nipy_system_dir()`
4. If `sys.prefix` is `/usr`, we add `/usr/local/share/nipy`. We need this because Python 2.6 in Debian / Ubuntu does default installs to `/usr/local`.
5. The result of `get_nipy_user_dir()`

Therefore, any paths found in `NIPY_DATA_PATH` will be searched before paths found in the user directory `config.ini`

ParametersNone :

Returnspaths : sequence of paths

Notes

We have to add `/usr/local/share/nipy` if sys.prefix is `/usr`, because Debian has patched distutils in Python 2.6 to do default distutils installs there:

- https://www.debian.org/doc/packaging-manuals/python-policy/ap-packaging_tools.html#s-distutils
- https://www.mail-archive.com/debian-python@lists.debian.org/msg05084.html

Examples

```
>>> pth = get_data_path()
```

make_datasource

nibabel.data.**make_datasource**(*pkg_def*, ***kwargs*)

Return datasource defined by *pkg_def* as found in *data_path*

data_path is the only allowed keyword argument.

pkg_def is a dictionary with at least one key - 'relpath'. 'relpath' is a relative path with unix forward slash separators.

The relative path to the data is found with:

```
names = pkg_def['name'].split('/')
rel_path = os.path.join(names)
```

We search for this relative path in the list of paths given by *data_path*. By default *data_path* is given by `get_data_path()` in this module.

If we can't find the relative path, raise a DataError

Parameterspkg_def : dict

dict containing at least the key 'relpath'. 'relpath' is the data path of the package relative to *data_path*. It is in unix path format (using forward slashes as directory separators). *pkg_def* can also contain optional keys 'name' (the name of the package), and / or a key 'install hint' that we use in the returned error message from trying to use the resulting datasource

data_path : sequence of strings or None, optional

sequence of paths in which to search for data. If None (the default), then use `get_data_path()`

Returnsdatasource : `VersionedDatasource`

An initialized `VersionedDatasource` instance

environment

Settings from the system environment relevant to NIPY

get_home_dir()	Return the closest possible equivalent to a 'home' directory.
get_nipy_system_dir()	Get systemwide NIPY configuration file directory
get_nipy_user_dir()	Get the NIPY user directory

get_home_dir

nibabel.environment.**get_home_dir**()

Return the closest possible equivalent to a 'home' directory.

The path may not exist; code using this routine should not expect the directory to exist.

ParametersNone :

Returnshome_dir : string

best guess at location of home directory

get_nipy_system_dir

nibabel.environment.**get_nipy_system_dir**()

Get systemwide NIPY configuration file directory

On posix systems this will be `/etc/nipy`. On Windows, the directory is less useful, but by default it will be `C:\etc\nipy`

The path may well not exist; code using this routine should not expect the directory to exist.

ParametersNone :

Returnsnipy_dir : string

path to systemwide NIPY configuration directory

Examples

```
>>> pth = get_nipy_system_dir()
```

get_nipy_user_dir

nibabel.environment.**get_nipy_user_dir**()

Get the NIPY user directory

This uses the logic in *get_home_dir* to find the home directory and the adds either .nipy or _nipy to the end of the path.

We check first in environment variable `NIPY_USER_DIR`, otherwise returning the default of `<homedir>/.nipy` (Unix) or `<homedir>/_nipy` (Windows)

The path may well not exist; code using this routine should not expect the directory to exist.

ParametersNone :

Returnsnipy_dir : string

path to user's NIPY configuration directory

Examples

```
>>> pth = get_nipy_user_dir()
```

9.5.6 Miscellaneous Helpers

arrayproxy	Array proxy base class
affines	Utility routines for working with points and affine transforms
batteryrunners	Battery runner classes and Report classes
data	Utilities to find files from NIPY data packages

Continued on next page

Table 9.47 – continued from previous page

dft	DICOM filesystem tools
fileholders	Fileholder class
filename_parser	Create filename pairs, triplets etc, with expected extensions
fileslice	Utilities for getting array slices out of file-like objects
onetime	Descriptor support for NIPY.
openers	Context manager openers for various fileobject types
optpkg	Routines to support optional packages
rstutils	ReStructured Text utilities
tmpdirs	Contexts for *with* statement providing temporary directories
tripwire	Class to raise error for missing modules or other misfortunes
wrapstruct	Class to wrap numpy structured array

arrayproxy

Array proxy base class

The proxy API is - at minimum:

- The object has a read-only attribute `shape`
- read only `is_proxy` attribute / property set to True
- the object returns the data array from `np.asarray(prox)`
- returns array slice from `prox[<slice_spec>]` where `<slice_spec>` is any ndarray slice specification that does not use numpy 'advanced indexing'.
- modifying no object outside `obj` will affect the result of `np.asarray(obj)`. Specifically:
  - Changes in position (`obj.tell()`) of passed file-like objects will not affect the output of from `np.asarray(proxy)`.
  - if you pass a header into the __init__, then modifying the original header will not affect the result of the array return.

See `nibabel.tests.test_proxy_api` for proxy API conformance checks.

ArrayProxy(*args, **kwargs)	Class to act as proxy for the array that can be read from a file
is_proxy(obj)	Return True if *obj* is an array proxy

ArrayProxy

class `nibabel.arrayproxy.`**`ArrayProxy`**(**args*, ***kwargs*)

Bases: `object`

Class to act as proxy for the array that can be read from a file

The array proxy allows us to freeze the passed fileobj and header such that it returns the expected data array.

This implementation assumes a contiguous array in the file object, with one of the numpy dtypes, starting at a given file position `offset` with single `slope` and `intercept` scaling to produce output values.

The class `__init__` requires a `header` object with methods:

•get_data_shape

•get_data_dtype

- get_data_offset
- get_slope_inter

The header should also have a 'copy' method. This requirement will go away when the deprecated 'header' propoerty goes away.

This implementation allows us to deal with Analyze and its variants, including Nifti1, and with the MGH format.

Other image types might need more specific classes to implement the API. See *nibabel.minc1*, *nibabel.ecat* and *nibabel.parrec* for examples.

Initialize array proxy instance

Parametersfile_like : object

File-like object or filename. If file-like object, should implement at least `read` and `seek`.

header : object

Header object implementing `get_data_shape`, `get_data_dtype`, `get_data_offset`, `get_slope_inter`

mmap : {True, False, 'c', 'r'}, optional, keyword only

mmap controls the use of numpy memory mapping for reading data. If False, do not try numpy `memmap` for data array. If one of {'c', 'r'}, try numpy memmap with `mode=mmap`. A *mmap* value of True gives the same behavior as `mmap='c'`. If *file_like* cannot be memory-mapped, ignore *mmap* value and read array from file.

scaling : {'fp', 'dv'}, optional, keyword only

Type of scaling to use - see header `get_data_scaling` method.

__init__(**args*, ***kwargs*)

Initialize array proxy instance

Parametersfile_like : object
File-like object or filename. If file-like object, should implement at least `read` and `seek`.
header : object
Header object implementing `get_data_shape`, `get_data_dtype`, `get_data_offset`, `get_slope_inter`
mmap : {True, False, 'c', 'r'}, optional, keyword only
mmap controls the use of numpy memory mapping for reading data. If False, do not try numpy `memmap` for data array. If one of {'c', 'r'}, try numpy memmap with `mode=mmap`. A *mmap* value of True gives the same behavior as `mmap='c'`. If *file_like* cannot be memory-mapped, ignore *mmap* value and read array from file.
scaling : {'fp', 'dv'}, optional, keyword only
Type of scaling to use - see header `get_data_scaling` method.

get_unscaled()

Read of data from file

This is an optional part of the proxy API

header

inter

is_proxy

offset

order = 'F'

shape

slope

is_proxy

nibabel.arrayproxy.**is_proxy**(*obj*)
Return True if *obj* is an array proxy

affines

Utility routines for working with points and affine transforms

append_diag(aff, steps[, starts])	Add diagonal elements *steps* and translations *starts* to affine
apply_affine(aff, pts)	Apply affine matrix *aff* to points *pts*
dot_reduce(*args)	Apply numpy dot product function from right to left on arrays
from_matvec(matrix[, vector])	Combine a matrix and vector into an homogeneous affine
to_matvec(transform)	Split a transform into its matrix and vector components.

append_diag

nibabel.affines.**append_diag**(*aff*, *steps*, *starts=()*)
Add diagonal elements *steps* and translations *starts* to affine

Typical use is in expanding 4x4 affines to larger dimensions. Nipy is the main consumer because it uses NxM affines, whereas we generally only use 4x4 affines; the routine is here for convenience.

Parametersaff : 2D array

N by M affine matrix

steps : scalar or sequence

diagonal elements to append.

starts : scalar or sequence

elements to append to last column of *aff*, representing translations corresponding to the *steps*. If empty, expands to a vector of zeros of the same length as *steps*

Returnsaff_plus : 2D array

Now P by Q where L = `len(steps)` and P == N+L, Q=N+L

Examples

```
>>> aff = np.eye(4)
>>> aff[:3,:3] = np.arange(9).reshape((3,3))
>>> append_diag(aff, [9, 10], [99,100])
array([[   0.,    1.,    2.,    0.,    0.,    0.],
       [   3.,    4.,    5.,    0.,    0.,    0.],
       [   6.,    7.,    8.,    0.,    0.,    0.],
       [   0.,    0.,    0.,    9.,    0.,   99.],
       [   0.,    0.,    0.,    0.,   10.,  100.],
       [   0.,    0.,    0.,    0.,    0.,    1.]])
```

apply_affine

nibabel.affines.**apply_affine**(*aff*, *pts*)

Apply affine matrix *aff* to points *pts*

Returns result of application of *aff* to the *right* of *pts*. The coordinate dimension of *pts* should be the last.

For the 3D case, *aff* will be shape (4,4) and *pts* will have final axis length 3 - maybe it will just be N by 3. The return value is the transformed points, in this case:

```
res = np.dot(aff[:3,:3], pts.T) + aff[:3,3:4]
transformed_pts = res.T
```

This routine is more general than 3D, in that *aff* can have any shape (N,N), and *pts* can have any shape, as long as the last dimension is for the coordinates, and is therefore length N-1.

Parametersaff : (N, N) array-like

Homogenous affine, for 3D points, will be 4 by 4. Contrary to first appearance, the affine will be applied on the left of *pts*.

pts : (..., N-1) array-like

Points, where the last dimension contains the coordinates of each point. For 3D, the last dimension will be length 3.

Returnstransformed_pts : (..., N-1) array

transformed points

Examples

```
>>> aff = np.array([[0,2,0,10],[3,0,0,11],[0,0,4,12],[0,0,0,1]])
>>> pts = np.array([[1,2,3],[2,3,4],[4,5,6],[6,7,8]])
>>> apply_affine(aff, pts)
array([[14, 14, 24],
       [16, 17, 28],
       [20, 23, 36],
       [24, 29, 44]]...)
```

Just to show that in the simple 3D case, it is equivalent to:

```
>>> (np.dot(aff[:3,:3], pts.T) + aff[:3,3:4]).T
array([[14, 14, 24],
       [16, 17, 28],
       [20, 23, 36],
       [24, 29, 44]]...)
```

But *pts* can be a more complicated shape:

```
>>> pts = pts.reshape((2,2,3))
>>> apply_affine(aff, pts)
array([[[14, 14, 24],
        [16, 17, 28]],

       [[20, 23, 36],
        [24, 29, 44]]]...)
```

dot_reduce

nibabel.affines.**dot_reduce**(**args*)

Apply numpy dot product function from right to left on arrays

For passed arrays $A, B, C, ...Z$ returns $A\dot{B}\dot{C}...\dot{Z}$ where "." is the numpy array dot product.

Parametersargs** : arrays

Arrays that can be passed to numpy `dot` function

Returnsdot_product : array

If there are N arguments, result of `arg[0].dot(arg[1].dot(arg[2].dot ... arg[N-2].dot(arg[N-1])))...`

from_matvec

nibabel.affines.**from_matvec**(*matrix*, *vector=None*)

Combine a matrix and vector into an homogeneous affine

Combine a rotation / scaling / shearing matrix and translation vector into a transform in homogeneous coordinates.

Parametersmatrix : array-like

An NxM array representing the the linear part of the transform. A transform from an M-dimensional space to an N-dimensional space.

vector : None or array-like, optional

None or an (N,) array representing the translation. None corresponds to an (N,) array of zeros.

Returnsxform : array

An (N+1, M+1) homogenous transform matrix.

See also:

to_matvec

Examples

```
>>> from_matvec(np.diag([2, 3, 4]), [9, 10, 11])
array([[ 2,  0,  0,  9],
       [ 0,  3,  0, 10],
       [ 0,  0,  4, 11],
       [ 0,  0,  0,  1]])
```

The *vector* argument is optional:

```
>>> from_matvec(np.diag([2, 3, 4]))
array([[2, 0, 0, 0],
       [0, 3, 0, 0],
       [0, 0, 4, 0],
       [0, 0, 0, 1]])
```

to_matvec

nibabel.affines.**to_matvec**(*transform*)

Split a transform into its matrix and vector components.

The tranformation must be represented in homogeneous coordinates and is split into its rotation matrix and translation vector components.

Parameterstransform : array-like

NxM transform matrix in homogeneous coordinates representing an affine transformation from an (N-1)-dimensional space to an (M-1)-dimensional space. An example is a 4x4 transform representing rotations and translations in 3 dimensions. A 4x3 matrix can represent a 2-dimensional plane embedded in 3 dimensional space.

Returnsmatrix : (N-1, M-1) array

Matrix component of *transform*

vector : (M-1,) array

Vector compoent of *transform*

See also:

from_matvec

Examples

```
>>> aff = np.diag([2, 3, 4, 1])
>>> aff[:3,3] = [9, 10, 11]
>>> to_matvec(aff)
(array([[2, 0, 0],
        [0, 3, 0],
        [0, 0, 4]]), array([ 9, 10, 11]))
```

batteryrunners

Battery runner classes and Report classes

These classes / objects are for generic checking / fixing batteries

The `BatteryRunner` class will run a series of checks on a single object.

A check is a callable, of signature `func(obj, fix=False)` which returns a tuple `(obj, Report)` for `func(obj, False)` or `func(obj, True)`, where the obj may be a modified object, or a different object, if `fix==True`.

To run checks only, and return problem report objects:

```
>>> def chk(obj, fix=False): # minimal check
...     return obj, Report()
>>> btrun = BatteryRunner((chk,))
>>> reports = btrun.check_only('a string')
```

To run checks and fixes, returning fixed object and problem report sequence, with possible fix messages:

```
>>> fixed_obj, report_seq = btrun.check_fix('a string')
```

Reports are iterable things, where the elements in the iterations are `Problems`, with attributes `error`, `problem_level`, `problem_msg`, and possibly empty `fix_msg`. The `problem_level` is an integer, giving the level of problem, from 0 (no problem) to 50 (very bad problem). The levels follow the log levels from the logging module (e.g 40 equivalent to "error" level, 50 to "critical"). The `error` can be one of `None` if no error to suggest, or an Exception class that the user might consider raising for this sitation. The `problem_msg` and `fix_msg` are human readable strings that should explain what happened.

More about `checks`

Checks are callables returning objects and reports, like `chk` below, such that:

```
obj, report = chk(obj, fix=False)
obj, report = chk(obj, fix=True)
```

For example, for the Analyze header, we need to check the datatype:

```
def chk_datatype(hdr, fix=True):
    rep = Report(hdr, HeaderDataError)
    code = int(hdr['datatype'])
    try:
        dtype = AnalyzeHeader._data_type_codes.dtype[code]
    except KeyError:
        rep.problem_level = 40
        rep.problem_msg = 'data code not recognized'
    else:
        if dtype.type is np.void:
            rep.problem_level = 40
            rep.problem_msg = 'data code not supported'
        else:
            return hdr, rep
    if fix:
        rep.fix_problem_msg = 'not attempting fix'
    return hdr, rep
```

or the bitpix:

```
def chk_bitpix(hdr, fix=True):
    rep = Report(HeaderDataError)
    code = int(hdr['datatype'])
    try:
        dt = AnalyzeHeader._data_type_codes.dtype[code]
    except KeyError:
        rep.problem_level = 10
        rep.problem_msg = 'no valid datatype to fix bitpix'
        return hdr, rep
    bitpix = dt.itemsize * 8
    if bitpix == hdr['bitpix']:
        return hdr, rep
    rep.problem_level = 10
    rep.problem_msg = 'bitpix does not match datatype')
    if fix:
        hdr['bitpix'] = bitpix # inplace modification
        rep.fix_msg = 'setting bitpix to match datatype'
    return hdr, ret
```

or the pixdims:

```
def chk_pixdims(hdr, fix=True):
    rep = Report(hdr, HeaderDataError)
    if not np.any(hdr['pixdim'][1:4] < 0):
        return hdr, rep
    rep.problem_level = 40
    rep.problem_msg = 'pixdim[1,2,3] should be positive'
    if fix:
        hdr['pixdim'][1:4] = np.abs(hdr['pixdim'][1:4])
        rep.fix_msg = 'setting to abs of pixdim values'
    return hdr, rep
```

BatteryRunner(checks)	Class to run set of checks
Report([error, problem_level, problem_msg, ...])	Initialize report with values

BatteryRunner

class nibabel.batteryrunners.**BatteryRunner**(*checks*)

Bases: object

Class to run set of checks

Initialize instance from sequence of *checks*

Parameterschecks : sequence

sequence of checks, where checks are callables matching signature `obj, rep = chk(obj, fix=False)`. Checks are run in the order they are passed.

Examples

```
>>> def chk(obj, fix=False): # minimal check
...     return obj, Report()
>>> btrun = BatteryRunner((chk,))
```

__init__(*checks*)

Initialize instance from sequence of *checks*

Parameterschecks : sequence

sequence of checks, where checks are callables matching signature `obj, rep = chk(obj, fix=False)`. Checks are run in the order they are passed.

Examples

```
>>> def chk(obj, fix=False): # minimal check
...     return obj, Report()
>>> btrun = BatteryRunner((chk,))
```

check_fix(*obj*)

Run checks, with fixes, on *obj* returning *obj*, reports

Parametersobj : anything

object on which to run checks, fixes

Returnsobj : anything

possibly modified or replaced *obj*, after fixes

reports : sequence

sequence of reports on checks, fixes

check_only(*obj*)
Run checks on *obj* returning reports
Parametersobj : anything
object on which to run checks
Returnsreports : sequence
sequence of report objects reporting on result of running checks (withou fixes) on *obj*

Report

class nibabel.batteryrunners.**Report**(*error=<type 'exceptions.Exception'>, problem_level=0, problem_msg='', fix_msg=''*)
Bases: object

Initialize report with values

Parameterserror : None or Exception

Error to raise if raising error for this check. If None, no error can be raised for this check (it was probably normal).

problem_level : int

level of problem. From 0 (no problem) to 50 (severe problem). If the report originates from a fix, then this is the level of the problem remaining after the fix. Default is 0

problem_msg : string

String describing problem detected. Default is ''

fix_msg : string

String describing any fix applied. Default is ''.

Examples

```
>>> rep = Report()
>>> rep.problem_level
0
>>> rep = Report(TypeError, 10)
>>> rep.problem_level
10
```

__init__(*error=<type 'exceptions.Exception'>, problem_level=0, problem_msg='', fix_msg=''*)
Initialize report with values
Parameterserror : None or Exception
Error to raise if raising error for this check. If None, no error can be raised for this check (it was probably normal).
problem_level : int
level of problem. From 0 (no problem) to 50 (severe problem). If the report originates from a fix, then this is the level of the problem remaining after the fix. Default is 0
problem_msg : string
String describing problem detected. Default is ''
fix_msg : string
String describing any fix applied. Default is ''.

Examples

```
>>> rep = Report()
>>> rep.problem_level
0
>>> rep = Report(TypeError, 10)
>>> rep.problem_level
10
```

log_raise(*logger*, *error_level=40*)
Log problem, raise error if problem >= *error_level*
Parameters **logger** : log
log object, implementing `log` method
error_level : int, optional
If `self.problem_level` >= *error_level*, raise error

message
formatted message string, including fix message if present

write_raise(*stream*, *error_level=40*, *log_level=30*)
Write report to *stream*
Parameters **stream** : file-like
implementing `write` method
error_level : int, optional
level at which to raise error for problem detected in `self`
log_level : int, optional
Such that if *log_level* is >= `self.problem_level` we write the report to *stream*, otherwise we write nothing.

dft

DICOM filesystem tools

CachingError	error while caching
DFTError	base class for DFT exceptions
InstanceStackError(series, i, si)	bad series of instance numbers
VolumeError	unsupported volume parameter
clear_cache()	
get_studies([base_dir, followlinks])	
update_cache(base_dir[, followlinks])	

CachingError

class nibabel.dft.**CachingError**
Bases: *nibabel.dft.DFTError*

error while caching

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

DFTError

class nibabel.dft.**DFTError**
Bases: exceptions.Exception

base class for DFT exceptions

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

InstanceStackError

class nibabel.dft.**InstanceStackError**(*series*, *i*, *si*)
Bases: *nibabel.dft.DFTError*

bad series of instance numbers

__init__(*series*, *i*, *si*)

VolumeError

class nibabel.dft.**VolumeError**
Bases: *nibabel.dft.DFTError*

unsupported volume parameter

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

clear_cache

nibabel.dft.**clear_cache**()

get_studies

nibabel.dft.**get_studies**(*base_dir=None*, *followlinks=False*)

update_cache

nibabel.dft.**update_cache**(*base_dir*, *followlinks=False*)

fileholders

Fileholder class

FileHolder([filename, fileobj, pos])	class to contain filename, fileobj and file position
FileHolderError	
copy_file_map(file_map)	Copy mapping of fileholders given by *file_map*

FileHolder

class nibabel.fileholders.**FileHolder**(*filename=None*, *fileobj=None*, *pos=0*)
Bases: object

class to contain filename, fileobj and file position

Initialize FileHolder instance

Parametersfilename : str, optional

filename. Default is None

fileobj : file-like object, optional

Should implement at least 'seek' (for the purposes for this class). Default is None

pos : int, optional

position in filename or fileobject at which to start reading or writing data; defaults to 0

__init__(*filename=None*, *fileobj=None*, *pos=0*)
Initialize FileHolder instance
Parametersfilename : str, optional
filename. Default is None
fileobj : file-like object, optional
Should implement at least 'seek' (for the purposes for this class). Default is None
pos : int, optional
position in filename or fileobject at which to start reading or writing data; defaults to 0

get_prepare_fileobj(**args*, ***kwargs*)
Return fileobj if present, or return fileobj from filename

Set position to that given in self.pos
Parameters*args : tuple
positional arguments to file open. Ignored if there is a defined `self.fileobj`. These might include the mode, such as 'rb'
****kwargs** : dict
named arguments to file open. Ignored if there is a defined `self.fileobj`
Returnsfileobj : file-like object
object has position set (via `fileobj.seek()`) to `self.pos`

same_file_as(*other*)
Test if *self* refers to same files / fileobj as *other*
Parametersother : object
object with *filename* and *fileobj* attributes
Returnstf : bool
True if *other* has the same filename (or both have None) and the same fileobj (or both have None

FileHolderError

class nibabel.fileholders.**FileHolderError**
Bases: exceptions.Exception

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

copy_file_map

nibabel.fileholders.**copy_file_map**(*file_map*)

Copy mapping of fileholders given by *file_map*

Parametersfile_map : mapping

mapping of `FileHolder` instances

Returnsfm_copy : dict

Copy of *file_map*, using shallow copy of `FileHolders`

filename_parser

Create filename pairs, triplets etc, with expected extensions

TypesFilenamesError	
parse_filename(filename, types_exts, ...[, ...])	Splits filename into tuple of
splitext_addext(filename[, addexts, match_case])	Split `/pth/fname.ext.gz` into `/pth/fname, .ext, .gz`
types_filenames(template_fname, types_exts)	Return filenames with standard extensions from template name

TypesFilenamesError

class nibabel.filename_parser.**TypesFilenamesError**

Bases: `exceptions.Exception`

__init__()

x.__init__(...) initializes x; see help(type(x)) for signature

parse_filename

nibabel.filename_parser.**parse_filename**(*filename*, *types_exts*, *trailing_suffixes*, *match_case=False*)

Splits filename into tuple of (fileroot, extension, trailing_suffix, guessed_name)

Parametersfilename : str

filename in which to search for type extensions

types_exts : sequence of sequences

sequence of (name, extension) str sequences defining type to extension mapping.

trailing_suffixes : sequence of strings

suffixes that should be ignored when looking for extensions

match_case : bool, optional

If True, match case of extensions and trailing suffixes when searching in *filename*, otherwise do case-insensitive match.

Returnspth : str

path with any matching extensions or trailing suffixes removed

ext : str

If there were any matching extensions, in *types_exts* return that; otherwise return extension derived from `os.path.splitext`.

trailing : str

If there were any matching *trailing_suffixes* return that matching suffix, otherwise ‘’

guessed_type : str

If we found a matching extension in *types_exts* return the corresponding `type`

Examples

```
>>> types_exts = (('t1', 'ext1'),('t2', 'ext2'))
>>> parse_filename('/path/fname.funny', types_exts, ())
('/path/fname', '.funny', None, None)
>>> parse_filename('/path/fnameext2', types_exts, ())
('/path/fname', 'ext2', None, 't2')
>>> parse_filename('/path/fnameext2', types_exts, ('.gz',))
('/path/fname', 'ext2', None, 't2')
>>> parse_filename('/path/fnameext2.gz', types_exts, ('.gz',))
('/path/fname', 'ext2', '.gz', 't2')
```

splitext_addext

`nibabel.filename_parser.`**`splitext_addext`**(*filename*, *addexts=('.gz', '.bz2')*, *match_case=False*)

Split `/pth/fname.ext.gz` into `/pth/fname`, `.ext`, `.gz`

where `.gz` may be any of passed *addext* trailing suffixes.

Parametersfilename : str

filename that may end in any or none of *addexts*

match_case : bool, optional

If True, match case of *addexts* and *filename*, otherwise do case-insensitive match.

Returnsfroot : str

Root of filename - e.g. `/pth/fname` in example above

ext : str

Extension, where extension is not in *addexts* - e.g. `.ext` in example above

addext : str

Any suffixes appearing in *addext* occuring at end of filename

Examples

```
>>> splitext_addext('fname.ext.gz')
('fname', '.ext', '.gz')
>>> splitext_addext('fname.ext')
('fname', '.ext', '')
>>> splitext_addext('fname.ext.foo', ('.foo', '.bar'))
('fname', '.ext', '.foo')
```

types_filenames

nibabel.filename_parser.**types_filenames**(*template_fname*, *types_exts*, *trailing_suffixes=('.gz', '.bz2')*, *enforce_extensions=True*, *match_case=False*)

Return filenames with standard extensions from template name

The typical case is returning image and header filenames for an Analyze image, that expects an 'image' file type with extension `.img`, and a 'header' file type, with extension `.hdr`.

Parameterstemplate_fname : str

template filename from which to construct output dict of filenames, with given *types_exts* type to extension mapping. If `self.enforce_extensions` is True, then filename must have one of the defined extensions from the types list. If `self.enforce_extensions` is False, then the other filenames are guessed at by adding extensions to the base filename. Ignored suffixes (from *trailing_suffixes*) append themselves to the end of all the filenames.

types_exts : sequence of sequences

sequence of (name, extension) str sequences defining type to extension mapping.

trailing_suffixes : sequence of strings, optional

suffixes that should be ignored when looking for extensions - default is `('.gz', '.bz2')`

enforce_extensions : {True, False}, optional

If True, raise an error when attempting to set value to type which has the wrong extension

match_case : bool, optional

If True, match case of extensions and trailing suffixes when searching in *template_fname*, otherwise do case-insensitive match.

Returnstypes_fnames : dict

dict with types as keys, and generated filenames as values. The types are given by the first elements of the tuples in *types_exts*.

Examples

```
>>> types_exts = (('t1','.ext1'),('t2', '.ext2'))
>>> tfns = types_filenames('/path/test.ext1', types_exts)
>>> tfns == {'t1': '/path/test.ext1', 't2': '/path/test.ext2'}
True
```

Bare file roots without extensions get them added

```
>>> tfns = types_filenames('/path/test', types_exts)
>>> tfns == {'t1': '/path/test.ext1', 't2': '/path/test.ext2'}
True
```

With enforce_extensions == False, allow first type to have any extension.

```
>>> tfns = types_filenames('/path/test.funny', types_exts,
...                        enforce_extensions=False)
>>> tfns == {'t1': '/path/test.funny', 't2': '/path/test.ext2'}
True
```

fileslice

Utilities for getting array slices out of file-like objects

calc_slicedefs(sliceobj, in_shape, itemsize, ...)	Return parameters for slicing array with *sliceobj* given memory layout
canonical_slicers(sliceobj, shape[, check_inds])	Return canonical version of *sliceobj* for array shape *shape*
fileslice(fileobj, sliceobj, shape, dtype[, ...])	Slice array in *fileobj* using *sliceobj* slicer and array definitions
fill_slicer(slicer, in_len)	Return slice object with Nones filled out to match *in_len*
is_fancy(sliceobj)	Returns True if sliceobj is attempting fancy indexing
optimize_read_slicers(sliceobj, in_shape, ...)	Calculates slices to read from disk, and apply after reading
optimize_slicer(slicer, dim_len, all_full, ...)	Return maybe modified slice and post-slice slicing for *slicer*
predict_shape(sliceobj, in_shape)	Predict shape of array from slicing array shape *shape* with *sliceobj*
read_segments(fileobj, segments, n_bytes)	Read *n_bytes* byte data implied by *segments* from *fileobj*
slice2len(slicer, in_len)	Output length after slicing original length *in_len* with *slicer*
slice2outax(ndim, sliceobj)	Matching output axes for input array ndim *ndim* and slice *sliceobj*
slicers2segments(read_slicers, in_shape, ...)	Get segments from *read_slicers* given input *in_shape* and memory steps
strided_scalar(shape[, scalar])	Return array shape *shape* where all entries point to value *scalar*
threshold_heuristic(slicer, dim_len, stride)	Whether to force full axis read or contiguous read of stepped slice

calc_slicedefs

nibabel.fileslice.**calc_slicedefs**(*sliceobj*, *in_shape*, *itemsize*, *offset*, *order*, *heuristic=<function threshold_heuristic>*)

Return parameters for slicing array with *sliceobj* given memory layout

Calculate the best combination of skips / (read + discard) to use for reading the data from disk / memory, then generate corresponding *segments*, the disk offsets and read lengths to read the memory. If we have chosen some (read + discard) optimization, then we need to discard the surplus values from the read array using *post_slicers*, a slicing tuple that takes the array as read from a file-like object, and returns the array we want.

Parameterssliceobj : object

something that can be used to slice an array as in `arr[sliceobj]`

in_shape : sequence

shape of underlying array to be sliced

itemsize : int

element size in array (in bytes)

offset : int

offset of array data in underlying file or memory buffer

order : {'C', 'F'}

memory layout of underlying array

heuristic : callable, optional

function taking slice object, dim_len, stride length as arguments, returning one of 'full', 'contiguous', None. See *optimize_slicer()* and *threshold_heuristic()*

Returnssegments : list

list of 2 element lists where lists are (offset, length), giving absolute memory offset in bytes and number of bytes to read

read_shape : tuple

shape with which to interpret memory as read from *segments*. Interpreting the memory read from *segments* with this shape, and a dtype, gives an intermediate array - call this `R`

post_slicers : tuple

Any new slicing to be applied to the array `R` after reading via *segments* and reshaping via *read_shape*. Slices are in terms of *read_shape*. If empty, no new slicing to apply

canonical_slicers

nibabel.fileslice.**canonical_slicers**(*sliceobj*, *shape*, *check_inds=True*)

Return canonical version of *sliceobj* for array shape *shape*

sliceobj is a slicer for an array `A` implied by *shape*.

•Expand *sliceobj* with `slice(None)` to add any missing (implied) axes in *sliceobj*

•Find any slicers in *sliceobj* that do a full axis slice and replace by `slice(None)`

•Replace any floating point values for slicing with integers

•Replace negative integer slice values with equivalent positive integers.

Does not handle fancy indexing (indexing with arrays or array-like indices)

Parametersssliceobj : object

something that can be used to slice an array as in `arr[sliceobj]`

shape : sequence

shape of array that will be indexed by *sliceobj*

check_inds : {True, False}, optional

Whether to check if integer indices are out of bounds

Returnscan_slicers : tuple

version of *sliceobj* for which Ellipses have been expanded, missing (implied) dimensions have been appended, and slice objects equivalent to `slice(None)` have been replaced by `slice(None)`, integer axes have been checked, and negative indices set to positive equivalent

fileslice

nibabel.fileslice.**fileslice**(*fileobj*, *sliceobj*, *shape*, *dtype*, *offset=0*, *order='C'*, *heuristic=<function threshold_heuristic>*)

Slice array in *fileobj* using *sliceobj* slicer and array definitions

fileobj contains the contiguous binary data for an array `A` of shape, dtype, memory layout *shape*, *dtype*, *order*, with the binary data starting at file offset *offset*.

Our job is to return the sliced array `A[sliceobj]` in the most efficient way in terms of memory and time.

Sometimes it will be quicker to read memory that we will later throw away, to save time we might lose doing short seeks on *fileobj*. Call these alternatives: (read + discard); and skip. This routine guesses when to (read+discard) or skip using the callable *heuristic*, with a default using a hard threshold for the memory gap large enough to prefer a skip.

Parametersfileobj : file-like object

binary file-like object. Implements `read` and `seek`

sliceobj : object

something that can be used to slice an array as in `arr[sliceobj]`

shape : sequence

shape of full array inside *fileobj*

dtype : dtype object

dtype of array inside *fileobj*

offset : int, optional

offset of array data within *fileobj*

order : {'C', 'F'}, optional

memory layout of array in *fileobj*

heuristic : callable, optional

function taking slice object, axis length, stride length as arguments, returning one of 'full', 'contiguous', None. See *optimize_slicer()* and see *threshold_heuristic()* for an example.

Returnssliced_arr : array

Array in *fileobj* as sliced with *sliceobj*

fill_slicer

nibabel.fileslice.**fill_slicer**(*slicer*, *in_len*)

Return slice object with Nones filled out to match *in_len*

Also fixes too large stop / start values according to slice() slicing rules.

The returned slicer can have a None as *slicer.stop* if *slicer.step* is negative and the input *slicer.stop* is None. This is because we can't represent the `stop` as an integer, because -1 has a different meaning.

Parametersslicer : slice object

in_len : int

length of axis on which *slicer* will be applied

Returnscan_slicer : slice object

slice with start, stop, step set to explicit values, with the exception of `stop` for negative step, which is None for the case of slicing down through the first element

is_fancy

nibabel.fileslice.**is_fancy**(*sliceobj*)

Returns True if sliceobj is attempting fancy indexing

Parametersliceobj : object

something that can be used to slice an array as in `arr[sliceobj]`

Returnstf: bool :

True if sliceobj represents fancy indexing, False for basic indexing

optimize_read_slicers

nibabel.fileslice.**optimize_read_slicers**(*sliceobj*, *in_shape*, *itemsize*, *heuristic*)

Calculates slices to read from disk, and apply after reading

Parameterssliceobj : object

something that can be used to slice an array as in `arr[sliceobj]`. Can be assumed to be canonical in the sense of `canonical_slicers`

in_shape : sequence

shape of underlying array to be sliced. Array for *in_shape* assumed to be already in 'F' order. Reorder shape / sliceobj for slicing a 'C' array before passing to this function.

itemsize : int

element size in array (bytes)

heuristic : callable

function taking slice object, axis length, and stride length as arguments, returning one of 'full', 'contiguous', None. See *optimize_slicer()*; see *threshold_heuristic()* for an example.

Returnsread_slicers : tuple

sliceobj maybe rephrased to fill out dimensions that are better read from disk and later trimmed to their original size with *post_slicers*. *read_slicers* implies a block of memory to be read from disk. The actual disk positions come from *slicers2segments* run over *read_slicers*. Includes any `newaxis` dimensions in *sliceobj*

post_slicers : tuple

Any new slicing to be applied to the read array after reading. The *post_slicers* discard any memory that we read to save time, but that we don't need for the slice. Include any `newaxis` dimension added by *sliceobj*

optimize_slicer

nibabel.fileslice.**optimize_slicer**(*slicer*, *dim_len*, *all_full*, *is_slowest*, *stride*, *heuristic=<function threshold_heuristic>*)

Return maybe modified slice and post-slice slicing for *slicer*

Parametersslicer : slice object or int

dim_len : int

length of axis along which to slice

all_full : bool

Whether dimensions up until now have been full (all elements)

is_slowest : bool

Whether this dimension is the slowest changing in memory / on disk

stride : int

size of one step along this axis

heuristic : callable, optional

function taking slice object, dim_len, stride length as arguments, returning one of 'full', 'contiguous', None. See *threshold_heuristic()* for an example.

Returnsto_read : slice object or int

maybe modified slice based on *slicer* expressing what data should be read from an underlying file or buffer. *to_read* must always have positive `step` (because we don't want to go backwards in the buffer / file)

post_slice : slice object

slice to be applied after array has been read. Applies any transformations in *slicer* that have not been applied in *to_read*. If axis will be dropped by *to_read* slicing, so no slicing would make sense, return string `dropped`

Notes

This is the heart of the algorithm for making segments from slice objects.

A contiguous slice is a slice with `slice.step in (1, -1)`

A full slice is a continuous slice returning all elements.

The main question we have to ask is whether we should transform *to_read*, *post_slice* to prefer a full read and partial slice. We only do this in the case of all_full==True. In this case we might benefit from reading a continuous chunk of data even if the slice is not continuous, or reading all the data even if the slice is not full. Apply a heuristic *heuristic* to decide whether to do this, and adapt *to_read* and *post_slice* slice accordingly.

Otherwise (apart from constraint to be positive) return *to_read* unaltered and *post_slice* as `slice(None)`

predict_shape

`nibabel.fileslice.`**`predict_shape`**(*sliceobj*, *in_shape*)

Predict shape of array from slicing array shape *shape* with *sliceobj*

Parameterssliceobj : object

something that can be used to slice an array as in `arr[sliceobj]`

in_shape : sequence

shape of array that could be sliced by *sliceobj*

Returnsout_shape : tuple

predicted shape arising from slicing array shape *in_shape* with *sliceobj*

read_segments

`nibabel.fileslice.`**`read_segments`**(*fileobj*, *segments*, *n_bytes*)

Read *n_bytes* byte data implied by *segments* from *fileobj*

Parametersfileobj : file-like object

Implements *seek* and *read*

segments : sequence

list of 2 sequences where sequences are (offset, length), giving absolute file offset in bytes and number of bytes to read

n_bytes : int

total number of bytes that will be read

Returnsbuffer : buffer object

object implementing buffer protocol, such as byte string or ndarray or mmap or ctypes `c_char_array`

slice2len

`nibabel.fileslice.`**`slice2len`**(*slicer*, *in_len*)

Output length after slicing original length *in_len* with *slicer* Parameters ———- slicer : slice object in_len : int

Returnsout_len : int

Length after slicing

Notes

Returns same as `len(np.arange(in_len)[slicer])`

slice2outax

`nibabel.fileslice.`**`slice2outax`**(*ndim*, *sliceobj*)

Matching output axes for input array ndim *ndim* and slice *sliceobj*

Parametersndim : int

number of axes in input array

sliceobj : object

something that can be used to slice an array as in `arr[sliceobj]`

Returnsout_ax_inds : tuple

Say `A` is a (pretend) input array of `ndim` dimensions. Say ``B = A[sliceobj]``. *out_ax_inds* has one value per axis in `A` giving corresponding axis in `B`.

slicers2segments

`nibabel.fileslice.`**`slicers2segments`**(*read_slicers*, *in_shape*, *offset*, *itemsize*)

Get segments from *read_slicers* given input *in_shape* and memory steps

Parametersread_slicers : object

something that can be used to slice an array as in `arr[sliceobj]` Slice objects can by be assumed canonical as in `canonical_slicers`, and positive as in `_positive_slice`

in_shape : sequence

shape of underlying array on disk before reading

offset : int

offset of array data in underlying file or memory buffer

itemsize : int

element size in array (in bytes)

Returnssegments : list

list of 2 element lists where lists are [offset, length], giving absolute memory offset in bytes and number of bytes to read

strided_scalar

nibabel.fileslice.**strided_scalar**(*shape*, *scalar=0.0*)

Return array shape *shape* where all entries point to value *scalar*

Parametersshape : sequence

Shape of output array.

scalar : scalar

Scalar value with which to fill array.

Returnsstrided_arr : array

Array of shape *shape* for which all values == *scalar*, built by setting all strides of *strided_arr* to 0, so the scalar is broadcast out to the full array *shape*. *strided_arr* is flagged as not *writeable*.

The array is set read-only to avoid a numpy error when broadcasting - see https://github.com/numpy/numpy/issues/6491

threshold_heuristic

nibabel.fileslice.**threshold_heuristic**(*slicer*, *dim_len*, *stride*, *skip_thresh=256*)

Whether to force full axis read or contiguous read of stepped slice

Allows *fileslice()* to sometimes read memory that it will throw away in order to get maximum speed. In other words, trade memory for fewer disk reads.

Parametersslicer : slice object, or int

If slice, can be assumed to be full as in `fill_slicer`

dim_len : int

length of axis being sliced

stride : int

memory distance between elements on this axis

skip_thresh : int, optional

Memory gap threshold in bytes above which to prefer skipping memory rather than reading it and later discarding.

Returnsaction : {'full', 'contiguous', None}

Gives the suggested optimization for reading the data

- 'full' - read whole axis
- 'contiguous' - read all elements between start and stop
- None - read only memory needed for output

Notes

Let's say we are in the middle of reading a file at the start of some memory length B bytes. We don't need the memory, and we are considering whether to read it anyway (then throw it away) (READ) or stop reading, skip B bytes and restart reading from there (SKIP).

After trying some more fancy algorithms, a hard threshold (*skip_thresh*) for the maximum skip distance seemed to work well, as measured by times on `nibabel.benchmarks.bench_fileslice`

onetime

Descriptor support for NIPY.

Utilities to support special Python descriptors [1,2], in particular the use of a useful pattern for properties we call 'one time properties'. These are object attributes which are declared as properties, but become regular attributes once they've been read the first time. They can thus be evaluated later in the object's life cycle, but once evaluated they become normal, static attributes with no function call overhead on access or any other constraints.

A special ResetMixin class is provided to add a .reset() method to users who may want to have their objects capable of resetting these computed properties to their 'untriggered' state.

References

[1] How-To Guide for Descriptors, Raymond Hettinger. http://users.rcn.com/python/download/Descriptor.htm

[2] Python data model, https://docs.python.org/reference/datamodel.html

OneTimeProperty(func)	A descriptor to make special properties that become normal attributes.
ResetMixin	A Mixin class to add a .reset() method to users of OneTimeProperty.
auto_attr(func)	Decorator to create OneTimeProperty attributes.
setattr_on_read(func)	Decorator to create OneTimeProperty attributes.

OneTimeProperty

class `nibabel.onetime.`**OneTimeProperty**(*func*)

Bases: `object`

A descriptor to make special properties that become normal attributes.

This is meant to be used mostly by the auto_attr decorator in this module.

Create a OneTimeProperty instance.

Parametersfunc : method

The method that will be called the first time to compute a value. Afterwards, the method's name will be a standard attribute holding the value of this computation.

__init__(*func*)

Create a OneTimeProperty instance.

Parametersfunc : method

The method that will be called the first time to compute a value. Afterwards, the method's name will be a standard attribute holding the value of this computation.

ResetMixin

class nibabel.onetime.**ResetMixin**
Bases: object

A Mixin class to add a .reset() method to users of OneTimeProperty.

By default, auto attributes once computed, become static. If they happen to depend on other parts of an object and those parts change, their values may now be invalid.

This class offers a .reset() method that users can call *explicitly* when they know the state of their objects may have changed and they want to ensure that *all* their special attributes should be invalidated. Once reset() is called, all their auto attributes are reset to their OneTimeProperty descriptors, and their accessor functions will be triggered again.

> **Warning:** If a class has a set of attributes that are OneTimeProperty, but that can be initialized from any one of them, do NOT use this mixin! For instance, UniformTimeSeries can be initialized with only sampling_rate and t0, sampling_interval and time are auto-computed. But if you were to reset() a UniformTimeSeries, it would lose all 4, and there would be then no way to break the circular dependency chains.
> If this becomes a problem in practice (for our analyzer objects it isn't, as they don't have the above pattern), we can extend reset() to check for a _no_reset set of names in the instance which are meant to be kept protected. But for now this is NOT done, so caveat emptor.

Examples

```
>>> class A(ResetMixin):
...     def __init__(self,x=1.0):
...         self.x = x
...
...     @auto_attr
...     def y(self):
...         print('*** y computation executed ***')
...         return self.x / 2.0
...
```

```
>>> a = A(10)
```

About to access y twice, the second time no computation is done: >>> a.y *** y computation executed *** 5.0 >>> a.y 5.0

Changing x >>> a.x = 20

a.y doesn't change to 10, since it is a static attribute: >>> a.y 5.0

We now reset a, and this will then force all auto attributes to recompute the next time we access them: >>> a.reset()

About to access y twice again after reset(): >>> a.y *** y computation executed *** 10.0 >>> a.y 10.0

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

reset()
Reset all OneTimeProperty attributes that may have fired already.

auto_attr

nibabel.onetime.**auto_attr**(*func*)

Decorator to create OneTimeProperty attributes.

Parametersfunc : method

The method that will be called the first time to compute a value. Afterwards, the method's name will be a standard attribute holding the value of this computation.

Examples

```
>>> class MagicProp(object):
...     @auto_attr
...     def a(self):
...         return 99
...
>>> x = MagicProp()
>>> 'a' in x.__dict__
False
>>> x.a
99
>>> 'a' in x.__dict__
True
```

setattr_on_read

nibabel.onetime.**setattr_on_read**(*func*)

Decorator to create OneTimeProperty attributes.

Parametersfunc : method

The method that will be called the first time to compute a value. Afterwards, the method's name will be a standard attribute holding the value of this computation.

Examples

```
>>> class MagicProp(object):
...     @auto_attr
...     def a(self):
...         return 99
...
>>> x = MagicProp()
>>> 'a' in x.__dict__
False
>>> x.a
99
>>> 'a' in x.__dict__
True
```

openers

Context manager openers for various fileobject types

BufferedGzipFile([filename, mode, ...])	GzipFile able to readinto buffer >= 2**32 bytes.
Opener(fileish, *args, **kwargs)	Class to accept, maybe open, and context-manage file-likes / filenames

BufferedGzipFile

class nibabel.openers.**BufferedGzipFile**(*filename=None*, *mode=None*, *compresslevel=9*, *fileobj=None*, *mtime=None*)

Bases: gzip.GzipFile

GzipFile able to readinto buffer >= 2**32 bytes.

This class only differs from gzip.GzipFile in Python 3.5.0.

This works around a known issue in Python 3.5. See https://bugs.python.org/issue25626

Constructor for the GzipFile class.

At least one of fileobj and filename must be given a non-trivial value.

The new class instance is based on fileobj, which can be a regular file, a StringIO object, or any other object which simulates a file. It defaults to None, in which case filename is opened to provide a file object.

When fileobj is not None, the filename argument is only used to be included in the gzip file header, which may includes the original filename of the uncompressed file. It defaults to the filename of fileobj, if discernible; otherwise, it defaults to the empty string, and in this case the original filename is not included in the header.

The mode argument can be any of 'r', 'rb', 'a', 'ab', 'w', or 'wb', depending on whether the file will be read or written. The default is the mode of fileobj if discernible; otherwise, the default is 'rb'. Be aware that only the 'rb', 'ab', and 'wb' values should be used for cross-platform portability.

The compresslevel argument is an integer from 0 to 9 controlling the level of compression; 1 is fastest and produces the least compression, and 9 is slowest and produces the most compression. 0 is no compression at all. The default is 9.

The mtime argument is an optional numeric timestamp to be written to the stream when compressing. All gzip compressed streams are required to contain a timestamp. If omitted or None, the current time is used. This module ignores the timestamp when decompressing; however, some programs, such as gunzip, make use of it. The format of the timestamp is the same as that of the return value of time.time() and of the st_mtime member of the object returned by os.stat().

__init__(*filename=None*, *mode=None*, *compresslevel=9*, *fileobj=None*, *mtime=None*)

Constructor for the GzipFile class.

At least one of fileobj and filename must be given a non-trivial value.

The new class instance is based on fileobj, which can be a regular file, a StringIO object, or any other object which simulates a file. It defaults to None, in which case filename is opened to provide a file object.

When fileobj is not None, the filename argument is only used to be included in the gzip file header, which may includes the original filename of the uncompressed file. It defaults to the filename of fileobj, if discernible; otherwise, it defaults to the empty string, and in this case the original filename is not included in the header.

The mode argument can be any of 'r', 'rb', 'a', 'ab', 'w', or 'wb', depending on whether the file will be read or written. The default is the mode of fileobj if discernible; otherwise, the default is 'rb'. Be aware that only the 'rb', 'ab', and 'wb' values should be used for cross-platform portability.

The compresslevel argument is an integer from 0 to 9 controlling the level of compression; 1 is fastest and produces the least compression, and 9 is slowest and produces the most compression. 0 is no compression at all. The default is 9.

The mtime argument is an optional numeric timestamp to be written to the stream when compressing. All gzip compressed streams are required to contain a timestamp. If omitted or None, the current time is used. This module ignores the timestamp when decompressing; however, some programs, such as gunzip, make use of it. The format of the timestamp is the same as that of the return value of time.time() and of the st_mtime member of the object returned by os.stat().

Opener

class nibabel.openers.**Opener**(*fileish*, **args*, ***kwargs*)
Bases: object

Class to accept, maybe open, and context-manage file-likes / filenames

Provides context manager to close files that the constructor opened for you.

Parametersfileish : str or file-like

if str, then open with suitable opening method. If file-like, accept as is

***args** : positional arguments

passed to opening method when *fileish* is str. mode, if not specified, is *rb*. compresslevel, if relevant, and not specified, is set from class variable default_compresslevel

****kwargs** : keyword arguments

passed to opening method when *fileish* is str. Change of defaults as for *args

__init__(*fileish*, **args*, ***kwargs*)

bz2_def = (<type 'bz2.BZ2File'>, ('mode', 'buffering', 'compresslevel'))

close(**args*, ***kwargs*)

close_if_mine()
Close self.fobj iff we opened it in the constructor

closed

compress_ext_icase = True
whether to ignore case looking for compression extensions

compress_ext_map = {'.bz2': (<type 'bz2.BZ2File'>, ('mode', 'buffering', 'compresslevel')), None: (<built-in function o

default_compresslevel = 1
default compression level when writing gz and bz2 files

fileno()

gz_def = (<function _gzip_open at 0x102b72050>, ('mode', 'compresslevel'))

mode

name
Return self.fobj.name or self._name if not present

self._name will be None if object was created with a fileobj, otherwise it will be the filename.

read(**args*, ***kwargs*)

seek(**args*, ***kwargs*)

tell(**args*, ***kwargs*)

write(**args*, ***kwargs*)

optpkg

Routines to support optional packages

optional_package(name[, trip_msg])	Return package-like thing and module setup for package *name*

optional_package

nibabel.optpkg.**optional_package**(*name*, *trip_msg=None*)

Return package-like thing and module setup for package *name*

Parametersname : str

package name

trip_msg : None or str

message to give when someone tries to use the return package, but we could not import it, and have returned a TripWire object instead. Default message if None.

Returnspkg_like : module or `TripWire` instance

If we can import the package, return it. Otherwise return an object raising an error when accessed

have_pkg : bool

True if import for package was successful, false otherwise

module_setup : function

callable usually set as `setup_module` in calling namespace, to allow skipping tests.

Examples

Typical use would be something like this at the top of a module using an optional package:

```
>>> from nibabel.optpkg import optional_package
>>> pkg, have_pkg, setup_module = optional_package('not_a_package')
```

Of course in this case the package doesn't exist, and so, in the module:

```
>>> have_pkg
False
```

and

```
>>> pkg.some_function()
Traceback (most recent call last):
    ...
TripWireError: We need package not_a_package for these functions, but ``import not_a_package`` ra
```

If the module does exist - we get the module

```
>>> pkg, _, _ = optional_package('os')
>>> hasattr(pkg, 'path')
True
```

Or a submodule if that's what we asked for

```
    >>> subpkg, _, _ = optional_package('os.path')
    >>> hasattr(subpkg, 'dirname')
    True
```

rstutils

ReStructured Text utilities

- Make ReST table given array of values

rst_table(cell_values[, row_names, ...])	Return string for ReST table with entries *cell_values*

rst_table

nibabel.rstutils.**rst_table**(*cell_values*, *row_names=None*, *col_names=None*, *title=''*, *val_fmt='{0:5.2f}'*, *format_chars=None*)

Return string for ReST table with entries *cell_values*

Parameterscell_values : (R, C) array-like

At least 2D. Can be greater than 2D, in which case you should adapt the *val_fmt* to deal with the multiple entries that will go in each cell

row_names : None or (R,) length sequence, optional

Row names. If None, use `row[0]` etc.

col_names : None or (C,) length sequence, optional

Column names. If None, use `col[0]` etc.

title : str, optional

Title for table. Add as heading above table

val_fmt : str, optional

Format string using string `format` method mini-language. Converts the result of `cell_values[r, c]` to a string to make the cell contents. Default assumes a floating point value in a 2D *cell_values*.

format_chars : None or dict, optional

With keys 'down', 'along', 'thick_long', 'cross' and 'title_heading'. Values are characters for: lines going down; lines going along; thick lines along; two lines crossing; and the title overline / underline. All missing values filled with rst defaults.

Returnstable_str : str

Multiline string with ascii table, suitable for printing

tmpdirs

Contexts for *with* statement providing temporary directories

InGivenDirectory([path])	Change directory to given directory for duration of `with` block
InTemporaryDirectory([suffix, prefix, dir])	Create, return, and change directory to a temporary directory
TemporaryDirectory([suffix, prefix, dir])	Create and return a temporary directory.

InGivenDirectory

class nibabel.tmpdirs.**InGivenDirectory**(*path=None*)
Bases: object

Change directory to given directory for duration of `with` block

Useful when you want to use *InTemporaryDirectory* for the final test, but you are still debugging. For example, you may want to do this in the end:

```
>>> with InTemporaryDirectory() as tmpdir:
...     # do something complicated which might break
...     pass
```

But indeed the complicated thing does break, and meanwhile the `InTemporaryDirectory` context manager wiped out the directory with the temporary files that you wanted for debugging. So, while debugging, you replace with something like:

```
>>> with InGivenDirectory() as tmpdir: # Use working directory by default
...     # do something complicated which might break
...     pass
```

You can then look at the temporary file outputs to debug what is happening, fix, and finally replace `InGivenDirectory` with `InTemporaryDirectory` again.

Initialize directory context manager

Parameterspath : None or str, optional

path to change directory to, for duration of `with` block. Defaults to `os.getcwd()` if None

__init__(*path=None*)
Initialize directory context manager
Parameterspath : None or str, optional
path to change directory to, for duration of `with` block. Defaults to `os.getcwd()` if None

InTemporaryDirectory

class nibabel.tmpdirs.**InTemporaryDirectory**(*suffix=''*, *prefix='tmp'*, *dir=None*)
Bases: *nibabel.tmpdirs.TemporaryDirectory*

Create, return, and change directory to a temporary directory

Examples

```
>>> import os
>>> my_cwd = os.getcwd()
>>> with InTemporaryDirectory() as tmpdir:
...     _ = open('test.txt', 'wt').write('some text')
...     assert os.path.isfile('test.txt')
...     assert os.path.isfile(os.path.join(tmpdir, 'test.txt'))
>>> os.path.exists(tmpdir)
False
>>> os.getcwd() == my_cwd
True
```

__init__(*suffix=''*, *prefix='tmp'*, *dir=None*)

TemporaryDirectory

class nibabel.tmpdirs.**TemporaryDirectory**(*suffix=''*, *prefix='tmp'*, *dir=None*)
Bases: object

Create and return a temporary directory. This has the same behavior as mkdtemp but can be used as a context manager.

Upon exiting the context, the directory and everthing contained in it are removed.

Examples

```
>>> import os
>>> with TemporaryDirectory() as tmpdir:
...     fname = os.path.join(tmpdir, 'example_file.txt')
...     with open(fname, 'wt') as fobj:
...         _ = fobj.write('a string\n')
>>> os.path.exists(tmpdir)
False
```

__init__(*suffix=''*, *prefix='tmp'*, *dir=None*)

cleanup()

tripwire

Class to raise error for missing modules or other misfortunes

TripWire(msg)	Class raising error if used
TripWireError	Exception if trying to use TripWire object
is_tripwire(obj)	Returns True if *obj* appears to be a TripWire object

TripWire

class nibabel.tripwire.**TripWire**(*msg*)
Bases: object

Class raising error if used

Standard use is to proxy modules that we could not import

Examples

```
>>> a_module = TripWire('We do not have a_module')
>>> a_module.do_silly_thing('with silly string')
Traceback (most recent call last):
    ...
TripWireError: We do not have a_module
```

__init__(*msg*)

TripWireError

class nibabel.tripwire.**TripWireError**
Bases: exceptions.AttributeError

Exception if trying to use TripWire object

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

is_tripwire

nibabel.tripwire.**is_tripwire**(*obj*)
Returns True if *obj* appears to be a TripWire object

Examples

```
>>> is_tripwire(object())
False
>>> is_tripwire(TripWire('some message'))
True
```

wrapstruct

Class to wrap numpy structured array

wrapstruct

The *WrapStruct* class is a wrapper around a numpy structured array type.

It implements:

- Mappingness from the underlying structured array fields
- from_fileobj, write_to methods to read and write data to fileobj
- A mechanism for setting checks and fixes to the data on object creation
- Endianness guessing, and on-the-fly swapping

The *LabeledWrapStruct* subclass adds:

- A pretty printing mechanism whereby field values can be displayed as corresponding strings (see *LabeledWrapStruct.get_value_label()* and LabeledWrapStruct.__str__())

Mappingness You can access and set fields of the contained structarr using standard __getitem__ / __setitem__ syntax:

wrapped['field'] = 10

Wrapped structures also implement general mappingness:

wrapped.keys() wrapped.items() wrapped.values()

Properties:

```
.endianness (read only)
.binaryblock (read only)
.structarr (read only)
```

Methods:

```
.as_byteswapped(endianness)
.check_fix()
.__str__
.__eq__
.__ne__
.get_value_label(name)
```

Class methods:

```
.diagnose_binaryblock
.as_byteswapped(endianness)
.write_to(fileobj)
.from_fileobj(fileobj)
.default_structarr() - return default structured array
.guessed_endian(structarr) - return guessed endian code from this structarr
```

Class variables: template_dtype - native endian version of dtype for contained structarr

Consistency checks We have a file, and we would like information as to whether there are any problems with the binary data in this file, and whether they are fixable. `WrapStruct` can hold checks for internal consistency of the contained data:

```
wrapped = WrapStruct.from_fileobj(open('myfile.bin'), check=False)
dx_result = WrapStruct.diagnose_binaryblock(wrapped.binaryblock)
```

This will run all known checks, with no fixes, returning a string with diagnostic output. See below for the `check=False` flag.

In creating a `WrapStruct` object, we often want to check the consistency of the contained data. The checks can test for problems of various levels of severity. If the problem is severe enough, it should raise an Error. So, with data that is consistent - no error:

```
wrapped = WrapStruct.from_fileobj(good_fileobj)
```

whereas:

```
wrapped = WrapStruct.from_fileobj(bad_fileobj)
```

would raise some error, with output to logging (see below).

If we want the created object, come what may:

```
hdr = WrapStruct.from_fileobj(bad_fileobj, check=False)
```

We set the error level (the level of problem that the `check=True` versions will accept as OK) from global defaults:

```
import nibabel as nib
nib.imageglobals.error_level = 30
```

The same for logging:

```
nib.imageglobals.logger = logger
```

LabeledWrapStruct([binaryblock, endianness, ...])	A WrapStruct with some fields having value labels for printing etc
WrapStruct([binaryblock, endianness, check])	Initialize WrapStruct from binary data block
WrapStructError	

LabeledWrapStruct

class nibabel.wrapstruct.**LabeledWrapStruct**(*binaryblock=None*, *endianness=None*, *check=True*)

Bases: *nibabel.wrapstruct.WrapStruct*

A WrapStruct with some fields having value labels for printing etc

Initialize WrapStruct from binary data block

Parametersbinaryblock : {None, string} optional

binary block to set into object. By default, None, in which case we insert the default empty block

endianness : {None, '<','>', other endian code} string, optional

endianness of the binaryblock. If None, guess endianness from the data.

check : bool, optional

Whether to check content of binary data in initialization. Default is True.

Examples

```
>>> wstr1 = WrapStruct() # a default structure
>>> wstr1.endianness == native_code
True
>>> wstr1['integer']
array(0, dtype=int16)
>>> wstr1['integer'] = 1
>>> wstr1['integer']
array(1, dtype=int16)
```

__init__(*binaryblock=None*, *endianness=None*, *check=True*)

Initialize WrapStruct from binary data block

Parametersbinaryblock : {None, string} optional

binary block to set into object. By default, None, in which case we insert the default empty block

endianness : {None, '<','>', other endian code} string, optional

endianness of the binaryblock. If None, guess endianness from the data.

check : bool, optional

Whether to check content of binary data in initialization. Default is True.

Examples

```
>>> wstr1 = WrapStruct() # a default structure
>>> wstr1.endianness == native_code
True
>>> wstr1['integer']
array(0, dtype=int16)
```

```
>>> wstr1['integer'] = 1
>>> wstr1['integer']
array(1, dtype=int16)
```

get_value_label(*fieldname*)
Returns label for coded field

A coded field is an int field containing codes that stand for discrete values that also have string labels.

Parametersfieldname : str
name of header field to get label for

Returnslabel : str
label for code value in header field *fieldname*

RaisesValueError :
if field is not coded.

Examples

```
>>> from nibabel.volumeutils import Recoder
>>> recoder = Recoder(((1, 'one'), (2, 'two')), ('code', 'label'))
>>> class C(LabeledWrapStruct):
...     template_dtype = np.dtype([('datatype', 'i2')])
...     _field_recoders = dict(datatype = recoder)
>>> hdr  = C()
>>> hdr.get_value_label('datatype')
'<unknown code 0>'
>>> hdr['datatype'] = 2
>>> hdr.get_value_label('datatype')
'two'
```

WrapStruct

class nibabel.wrapstruct.**WrapStruct**(*binaryblock=None*, *endianness=None*, *check=True*)
Bases: object

Initialize WrapStruct from binary data block

Parametersbinaryblock : {None, string} optional

binary block to set into object. By default, None, in which case we insert the default empty block

endianness : {None, '<','>', other endian code} string, optional

endianness of the binaryblock. If None, guess endianness from the data.

check : bool, optional

Whether to check content of binary data in initialization. Default is True.

Examples

```
>>> wstr1 = WrapStruct() # a default structure
>>> wstr1.endianness == native_code
True
>>> wstr1['integer']
```

```
array(0, dtype=int16)
>>> wstr1['integer'] = 1
>>> wstr1['integer']
array(1, dtype=int16)
```

__init__(*binaryblock=None*, *endianness=None*, *check=True*)

Initialize WrapStruct from binary data block

Parametersbinaryblock : {None, string} optional
binary block to set into object. By default, None, in which case we insert the default empty block

endianness : {None, '<','>', other endian code} string, optional
endianness of the binaryblock. If None, guess endianness from the data.

check : bool, optional
Whether to check content of binary data in initialization. Default is True.

Examples

```
>>> wstr1 = WrapStruct() # a default structure
>>> wstr1.endianness == native_code
True
>>> wstr1['integer']
array(0, dtype=int16)
>>> wstr1['integer'] = 1
>>> wstr1['integer']
array(1, dtype=int16)
```

as_byteswapped(*endianness=None*)

return new byteswapped object with given `endianness`

Guaranteed to make a copy even if endianness is the same as the current endianness.

Parametersendianness : None or string, optional
endian code to which to swap. None means swap from current endianness, and is the default

Returnswstr : `WrapStruct`
`WrapStruct` object with given endianness

Examples

```
>>> wstr = WrapStruct()
>>> wstr.endianness == native_code
True
>>> bs_wstr = wstr.as_byteswapped()
>>> bs_wstr.endianness == swapped_code
True
>>> bs_wstr = wstr.as_byteswapped(swapped_code)
>>> bs_wstr.endianness == swapped_code
True
>>> bs_wstr is wstr
False
>>> bs_wstr == wstr
True
```

If you write to the resulting byteswapped data, it does not change the original.

```
>>> bs_wstr['integer'] = 3
>>> bs_wstr == wstr
False
```

If you swap to the same endianness, it returns a copy

```
>>> nbs_wstr = wstr.as_byteswapped(native_code)
>>> nbs_wstr.endianness == native_code
True
>>> nbs_wstr is wstr
False
```

binaryblock
binary block of data as string
Returnsbinaryblock : string
string giving binary data block

Examples

```
>>> # Make default empty structure
>>> wstr = WrapStruct()
>>> len(wstr.binaryblock)
2
```

check_fix(*logger=None*, *error_level=None*)
Check structured data with checks

copy()
Return copy of structure

```
>>> wstr = WrapStruct()
>>> wstr['integer'] = 3
>>> wstr2 = wstr.copy()
>>> wstr2 is wstr
False
>>> wstr2['integer']
array(3, dtype=int16)
```

classmethod default_structarr(*klass*, *endianness=None*)
Return structured array for default structure, with given endianness

classmethod diagnose_binaryblock(*klass*, *binaryblock*, *endianness=None*)
Run checks over binary data, return string

endianness
endian code of binary data

The endianness code gives the current byte order interpretation of the binary data.

Notes

Endianness gives endian interpretation of binary data. It is read only because the only common use case is to set the endianness on initialization, or occasionally byteswapping the data - but this is done via the as_byteswapped method

Examples

```
>>> wstr = WrapStruct()
>>> code = wstr.endianness
>>> code == native_code
True
```

classmethod from_fileobj(*klass*, *fileobj*, *endianness=None*, *check=True*)
Return read structure with given or guessed endiancode

Parametersfileobj : file-like object
Needs to implement `read` method

endianness : None or endian code, optional
Code specifying endianness of read data

Returnswstr : WrapStruct object
WrapStruct object initialized from data in fileobj

get(*k*, *d=None*)
Return value for the key k if present or d otherwise

classmethod guessed_endian(*mapping*)
Guess intended endianness from mapping-like `mapping`

Parameterswstr : mapping-like
Something implementing a mapping. We will guess the endianness from looking at the field values

Returnsendianness : {'<', '>'}
Guessed endianness of binary data in `wstr`

items()
Return items from structured data

keys()
Return keys from structured data

structarr
Structured data, with data fields

Examples

```
>>> wstr1 = WrapStruct() # with default data
>>> an_int = wstr1.structarr['integer']
>>> wstr1.structarr = None
Traceback (most recent call last):
   ...
AttributeError: can't set attribute
```

template_dtype = dtype([('integer', '<i2')])

values()
Return values from structured data

write_to(*fileobj*)
Write structure to fileobj

Write starts at fileobj current file position.

Parametersfileobj : file-like object
Should implement `write` method

ReturnsNone :

Examples

```
>>> wstr = WrapStruct()
>>> from io import BytesIO
>>> str_io = BytesIO()
>>> wstr.write_to(str_io)
>>> wstr.binaryblock == str_io.getvalue()
True
```

WrapStructError

class nibabel.wrapstruct.**WrapStructError**
Bases: exceptions.Exception

__init__()
x.__init__(...) initializes x; see help(type(x)) for signature

9.5.7 Alphabetical API reference

API Reference

benchmarks

Module: benchmarks.bench_array_to_file Benchmarks for array_to_file routine

Run benchmarks with:

```
import nibabel as nib
nib.bench()
```

If you have doctests enabled by default in nose (with a noserc file or environment variable), and you have a numpy version <= 1.6.1, this will also run the doctests, let's hope they pass.

Run this benchmark with:

nosetests -s –match '(?:^|[b_.//-])[Bb]ench' /path/to/bench_load_save.py

---

bench_array_to_file()

Module: benchmarks.bench_fileslice Benchmarks for fileslicing

import nibabel as nib nib.bench()

If you have doctests enabled by default in nose (with a noserc file or environment variable), and you have a numpy version <= 1.6.1, this will also run the doctests, let's hope they pass.

Run this benchmark with:

nosetests -s –match '(?:^|[b_.//-])[Bb]ench' /path/to/bench_fileslice.py

---

bench_fileslice([bytes, file_, gz, bz2])

Continued on next page

Table 9.64 – continued from previous page

run_slices(file_like[, repeat, offset, order])	

Module: benchmarks.bench_finite_range Benchmarks for finite_range routine

Run benchmarks with:

```
import nibabel as nib
nib.bench()
```

If you have doctests enabled by default in nose (with a noserc file or environment variable), and you have a numpy version <= 1.6.1, this will also run the doctests, let's hope they pass.

Run this benchmark with:

nosetests -s –match '(?:^|[b_.//-])[Bb]ench' /path/to/bench_finite_range

bench_finite_range()	

Module: benchmarks.bench_load_save Benchmarks for load and save of image arrays

Run benchmarks with:

```
import nibabel as nib
nib.bench()
```

If you have doctests enabled by default in nose (with a noserc file or environment variable), and you have a numpy version <= 1.6.1, this will also run the doctests, let's hope they pass.

Run this benchmark with:

nosetests -s –match '(?:^|[b_.//-])[Bb]ench' /path/to/bench_load_save.py

bench_load_save()	

Module: benchmarks.butils Benchmarking utilities

print_git_title(title)	Prints title string with git hash if possible, and underline

bench_array_to_file
nibabel.benchmarks.bench_array_to_file.**bench_array_to_file**()

bench_fileslice
nibabel.benchmarks.bench_fileslice.**bench_fileslice**(*bytes=True*, *file_=True*, *gz=True*, *bz2=False*)

run_slices
nibabel.benchmarks.bench_fileslice.**run_slices**(*file_like*, *repeat=3*, *offset=0*, *order='F'*)

bench_finite_range
nibabel.benchmarks.bench_finite_range.**bench_finite_range**()

bench_load_save
nibabel.benchmarks.bench_load_save.**bench_load_save**()

print_git_title
nibabel.benchmarks.butils.**print_git_title**(*title*)
Prints title string with git hash if possible, and underline

checkwarns

Contexts for *with* statement allowing checks for warnings

ErrorWarnings([record, module])	Context manager to check for warnings as errors.
IgnoreWarnings([record, module])	Context manager to ignore warnings

ErrorWarnings
class nibabel.checkwarns.**ErrorWarnings**(*record=True*, *module=None*)
Bases: warnings.catch_warnings

Context manager to check for warnings as errors. Usually used with assert_raises in the with block

Examples

```
>>> with ErrorWarnings():
...     try:
...         warnings.warn('Message', UserWarning)
...     except UserWarning:
...         print('I consider myself warned')
I consider myself warned
```

__init__(*record=True*, *module=None*)

filter = 'error'

IgnoreWarnings
class nibabel.checkwarns.**IgnoreWarnings**(*record=True*, *module=None*)
Bases: *nibabel.checkwarns.ErrorWarnings*

Context manager to ignore warnings

Examples

```
>>> with IgnoreWarnings():
...     warnings.warn('Message', UserWarning)
```

(and you get no warning)

__init__(*record=True*, *module=None*)

filter = 'ignore'

deprecated

Module to help with deprecating classes and modules

FutureWarningMixin(*args, **kwargs)	Insert FutureWarning for object creation
ModuleProxy(module_name)	Proxy for module that may not yet have been imported

FutureWarningMixin

class nibabel.deprecated.**FutureWarningMixin**(**args*, ***kwargs*)

Bases: object

Insert FutureWarning for object creation

Examples

```
>>> class C(object): pass
>>> class D(FutureWarningMixin, C):
...     warn_message = "Please, don't use this class"
```

Record the warning

```
>>> with warnings.catch_warnings(record=True) as warns:
...     d = D()
...     warns[0].message
FutureWarning("Please, don't use this class",)
```

__init__(**args*, ***kwargs*)

warn_message = 'This class will be removed in future versions'

ModuleProxy

class nibabel.deprecated.**ModuleProxy**(*module_name*)

Bases: object

Proxy for module that may not yet have been imported

Parametersmodule_name : str

Full module name e.g. nibabel.minc

Examples

::arr = np.arange(24).reshape((2, 3, 4)) minc = ModuleProxy('nibabel.minc') minc_image = minc.Minc1Image(arr, np.eye(4))

So, the minc object is a proxy that will import the required module when you do attribute access and return the attributes of the imported module.

__init__(*module_name*)

keywordonly

Decorator for labeling keyword arguments as keyword only

kw_only_func(n)	Return function decorator enforcing maximum of *n* positional arguments
kw_only_meth(n)	Return method decorator enforcing maximum of *n* positional arguments

kw_only_func

nibabel.keywordonly.**kw_only_func**(*n*)

Return function decorator enforcing maximum of *n* positional arguments

kw_only_meth

nibabel.keywordonly.**kw_only_meth**(*n*)

Return method decorator enforcing maximum of *n* positional arguments

The method has at least one positional argument `self` or `cls`; allow for that.

minc

Deprecated MINC1 module

---

mriutils

Utilities for calculations related to MRI

MRIError	
calculate_dwell_time(water_fat_shift, ...)	Calculate the dwell time

MRIError

class nibabel.mriutils.**MRIError**

Bases: exceptions.ValueError

__init__()

x.__init__(...) initializes x; see help(type(x)) for signature

calculate_dwell_time

nibabel.mriutils.**calculate_dwell_time**(*water_fat_shift*, *echo_train_length*, *field_strength*)

Calculate the dwell time

Parameterswater_fat_shift : float

The water fat shift of the recording, in pixels.

echo_train_length : int

The echo train length of the imaging sequence.

field_strength : float

Strength of the magnet in Tesla, e.g. 3.0 for a 3T magnet recording.

Returnsdwell_time : float

The dwell time in seconds.

RaisesMRIError :

if values are out of range

py3k

Python 3 compatibility tools.

Copied from numpy/compat/py3k

Please prefer the routines in externals/six.py when possible

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asbytes_nested(x)
asunicode(s)
asunicode_nested(x)
getexception()
ints2bytes(seq)
isfileobj(f)
open_latin1(filename[, mode])

asbytes_nested
nibabel.py3k.**asbytes_nested**(*x*)

asunicode
nibabel.py3k.**asunicode**(*s*)

asunicode_nested
nibabel.py3k.**asunicode_nested**(*x*)

getexception
nibabel.py3k.**getexception**()

ints2bytes
nibabel.py3k.**ints2bytes**(*seq*)

isfileobj
nibabel.py3k.**isfileobj**(*f*)

open_latin1
nibabel.py3k.**open_latin1**(*filename*, *mode='r'*)

spaces

Routines to work with spaces

A space is defined by coordinate axes.

A voxel space can be expressed by a shape implying an array, where the axes are the axes of the array.

A mapped voxel space (mapped voxels) is either:

- an image, with attributes `shape` (the voxel space) and `affine` (the mapping), or
- a length 2 sequence with the same information (shape, affine).

slice2volume(index, axis[, shape])	Affine expressing selection of a single slice from 3D volume
vox2out_vox(mapped_voxels[, voxel_sizes])	output-aligned shape, affine for input implied by *mapped_voxels*

slice2volume

nibabel.spaces.**slice2volume**(*index*, *axis*, *shape=None*)

Affine expressing selection of a single slice from 3D volume

Imagine we have taken a slice from an image data array, `s = data[:, :, index]`. This function returns the affine to map the array coordinates of `s` to the array coordinates of `data`.

This can be useful for resampling a single slice from a volume. For example, to resample slice `k` in the space of `img1` from the matching spatial voxel values in `img2`, you might do something like:

```
slice_shape = img1.shape[:2]
slice_aff = slice2volume(k, 2)
whole_aff = np.linalg.inv(img2.affine).dot(img1.affine.dot(slice_aff))
```

and then use `whole_aff` in `scipy.ndimage.affine_transform`:

rzs, trans = to_matvec(whole_aff) data = img2.get_data() new_slice = scipy.ndimage.affine_transform(data, rzs, trans, slice_shape)

Parametersindex : int

index of selected slice

axis : {0, 1, 2}

axis to which *index* applies

Returnsslice_aff : shape (4, 3) affine

Affine relating input coordinates in a slice to output coordinates in the embedded volume

vox2out_vox

nibabel.spaces.**vox2out_vox**(*mapped_voxels*, *voxel_sizes=None*)

output-aligned shape, affine for input implied by *mapped_voxels*

The input (voxel) space, and the affine mapping to output space, are given in *mapped_voxels*.

The output space is implied by the affine, we don't need to know what that is, we just return something with the same (implied) output space.

Our job is to work out another voxel space where the voxel array axes and the output axes are aligned (top left 3 x 3 of affine is diagonal with all positive entries) and which contains all the voxels of the implied input image at their correct output space positions, once resampled into the output voxel space.

Parametersmapped_voxels : object or length 2 sequence

If object, has attributes `shape` giving input voxel shape, and `affine` giving mapping of input voxels to output space. If length 2 sequence, elements are (shape, affine) with same meaning as above. The affine is a (4, 4) array-like.

voxel_sizes : None or sequence

Gives the diagonal entries of *output_affine* (except the trailing 1 for the homogenous coordinates) (`output_affine == np.diag(voxel_sizes + [1])`). If None, return identity *output_affine*.

Returnsoutput_shape : sequence

Shape of output image that has voxel axes aligned to original image output space axes, and encloses all the voxel data from the original image implied by input shape.

output_affine : (4, 4) array

Affine of output image that has voxel axes aligned to the output axes implied by input affine. Top-left 3 x 3 part of affine is diagonal with all positive entries. The entries come from *voxel_sizes* if specified, or are all 1. If the image is < 3D, then the missing dimensions will have a 1 in the matching diagonal.

n

Symbols

A

B

C

D

E

F

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H

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K

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M

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O

P

Q

R

S

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V

W

X