



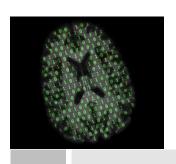
## **NIfTI**

- NIfTI (Neuroimaging Informatics Technology Initiative) format
  - Standardized representation of images
  - Most commonly used type of analytic file
  - Developed to facilitate cross-platform, crosssoftware interpretability
  - 3-dimensional (3D) array: stacking individual slices on top of each other
  - DICOM: one sheet of paper, NIfTI: stack of papers



# **DICOM versus NIfTI**

	DICOM	NIfTI
File extension	.dcm	.nii .nii.gz
File represents	One slice of the brain	3D image of the brain
Header contains	Many fields, protected health information, hospital-related meta-data	Image meta-data, no patient information
Storage	Different folders per subject, more complex data structures	Different files (can be in the same directory)



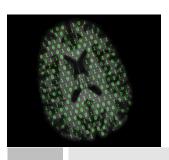
#### From DICOM to NifTI

- DICOM to NIfTI using the dicom2nifti
   function in the oro.dicom package
- □ The nifti object becomes an R object
- $\square$  After saving a file to a <code>nifti</code> file it can be used without R



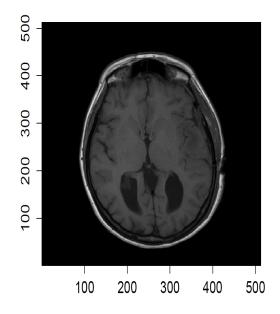
#### Recall: Loading Multiple DICOM Files

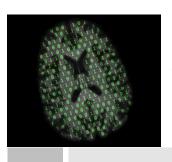
```
Neurohacking data
   BRAINIX
       DICOM
          т1
              IM-0001-0001.dcm
              IM-0001-0022.dcm
          ROI
          FLAIR
          T2
setwd ("~/Neurohacking data/BRAINIX/DICOM")
all slices T1 = readDICOM("T1/")
dim(all slices T1$img[[11]])
[1] 512 512
hdr=all slices T1$hdr[[11]]
hdr[hdr$name == "PixelSpacing", "value"]
[1] "0.46875 0.46875"
```



## From DICOM to NIfTI

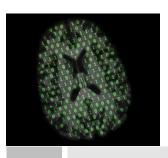
```
nii_T1=dicom2nifti(all_slices_T1)
d=dim(nii_T1); d; class(nii_T1)
[1] 512 512 22
[1] "nifti"
image(1:d[1],1:d[2],nii_T1[,,
11],col=gray(0:64/64),xlab="",ylab="")
```





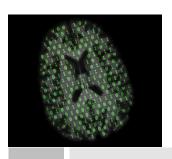
#### Write and Read NIfTI Files

- Use the writeNIfTI, readNIfTI
  functions in the oro.nifti package
- Writes, reads the nifti R object to a NIfTI file
- Default for writeNIfTI is to save compressed NIfTI files



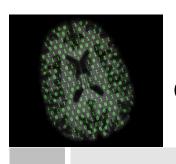
#### Write and Read NIfTI Files

```
library(oro.nifti)
setwd("~/Neurohacking data/BRAINIX/NIfTI")
fname="Output 3D File"
writeNIfTI(nim=nii T1, filename=fname)
list.files(getwd(), pattern = "Output 3D File")
[1] "Output 3D File.nii.gz"
list.files(getwd(), pattern = "T")
[1] "T1.nii.gz" "T2.nii.gz"
nii T2=readNIfTI("T2.nii.gz", reorient=FALSE)
dim(nii T2)
[1] 512 512 22
```



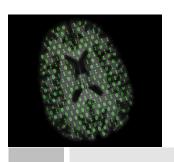
## **Compressed Image Files**

- Files are in compressed format with the extension .nii.gz
- Saves disk space, makes read/write data very fast
- □ Excellent for scripting, analysis of image population
- A non-compressed file can be obtained using the argument gzipped=FALSE in the function writeNifTI
- No extension for file name in writeNifTI



## dcm2nii

- If you do not like R you can use the dcm2nii software as part of the MRIcron platform
- □ Converts DICOM to NIfTI files
- Can handle multiple formats and file types
- But, if you do not R like then you should probably not take this course



## **Other Formats**

- Files from Philips scanners are PAR/REC files (not DICOM)
- $\square$  r2a can be used to convert PAR/REC files to NIfTI files
- NIfTI was based on the ANALYZE format: older, format header and image were in separate files
- □ We prefer NIfTI: one file, can be compressed
- NRRD (Nearly Raw Raster Data) is another, less common format: most neuroimaging software can read NRRD