Description of Source Data

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1 Structure of source Data

Results are structured in the file:

/vol/biomedic3/bglocker/nnUNet

```
-rwxr-xr-x   1 bglocker biomedia 236 Sep 24 15:16 exports
drwxr-sr-x   9 bglocker biomedia   9 Nov 25 10:55 nnUNet_preprocessed
drwxr-sr-x   9 bglocker biomedia  10 Nov 25 10:50 nnUNet_raw
drwxr-sr-x   9 bglocker biomedia   9 Nov 25 12:20 nnUNet_results
drwxr-sr-x  11 bglocker biomedia  11 Dec 16 09:10 nnUNet_testing
-rw-r--r--   1 bglocker biomedia 644 Oct 20 07:20 run_nnunet_0.sh
-rw-r--r--   1 bglocker biomedia 644 Oct 20 07:20 run_nnunet_1.sh
-rw-r--r--   1 bglocker biomedia 644 Oct 20 07:20 run_nnunet_2.sh
-rw-r--r--   1 bglocker biomedia 644 Oct 20 07:21 run_nnunet_3.sh
-rw-r--r--   1 bglocker biomedia 644 Oct 20 07:21 run_nnunet_4.sh
```

2 nnUNet_raw

nnUNet_raw has the original (training) images with manual annotations. Each Dataset below is treated as a binary segmentation problem. See Section5

```
drwxr-sr-x  4 bglocker biomedia   5 Sep 17 13:47 Dataset001_Anorectum
drwxr-sr-x  3 bglocker biomedia   5 Sep 17 20:24 Dataset002_Bladder
drwxr-sr-x  3 bglocker biomedia   5 Sep 17 20:27 Dataset003_CTVn
drwxr-sr-x  3 bglocker biomedia   5 Sep 17 20:28 Dataset004_CTVp
drwxr-sr-x  3 bglocker biomedia   5 Sep 17 20:29 Dataset005_Parametrium
-rw-r--r--  1 bglocker biomedia 135 Nov 25 10:50 note
```

3 nnUNet_results

The raw files from Section2 are used to train an nnUNet model. Which does a 5-fold cross validation, resulting in five models, each trained on 80 subjects and tested on 20 (there is a total of 100 subjects with manual annotations).

3.1 Script

Slurm script

Each of the scripts are presented as bash scripts in `/vol/biomedic3/bglocker/nnUNet/run_nnunet_*.sh`. These are used to schedule the python program into the Slurm scheduler for running in the cloud.

```
#!/bin/bash

# Example of running python script in a batch mode
#SBATCH -c 4                            # Number of CPU Cores
#SBATCH -p gpus                         # Partition (queue)
#SBATCH --gres gpu:1                    # gpu:n, where n = number of GPUs
#SBATCH --mem 12288                     # memory pool for all cores
#SBATCH --nodelist lory                     # SLURM node
#SBATCH --output=slurm.%N.%j.log        # Standard output and error log

# Source virtual environment (pip)
source /vol/biomedic3/bglocker/coding/envs/nnunet/bin/activate

# Set env variables
source /vol/biomedic3/bglocker/nnUNet/exports

# Run python script
nnUNetv2_train 1 3d_fullres 4 # where 4 refers to which dataset we're
                              # training
```

- Source virtual environment

  This is activating the already created python environment.

- Set env variables

  contains paths for raw, results and preprocessed directories

- Run python scripts

  runs the script at `/vol/biomedic3/bglocker/coding/envs/nnunet`

Python script

No access

4 nnUNet_testing

The models are then tested against 10 hold out manual semgentations with no manual segmentations.

5 Viewing the Data

The viewing tool used is ItkSnap, which was developed as an open source tool for viewing medical imaging scans. The view (Figure1) shows how you would see input data.

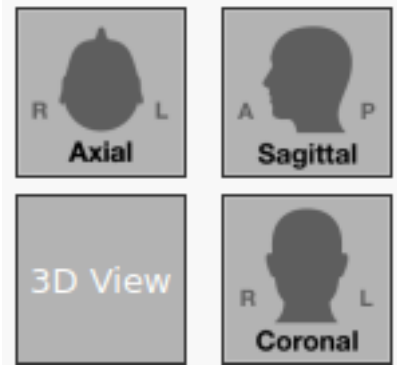

Figure 1: view of all input data

With that we can use this tool to view input data. Here, the R and L stand for right and left respectively, and the A and P stand for Anterior and Posterior. We can provide a few other examples of viewing data displayed below in Figure2. We are further provided with manual annotation of the substructures. Figure3 shows an example of the annotation of the Anorectum. You can enable the 3D visual model through `Edit > 3D Panel > Toggle 3D view`.

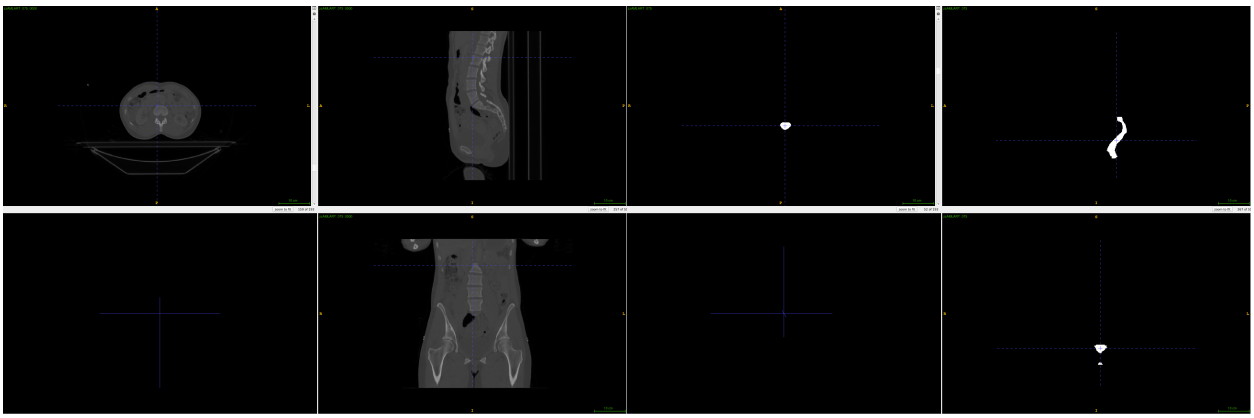

Figure 2: ItkSnap view of the Anorectum Raw Image

Figure 3: ItkSnap view of the Anorectum Raw Image

6 Viewing the data in python

6.1 Reading the data

Please view the script at `research/source/code/performance/geometric/fetch-and-pre-process-data.py`

6.2 What should a medical image contain as data?

"A medical image is the representation of the internal structure or function of an anatomic region in the form of an array of picture elements called pixels or voxels. It is a discrete repre- sentation resulting from a sampling/reconstruction process that maps numerical values to positions of the space. The number of pixels used to describe the field-of-view of a certain acquisition modality is an expression of the detail with which the anatomy or function can be depicted. What the numerical value of the pixel expresses depends on the imaging modality, the acquisition protocol, the reconstruction, and eventually, the post-processing." [3]

6.2.1 Components

- *Pixel Depth*: "number of bits used to encode the information of each pixel" [3]
- *Photometric Interpretation*: "specifies how the pixel data should be interpreted for the correct image display as a monochrome or color image. To specify if color information is or is not stored in the image pixel values, we introduce the concept of samples per pixel (also known as number of channels). Monochrome images have one sample per pixel and no color information stored in the image. A scale of shades of gray from black to white is used to display the images. The number of shades of gray depends clearly from the number of bits used to store the sample that, in this case, coincide with the pixel depth" [3]

  For our case, this will be grey scale
- *Metadata*: information that describe the image
- *Pixel Data*: the section where the numerical values of the pixels are stored

6.3 NIfTI file format

The files are stored in a `.nii` format. This is a NIfTI file format which has had more prominence than the dicom file format recently [4].

- "NIfTI is simple and easy to support"
- "Neuroimaging Informatics Technology Initiativ"[3]
- "allows spatial orientation information to be stored more fully"[4]. Therefore, NIfTI-compliant software should reduce the chance of making "left–right ambiguity"[3, 4]

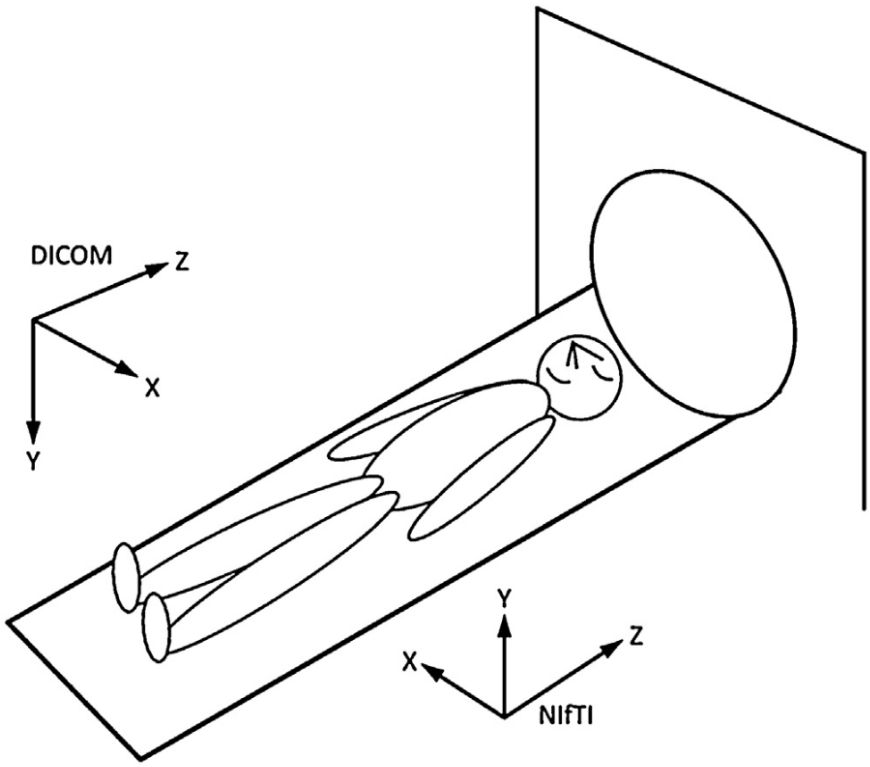

Fig. 1. DICOM Patient Coordinate System (PCS) and NIfTI coordinate system when Patient Position is Head First Supine (HFS). The arrows of axes indicate the positive directions, LPS for DICOM and RAS for NIfTI. For DICOM images in the MR modality, the origin (coordinate 0, 0, 0) refers to the magnet isocenter. For DICOM CT it refers to the table center. After warping to standard space, the NIfTI format specifies that the origin should be set to the location of the anterior commissure. Note that, despite the axis direction difference, both DICOM and NIfTI coordinates systems are so-called right-handed systems, which is different from Analyze coordinate system.

Figure 4: taken from [4]

6.4 Header File

One may observe the header of the file:

```
{
    'ITK_FileNotes': ''
    'ITK_original_direction': '[UNKNOWN_PRINT_CHARACTERISTICS]\n'
    'ITK_original_spacing': '[UNKNOWN_PRINT_CHARACTERISTICS]\n'
    'aux_file': ''
    'bitpix': '32'
    'cal_max': '0'
    'cal_min': '0'
    'datatype': '8'
    'descrip': ''
    'dim[0]': '3'
    'dim[1]': '512'
```

```
    'dim[2]': '512'
    'dim[3]': '193'
    'dim[4]': '1'
    'dim[5]': '1'
    'dim[6]': '1'
    'dim[7]': '1'
    'dim_info': '0'
    'intent_code': '0'
    'intent_name': ''
    'intent_p1': '0'
    'intent_p2': '0'
    'intent_p3': '0'
    'nifti_type': '1'
    'pixdim[0]': '0'
    'pixdim[1]': '1.26953'
    'pixdim[2]': '1.26953'
    'pixdim[3]': '2.5'
    'pixdim[4]': '0'
    'pixdim[5]': '0'
    'pixdim[6]': '0'
    'pixdim[7]': '0'
    'qfac': '[UNKNOWN_PRINT_CHARACTERISTICS]\n'
    'qform_code': '1'
    'qform_code_name': 'NIFTI_XFORM_SCANNER_ANAT'
    'qoffset_x': '325'
    'qoffset_y': '325'
    'qoffset_z': '-155'
    'qto_xyz': '[UNKNOWN_PRINT_CHARACTERISTICS]\n'
    'quatern_b': '0'
    'quatern_c': '0'
    'quatern_d': '1'
    'scl_inter': '0'
    'scl_slope': '1'
    'sform_code': '1'
    'sform_code_name': 'NIFTI_XFORM_SCANNER_ANAT'
    'slice_code': '0'
    'slice_duration': '0'
    'slice_end': '0'
    'slice_start': '0'
    'srow_x': '-1.26953 0 0 325'
    'srow_y': '0 -1.26953 0 325'
    'srow_z': '0 0 2.5 -155'
    'toffset': '0'
    'vox_offset': '352'
    'xyzt_units': '2'
}
```

Table 2
Several important NIfTI header items. Each item has fixed length, and fixed location inside the header.

Name	Meaning	Value example
dim	Image dimension	4 64 64 38 200 1 1 1
pixdim	Voxel size and time interval	1 3 3 3 2 0 0 0
slice_code	Slice order code	0 to 6
descrip	Human readable text	'time = 091230;phase = –y;'
quatern_*b*	Quaternion *b*, *c*, *d*	0
quatern_*c*	parameters	0
quatern_*d*		0
qoffset_*x*	Quaternion transform	–100
qoffset_*y*	offset	–120
qoffset_*z*		–40.2
srow_*x*	Three rows of affine	3 0 0 –100
srow_*y*	transform	0 3 0 –120
srow_*z*		0 0 3 –40.2

Figure 5: taken from [4] with further information available from [2]

6.4.1 Dimension

Starting indexing at 0, we have:

$$dim = \begin{bmatrix} 3 \\ 512 \\ 512 \\ 193 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix}$$

From Page 3 of [1]

- dim[3] $\neq 1$, therefore this is not a single slice. Instead, dim[3] > 1, so there is several slices.
- dim[5] $= 1$, therefore, this is a statistical parameter stored in `intent_p1/2/3`. These are all set to 0, therefore, this is a null dimension.

6.4.2 PixDim

BitPix (32) is the "number of bits per voxel [...], which MUST correspond with the datatype field" [2]. PixDim is the grid spacing [2]. We indicate the units of pixdim with "char xyzt_units" [2] which is 2 in our case. We have no temporal dimension because "dimensions 1,2,3 are for x,y,z; dimension 4 is for time (t)" [2]. A value of 2 means "#define NIFTI_UNITS_MM 2" [2] where bits 0 .. 2 specify the units of our dimensions, so $2 \equiv 010_2$ hence we measure our dimensions in mm.

6.4.3 The Rest

The rest are not relevant to our cause - the library supposedly does everything else for us.

6.5 What do the pixels values mean in NIfTI

6.5.1 ImagesTr

When you read in the data for the `.nii` then you get a list of 2658 unique values. This is not as simple as binary segmentation task of 0s and 1s, we have negatives from -1000 to positives up to 3140. Yeah duh, I mistakenly was analyzing the raw input which will have variable pixel strengths depending on the part of the body it is displaying.

6.5.2 LabelsTr

```
>>> values, count = fetch.np.unique(itk_image, return_counts=True)
>>> values
array([0, 1], dtype=uint8)
>>> count
array([50579427,     14365])
```

References

[1] Hester Breman. *NIfTI-1 Data Format*. URL: `https://nifti.nimh.nih.gov/nifti-1/documentation/nifti1diagrams/`.

[2] Bob Cox. *nifti-1 header field-by-field documentation*. URL: `https://nifti.nimh.nih.gov/pub/dist/src/niftilib/nifti1.h`.

[3] Michele Larobina and Loredana Murino. "Medical Image File Formats". In: *Journal of Digital Imaging* 27 (2013). URL: `https://link.springer.com/article/10.1007/s10278-013-9657-9`.

[4] Xiangrui Li et al. "The first step for neuroimaging data analysis: DICOM to NIfTI conversion". In: *Journal of Neuroscience Methods* 264 (2016). URL: `https://pubmed.ncbi.nlm.nih.gov/26945974/`.