
NiftyPET Documentation

Release 2.0.0

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Dec 14, 2021

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NiftyPET is a software platform and a Python namespace package encompassing sub-packages for high-throughput PET image reconstruction, manipulation, processing and analysis with high quantitative accuracy and precision. One of its key applications is **brain imaging in dementia** with the use of amyloid tracers. See below for the description of the above amyloid PET image reconstructed using *NiftyPET*, superimposed on the MR T1 weighted image*⁰.

Note: Latest Research:

Advanced quantitative evaluation of PET systems using the ACR phantom and NiftyPET software

NiftyPET includes two packages:

- **nimpa**: <https://github.com/NiftyPET/NIMPA> (neuro-image manipulation, processing and analysis)
- **nipet**: <https://github.com/NiftyPET/NIPET> (quantitative PET neuroimaging)

The core routines are written in CUDA C and embedded in Python C extensions to enable user-friendly and high-throughput executions on NVIDIA graphics processing units (GPU). For the scientific aspects of this software platform see section *Scientific Output*.

Although, *NiftyPET* is dedicated to high-throughput image reconstruction and analysis of brain images, it can equally well be used for **whole body imaging**. Strong emphasis is put on the data, which are acquired using positron emission tomography (PET) and magnetic resonance (MR), especially using the hybrid and simultaneous PET/MR scanners.

This software platform covers the entire processing pipeline, from the raw list-mode (LM) PET data through to the final image statistic of interest (e.g., regional SUV), including LM bootstrapping and multiple independent reconstructions to facilitate voxel-wise estimation of uncertainties.

⁰ The above dynamic transaxial and coronal images show the activity of ¹⁸F-florbetapir during the one-hour dynamic acquisition. Note that the signal in the brain white matter dominates over the signal in the grey matter towards the end of the acquisition, which is a typical presentation of a negative amyloid beta (Abeta) scan.

INTRODUCTION

NiftyPET is an open source software solution for standalone and high-throughput PET image reconstruction and analysis. The key computational routines are written in CUDA C for fast and efficient processing on NVIDIA GPU devices. The routines are then embedded in Python C extensions to be readily available for high level programming in Python^{*0}.

1.1 Aim

The purpose of this software platform is to enable rapid processing of raw data as well as image data for fully controlled quantitative PET image reconstruction and analysis. *NiftyPET* includes two stand-alone and independent Python packages: *nipet* and *nimpa*, which are dedicated to high-throughput image reconstruction and analysis. Strong emphasis is put on the data, which are acquired using positron emission tomography (PET) and magnetic resonance (MR), especially the hybrid and simultaneous PET/MR scanners.

This documentation intends to present all the processing chains required not only for generating a final PET image from raw data acquired on a PET/MR scanner, but also further process the image to obtain a final statistic, such as global or regional SUV (standardised uptake value) or SUVr (SUV ratio).

The *nipet* (neuro-imaging PET) Python package contains all the routines needed for robust quantitative image reconstruction from raw data with added quality control of any processing segments, e.g., photon scatter or randoms corrections. The raw data typically includes large list-mode (LM) data (usually taking up GBs), data for detector normalisation, and data for attenuation correction, i.e., the attenuation map, also called the -map.

The *nimpa* (neuro-image manipulation, processing and analysis) package contains all the routines for image input/output, image trimming and up-sampling for regional signal extraction (e.g. from a region of interest-ROI), image registration, and importantly, for partial volume correction (PVC).

The key aspect of *nipet* is the fast LM processing for efficient uncertainty estimation of statistic based on image or projection data. Significant emphasis is placed on reconstruction for scanners with extended axial field of view (FOV), such as the latest PET/MR systems, e.g., the Siemens Biograph *mMR* or the GE *Signa*^{†0}.

The processing chains include:

1. list-mode data processing;
2. accurate attenuation coefficient map generation (with pseudo-CT for PET/MR);
3. detector normalisation with dead time correction;
4. exact forward and back projection between sinogram and image space;
5. estimation of reduced-variance random events;
6. high accuracy fully 3D estimation of scatter events;

⁰ Python 2.7 is supported in version 1.0, while Python 3 support is added in version 2.0+ of *NiftyPET*

[†] Currently the GE *Signa* is not yet fully supported in *NiftyPET*.

7. voxel-based partial volume correction;
8. region- and voxel-level image analysis.

Due to its speed and additional functionalities, *NiftyPET* allows practical and efficient generation of multiple bootstrap realisations of raw and image datasets, being processed within arbitrarily complex reconstruction and analysis chains [1]. Based on these datasets, distributions of any statistic can be formed indicating the uncertainty of any given parameter of interest, for example, the regional SUVR in amyloid brain imaging.

1.2 Software infrastructure

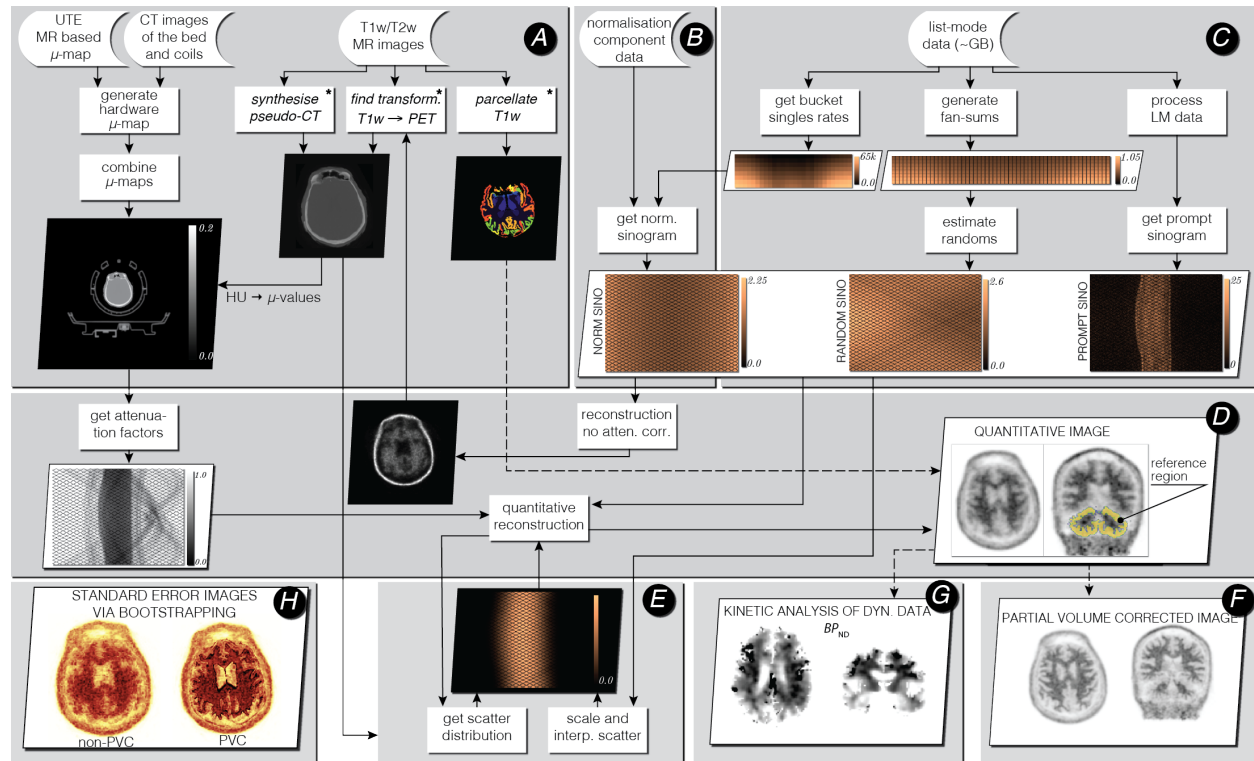


Fig. 1.1: Infrastructure for standalone PET image reconstruction and analysis of PET/MR brain data using amyloid PET tracer. The processing stages (A-H) are explained below. The asterisk (*) indicates external software packages.

For demonstration purposes, all the processing stages presented in the above figure use an amyloid brain scan acquired on the Siemens Biograph mMR. The participant was taking part in “Insight 46”—a neuroscience sub-study of the Medical Research Council National Survey of Health and Development [2].

The input data include the attenuation coefficient maps (μ -maps) of the hardware and subject (stage A), normalisation component data (stage B) and the list-mode data (stage C). Optionally, T1 and/or T2 weighted MR images are provided for brain parcellation used in reconstruction and analysis stage D and partial volume correction (PVC) stage F. The T1w image is also used for generating an accurate subject’s s -map.

In stage B the normalisation component data (relatively small file) is used to generate single factors for each sinogram bin, with the use of bucket singles obtained from list-mode (LM) processing in stage C. The LM processing stage C generates prompt and delayed sinograms and fan sums, which are used for estimating reduced-variance randoms for each sinogram bin.

Great emphasis was put on the quantitative image reconstruction and analysis in stages D-H (for more details see [3]):

- forward and back projectors used for image reconstruction (stage **D**); the attenuation factors are generated with the forward projector.
- fully 3D estimation of scatter events (stage **E**), with high resolution ray tracing in image and projection space; the estimation is based on voxel-driven scatter model (VSM) and is coupled with image reconstruction, i.e., the scatter is updated every time a better image estimation of the radiotracer distribution is available.
- voxel-wise partial volume correction using MRI brain parcellations (stage **F**), based on the iterative Yang method and given point spread function (PSF) of the whole imaging system (including the hardware and the reconstruction algorithm).
- kinetic analysis using dynamic multi-frame PET data (stage **G**).
- voxel-wise uncertainty estimation based on efficient generation of bootstrap LM data replicates (stage **H**).

INSTALLATION

Note: Quick note on ways of installation

Requirements:

- An NVIDIA GPU with the [CUDA SDK/Toolkit](#) (including drivers) installed
- [Git](#)
- Python 3.6 or greater (e.g. via [Anaconda](#) or [Miniconda](#))

Installation:

```
pip install niftyPET
```

This will install all relevant packages, including [nipet](#) and [nimpa](#).

Tip: Installation (advanced):

```
git clone https://github.com/NiftyPET/NIMPA.git
git clone https://github.com/NiftyPET/NIPET.git

export PATHTOOLS=$HOME/NiftyPET_tools
export HMUDIR=$HOME/mmr_hardwareumaps

conda install -c conda-forge python=3 \
    numpy scipy scikit-image matplotlib ipykernel ipywidgets
pip install --verbose -e ./NIMPA
pip install --verbose -e ./NIPET
```

This will install an "editable" distribution at the source locations for both [nimpa](#) and [nipet](#) (allowing easy modification and/or updating using `git pull`).

Detailed steps for installation are given below.

NiftyPET is a [Python namespace package](#), primarily encompassing the two packages [nimpa](#) and [nipet](#). Currently, these are available for Python 3.6 or greater for Linux and Windows systems. It has been deployed and tested on CentOS 6.8 and 7, Ubuntu 14.04, 16.04, 18.04 and 20.04, as well as Windows 10 (limited) – including Python C extensions for the core CUDA routines. Linux systems are recommended due to their robustness and stability (support for Windows is comparatively limited).

2.1 Dependencies

2.1.1 Hardware

- **GPU device:** One or more GPU devices from NVIDIA with a CUDA compute capability of at least 3.5. It is also recommended to have at least 5 GB of GPU memory. The following devices have been tested with *NiftyPET*:
 - NVIDIA Tesla K20/K40/V100
 - NVIDIA Titan Xp/RTX
 - NVIDIA Quadro P4000/P6000
 - NVIDIA GeForce GTX 1060/1080/1080 Ti/1080 Max-Q
- **CPU host:** The GPU device can be accessed by a CPU host, with a reasonable computing power for some other image processing routines (e.g. image registration, etc.). It is recommended to have at least 16 GB of RAM, although we have managed to run dynamic reconstruction using old PC workstations with as little as 11 GB of RAM.

2.1.2 Software

NiftyPET installation needs the following software pre-installed:

- **C/C++ compiler**

GCC and *Clang* are commonly using on Linux systems, and *Visual Studio* on Windows.

- Ubuntu Linux:

```
apt-get install build-essential
```

- CentOS Linux:

```
yum group install "Development Tools"
```

- Windows: [Visual Studio](#)

- **CUDA GPU & Software**

The [CUDA SDK/Toolkit](#) (click the link to download) is a parallel computing platform and programming model. This includes the CUDA compiler (nvcc) and runtime API. For extra guidance, consult the [CUDA documentation](#).

Tip: In CentOS, it is necessary to install DKMS (Dynamic Kernel Module Support). Download from [here](#) and install as follows:

```
rpm -ivh epel-release-latest-7.noarch.rpm
yum -y install dkms
```

Tip: Make sure that CUDA is installed with appropriate paths to CUDA resources setup, e.g. on Linux systems:

```
export PATH="/usr/local/cuda/bin:$PATH"
export LD_LIBRARY_PATH="/usr/local/cuda/lib64:$LD_LIBRARY_PATH"
```

This can be added to `~/.profile` or `~/.bashrc` files. For more details see <http://docs.nvidia.com/cuda/cuda-installation-guide-linux/index.html#post-installation-actions>.

- **Git**

Git is a version control system used for downloading *NiftyPET* and other necessary tools, i.e. *NiftyReg* and *dcm2niix*. For more details on installing git see <https://git-scm.com/book/en/v2/Getting-Started-Installing-Git>.

On Linux systems it can be installed as follows:

- Ubuntu Linux:

```
apt-get install git
```

- CentOS Linux:

```
yum install git
```

- Windows: [Git](#)

- **Python 3.6 or greater**

A free high-level programming language, through which all the GPU routines are available for the user. The easiest way to run *NiftyPET* in Python is by using the [Anaconda](#) or [Miniconda](#) distributions.

Tip: *Optional Python packages*

Jupyter Notebook (notebook) is a useful development interface.

Additionally, when using Anacoda or Minconda, it is recommended to use `conda` to install some dependencies rather than rely on *NiftyPET* to automatically install them via `pip`.

```
# useful mathematical & plotting libraries
conda install -c conda-forge python=3 numpy scipy scikit-image matplotlib nibabel_
↪pydicom
# jupyter noebook support
conda install -c conda-forge python=3 ipykernel ipywidgets
```

2.2 *NiftyPET* installation

Tip: To avoid prompts during installation, specify configuration directories in advance:

```
export PATHTOOLS=$HOME/NiftyPET_tools
export HMUDIR=$HOME/mmr_hardwareumaps
```

2.2.1 Using pip

To install the entire suite of packages, use:

```
pip install niftyPET
```

Tip: Instead of installing everything, follow these steps to install individual components separately.

- `nimpa`

```
pip install --verbose nimpa
```

- `nipet`

The core of *NiftyPET* image reconstruction.

```
pip install --verbose nipet
```

This will also install `nimpa` if not already present.

2.2.2 From source

The source code of full version of `nimpa` and `nipet` packages can be downloaded to a specific folder using `git` as follows:

```
git clone https://github.com/NiftyPET/NIMPA.git
git clone https://github.com/NiftyPET/NIPET.git
```

After a successful download, navigate to folder `nimpa` and run inside one of the following:

- 1) `pip install --verbose .`
- 2) `pip install --verbose -e .`

The last option with the `-e` makes the installation "editable", allowing the user to modify the source code themselves or by pulling newer versions from `git` using `git pull`.

Identically for `nipet`, run one of the following:

- 1) `pip install --verbose .`
- 2) `pip install --verbose -e .`

The installation will download and call on `cmake`, which will run automatically and generate Ninja files, and then run `ninja` to build all the CUDA C routines and Python C extensions. Following this, the compiled Python modules will be installed into the specific Python package location.

2.2.3 Third party software installed with *NiftyPET*

NiftyPET will automatically install additional third party software (used for capabilities such as image registration and conversion). *NiftyReg* and *dcm2niix* will be installed in the `NiftyPET_tools` folder specified during the installation process:

- **dcm2niix:** conversion of DICOM images to NIfTI images (v1.0.20171204). If for some reason the automatic installation fails (e.g., due to a problem with dependencies), try to download the source code from <https://github.com/rordenlab/dcm2niix> and compile it, or use the pre-compiled version with current release available at <https://github.com/rordenlab/dcm2niix/releases/>.
- **NiftyReg:** image registration and resampling tool. The stable version (16 Nov 2017) is fetched and installed automatically from <https://github.com/KCL-BMEIS/niftyreg>. Some details for a manual install can be found at http://cmictig.cs.ucl.ac.uk/wiki/index.php/NiftyReg_install (can be outdated).

2.2.4 Conda environments

One of the advantages of using conda is the possibility of having separate environments for different versions of Python and/or packages installed in them. Thus conda environments enable the user to set up *NiftyPET* differently for various applications (e.g., different image resolution, radio-pharmaceutical-optimised attenuation and/or scatter correction, etc.). Below is an example of installation of *NiftyPET* into environment called *niftypet*.

Create environment called, for example, *niftypet*, by running this command:

```
conda create --name niftypet
```

Activate the conda environment:

```
conda activate niftypet
```

Note: On Windows, this may be simply `activate niftypet`, and on Linux `source activate niftypet`.

Tip: It may be quicker to also install additional required packages with conda (rather than relying on pip to automatically do this during installation of *niftypet*):

```
# useful mathematical & plotting libraries
conda install -c conda-forge python=3 numpy scipy scikit-image matplotlib nibabel pydicom
# jupyter notebook support
conda install -c conda-forge python=3 ipykernel ipywidgets
```

NiftyPET can now be installed as described above in *NiftyPET installation*, while making sure that the conda environment is active.

Warning: Make sure to `conda activate niftypet` whenever opening a new terminal to ensure the correct environment is active.

2.2.5 Jupyter Notebook

Jupyter Notebooks are useful for sharing and replicating image reconstruction methods written in Python. They allow introspection, plotting and sharing of any intermediate results (e.g. sinograms and images generated during the reconstruction pipeline) or any end results. It is easiest to use conda to install Jupyter in the base environment in order to automatically pick up kernels for all other environments (conda install --name base notebook). See <http://jupyter.readthedocs.io/en/latest/tryjupyter.html> for more details and <http://jupyter.readthedocs.io/en/latest/install.html> for a manual installation.

Warning: When using Jupyter, make sure to select the correct *kernel* (corresponding to the desired conda environment name) within the notebook.

2.3 Post-installation checks

2.3.1 Configuration

A `.niftyPET` folder is created during the installation (in `$HOME` or `%APPDATA%`). Additional subfolders may be present corresponding to the conda environment name. Configuration information is stored in `resources.py` within this folder.

Warning: It is recommended to rerun `pip install` rather than manually editing paths and device properties in `resources.py`.

Default CUDA device

The default CUDA device used for GPU calculations is chosen during the installation together with the corresponding optimal `nvcc` (CUDA compiler) flags. For example, for the NVIDIA Titan Xp with compute capability of 6.1, `resources.py` will have a section showing:

```
# DO NOT MODIFY BELOW--DONE AUTOMATICALLY
### start GPU properties ###
DEV_ID = 0
CC_ARCH = '-gencode=arch=compute_61,code=compute_61;'
### stop GPU properties ###
```

Any available (installed) CUDA device can be chosen within Python for any image reconstruction or part of the reconstruction pipeline.

Search paths for third-party software

Paths to tools for image registration, resampling, and conversion (DICOM -> NIFTI) can also be found in `resources.py`:

```
# paths to apps and tools needed by NiftyPET
### start NiftyPET tools ###
PATHTOOLS = '/path/to/NiftyPET_tools/'
RESPATH = '/path/to/NiftyPET_tools/niftyreg/bin/reg_resample'
```

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```
REGPATH = '/path/to/NiftyPET_tools/niftyreg/bin/reg_aladin'  
DCM2NIIX = '/path/to/NiftyPET_tools/dcm2niix/bin/dcm2niix'  
HMUDIR = '/path/to/mmr_hardware_mumaps'  
### end NiftyPET tools ###
```

Note that the proprietary hardware μ -maps (HMUDIR) are not distributed with this software, and have to be obtained from the Siemens Biograph mMR scanner.

SCIENTIFIC OUTPUT

3.1 Scientific aspects of NiftyPET

The core routines are written in CUDA C and embedded in Python C extensions to enable user-friendly and high-throughput executions on NVIDIA graphics processing units (GPU). The scientific aspects of this software platform are covered in two open-access publications:

- *NiftyPET: a High-throughput Software Platform for High Quantitative Accuracy and Precision PET Imaging and Analysis* Neuroinformatics (2018) 16:95. <https://doi.org/10.1007/s12021-017-9352-y>
- *Rapid processing of PET list-mode data for efficient uncertainty estimation and data analysis* Physics in Medicine & Biology (2016). <https://doi.org/10.1088/0031-9155/61/13/N322>

3.2 Advanced imaging with the ACR phantom

Quantitative measurement of the spatial resolution using the measured knife-edge response $K(x)$, for any phantom insert with different attenuation and activity properties, thus facilitating comprehensive and quantitative characterisation of PET/MR or (PET/CT) scanners in multisite clinical studies, e.g., in the [Dementias Platform UK](#) network.

P.J. Markiewicz, C. da Costa-Luis, J. Dickson, A. Barnes, G. Krokos, J. MacKewn, T. Clark, C. Wimberley, G. MacNaught, M.M. Yaqub, J.D. Gispert, B. F. Hutton, P. Marsden, A. Hammers, A.J. Reader, S. Ourselin, K. Herholz, J.C. Matthews, F. Barkhof. **Advanced quantitative evaluation of PET systems using the ACR phantom and NiftyPET software**. Med. Phys., accepted for publication.

3.3 MR-PET registration uncertainty analysis

Novel MR-PET registration uncertainty analysis, indicating that registration software has the biggest effect on MR-PET registration precision, followed by reconstruction parameters (i.e., iterations, smoothing) and PET count level. Although PVC can significantly improve the PET signal, it also increases PET signal variability since it relies on precise MR-PET registration. More details can be found in [4]:

P.J. Markiewicz, J.C. Matthews, J. Ashburner, D.M. Cash, D.L. Thomas, E. De Vita, A. Barnes, M.J. Cardoso, M. Modat, R. Brown, K. Thielemans, C. da Costa-Luis, I. Lopes Alves, J.D. Gispert, M.E. Schmidt, P. Marsden, A. Hammers, S. Ourselin, and F. Barkhof (2021). **Uncertainty analysis of MR-PET image registration for precision neuro-PET imaging**. Neuroimage 655 232, 117821. <https://doi.org/10.1016/j.neuroimage.2021.117821>

3.4 Fast PET image reconstruction

An example application of *NiftyPET* in the development of novel image reconstruction using advanced randomized optimization algorithms to solve the PET reconstruction problem for a very large class of non-smooth priors [5]:

M.J. Ehrhardt, P.J. Markiewicz, C-B. Schönlieb (2019). **Faster PET reconstruction with non-smooth priors by randomization and preconditioning.** Phys. Med. Biol. 64(22), <https://doi.org/10.1088/1361-6560/ab3d07>

3.5 Dynamic PET image reconstruction

Dynamic PET image reconstruction for reduced acquisition time PET pharmacokinetic modelling [6]:

C.J. Scott, J. Jiao, A. Melbourne, N. Burgos, D.M. Cash, E. De Vita, P.J. Markiewicz, A. O'Connor, D.L. Thomas, P.S.J. Weston, J.M. Schott, B.F. Hutton, S.Ourselin (2018) **Reduced acquisition time PET pharmacokinetic modelling using simultaneous ASL–MRI: proof of concept.** Journal of Cerebral Blood Flow & Metabolism. <https://doi.org/10.1177/0271678X18797343>

NIFTYPET EXAMPLE

This is a full demo of NiftyPET's default *OSEM* ($n_{\max} = 14$ subsets, span 11, Siemens Biograph mMR resolution), as well as a custom, explicit *MLEM* incorporating RM (resolution modelling).

Mathematically:

$$\theta^{(k+1)} = \frac{\theta^{(k)}}{\sum_n \mathbf{H}^T \mathbf{X}_n^T \mathbf{A}^T \mathbf{N}^T \mathbf{1}} \circ \sum_n \mathbf{H}^T \mathbf{X}_n^T \mathbf{A}^T \mathbf{N}^T \frac{\mathbf{m}}{\mathbf{N} \mathbf{A} \mathbf{X}_n \mathbf{H} \theta^{(k)} + \mathbf{r} + \mathbf{s}},$$

- k is iteration number
- H applies a Gaussian PSF
- X_n is the system matrix for subset n (MLEM has just one subset)
- m, r, s are measured, randoms, and scatter

-
- Author: Casper O. da Costa-Luis casper.dcl@physics.org | casper.dcl@ieee.org | casper.dcl@kcl.ac.uk
 - Date: 2019-21
-

4.1 Imports

In addition to NiftyPET, this is recommended:

```
pip install brainweb # basic registration
pip install spm12    # MATLAB-based registration
```

```
[1]: # imports & helper functions
from __future__ import print_function, division
%matplotlib notebook
from collections import OrderedDict
from glob import glob
from os import path
import functools
import logging
import os

if os.getenv("OMP_NUM_THREADS", None) != "1":
```

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```

    raise EnvironmentError("should run `export OMP_NUM_THREADS=1` before notebook launch
    ↪")

from miutil.plot import apply_cmap, imscroll
from niftypet import nipet
from niftypet.nimpa import getnii
from scipy.ndimage.filters import gaussian_filter
from tqdm.auto import trange
import matplotlib.pyplot as plt
import numpy as np
import pydicom

logging.basicConfig(level=logging.INFO)
print(nipet.gpuinfo())
# get all the scanner parameters
mMRpars = nipet.get_mmrparams()
# conversion for Gaussian sigma/[voxel] to FWHM/[mm]
SIGMA2FWHMmm = (8 * np.log(2))**0.5 * np.array([mMRpars['Cnt']['SO_VX' + i] for i in 'ZYX
    ↪']) * 10

def div_nzer(x, y):
    return np.divide(x, y, out=np.zeros_like(y), where=y!=0)

def trimVol(x):
    return x[:, 100:-100, 100:-100]

def mapVol(vol, cmap=None, vmin=0, vmax=None):
    msk = ~np.isnan(vol)
    if vmin is None:
        vmin = vol[msk].min()
    if vmax is None:
        vmax = vol[msk].max()
    vol = (np.clip(vol, vmin, vmax) - vmin) / (vmax - vmin)
    return apply_cmap(**{cmap: vol}) if cmap is not None else vol

def register_spm(ref_file, mov_file, opth):
    """
    ref_file : e.g. recon['fpet']
    mov_file : e.g. datain['Tlnii']
    """
    from spm12.regseg import coreg_spm, resample_spm
    reg = coreg_spm(ref_file, mov_file, outpath=opth, save_arr=False, save_txt=False)
    return getnii(resample_spm(ref_file, mov_file, reg['affine'], outpath=opth,
        ↪del_ref_uncmpr=True, del_flo_uncmpr=True, del_out_
        ↪uncmpr=True))

def register_dipy(ref_file, mov_file, ROI=None):
    """
    ref_file : e.g. recon['fpet']
    mov_file : e.g. datain['Tlnii']
    """
    from brainweb import register

```

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```

    return register(getnii(mov_file), getnii(ref_file), ROI=ROI or ((0, None), (100, -
→100), (100, -100)))

[('GeForce GTX 1070 with Max-Q Design', 8119, 6, 1)]

```

4.2 Load & Process Raw Data

```

[2]: folderin = "amyloidPET_FBP_TP0"
    folderout = "." # realtive to `{folderin}/niftyout`
    itr = 7 # number of iterations (will be multiplied by 14 for MLEM)
    fwhm = 2.5 # mm (for resolution modelling)
    totCnt = None # bootstrap sample (e.g. `300e6`) counts

```

```

[3]: # datain
    folderin = path.expanduser(folderin)

    # automatically categorise the input data
    datain = nipet.classify_input(folderin, mMRpars, recurse=-1)

    # output path
    opth = path.join(datain['corepath'], "niftyout")

    datain

```

```

INFO:niftyPET.nipet.mmraux:got LM interfile.
INFO:niftyPET.nipet.mmraux:got CSA info.

```

```

[3]: {'corepath': 'amyloidPET_FBP_TP0',
      'lm_dcm': 'amyloidPET_FBP_TP0/LM/17598013_1946_20150604155500.000000.dcm',
      'lm_bf': 'amyloidPET_FBP_TP0/LM/17598013_1946_20150604155500.000000.bf',
      'hmumap': 'amyloidPET_FBP_TP0/niftyout/mumap-hdw/hmumap.npz',
      'sinos': 'amyloidPET_FBP_TP0/niftyout/sino/sinos_s11_frm-0-0.npz',
      'nrm_dcm': 'amyloidPET_FBP_TP0/norm/17598013_1946_20150604082431.000000.dcm',
      'nrm_bf': 'amyloidPET_FBP_TP0/norm/17598013_1946_20150604082431.000000.bf',
      'pCT': 'amyloidPET_FBP_TP0/pCT/17598013_pCT_synth.nii.gz',
      'T1l1b1': 'amyloidPET_FBP_TP0/prcl/n4_bias_corrected_T1_NeuroMorph_Parcellation.nii.gz',
      'T1nii': 'amyloidPET_FBP_TP0/T1w_N4/t1_S00113_17598013_N4bias_cut.nii.gz',
      'T1N4': 'amyloidPET_FBP_TP0/T1w_N4/t1_S00113_17598013_N4bias_cut.nii.gz',
      'mumapDCM': 'amyloidPET_FBP_TP0/umap',
      '#mumapDCM': 192}

```

```

[4]: # hardware mu-map (bed, head/neck coils)
    mu_h = nipet.hdw_mumap(datain, [1,2,4], mMRpars, outpath=opth, use_stored=True)

    INFO:niftyPET.nipet.img.mmring:loaded hardware mu-map from file: amyloidPET_FBP_TP0/
→niftyout/mumap-hdw/hmumap.npz

```

```

[5]: # MR-based human mu-map

    # UTE-based object mu-map aligned (need UTE sequence or T1 for pseudo-CT)
    #mu_o = nipet.align_mumap(

```

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```
# datain,
# scanner_params=mMRpars,
# outpath=opth,
# t0=0, t1=0, # when both times are 0, will use full data
# itr=2,      # number of iterations used for recon to which registering MR/UTE
# petopt='ac', # what PET image to use (ac-just attenuation corrected)
# musrc='ute', # source of mu-map (ute/pct)
# ute_name='UTE2', # which UTE to use (UTE1/2 shorter/faster)
# verbose=True,
#)
```

```
# the same as above without any faff though (no alignment)
mu_o = nipet.obj_mumap(datain, mMRpars, outpath=opth, store=True)
```

```
INFO:nifypet.nipet.mmraux:gantry offset from DICOM:
[0.00147903 0.00593885 0.0170666 ]
INFO:nifypet.nipet.mmraux:table position origin from DICOM:
[-1179.    0.    0.]
INFO:nifypet.nipet.mmraux:got LM interfile.
INFO:nifypet.nipet.mmraux:got CSA info.
pixdim[0] (qfac) should be 1 (default) or -1; setting qfac to 1
INFO:nibabel.global.pixdim[0] (qfac) should be 1 (default) or -1; setting qfac to 1
```

```
[6]: # create histogram
mMRpars['Cnt']['BTP'] = 0
m = nipet.mmhist(datain, mMRpars, outpath=opth, store=True, use_stored=True)
if totCnt:
    mMRpars['Cnt']['BTP'] = 2 # enable parametric bootstrap
    mMRpars['Cnt']['BTPRT'] = totCnt / m['psino'].sum() # ratio count level relative to
    ↳ the original
    m = nipet.mmhist(datain, mMRpars, outpath=path.join(opth, 'BTP', '%.3g' % totCnt),
    ↳ store=True)
```

4.2.1 Visualisations

```
[7]: try: # needs HW mu-maps
    imscroll(mu_o['im'] + mu_h['im'], cmap='bone') # title=r"$\mu$-map"
except:
    imscroll(mu_o['im'], cmap='bone')

<IPython.core.display.Javascript object>

<IPython.core.display.HTML object>
```

```
[8]: # sinogram index (<127 for direct sinograms, >=127 for oblique sinograms)
imshow([m['psino'], m['dsino']],
       titles=["Prompt sinogram (%.3gM)" % (m['psino'].sum() / 1e6),
              "Delayed sinogram (%.3gM)" % (m['dsino'].sum() / 1e6)],
       cmap='inferno',
       #colorbars=[1]*2,
       fig=plt.figure(figsize=(9.5, 3.5), tight_layout=True, frameon=False));
```

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```

axs = plt.gcf().axes
axs[-1].set_xlabel("bins")
[i.set_ylabel("angles") for i in axs];
<IPython.core.display.Javascript object>
<IPython.core.display.HTML object>

```

4.3 Reconstruction

4.3.1 OSEM

```

[9]: # built-in default: 14 subsets
fcomment = f"_fwhm-{fwhm}_recon"
outpath = path.join(opth, folderout)
recon = glob(
    f"{outpath}/PET/single-frame/a_t-*-*sec_itr-{itr}{fcomment}.nii.gz"
)
if recon:
    recon = {'fpet': recon[0], 'im': getnii(recon[0])}
else:
    recon = nipet.mmchain(
        datain, mMRpars,
        #frames=['timings', [3000, 3600]],
        itr=itr,
        #store_itr=range(itr),
        histo=m,
        mu_h=mu_h,
        mu_o=mu_o,
        psf=fwhm,
        #recomod=1, # no scatter & rand
        outpath=outpath,
        fcomment=fcomment,
        store_img=True)

```

Registration

```

[10]: # convert DCM to NII if required
if 'T1nii' not in datain:
    !{mMRpars['Cnt']}['DCM2NII'] -z y -f 'T1' {datain['T1DCM']}
    extra = nipet.classify_input(datain['T1DCM'], mMRpars)
    extra.pop('corepath')
    datain.update(extra)

#filepaths = sorted(glob(path.join(datain['T1DCM'], '*.IMA')))
#arr = np.asanyarray([pydicom.dcmread(i).pixel_array for i in filepaths]).transpose(1, 2,
→ 0)

```

```
[11]: # SPM12
regout = f"{opth}/affine_ref-a_t-*sec_itr-21_fwhm-4.5_recon.nii.gz"
regim = getnii(regout) if path.exists(regout) else register_spm(recon['fpet'], datain[
    ↪ 'T1nii'], opth)

# Simple Alternative: DIPY CoM
#regim = register_dipy(recon['fpet'], datain['T1nii'])

INFO:spm12.regseg:matrix M given in the form of Numpy array
```

Figures

```
[12]: vmax = np.percentile(recon['im'], 99.95)
imscroll({
    "PET": mapVol(trimVol(recon['im']), 'magma', vmax=vmax),
    "Smoothed": mapVol(gaussian_filter(trimVol(recon['im']), 4.5 / SIGMA2FWHMmm), 'magma
    ↪ ', vmax=vmax),
    "$\\mu$ Map": mapVol(trimVol(mu_o['im']), 'bone'),
    "T1": mapVol(trimVol(regim), 'Greys_r'),
},
fig=plt.figure(figsize=(9.5, 3.5), tight_layout=True, frameon=False),
);
```

<IPython.core.display.Javascript object>

<IPython.core.display.HTML object>

```
[13]: # rgb => PET, mu_o, T1
def norMax(x, scale=1):
    x = trimVol(x).transpose(2, 0, 1)[..., None]
    return x * (scale / x[~np.isnan(x)].max())
imscroll([np.concatenate([norMax(recon['im']), norMax(mu_o['im'], 0.15), norMax(regim, 0.
    ↪ 75)], axis=-1)]);
```

<IPython.core.display.Javascript object>

<IPython.core.display.HTML object>

4.3.2 MLEM

```
[14]: ## Attenuation, Normalisation & Sensitivity

A = nipet.frwd_prj(mu_h['im'] + mu_o['im'], mMRpars, attenuation=True)
N = nipet.mmnorm.get_norm_sino(datain, mMRpars, m)
AN = A * N
sim = nipet.back_prj(AN, mMRpars)
msk = nipet.img.mmring.get_cylinder(mMRpars['Cnt'], rad=29., xo=0., yo=0., unival=1, gpu_
    ↪ dim=False) <= 0.9

## Randoms

r = nipet.randoms(m, mMRpars)[0]
```

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```

print("Randoms: %.3g%%" % (r.sum() / m['psino'].sum() * 100))

## Scatter

# One OSEM iteration estimate (implicitly using voxel-driven scatter model)
eim = nipet.mmrchain(datain, mMRpars, mu_h=mu_h, mu_o=mu_o, histo=m, itr=1,
    ↳outpath=opath)['im']

# Recalculate scatter
s = nipet.vsm(datain, (mu_h['im'], mu_o['im']), eim, mMRpars, m, r)
print("Scatter: %.3g%%" % (s.sum() / m['psino'].sum() * 100))

INFO:niftyPET.nipet.img.auximg:using object mu-map from dictionary
INFO:niftyPET.nipet.img.auximg:using hardware mu-map from dictionary
INFO:niftyPET.nipet.img.pipe:using the provided mu-map the same way for all frames.
INFO:niftyPET.nipet.img.pipe:dynamic frame times t0=0, t1=3601:
INFO:niftyPET.nipet.img.pipe:-----
using provided histogram
-----
INFO:niftyPET.nipet.prj.mmrrec:reconstruction in mode: 3

Randoms: 52.1%

INFO:niftyPET.nipet.prj.mmrrec:----- OSEM (1) -----
INFO:niftyPET.nipet.mmrax:got LM interfile.
INFO:niftyPET.nipet.mmrax:got CSA info.

OSEM:   0%|          | 0/1 [00:00<?, ?it/s]

INFO:niftyPET.nipet.prj.mmrrec:recon time: 7.3
INFO:niftyPET.nipet.prj.mmrrec:applying decay correction of: 1.2014266465888763
INFO:niftyPET.nipet.prj.mmrrec:applying quantification factor: 5570.410609255673 to the
    ↳whole image
INFO:niftyPET.nipet.prj.mmrrec:for the frame duration of: 3601

Scatter: 13.7%

```

```

[15]: imscroll(OrderedDict([("Prompts", m['psino']), ("Delayed", m['dsino']), ("Attenuation",
    ↳A)]),
        cmap='inferno', fig=plt.figure(figsize=(9.5, 3), tight_layout=True,
    ↳frameon=False));
imshow(OrderedDict([("Scatter", s), ("Randoms", r), ("Normalisation", N)]),
        cmap='inferno', fig=plt.figure(figsize=(9.5, 3), tight_layout=True,
    ↳frameon=False));

<IPython.core.display.Javascript object>

<IPython.core.display.HTML object>

<IPython.core.display.Javascript object>

<IPython.core.display.HTML object>

```

```

[16]: ## MLEM with RM

psf = functools.partial(gaussian_filter, sigma=fwhm / SIGMA2FWHMmm)

```

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```
sim_inv = div_nzer(1, psf(sim))
sim_inv[msk] = 0
rs_AN = div_nzer(r + s, AN)
recon_mlem = [np.ones_like(sim)]
for k in trange(itr * 14, desc="MLEM"):
    fprj = nipet.frwd_prj(psf(recon_mlem[-1]), mMRpars) + rs_AN
    recon_mlem.append(recon_mlem[-1] * sim_inv * psf(nipet.back_prj(div_nzer(m['psino'],
↪fprj), mMRpars)))
```

MLEM: 0%| | 0/98 [00:00<?, ?it/s]

```
[17]: # central slice across iterations
import matplotlib.pyplot as plt
import numpy as np
from nipet.core import nipet

recon_mlem = [np.ones_like(sim)]
for k in trange(itr * 14, desc="MLEM"):
    fprj = nipet.frwd_prj(psf(recon_mlem[-1]), mMRpars) + rs_AN
    recon_mlem.append(recon_mlem[-1] * sim_inv * psf(nipet.back_prj(div_nzer(m['psino'],
↪fprj), mMRpars)))

# central slice across iterations
imshow(
    np.asarray([trimVol(i) for i in recon_mlem[1:14]]),
    titles=["iter %d" % i for i in range(1, len(recon_mlem), 14)],
    cmap='magma', fig=plt.figure(figsize=(9.5, 2), tight_layout=True, frameon=False));

<IPython.core.display.Javascript object>

<IPython.core.display.HTML object>
```

ACCESSING AND QUERYING GPU DEVICES

`IPython` is an interactive Python prompt, particularly useful for PET/MR imaging. Start `IPython` by issuing `ipython` in the terminal to obtain the following:

```
Python 2.7.15 |Anaconda custom (64-bit)| (default, May 1 2018, 23:32:55)
Type "copyright", "credits" or "license" for more information.

IPython 5.7.0 -- An enhanced Interactive Python.
?          -> Introduction and overview of IPython's features.
%quickref  -> Quick reference.
help       -> Python's own help system.
object?    -> Details about 'object', use 'object??' for extra details.

In [1]:
```

Note: At this stage Python 2.7 is supported. Support for Python 3 is coming soon.

Import `nimpa` package from Python *NiftyPET* namespace and run the :

```
from niftypet import nimpa
nimpa.gpuinfo()
```

which for two NVIDIA GPU devices used for this documentation (TITAN Xp and Quadro K4200) will produce:

```
In [1]: from niftypet import nimpa
...:   nimpa.gpuinfo()
...:
Out[1]: [('TITAN X (Pascal)', 12788L, 6L, 1L), ('Quadro K4200', 4231L, 3L, 0L)]

In [2]:
```

Please note that only the first device is supported, i.e., the compute capability is ≥ 3.5 :

```
In [3]: nimpa.gpuinfo()[0][2:]
Out[3]: (6L, 1L)
```

The same function is available in `nipet`, i.e.:

```
from niftypet import nipet
nipet.gpuinfo()
```

It's also possible to get extended information about the installed GPU devices by running either

```
nipet.gpuinfo(extended=True)
```

or

```
nimpa.gpuinfo(extended=True)
```

For the above GPU devices, the following will be obtained:

```
In [4]: nimpa.gpuinfo(extended=True)
i> there are 2 GPU devices.

-----
CUDA device: TITAN X (Pascal), ID = 0
-----
i> total memory [MB]:12788.50
i> shared memory/block [kB]: 49.15
i> registers (32bit)/thread block: 65536
i> warp size: 32
i> compute capability: 6.1
i> clock rate [MHz]: 1531.00
i> ECC enabled? 0
i> max # threads/block: 1024

i> Memory available: 12788.50[MB]
    Used: 504.37[MB]
    Free:12284.13[MB]

-----
CUDA device: Quadro K4200, ID = 1
-----
i> total memory [MB]:4231.99
i> shared memory/block [kB]: 49.15
i> registers (32bit)/thread block: 65536
i> warp size: 32
i> compute capability: 3.0
i> clock rate [MHz]: 784.00
i> ECC enabled? 0
i> max # threads/block: 1024

i> Memory available: 4231.99[MB]
    Used:1117.06[MB]
    Free:3114.93[MB]

[('TITAN X (Pascal)', 12788L, 6L, 1L), ('Quadro K4200', 4231L, 3L, 0L)]
Out[4]: [('TITAN X (Pascal)', 12788L, 6L, 1L), ('Quadro K4200', 4231L, 3L, 0L)]
```

DICOM ANONYMISATION

DICOM data [anonymisation](#) or [pseudonymisation](#) is a process of removing sensitive personal information from DICOM attributes. This ensures compliance with the EU's General Data Protection Regulation ([GDPR](#)); so that the people who are imaged remain anonymous when their image data is distributed for wider scientific or clinical research.

The difference between anonymisation and pseudonymisation is that the former does not allow re-identification, while the latter does. In pseudonymisation the personally identifiable information is replaced with artificial identifiers, which must be kept separately and safely. Importantly, however, it has to be recognised that with current machine learning techniques, absolute protection of digital imaging data is almost impossible. For example, in an MR study of the head, effective anonymisation would also need to involve irreversible image deformation of the face [7].

6.1 Anonymisation in *NiftyPET*

The anonymisation can be achieved using function `dcmanonym` in sub-package `nimpa` through the use of [Pydicom](#). For example, sensitive information, such as the patient's name, date of birth, etc., can be checked and displayed by:

```
from niftyPET import nimpa
dcmPath = '/path/to/DICOM-file'
nimpa.dcmanonym(dcmPath, displayonly=True)
```

If it needs anonymisation or pseudonymisation, the sensitive information, such as the patient's name, date of birth (dob) and physician's name, has to be replaced by the user-defined strings, i.e.:

```
nimpa.dcmanonym(dcmPath,
                patient='Anonymous',
                physician='DR. Anonymous',
                dob='19000101',
                verbose=True)
```

The argument `dcmPath` in the above call, can be not only the path (a Python string) to a single DICOM file, but also it can be a Python list of DICOM file paths, the path to a folder containing DICOM files, or a dictionary `dataIn` containing all the data (including raw data) needed for a standalone image reconstruction. For example, assuming that the scanner (here the Biograph mMR) is initialised and the path to raw data is provided, i.e.:

```
from niftyPET import nipet
from niftyPET import nimpa

# get all the scanner parameters
mMRparams = nipet.get_mmrparams()
folderin = '/path/to/raw-data'
```

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```
# automatically categorise the input data
datain = nipet.classify_input(folderin, mMRparams)
```

then all the DICOM data required for reconstruction can be anonymised simply by:

```
nimpa.dcmanonym(datain,
                 patient='RandomID',
                 physician='Dr. Hopefully Nice',
                 dob='19800101',
                 verbose=True)
```

Please note, that the anonymisation of the Biograph mMR data goes somewhat deeper than just modifying the DICOM attributes—it also extracts the specific CSA headers and searches them for the patient’s name.

LIST-MODE PROCESSING AND MOTION DETECTION

The list-mode (LM) data is usually of large size in the order of GB. In NiftyPET, the LM data is hidden within image reconstruction function (see *Basic PET image reconstruction*) and processed automatically. However, the LM data can be processed separately to obtain histogrammed data (sinograms) as well as other statistics of the PET acquisition, including the head curves and motion detection.

After the following initialisation and input data specification (an example of amyloid brain acquisition is provided at *Raw brain PET data* [8]):

```
import sys, os, logging
from niftyPET import nipet

# control the logging output
logging.basicConfig(level=logging.INFO)

# get all the scanner parameters (mMR)
mMRpars = nipet.get_mmrparams()

# Enter the path to the input data folder
folderin = '/path/to/input/data/folder/'

# automatically categorise the input data
datain = nipet.classify_input(folderin, mMRpars)
```

the LM data processing can be performed by running the following line:

```
hst = nipet.mmrhist(datain, mMRpars)
```

The direct prompt and delayed sinograms can be viewed by choosing the sinogram index below 127 and from 127 up to 836 for oblique sinograms, i.e.:

```
# sinogram index (<127 for direct sinograms, >=127 for oblique sinograms)
si = 60

# prompt sinogram
matshow(hst['psino'][si,:,:], cmap='inferno')
colorbar()
xlabel('bins')
ylabel('angles')

# delayed sinogram
matshow(hst['dsino'][si,:,:], cmap='inferno')
```

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```
colorbar()
xlabel('bins')
ylabel('angles')
```

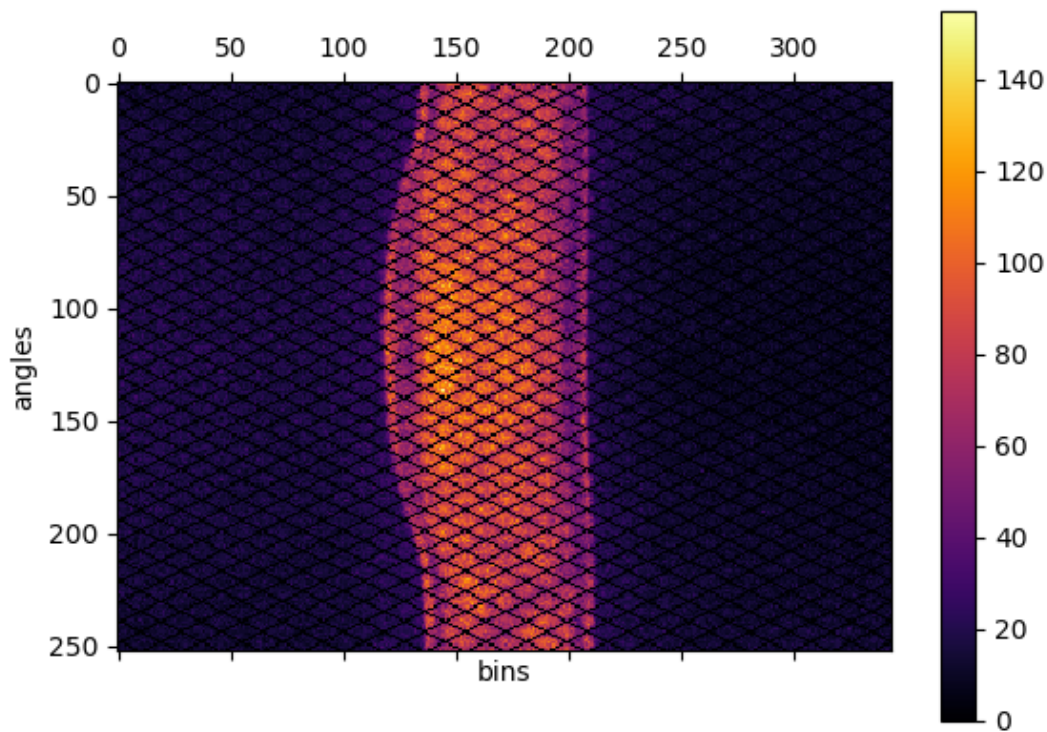


Fig. 7.1: Direct prompt sinogram for 60 minute amyloid PET acquisition.

The head-curve, which is the total number of counts detected per second across the acquisition time, for the prompt and delayed data can be plotted as follows:

```
plot(hst['phc'], label='prompt')
plot(hst['dhc'], label='delayed')
legend()
grid('on')
xlabel('time')
ylabel('counts')
```

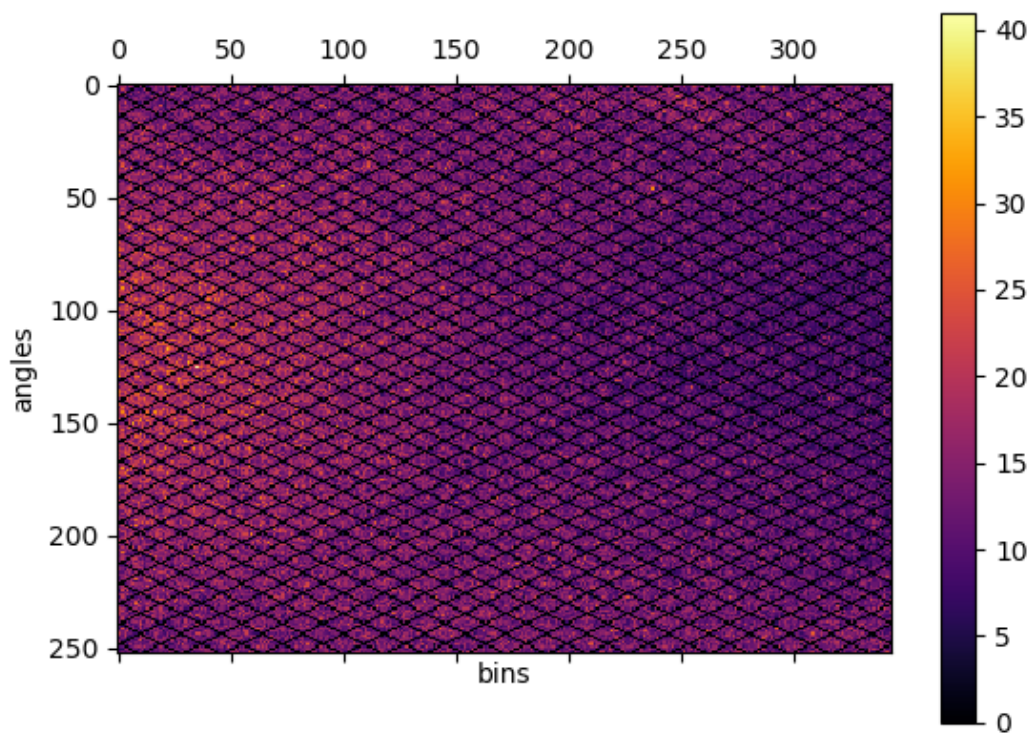


Fig. 7.2: Direct delayed sinogram for 60 minute PET acquisition.

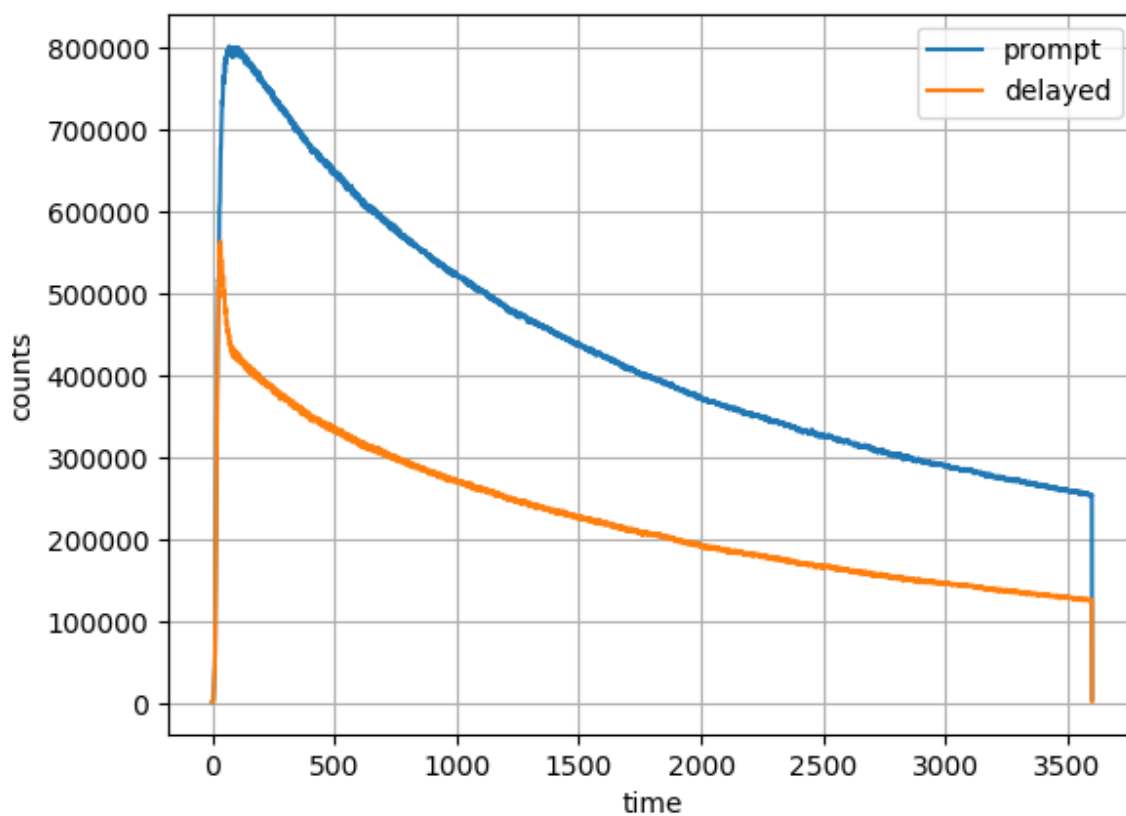


Fig. 7.3: Head curve for prompt and delayed events for the 60-minute acquisition.

7.1 Motion detection

In order to get a general idea about the potential motion during the acquisition, the LM processing includes the centre of mass of the radiodistribution along the axial direction as one of the main directions of motion. This centre of mass information can be plotted as follows for the available dataset (*Raw brain PET data*):

```
plot(hst['cmass'])  
grid('on')  
xlabel('time')  
ylabel('Centre of mas of radiodistribution')
```

which for the provided one-hour amyloid acquisition will produce:

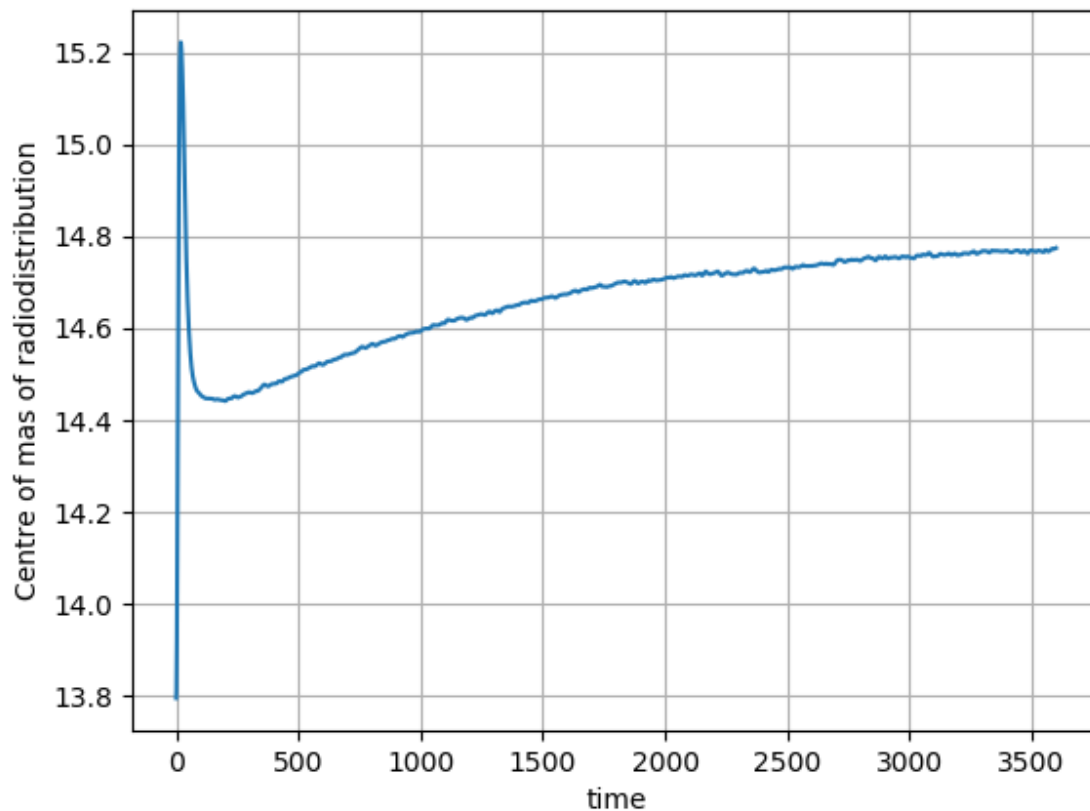


Fig. 7.4: The centre of mass of the radiodistribution for the 60-minute amyloid PET acquisition. Very little motion is observed—the smooth, exponentially varying curve is due to the tracer kinetics.

For another amyloid acquisition with motion, the curve can look like this:

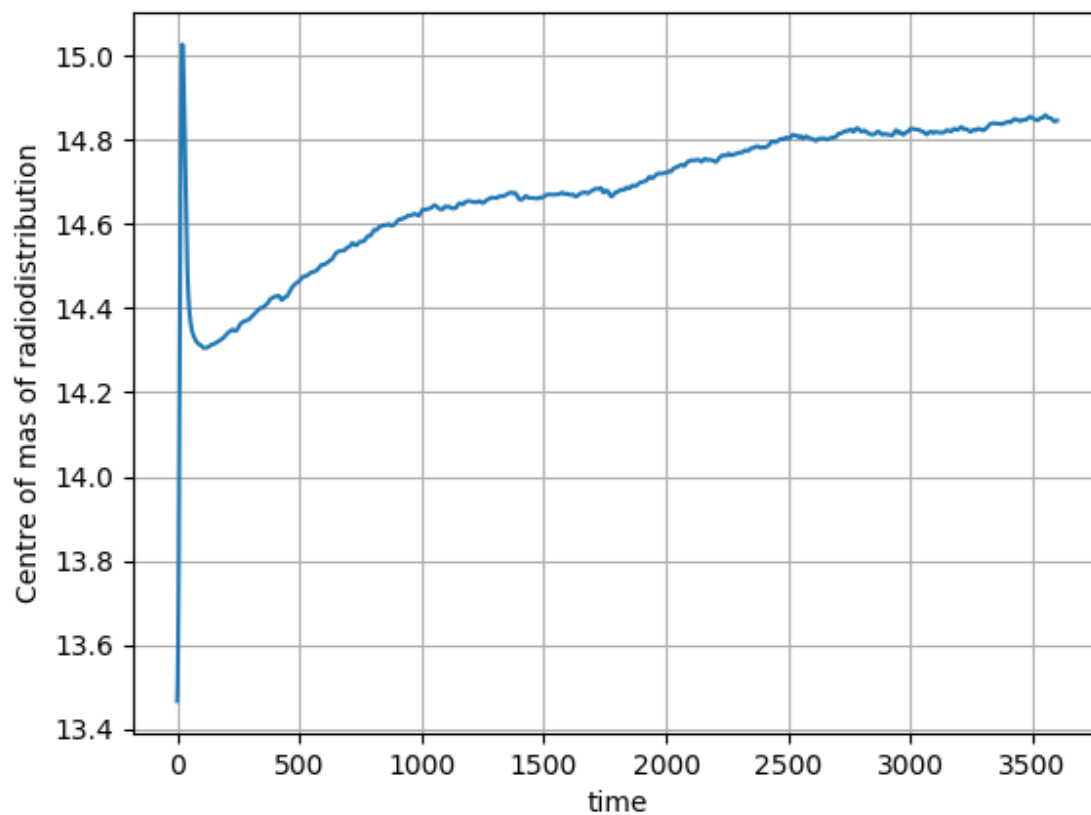


Fig. 7.5: The centre of mass of the radiodistribution for another 60-minute amyloid PET acquisition in which motion occurred. The motion is observed by the ‘breaks’, in particular seen around 1760 second (the 29th minute) of the curve on top of the smooth exponential due to the tracer pharmacokinetics.

BASIC PET IMAGE RECONSTRUCTION

For basic Siemens Biograph mMR image reconstruction, *NiftyPET* requires:

- (1) PET list-mode data;
- (2) component-based normalisation file(s);
- (3) the -map image (the linear attenuation map as a 3D image).

An example of downloadable raw PET data of amyloid brain scan is provided in [Raw brain PET data](#) [8].

8.1 Initialisation

Prior to dealing with the raw input data, required packages need to be imported and the Siemens Biograph mMR scanner constants and parameters (transaxial and axial lookup tables, LUTs) have to be loaded:

```
import sys, os, logging
import numpy as np

# NiftyPET image reconstruction package (nipet)
from niftyPET import nipet
# NiftyPET image manipulation and analysis (nimpa)
from niftyPET import nimpa

# control the logging output
logging.basicConfig(level=logging.INFO)

# get all the scanner parameters
mMRpars = nipet.get_mmrparams()
```

8.2 Sorting and classification of input data

All the part of the input data is aimed to be automatically recognised and sorted in Python dictionary. This can be obtained by providing a path to the folder containing the unzipped file of the freely provided raw PET data in [Raw brain PET data](#). The data is then automatically explored and sorted in the output dictionary datain:

```
# Enter the path to the input data folder
folderin = '/path/to/input/data/folder/'
```

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```
# automatically categorise the input data
datain = nipet.classify_input(folderin, mMRpars)
```

The output of datain for the above PET data should be as follows:

```
In [5]: datain
Out[5]:
{'#mumapDCM': 192,
 'corepath': '/data/amyloid_brain',
 'lm_bf': '/data/amyloid_brain/LM/17598013_1946_20150604155500.000000.bf',
 'lm_dcm': '/data/amyloid_brain/LM/17598013_1946_20150604155500.000000.dcm',
 'mumapDCM': '/data/amyloid_brain/umap',
 'nrm_bf': '/data/amyloid_brain/norm/17598013_1946_20150604082431.000000.bf',
 'nrm_dcm': '/data/amyloid_brain/norm/17598013_1946_20150604082431.000000.dcm'}
```

The parts of the recognised and categorised input data include:

Type	Path
corepath	the core path of the input folder
#mumapDCM	the number of DICOM files for the -map, usually 192
mumapDCM	path to the MR-based DICOM -map
lm_bf	path to the list-mode binary file
lm_dcm	the path to the DICOM header of the list-mode binary file
nrm_bf	path to the binary file for component based normalisation
nrm_dcm	path to the DICOM header for the normalisation

Note: The raw mMR PET data can also be represented by a single *.ima DICOM file instead of the *.dcm and *.bf pairs for list-mode and normalisation data, which will be reflected in datain.

8.3 Specifying output folder

The path to the output folder where the products of *NiftyPET* go, as well as the verbose mode can be specified as follows:

```
# output path
opath = os.path.join( datain['corepath'], 'output')

# switch on verbose mode
logging.getLogger().setLevel(logging.DEBUG)
```

With the setting as above, the output folder output will be created within the input data folder.

8.4 Obtaining the hardware and object -maps

Since MR cannot image the scanner hardware, i.e., the patient table, head and neck coils, etc., the high resolution CT-based mu-maps are provided by the scanner manufacturer. These then have to be appropriately resampled to the table and coils position as used in any given imaging setting. The hardware and object -maps are obtained as follow:

```
# obtain the hardware mu-map (the bed and the head&neck coil)
muhdct = nipet.hdw_mumap(datain, [1,2,4], mMRpars, outpath=opath, use_stored=True)

# obtain the MR-based human mu-map
muodct = nipet.obj_mumap(datain, mMRpars, outpath=opath, store=True)
```

The argument [1,2,4] for Obtaining the hardware -map correspond to the hardware bits used in imaging, i.e.:

- (1) Head and neck lower coil
- (2) Head and neck upper coil
- (3) Spine coil
- (4) Table

Currently, the different parts have to be entered manually (they are not automatically recognised which are in use).

The option `use_stored=True` allows to reuse the already created hardware -map, without recalculating it (the resampling can take more than a minute).

Both output dictionaries `muhdct` and `muodct` will contain images among other parameters, such as the image affine matrix and image file paths.

In order to check if both -maps were properly loaded, the maps can be plotted together transaxially by choosing the axial index `iz` along the z -axis, as follows:

```
# axial index
iz = 60

# plot image with a colour bar
matshow(muhdct['im'][iz,:,:] + muodct['im'][iz,:,:], cmap='bone')
colorbar()
```

This will produce the following image:

The sagittal image can be generated in a similar way, but choosing the slice along the x -axis, i.e.:

```
# axial index
ix = 170

# plot image with a colour bar
matshow(muhdct['im'][:, :, ix] + muodct['im'][:, :, ix], cmap='bone')
colorbar()
```

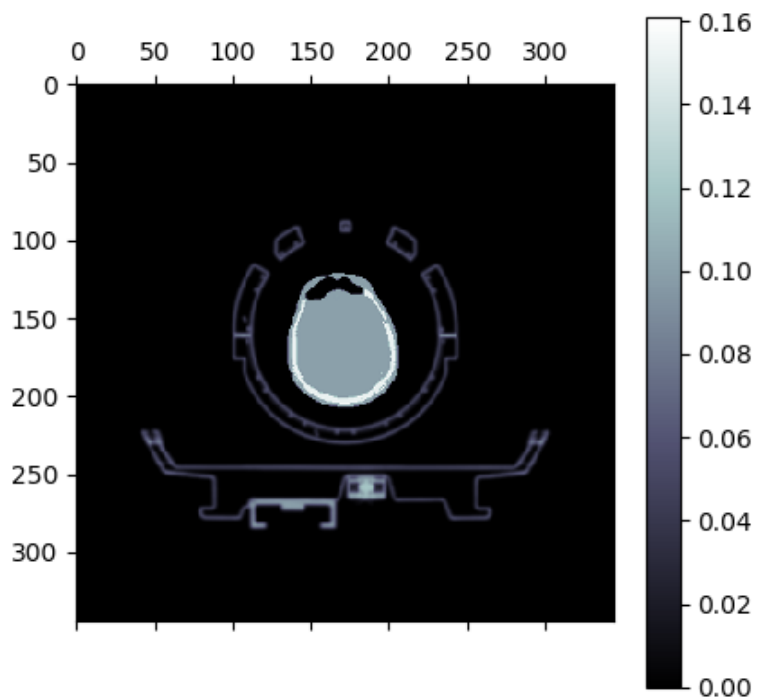


Fig. 8.1: Composite of the hardware and object -maps. Observed can be the human head between the upper and lower head&neck coils, and the patient table below.

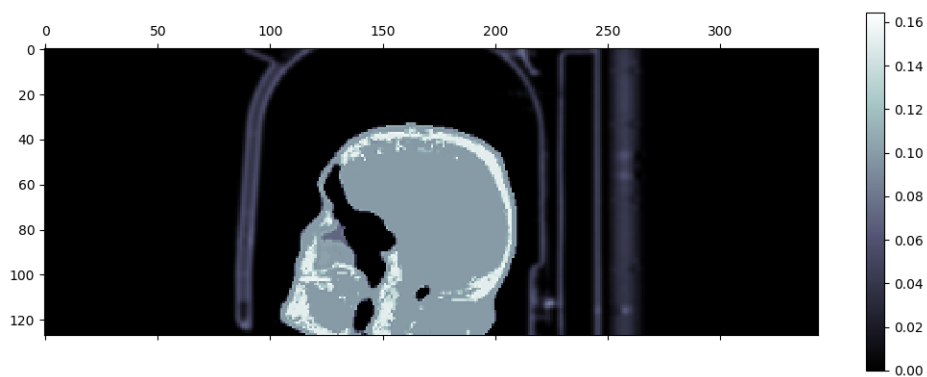


Fig. 8.2: Sagittal view of the composite of the hardware and object -maps. Observed can be the human head between the upper and lower head&neck coils, and the patient table on the right of the head.

8.5 Static image reconstruction

The code below provides full image reconstruction for the last 10 minutes of the acquisition to get an estimate of the amyloid load through the ratio image (SUVr).

```
recon = nipet.mmchain(
    datain, mMRpars,
    frames = ['timings', [3000, 3600]],
    mu_h = muhdct,
    mu_o = muodct,
    itr=4,
    fwhm=0.0,
    outpath = opth,
    fcomment = 'niftyPET-recon',
    store_img = True)
```

The input arguments are as follows:

argument	description
datain	input data (list-mode, normalisation and the -map)
mMRpars	scanner parameters (scanner constants and LUTs)
frames	definitions of time frame(s);
mu_h	hardware -map
mu_o	object -map
itr	number of iterations of OSEM (14 subsets).
fwhm	full width at half-maximum for the image post-smoothing
outpath	path to the output folder
fcomment	prefix for all the generated output files
store_img	store images (yes/no)

- the argument `timings` indicates that the start/stop times in the following sublist is user-specified and can be done for multiple time frames (see section [Dynamic time frame definitions](#)).

The reconstructed image can be viewed as follow:

```
matshow(recon['im'][60,:,:], cmap='magma')
colorbar()
```

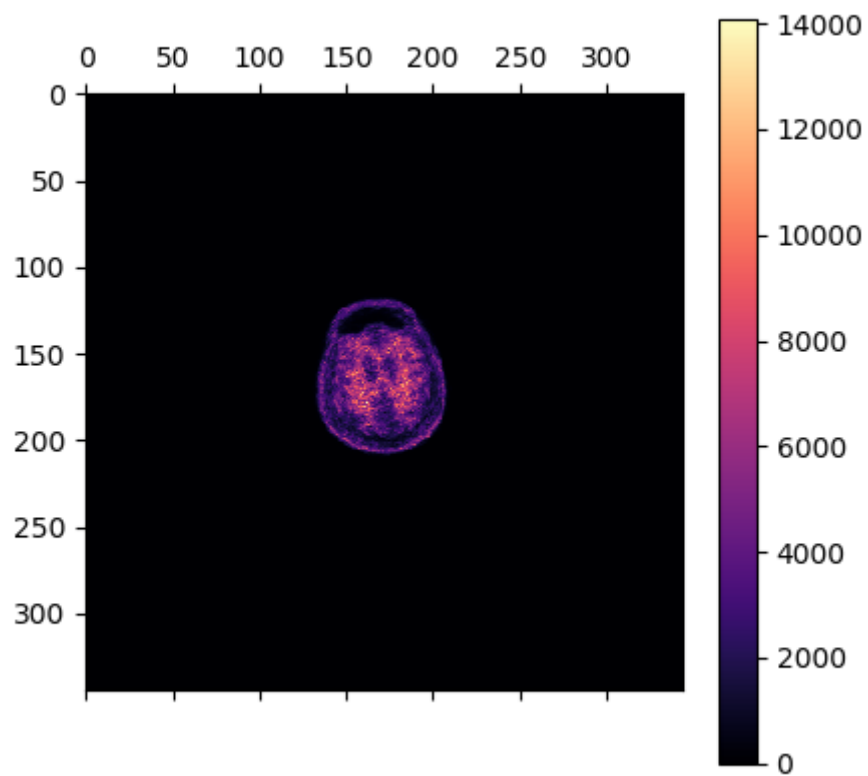


Fig. 8.3: The transaxial slice of the amyloid PET reconstructed image. Voxel intensities are in Bq.

DYNAMIC IMAGE RECONSTRUCTION

Dynamic imaging involves reconstruction of a series of static images across the whole duration of the acquisition time (usually not less than one hour) by dividing the time into usually non-overlapping dynamic time frames. It is assumed that the average tracer concentration during any frame is representative of the whole frame and any concentration changes within the frame are considered minor relative to the changes across the whole acquisition.

Dynamic reconstruction of the Biograph mMR data uses the same function, `nipet.mmrchain` as shown in section [Static image reconstruction](#) for the mMR chain processing. In addition to the basic parameters used, additional parameters need to be defined for dynamic reconstruction.

9.1 Dynamic time frame definitions

The extra parameters include the definition of the dynamic time frames. For example, for identical acquisitions, as the provided amyloid PET data (see [Raw brain PET data](#)), the one-hour dynamic PET data was divided into 31 dynamic frames in [6], i.e.: $4 \times 15\text{s}$, $8 \times 30\text{s}$, $9 \times 60\text{s}$, $2 \times 180\text{s}$, $8 \times 300\text{s}$, which makes the total of 3600s (one hour).

These definitions can then be represented using Python lists in three ways:

1. the simplest way—a 1-D list, with elements representing the consecutive frame durations in seconds, i.e., for the above definitions it will be:

```
frmdef_1D = [
    15, 15, 15, 15,
    30, 30, 30, 30,
    30, 30, 30, 30,
    60, 60, 60,
    60, 60, 60,
    60, 60, 60,
    180, 180,
    300, 300, 300, 300,
    300, 300, 300, 300
]
```

2. a more elegant representation is by using a 2-D Python list, starting with a string 'def', followed by two-element sub-lists with the repetition number and the duration in seconds [s], respectively, i.e.:

```
frmdef_2D = ['def', [4, 15], [8, 30], [9, 60], [2, 180], [8, 300]]
```

3. and the last most flexible representation is by using again a 2-D list, starting with a string 'timings' or 'fluid', followed by two-element sub-lists with the start time, t_0 and the end time t_1 for each frame, i.e.:

```
frmdef_t = [  
    'timings',  
    [0, 15],  
    [15, 30],  
    [30, 45],  
    [45, 60],  
    [60, 90],  
    [90, 120],  
    [120, 150],  
    [150, 180],  
    [180, 210],  
    [210, 240],  
    [240, 270],  
    [270, 300],  
    [300, 360],  
    [360, 420],  
    [420, 480],  
    [480, 540],  
    [540, 600],  
    [600, 660],  
    [660, 720],  
    [720, 780],  
    [780, 840],  
    [840, 1020],  
    [1020, 1200],  
    [1200, 1500],  
    [1500, 1800],  
    [1800, 2100],  
    [2100, 2400],  
    [2400, 2700],  
    [2700, 3000],  
    [3000, 3300],  
    [3300, 3600]  
]
```

The last representation is the most flexible as it allows the time frames to be defined independent of each other. This is especially useful when defining overlapping time frames or frames which are not necessarily consecutive time-wise.

All the definitions can be summarised in one dictionary using the above `frmdef_1D` or `frmdef_2D` definitions, i.e.:

```
# import the NiftyPET sub-package if it is not loaded yet  
from niftyPET import nipet  
  
# frame dictionary  
frmdct = nipet.dynamic_timings(frmdef_1D)
```

or

```
# frame dictionary  
frmdct = nipet.dynamic_timings(frmdef_2D)
```

resulting in:

```

In [1]: frmdct
Out[1]:
{'frames': array([ 15,  15,  15,  15,  30,  30,  30,  30,  30,  30,  30,  30,  30,
↪ 60,
               60,  60,  60,  60,  60,  60,  60,  60, 180, 180, 300, 300, 300,
               300, 300, 300, 300, 300], dtype=uint16),
'timings': ['timings',
            [0, 15],
            [15, 30],
            [30, 45],
            [45, 60],
            [60, 90],
            [90, 120],
            [120, 150],
            [150, 180],
            [180, 210],
            [210, 240],
            [240, 270],
            [270, 300],
            [300, 360],
            [360, 420],
            [420, 480],
            [480, 540],
            [540, 600],
            [600, 660],
            [660, 720],
            [720, 780],
            [780, 840],
            [840, 1020],
            [1020, 1200],
            [1200, 1500],
            [1500, 1800],
            [1800, 2100],
            [2100, 2400],
            [2400, 2700],
            [2700, 3000],
            [3000, 3300],
            [3300, 3600]],
'total': 3600}

```

Please note, that internally, consecutive dynamic frames are represented as an array of unsigned 16-bit integers.

9.2 Dynamic reconstruction

The dynamic reconstruction can be invoked after the following setting-up and pre-processing:

```

import os
import logging
from niftyPET import nipet
from niftyPET import nimpa

```

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```

logging.basicConfig(level=logging.INFO)
# dynamic frames for kinetic analysis
frmdef = ['def', [4, 15], [8, 30], [9, 60], [2, 180], [8, 300]]

# get all the constants and LUTs
mMRpars = nipet.get_mmrparams()

#-----
# GET THE INPUT
folderin = '/path/to/amyloid_brain'

# recognise the input data as much as possible
datain = nipet.classify_input(folderin, mMRpars)
#-----

# switch on verbose mode
logging.getLogger().setLevel(logging.DEBUG)

# output path
opath = os.path.join( datain['corepath'], 'output')

#-----
# GET THE MU-MAPS
muhdct = nipet.hdw_mumap(datain, [1,2,4], mMRpars, outputpath=opath, use_
↪stored=True)

# UTE-based object mu-map
muodct = nipet.obj_mumap(datain, mMRpars, outputpath=opath, store=True)
#-----

```

Since multiple image frames are reconstructed, the `mmrchain` function apart from 4-D NIfTI image storing, also enables to store intermediate 3-D NIfTI images for each dynamic frame using the option `store_img_intrmd = True`:

```

recon = nipet.mmrchain(
    datain,
    mMRpars,
    frames = frmdef,
    mu_h = muhdct,
    mu_o = muodct,
    itr = 4,
    fwhm = 0.,
    outputpath = opath,
    fcomment = '_dyn',
    store_img = True,
    store_img_intrmd = True)

```

The path to the reconstructed 4-D image can be accessed through the output dictionary, `recon`:

```

In [2]: recon['im'].shape
Out[2]: (31, 127, 344, 344)

```

or the stored 4-D NIfTI image in:


```
In [19]: recon['fpet']
Out[19]: '/path/to/NIfTI-output'
```

9.3 Time offset due to injection delay

In most cases the injection is performed with some delay relative to the time of starting the scan. Also, the first recorded counts will be random events, as the activity is detected from outside the field of view (FOV). The offset caused by the injection delay and random events, can be separated and omitted by running first list mode processing with histogramming, followed by estimating the time offset and accounting for it in the timings of the frames:

```
# histogram the list mode data (in <datain> dictionary) using scanner_
↳parameters (<mMRpars>)
hst = nipet.mmhist(datain, mMRpars)

# offset for the time from which meaningful events are detected
toff = nipet.lm.get_time_offset(hst)

# dynamic frame timings
frm_timings = nipet.lm.dynamic_timings(frmdef, offset=toff)
```

The reconstruction is then performed with the augmented timings in the following way:

```
recon = nipet.mmchain(
    datain,
    mMRpars,
    frames = frm_timings,
    mu_h = muhdc,
    mu_o = muodc,
    itr = 4,
    fwhm = 0.,
    outpath = oph,
    fcomment = '_dyn',
    store_img = True,
    store_img_intrmd = True)
```

Note, that the reconstruction pipeline accepts different definitions of the dynamic frames as shown above.

9.4 Visualisation of dynamic frame timings

The time frames can be visualised with one line of code:

```
# draw the frame timings over the head-curve
nipet.lm.draw_frames(hst, frm_timings)
```

which plots the timings of dynamic frames over the prompts, delayed and the difference between the two as shown below in Fig. 9.1.

In order to zoom in to a particular time interval, e.g., from 0s to 150s, and visualise clearly the time offset, the following line of code can be used:

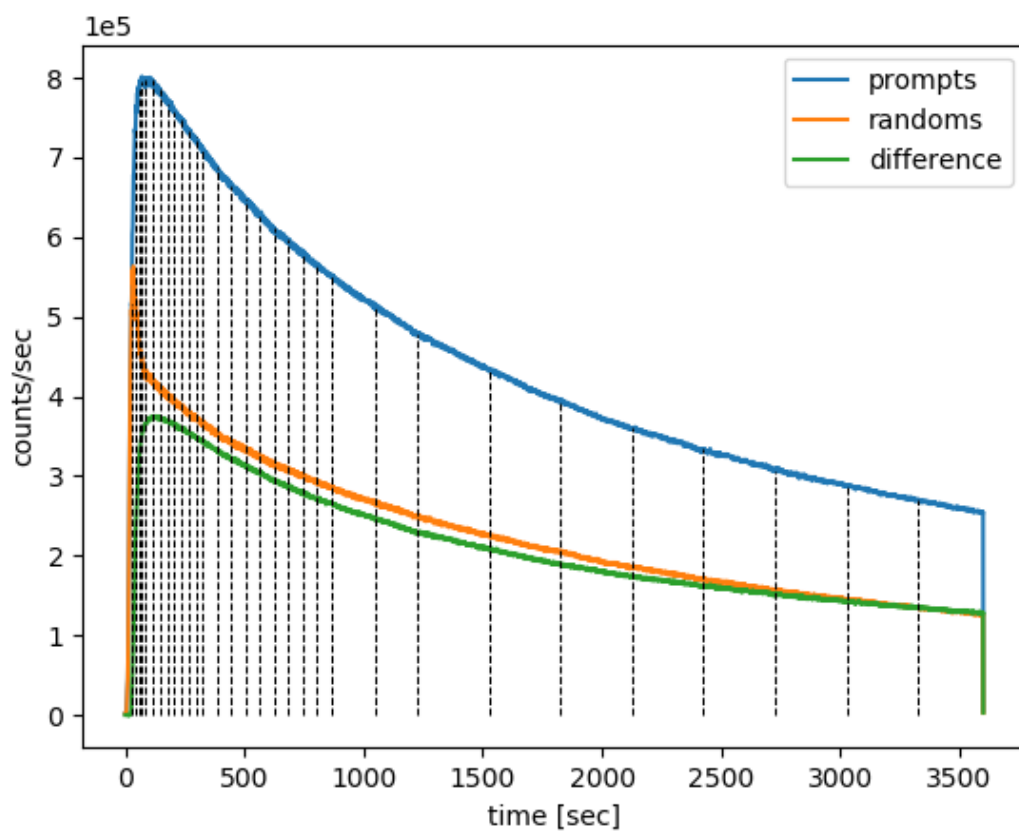


Fig. 9.1: The dynamic frame intervals are marked with dashed horizontal black curves on top of the head-curve (prompts and delayed per second).

```
# draw the frame timings over the head-curve, with time limits of tlim
nipet.lm.draw_frames(hst, frm_timings, tlim = [0, 150])
```

resulting in the following plot (Fig. 9.2):

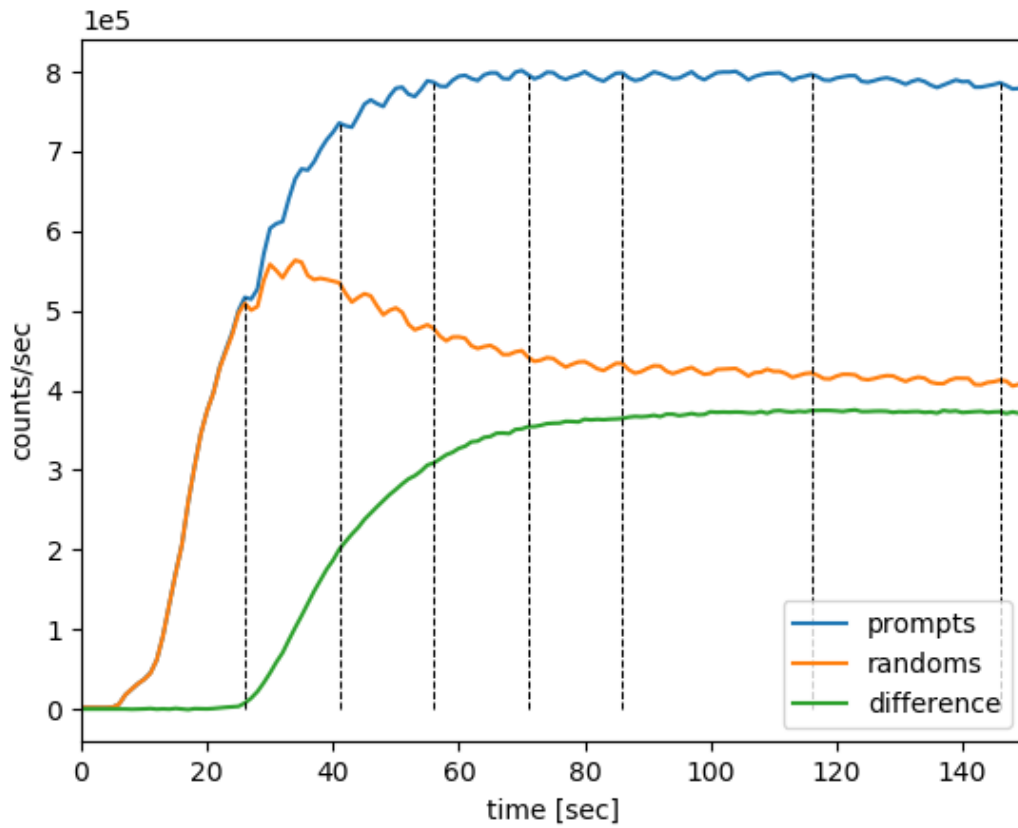


Fig. 9.2: The dynamic frame intervals are marked with dashed horizontal black curves on top of the part of head-curve (prompts and delayed per second). Note that almost 30s of list mode data from the beginning is discarded.

CORRECTIONS FOR QUANTITATIVE PET

10.1 Decay correction

During any PET acquisition, the radio-tracer activity, A_t , decays according to:

$$A_t = A_0 e^{-\lambda t},$$

where A_0 is the reference activity at time t_0 . The decay constant λ is defined as:

$$\lambda = \frac{\ln(2)}{T_{1/2}},$$

where $T_{1/2}$ is the half-life of the radionuclide.

Likewise, for activity A_t at time t , the original activity is simply:

$$A_0 = A_t e^{\lambda t}.$$

10.1.1 Real PET acquisition example

Consider the one-hour dynamic amyloid PET data provided in *Raw brain PET data*. The injected radioactivity at $t_0 = 0$ was $A_0 = 409$ MBq, and since the used amyloid tracer is ^{18}F -based, the half life for the radioisotope is $T_{1/2} = 6586.272$ s (≈ 110 min), and hence $\lambda = 1.052 \times 10^{-4} \text{ s}^{-1}$. The radioactive decay from the injected activity is shown in black in Fig. 10.1.

Consider also a time frame of the last 10 minutes of acquisition, from $t_1 = 3000$ to $t_2 = 3500$ seconds, as shown in Fig. 10.1. In order to correct for the decay not only within the time frame, but also relative to the beginning of the scan at injection, the measurable activity of the time frame needs to be compared to the ideal case of no radioactive decay.

In this example, the ideal radioactivity would remain constant at $A_0 = 409$ MBq, as is shown by the horizontal dashed line. Therefore, for the considered duration of the time frame, the measurable ideal activity would be $A_0 \Delta t$.

In the real case scenario, however, the activity decays, and the measurable activity with the time frame is:

$$\begin{aligned} \int_{t_1}^{t_2} A_0 e^{-\lambda t} dt &= -\frac{1}{\lambda} e^{-\lambda t} \Big|_{t_1}^{t_2} \\ &= \frac{A_0}{\lambda} (e^{-\lambda t_1} - e^{-\lambda t_2}) \end{aligned}$$

The decay correction, $C_{\text{decay}}^{t_0}$, for the time frame relative to the beginning of scan (injection), $t_0 = 0$, is simply the ratio of the two activities, i.e., the ideal one to the decaying, Δt , of the frame:

$$\begin{aligned} C_{\text{decay}}^{t_0} &= \frac{A_0 \Delta t}{A_0 (e^{-\lambda t_1} - e^{-\lambda t_2}) / \lambda} \\ &= \frac{\lambda \Delta t}{e^{-\lambda t_1} (1 - e^{-\lambda \Delta t})}, \end{aligned}$$

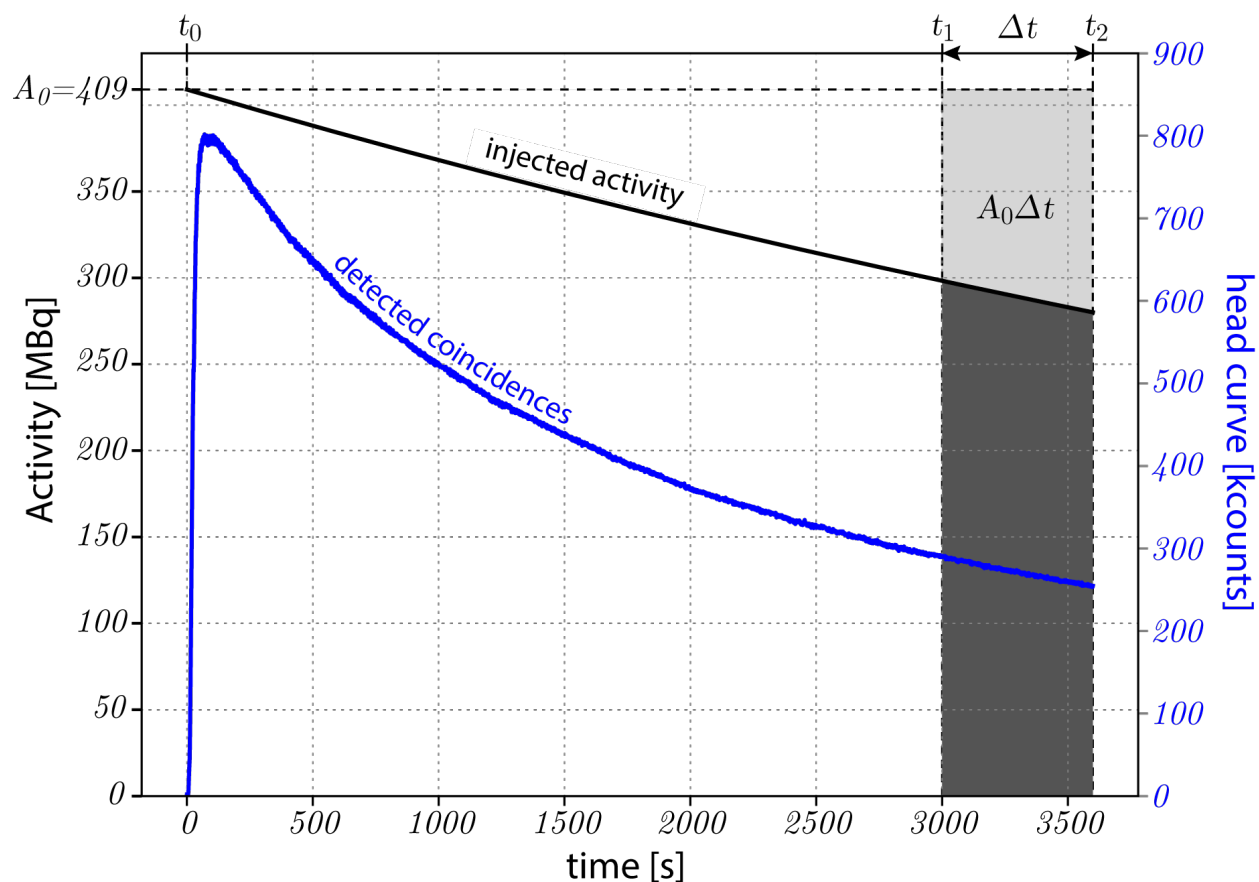


Fig. 10.1: Radioactive decay, shown in black, from the injected activity of $A_0 = 409$ MBq. The recorded prompt events are shown in blue. The decay correction calculations are shown for a frame of the last 10 minutes of acquisition. **Please note** that the injected activity is significantly greater than the recorded events (coincidences) as the field of view of the scanner allows only part of the body to be scanned. **Note** also the significantly different distribution of the detected coincidences, which is decaying considerably faster than the injected activity, and which is due to tracer clearance from the participant's head, dead-time and other factors.

and finally obtaining:

$$C_{\text{decay}}^{t_0} = \frac{\lambda e^{\lambda t_1} \Delta t}{1 - e^{-\lambda \Delta t}}.$$

See also <http://www.turkupetcentre.net/petanalysis/decay.html>.

10.1.2 Controlling decay correction in *NiftyPET*

The decay correction is by default applied automatically with the reference to the beginning of scan as recorded in the list-mode data. It does not need to be the injection time, i.e., in case of static scans, when the patient waits a time post-injection before is scanned. In *NiftyPET* decay correction is controlled by the dictionary entry `Cnt['DCYCRR']`. For example, if the scanner is initialised as follows:

```
# NiftyPET image reconstruction package (nipet)
from niftyPET import nipet
# NiftyPET image manipulation and analysis (nimpa)
from niftyPET import nimpa

# get all the Biograph mMR parameters
mMRpars = nipet.get_mmrparams()
```

Then the default decay correction can be switched off, if the following line:

```
mMRpars['Cnt']['DCYCRR'] = False,
```

is placed before image reconstruction. By default `mMRpars['Cnt']['DCYCRR'] = True`.

INTRODUCTION

A phantom-imaging platform, composed of a collection of software tools, for a novel automated and high precision imaging of the American College of Radiology (ACR) PET phantom for PET/MR and PET/CT systems is presented in the next sections.

The key aspect of the analysis is quantitative measurement of the spatial resolution using the measured knife-edge response $K(x)$, for any phantom insert with different attenuation and activity properties, and thus facilitating comprehensive and quantitative characterisation of PET/MR or (PET/CT) scanners in multisite clinical studies, e.g., in the [Dementias Platform UK](#) network.

PHANTOM IMAGE RECONSTRUCTION AND REGISTRATION

Import all packages needed for PET image reconstruction and registration

```
[7]: import numpy as np
import os, sys
import time
import glob
from pathlib import Path
import matplotlib.pyplot as plt
%matplotlib inline
from miutil import plot

import scipy.ndimage as ndi
import nibabel as nib
from scipy import ndimage

# > NiftyPET image reconstruction/analysis
from niftyPET import nipet
from niftyPET import nimpa

# > image registration and resampling
import dipy
from dipy.align import resample
from dipy.align import (affine_registration, center_of_mass, translation,
                        rigid, affine)

# > import tools for ACR parameters,
# > templates generation and I/O
import acr_params as pars
import acr_templates as ast
import acr_ioaux as ioaux
```

12.1 Imaging initialisation

Download the ACR raw and design data from [the Zenodo repository](#), and point to the top directory of this dataset as shown below.

```
[11]: # > core path with ACR phantom inputs
      cpth = Path('/sdata/ACR_data_design')

      # > get dictionary of constants, Cntd, for ACR phantom imaging
      Cntd = pars.get_params(cpth)

      # > get all the constants and LUTs for the mMR scanner
      mMRpars = nipet.get_mmrparams()

      # > standard and exploratory output
      outname = 'output_s'

      # > update the dictionary of constants with I/O paths
      Cntd = ioaux.get_paths(Cntd, mMRpars, cpth, outdir=outname)

      # > generate hardware mu-map for the phantom
      muhdct = nipet.hdw_mumap(Cntd['datain'], [3,4], mMRpars,
                               <-stored=True)
                               <-stored=True)
```

12.2 List-mode histogramming

Run the histogramming and show the sum of sinograms as well as the head curve (total counts per second):

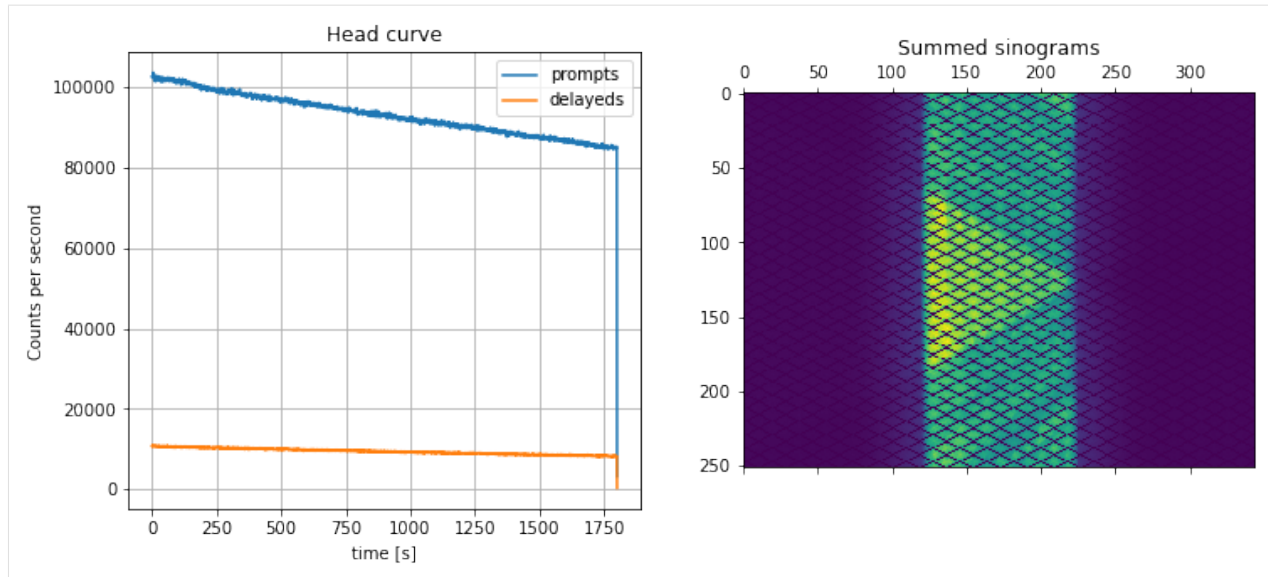
```
[28]: # > histogram the raw PET list-mode data
      hst = nipet.mmrhist(Cntd['datain'], mMRpars)

      fig, axs = plt.subplots(1,2, figsize=(12, 5))

      # > plot the headcurve
      axs[0].plot(hst['phc'], label='prompts')
      axs[0].plot(hst['dhc'], label='delayeds')
      axs[0].grid('on')
      axs[0].legend()
      axs[0].set_xlabel('time [s]')
      axs[0].set_ylabel('Counts per second')
      axs[0].set_title('Head curve')

      # > show the sum of all sinograms
      axs[1].matshow(np.sum(hst['psino'], axis=0))
      axs[1].set_title('Summed sinograms')
```

```
[28]: Text(0.5, 1.0, 'Summed sinograms')
```



12.3 NAC PET image reconstruction

The non-attenuation corrected (NAC) PET image (the attenuation of the patient bed is accounted for) is reconstructed for the purposes of image registration, so that an accurate attenuation can be performed using aligned μ -map as well as having accurate and precise sampling of the phantom volumes of interest (VOI).

```
[21]: # > reconstruct the phantom without object attenuation correction
if not 'imupd' in Cntd:
    recon = nipet.mmchain(
        Cntd['datain'],
        mMRpars,
        histo=hst,
        mu_h = muhdc,
        itr=Cntd['itr_nac'],
        fwhm=Cntd['fwhm_nac'],
        recmod=1,
        outpath=Cntd['opth'],
        fout=Cntd['fnac'],
        store_img = True,
        trim=True,
        trim_scale=Cntd['sclt'],
        trim_interp=1,
        trim_store=True,
    )
    nacim = recon['trimmed']['im']
else:
    nacim = nimpa.getnii(Cntd['fnacup'])

# > update the dictionary of constants with the recon
Cntd = ioaux.get_paths(Cntd, mMRpars, cpth, outdir=outname)
```

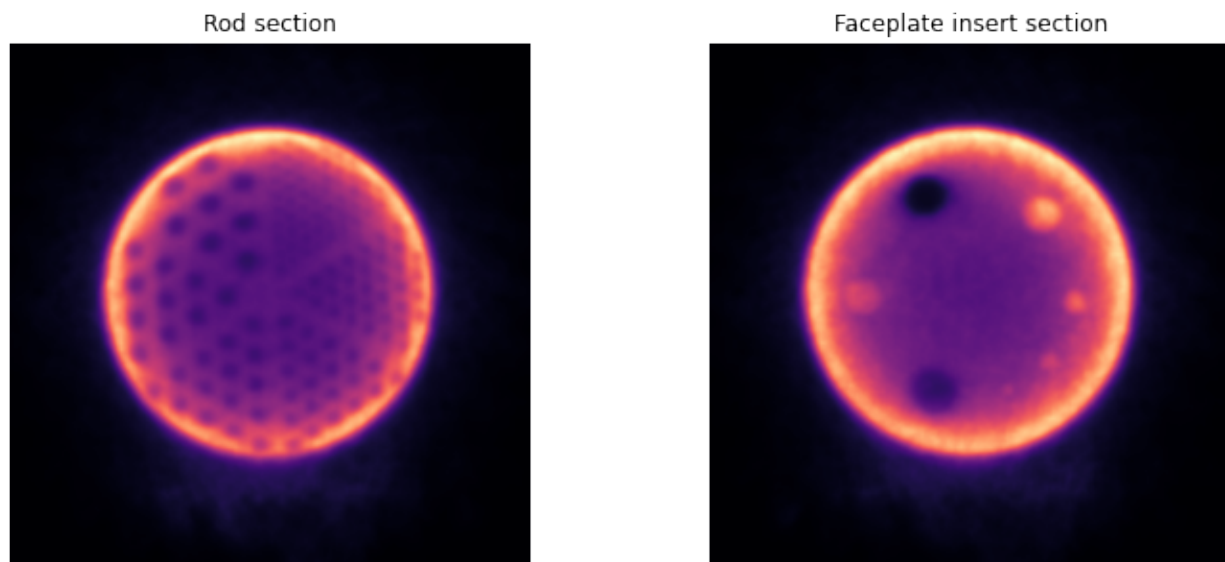
12.3.1 Plot the reconstructed NAC image

```
[25]: # > plot the NAC PET reconstruction and template
fig, axs = plt.subplots(1,2, figsize=(12, 5))

axs[0].imshow(np.sum(nacim[90:240],axis=0), cmap='magma')
axs[0].set_axis_off()
axs[0].set_title('Rod section')

axs[1].imshow(np.sum(nacim[370:440],axis=0), cmap='magma')
axs[1].set_axis_off()
axs[1].set_title('Faceplate insert section')
```

```
[25]: Text(0.5, 1.0, 'Faceplate insert section')
```



12.4 Generate μ -map and NAC PET templates

Run the functions to generate the core μ -map of the ACR phantom together with the NAC PET template facilitating an accurate image registration. The paths of the generated templates are stored in `Cntd['out']['facrmu']` and `Cntd['out']['facrdmu']` for μ -maps and `Cntd['out']['facrad']` for the NAC PET template.

```
[ ]: # > generate the mu-map and NAC PET templates
ast.create_mumap_core(Cntd, return_raw=True)
ast.create_nac_core(Cntd, return_raw=True)
```

12.4.1 Plot the templates

Please note, that the μ -map template is larger by the acrylic material compared to the NAC template which only represents the air or active water.

```
[33]: # > get the template images to arrays
tnac = nimpa.getnii(Cntd['out']['facrad'])
tmu = nimpa.getnii(Cntd['out']['facrdmu'])

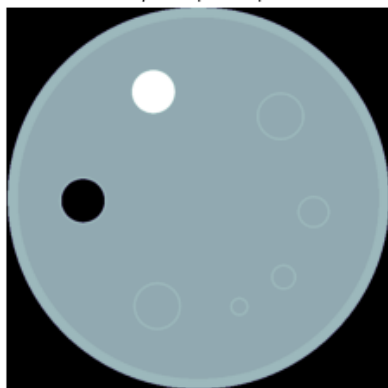
# > plot the NAC PET reconstruction and template
fig, axs = plt.subplots(2,2, figsize=(16, 9))
axs[0,0].imshow(tmu[450,...], cmap='bone')
axs[0,0].set_axis_off()
axs[0,0].set_title('Core  $\mu$ -map template')

axs[0,1].imshow(tnac[450,...], cmap='inferno')
axs[0,1].set_title('NAC Template')
axs[0,1].set_axis_off()

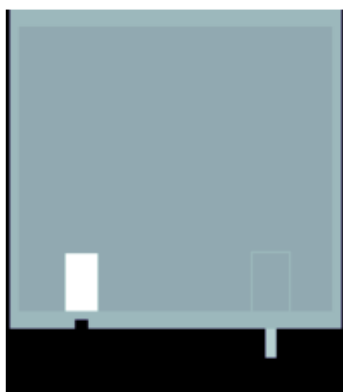
axs[1,0].imshow(tmu[...,230], cmap='bone')
axs[1,0].set_axis_off()

axs[1,1].imshow(tnac[...,230], cmap='inferno')
axs[1,1].set_axis_off()
```

Core μ -map template



NAC Template



12.5 Stage I image registration

In this stage I registration the core phantom is aligned in order to perform accurate attenuation correction using aligned μ -map and to perform the analysis in the native PET space. For more accurate registration, an NAC phantom core template is used and registered to the reference NAC PET image. In this stage of registration the resolution rods are not yet accounted for.

The registration is performed using Python imaging library [DIPY](#), using mutual information as the cost function.

Since the registration is performed in high resolution image grid, it will take a longer time, up to one hour, depending on the computing resources.

The aligned μ -map is resampled to the native (original) PET space, before upsampling, and is used for the next quantitative image reconstruction.

```
[17]: # > setup the registration pipeline
pipeline = [center_of_mass, translation, rigid]

# > registration output folder
dipy_fldr = os.path.dirname(Cntd['out']['faff'])

# > smooth and save the template image for improved registration
fsmo = os.path.basename(Cntd['out']['facrad']).split('.nii')[0]+'_smth'+str(Cntd['fwhm_
→tpl'])+'.replace('.', '-')+'.mm.nii.gz'
fsmo = os.path.join(dipy_fldr, fsmo)
_ = nimpa.imsmooth(Cntd['out']['facrad'], fwhm=Cntd['fwhm_tpl'], fout=fsmo, dev_
→id=False)

#=====
if not os.path.isfile(Cntd['out']['faff']):

    # > perform the registration, which can take longer time
    txim, txaff = affine_registration(
        fsmo,
        Cntd['fnacup'],
        nbins=32,
        metric='MI',
        pipeline=pipeline,
        level_iters=Cntd['dipy_its'],
        sigmas=Cntd['dipy_sgms'],
        factors=Cntd['dipy_fcts'])

    # > save the registration affine
    np.save(Cntd['out']['faff'], txaff)

else:
    txaff = np.load(Cntd['out']['faff'])
#=====

# > smooth the template mu-map
fwhm = 3
fsmo = os.path.basename(Cntd['out']['facrdmu']).split('.nii')[0]+'_smo-'+str(fwhm)+'_nii.
→gz'
fsmo = os.path.join(dipy_fldr, fsmo)
```

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```

_ = nimpa.imsmooth(Cntd['out']['facrdmu'], fwhm=fwhm, fout=fsmo, dev_id=False)

# > resample the ACR designed mu-map to the original PET space (2mm voxel size)
# > this mu-map will be used in image reconstruction
new = dipy.align.resample(fsmo, Cntd['fnac'], between_affine=txaff)
nib.save(new, Cntd['out']['fmuo'])

# FOR QUALITY CONTROL:
# > resample the ACR designed mu-map to the upsampled PET space
new = dipy.align.resample(fsmo, Cntd['fnacup'], between_affine=txaff)
nib.save(new, Cntd['out']['fmuo_hires'])

# > resample the NAC template to the upsampled PET space
new = dipy.align.resample(Cntd['out']['facrad'], Cntd['fnacup'], between_affine=txaff)
ftnac = os.path.join(dipy_fldr, 'acr-activity-dipy.nii.gz')
nib.save(new, ftnac)

```

```

-----
NameError                                Traceback (most recent call last)
<ipython-input-17-4721ca7750f5> in <module>
    51 new = dipy.align.resample(Cntd['out']['facrad'], Cntd['fnacup'], between_
-> affine=txaff)
    52 ftnac = os.path.join(dipy_fldr, 'acr-activity-dipy.nii.gz')
--> 53 nib.save(new, ftnac)

NameError: name 'ftanc' is not defined

```

12.5.1 Visualisation of the registration

```

[20]: # > get the aligned NAC template
tnac = nimpa.getnii(ftnac)

# > plot the NAC PET reconstruction and template
fig, axs = plt.subplots(2,3, figsize=(12, 9))
axs[0,0].set_axis_off()
axs[0,1].set_axis_off()
axs[0,2].set_axis_off()
axs[1,0].set_axis_off()
axs[1,1].set_axis_off()
axs[1,2].set_axis_off()

#itx = 480
itx = 440
axs[0,0].imshow(tnac[itx,...], 'bone', interpolation='none')
axs[0,1].imshow(nacim[itx,...], 'inferno', interpolation='none')
axs[0,2].imshow(tnac[itx,...], 'bone', interpolation='none')
axs[0,2].imshow(nacim[itx,...], 'inferno', interpolation='none', alpha=0.5)

iax = 320
axs[1,0].imshow(tnac[...,iax], 'bone', interpolation='none')
axs[1,1].imshow(nacim[...,iax], 'inferno', interpolation='none', vmax=0.5*nacim[...,iax].
-> max())

```

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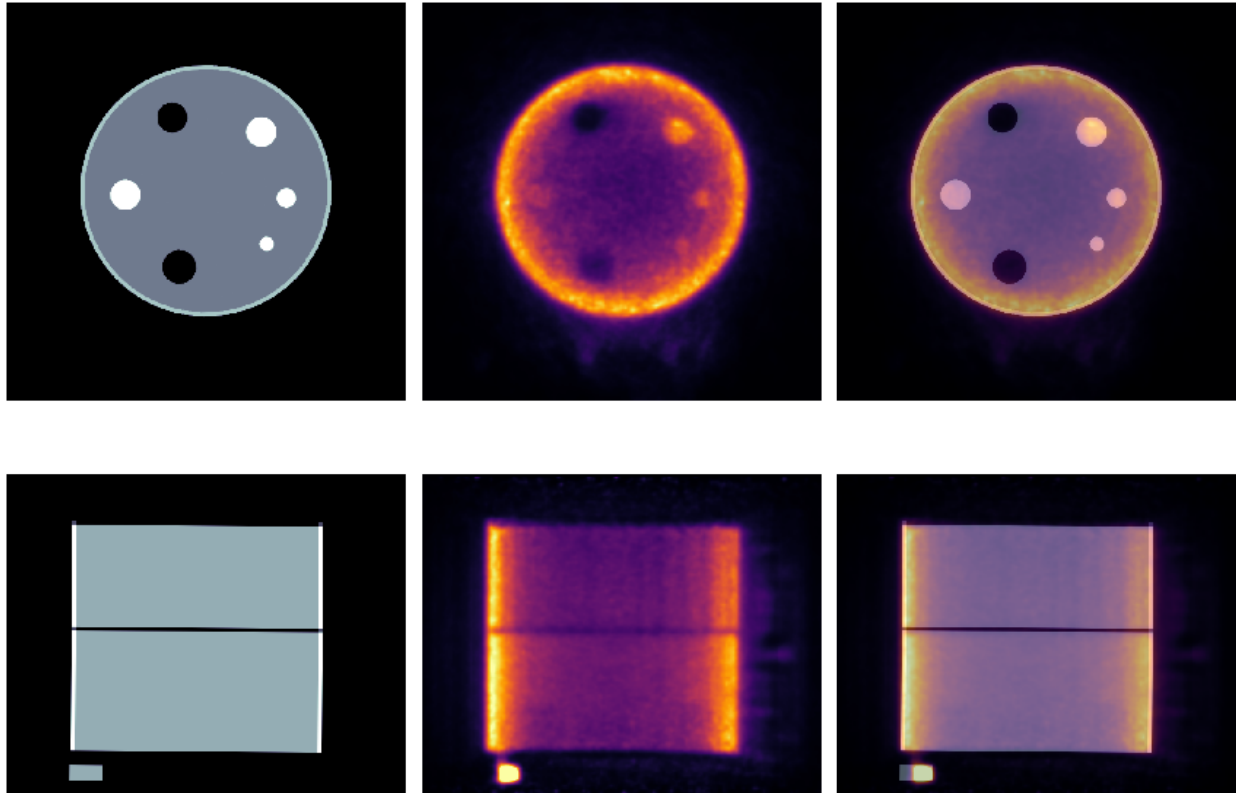
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```

axs[1,2].imshow(tnac[...,:iax], 'bone', interpolation='none')
axs[1,2].imshow(nacim[...,:iax], 'inferno', interpolation='none', vmax=0.5*nacim[...,:iax].
    ↪max(), alpha=0.5)

plt.tight_layout()

```



12.6 Quantitative reconstruction for stage II registration

This reconstruction is performed for stage II registration and uses the above generated μ -map for attenuation and scatter corrections. Note that the μ -map is not fully representative of the real attenuation since the rods are not yet accounted for. However, since the acrylic rods have slightly higher linear attenuation coefficient, the reconstructed rods will have slightly higher contrast due to the underestimated attenuation (assumed water at this stage).

```

[35]: #-----
# > check if reconstruction is needed
if not os.path.isfile(Cntd['fqnt']):

    # > get the mu-map
    mudct = nipet.img.obtain_image(Cntd['out']['fmuo'])
    mudct['im'] = np.float32(mudct['im'])

    recon = nipet.mmrchain(
        Cntd['datain'],
        mMRpars,

```

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```

        histo=hst,
        mu_h = muhdct,
        mu_o = mudct,
        itr=Cntd['itr_qnt'],
        fwhm=Cntd['fwhm_qnt'],
        recmod = 3,
        outpath = Cntd['opth'],
        fout=Cntd['fqnt'],
        store_img = True,
    )
#-----

# > trim and upsample the QNT image with the same parameters as the NAC image
imup = nimpa.imtrimup(
    Cntd['fqnt'],
    refim=Cntd['fnacup'],
    scale=Cntd['sclt'],
    int_order=1,
    fcomment_pfx=os.path.basename(Cntd['fqnt']).split('.')[0]+'_',
    store_img=True)

# > updated dictionary Cntd with the generated outputs relative to PET
Cntd = ioaux.get_paths(Cntd, mMRpars, cpth, outdir=outname)

```

```

-----
Correcting for trimming outside the original image (z-axis)'
-----

```

12.7 Generate the resolution rod template

The generation of the template for the resolution rods is followed by extracting the resolution rod part from the quantitative PET reconstructed above.

```

[37]: # > create the rods' template for the mu-map
      ast.create_reso(Cntd, return_raw=False)

      # > extract the resolution part from the QNT PET image to perform second
      # > stage of the registration for the resolution rod part
      exprf = ioaux.extract_reso_part(Cntd, offset=15)

```

12.7.1 Plot the resolution rod template and the target PET

```

[38]: resim = nimpa.getnii(Cntd['out']['fpet_res'])
      tres = nimpa.getnii(Cntd['out']['fresdQmu'])

[76]: # > plot the QNT PET reconstruction and resolution rod templates
      fig, axs = plt.subplots(2,2, figsize=(16, 9))
      axs[0,0].imshow(np.sum(resim[90:240,...], axis=0), cmap='inferno')

```

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```

axs[0,0].set_axis_off()
axs[0,0].set_title('Rod PET extracted part')

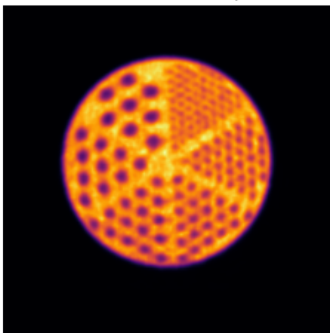
axs[0,1].imshow(tres[200,...], cmap='inferno')
axs[0,1].set_title('Rod PET template')
axs[0,1].set_axis_off()

axs[1,0].imshow(np.sum(resim[...,240:260],axis=2), cmap='inferno')
axs[1,0].set_axis_off()

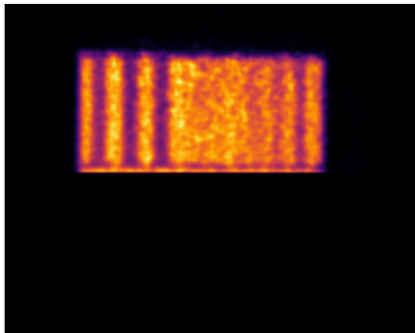
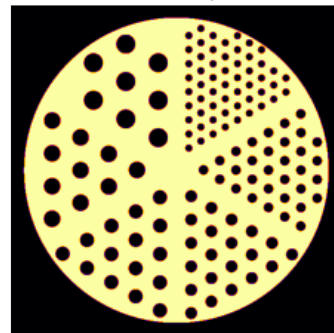
axs[1,1].imshow(tres[...,250], cmap='inferno')
axs[1,1].set_axis_off()

```

Rod PET extracted part



Rod PET template



12.8 Stage II image registration

This stage uses the extracted resolution PET part of the phantom and registers to it the resolution rod template, generated above.

```

[83]: # > RESOLUTION RODS REGISTRATION

pipeline = [center_of_mass, translation, rigid]

dipy_fldr = os.path.dirname(Cntd['out']['faff_res'])
fsmo = os.path.basename(Cntd['out']['fresdQmu']).split('.')[0]+'_smth'+str(Cntd['fwhm_
    ↳ tmp1']).replace('.', '-')+'.mm.nii.gz'

```

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```

fsmo = os.path.join(dipy_fldr, fsmo)
smoim = nimpa.imsmooth(Cntd['out']['fresdQmu'], fwhm=Cntd['fwhm_tmpl'], fout=fsmo, dev_
    ↪id=False)

#=====
if not os.path.isfile(Cntd['out']['faff_res']):
    txim, txaff = affine_registration(
        fsmo,
        Cntd['out']['fpet_res'],
        nbins=32,
        metric='MI',
        pipeline=pipeline,
        level_iters=Cntd['dipy_rods_itrs'],
        sigmas=Cntd['dipy_sgms'],
        factors=Cntd['dipy_fcts'])

    # > save the affine to Numpy format
    np.save(Cntd['out']['faff_res'], txaff)

else:
    txaff = np.load(Cntd['out']['faff_res'])
#=====

# > --- resolution rods mu-map in native PET space ---
fwhm = 3
fsmo = os.path.basename(Cntd['out']['fresdWmu']).split('.')[0]+'_smo-'+str(fwhm)+'.'
    ↪nii.gz'
fsmo = os.path.join(dipy_fldr, fsmo)
_ = nimpa.imsmooth(Cntd['out']['fresdWmu'], fwhm=fwhm, fout=fsmo, dev_id=False)

new = dipy.align.resample(fsmo, Cntd['fnac'], between_affine=txaff)
nib.save(new, Cntd['out']['fmur'])
#> ---

# > for quality control
# > rods themselves
new = dipy.align.resample(Cntd['out']['fresdmu'], Cntd['out']['fpet_res'], between_
    ↪affine=txaff)
frod = os.path.join(dipy_fldr, 'acr-rods-dipy-QC.nii.gz')
nib.save(new, frod)

# > activity among rods
new = dipy.align.resample(Cntd['out']['fresdQmu'], Cntd['out']['fpet_res'], between_
    ↪affine=txaff)
frodq = os.path.join(dipy_fldr, 'acr-reso-qnt-dipy-QC.nii.gz')
nib.save(new, frodq)

```

12.8.1 Visual QC of the registration

First get the images in Numpy arrays

```
[ ]: # > get the quantitative PET image of the rods part
    imq = nimpa.getnii(Cntd['out']['fpet_res'])

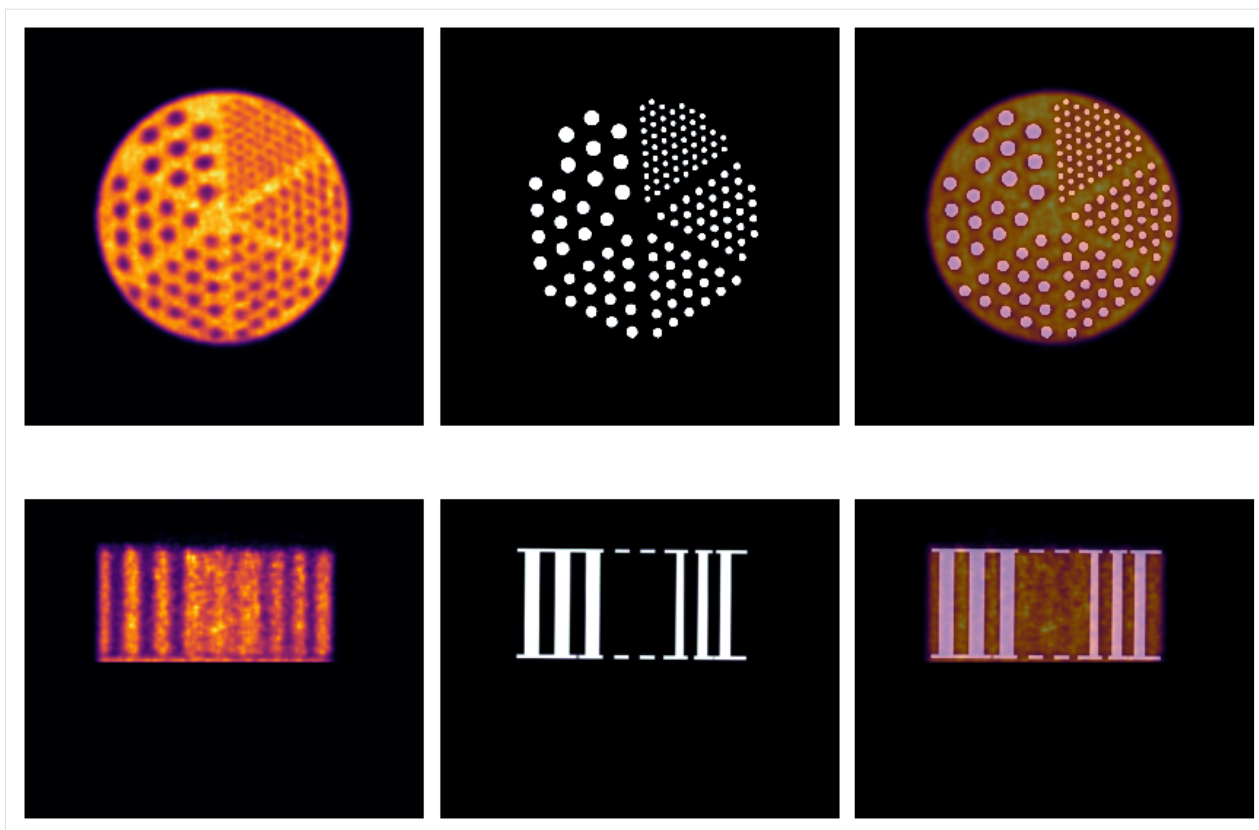
    # > QC: get the array data of aligned template of the rods only
    rod = nimpa.getnii(frod)
```

```
[123]: # > plot the NAC PET reconstruction and template
    fig, axs = plt.subplots(2,3, figsize=(12, 9))
    axs[0,0].set_axis_off()
    axs[0,1].set_axis_off()
    axs[0,2].set_axis_off()
    axs[1,0].set_axis_off()
    axs[1,1].set_axis_off()
    axs[1,2].set_axis_off()

    itx = 150
    axs[0,0].imshow(np.sum(imq[100:200,...],axis=0), 'inferno')
    axs[0,1].imshow(rod[itx,...], 'bone', interpolation='none')
    axs[0,2].imshow(np.sum(imq[100:200,...],axis=0), 'inferno')
    axs[0,2].imshow(rod[itx,...], 'bone', interpolation='none', alpha=0.5)

    iax = 240
    axs[1,0].imshow(np.sum(imq[...,iax:iax+5],axis=2), 'inferno')
    axs[1,1].imshow(rod[...,iax+4], 'bone')
    axs[1,2].imshow(rod[...,iax+4], 'bone')
    axs[1,2].imshow(np.sum(imq[...,iax:iax+10],axis=2), 'inferno', alpha=0.5)

    plt.tight_layout()
```



12.9 Compose the final μ -map

The complete μ -map is composed from the main core μ -map and the resolution rods' μ -map, following the two-stage registration. It is found as follows:

```
[125]: #=====
#> complete mu-map by combining the core and resolution rods mu-maps
#=====
acr = nimpa.getnii(Cntd['out']['fmuo'], output='all')
res = nimpa.getnii(Cntd['out']['fmur'])

msk = res>=Cntd['mu_water']-0.0001
acrf = acr['im'].copy()
acrf[msk] = res[msk]

# > ACR full mu-map
acrf = np.float32(acrf)

# > saving the complete mu-map to the path in Cntd['out']['fmuf']
nimpa.array2nii(
    acrf,
    acr['affine'],
    Cntd['out']['fmuf'],
    trnsp = (acr['transpose'].index(0), acr['transpose'].index(1), acr['transpose'].
    ↪ index(2)),
```

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```
flip = acr['flip'])
#=====
```

12.9.1 Visualisation of the μ -map alignment

The alignment is shown for the original native PET space of voxel size ~2 mm.

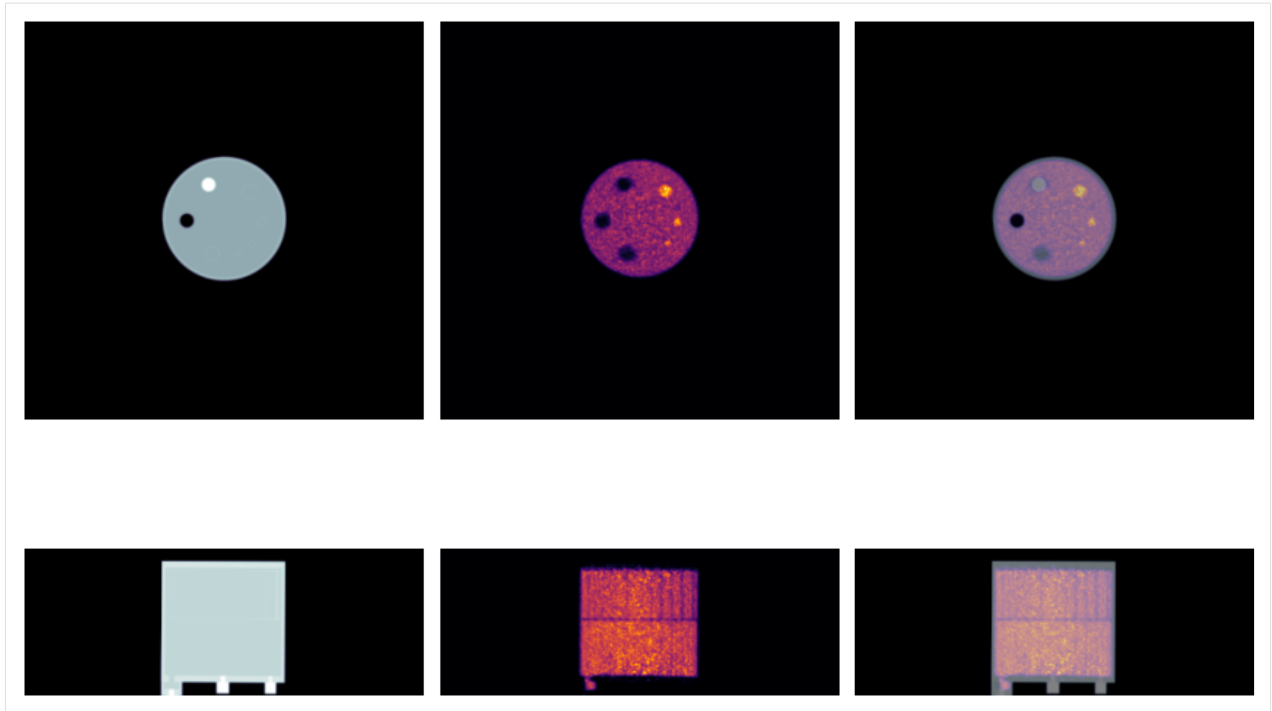
```
[129]: # > get the aligned NAC template
muf = nimpa.getnii(Cntd['out']['fmuf'])
imq = nimpa.getnii(Cntd['fqnt'])

# > plot the NAC PET reconstruction and template
fig, axs = plt.subplots(2,3, figsize=(12, 9))
axs[0,0].set_axis_off()
axs[0,1].set_axis_off()
axs[0,2].set_axis_off()
axs[1,0].set_axis_off()
axs[1,1].set_axis_off()
axs[1,2].set_axis_off()

itx = 100
axs[0,0].imshow(muf[itx,...], 'bone')
axs[0,1].imshow(imq[itx,...], 'inferno')
axs[0,2].imshow(muf[itx,...], 'bone')
axs[0,2].imshow(imq[itx,...], 'inferno', alpha=0.5)

iax = 171
axs[1,0].imshow(muf[...,iax], 'bone')
axs[1,1].imshow(imq[...,iax], 'inferno')
axs[1,2].imshow(muf[...,iax], 'bone')
axs[1,2].imshow(imq[...,iax], 'inferno', alpha=0.5)

plt.tight_layout()
```

12.10 Reuse of registraion for VOI sampling

The affine matrices of the two rigid body registrations are also used for aligning the sampling templates to the quantitatively reconstructed PET image, and hence making the alignment consistent between attenuation correction and VOI sampling.

The sampling and analysis is shown in the next section.

ADVANCED ANALYSIS

The advanced analysis is performed after having reconstructed the PET image with the correct and complete μ -map. The affine transformations (i.e., representing the rigid body alignment) of the two-stage registration are used again for aligning the concentric ring volumes of interest (VOI).

13.1 Imports

```
[1]: # > get all the imports
import numpy as np
import os
import glob
from pathlib import Path
import matplotlib.pyplot as plt
%matplotlib inline

from niftypet import nipet
from niftypet import nimpa

# > import tools for ACR parameters,
# > templates generation and I/O
import acr_params as pars
import acr_templates as ast
import acr_ioaux as ioaux
```

13.2 Initialisation

Initialise the scanner parameters and look-up tables, the path to the phantom data and design, and phantom constants, etc.

```
[2]: # > get all the constants and LUTs for the mMR scanner
mMRpars = nipet.get_mmrparams()

# > core path with ACR phantom inputs
cpth = Path('/sdata/ACR_data_design')

# > standard and exploratory output
outname = 'output_s'
```

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```
# > get dictionary of constants, Cntd, for ACR phantom imaging
Cntd = pars.get_params(cpth)

# > update the dictionary of constants with I/O paths
Cntd = ioaux.get_paths(Cntd, mMRpars, cpth, outdir=outname)
```

13.3 Quantitative PET reconstruction

Reconstruct the quantitative PET for iterations 4, 8 and 16 as given in `Cntd['itr_qnt2']`. Uses the complete μ -map as saved at path `Cntd['out']['fmuf']`.

```
[3]: # > adjust the time frame as needed
time_frame = [0, 1800]

# > output file name
facr = 'ACR_QNT_t{}-{}'.format(time_frame[0], time_frame[1])

if not os.path.isfile(os.path.join(os.path.dirname(Cntd['fqnt']), facr+'.nii.gz')):
    # > generate hardware mu-map for the phantom
    muhdct = nipet.hdw_mumap(Cntd['datain'], [3,4], mMRpars,
        outpath=Cntd['opth'], use_
        ↪stored=True)

    # > run reconstruction
    recon = nipet.mmrchain(
        Cntd['datain'],                # > all the input data in dictionary
        mMRpars,
        frames=['fluid', [0,1800]],
        mu_h=muhdct,
        mu_o=Cntd['out']['fmuf'],
        itr=max(Cntd['itr_qnt2']),
        store_itr=Cntd['itr_qnt2'],    # > list of all iterations after which image is_
        ↪saved
        recmod=3,
        outpath = Cntd['opth'],
        fout=facr,
        store_img = True)
```

13.4 Scaling up PET images to high resolution grid

The PET images are trimmed and upsampled to ~0.5 mm resolution grid to facilitate accurate and precise concentric ring VOI sampling.

```
[ ]: # > TRIM/UPSCALE

# > get PET images for different iterations to be upsacled
fims = glob.glob(os.path.join(Cntd['opth'], 'PET', 'single-frame', facr+'*inrecon*'))
```

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```

for fim in fims:
    imu = nimpa.imtrimup(
        fim,
        refim=Cntd['fnacup'],
        scale=Cntd['sclt'],
        int_order=1,
        fcomment_pfx=os.path.basename(fim).split('.')[0]+'_',
        store_img=True)

```

13.4.1 Plot upscaled PET images

Notice, the increased noise with a greater number of iterations, but also greater contrast achieved, especially seen on the summed images below.

[4]: #> get upscaled images for 4 and 16 OSEM iterations

```

fqnt4 = glob.glob(os.path.join(Cntd['opth'], 'PET', 'single-frame', 'trimmed', facr+
    ↳ '*itr4*inrecon*'))[0]
qntim4 = nimpa.getnii(fqnt4)
fqnt16 = glob.glob(os.path.join(Cntd['opth'], 'PET', 'single-frame', 'trimmed', facr+
    ↳ '*itr16*inrecon*'))[0]
qntim16 = nimpa.getnii(fqnt16)

```

[5]: #> RODS

```

# > plot the NAC PET reconstruction and template
fig, axs = plt.subplots(2,2, figsize=(12, 10))

axs[0,0].imshow(np.sum(qntim4[90:240],axis=0), cmap='magma')
axs[0,0].set_axis_off()
axs[0,0].set_title('Summed rod section, 4 iters')

axs[0,1].imshow(qntim4[160,...], cmap='magma')
axs[0,1].set_axis_off()
axs[0,1].set_title('Rod section, 4 iters')

axs[1,0].imshow(np.sum(qntim16[90:240],axis=0), cmap='magma')
axs[1,0].set_axis_off()
axs[1,0].set_title('Summed rod section, 16 iters')

axs[1,1].imshow(qntim16[160,...], cmap='magma')
axs[1,1].set_axis_off()
axs[1,1].set_title('Rod section, 16 iters')

# FACEPLATE
# > plot the NAC PET reconstruction and template
fig, axs = plt.subplots(2,2, figsize=(12, 10))

axs[0,0].imshow(np.sum(qntim4[370:440],axis=0), cmap='magma')
axs[0,0].set_axis_off()
axs[0,0].set_title('Summed faceplate section, 4 iters')

```

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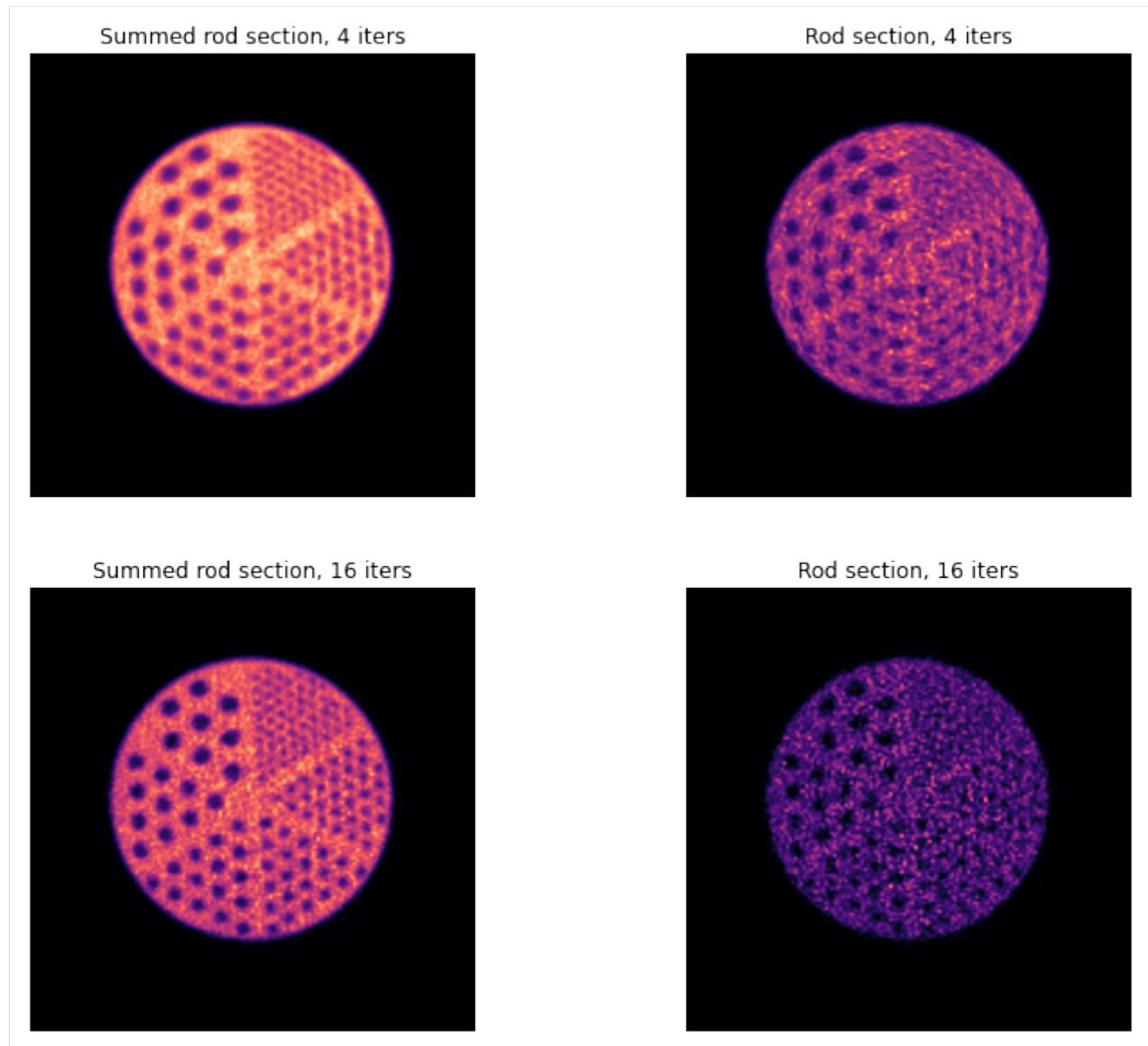
```
axs[0,1].imshow(qntim4[400,...], cmap='magma')
axs[0,1].set_axis_off()
axs[0,1].set_title('Faceplate section, 4 iters')

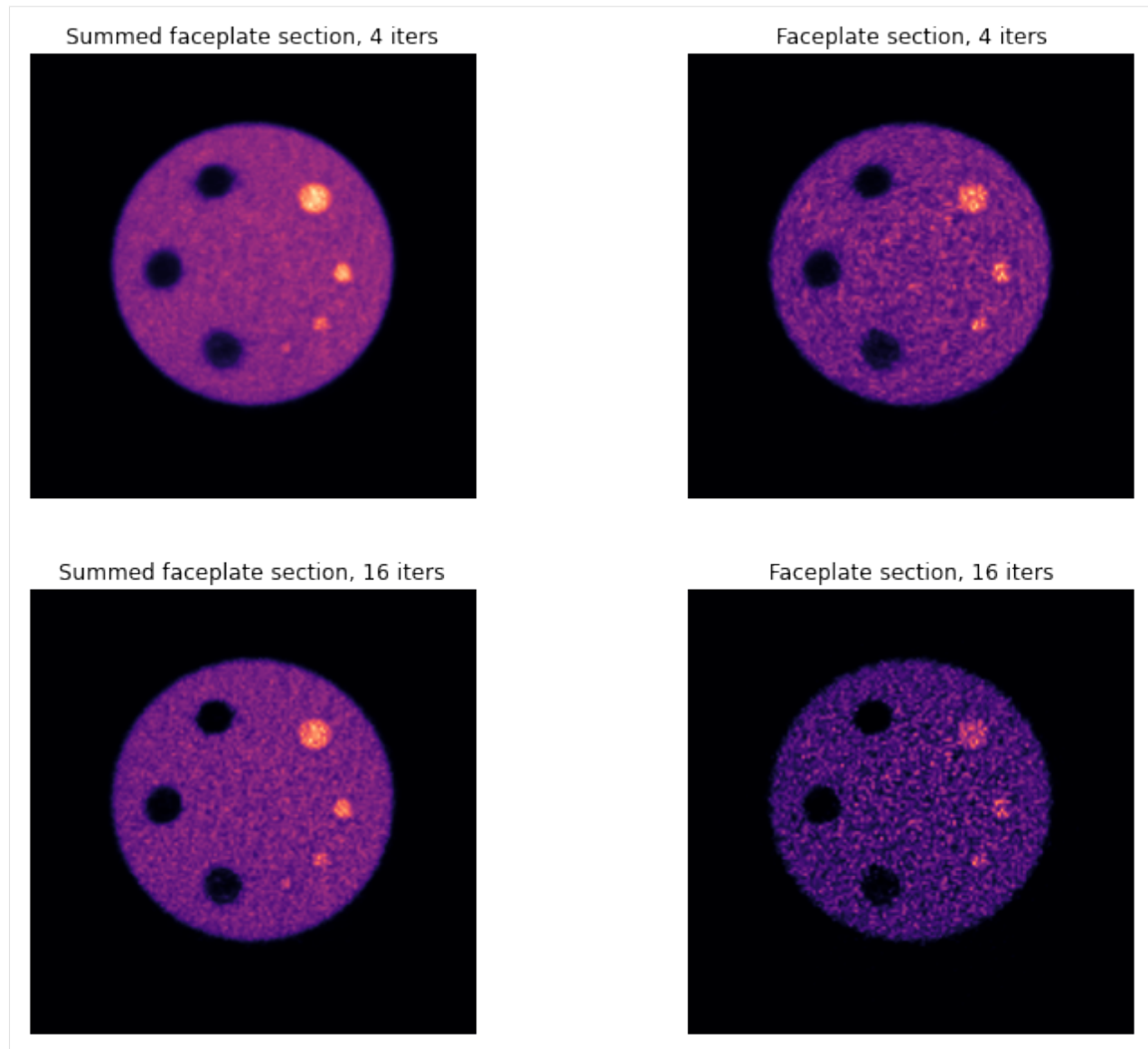
axs[1,0].imshow(np.sum(qntim16[370:440],axis=0), cmap='magma')
axs[1,0].set_axis_off()
axs[1,0].set_title('Summed faceplate section, 16 iters')

axs[1,1].imshow(qntim16[400,...], cmap='magma')
axs[1,1].set_axis_off()
axs[1,1].set_title('Faceplate section, 16 iters')

#axs[1,1].imshow(np.sum(qntim4[],axis=0), cmap='magma')
#axs[1,1].set_axis_off()
#axs[1,1].set_title('Summed faceplate insert section')
```

```
[5]: Text(0.5, 1.0, 'Faceplate section, 16 iters')
```





13.5 Generate the sampling templates

The templates are generated from high resolution PNG files and by repeating it in axial direction 3D NIfTI templates are generated.

```
[ ]: # > refresh all the input data and intermediate output
Cntd = pars.get_params(cpth)
Cntd = ioaux.get_paths(Cntd, mMRpars, cpth, outdir=outname)

# SAMPLING TEMPLATES
#> get the templates
ast.create_sampl_res(Cntd)
ast.create_sampl(Cntd)
```


13.6 Generate sampling VOIs

The concentric sampling VOIs are generate by aligning all the templates to the upsampled PET

```
[6]: #> create the VOIs by resampling the templates
      vois = ioaux.sampling_masks(Cntd, use_stored=True)

      i> using sampling folder: /sdata/ACR_data_design/raw/output_s/PET/single-frame/sampling_
      ↪ masks
      /sdata/ACR_data_design/templates/ACR-smpl/acr-res-sampling-0-2mm.nii.gz
      /sdata/ACR_data_design/templates/ACR-smpl/acr-all-sampling-0-2mm.nii.gz
      /sdata/ACR_data_design/templates/ACR-smpl/acr-insrt3-sampling-0-2mm.nii.gz
      /sdata/ACR_data_design/templates/ACR-smpl/acr-ibckg-sampling-0-2mm.nii.gz
```

13.7 Visualisation of VOI sampling

The left column shows the summed resolution rods and insert parts of the ACR phantom. The right column shows the sampling concentric rings for the largest rods and the largest hot insert.

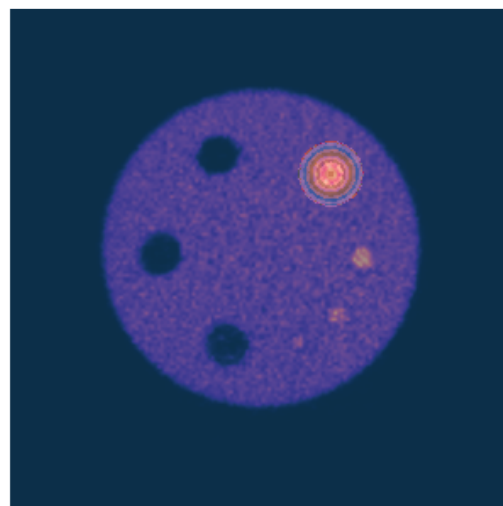
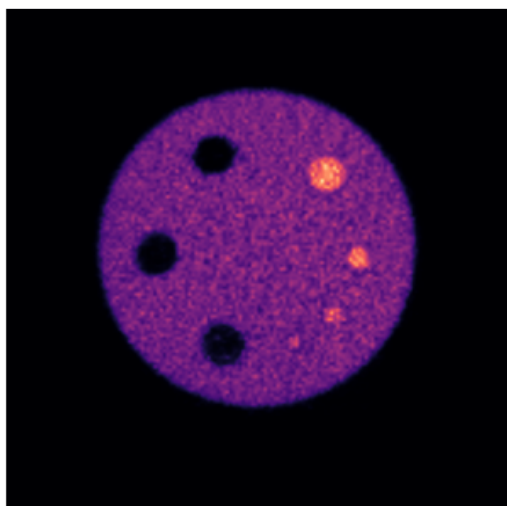
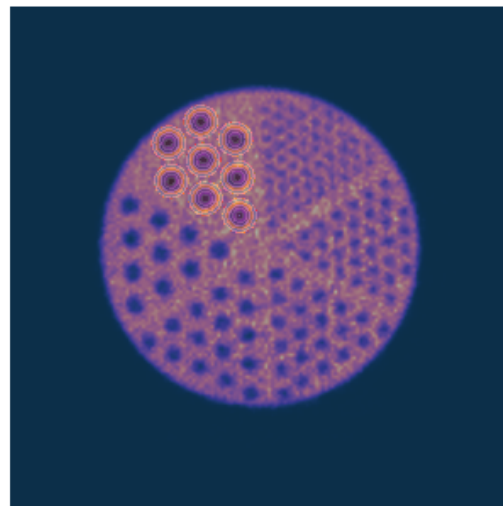
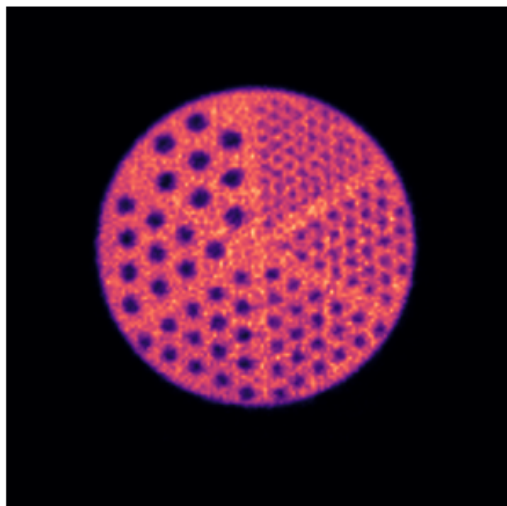
```
[7]: fig, axs = plt.subplots(2,2, figsize=(14, 12))

      axs[0,0].imshow(np.sum(qntim16[90:240],axis=0), cmap='magma')
      axs[0,0].set_axis_off()

      axs[0,1].imshow(np.sum(qntim16[90:240],axis=0), cmap='magma')
      axs[0,1].imshow(vois['fst_res'][150,...]*(vois['fst_res'][150,...]>=60), vmin=50, cmap=
      ↪ 'tab20', alpha=0.4)
      axs[0,1].set_axis_off()

      axs[1,0].imshow(np.sum(qntim16[370:440],axis=0), cmap='magma')
      axs[1,0].set_axis_off()

      axs[1,1].imshow(np.sum(qntim16[370:440],axis=0), cmap='magma')
      axs[1,1].imshow(vois['fst_insrt'][400,...]*(vois['fst_insrt'][400,...]<20), vmin=0, cmap=
      ↪ 'tab20', alpha=0.4)
      axs[1,1].set_axis_off()
```



RAW BRAIN PET DATA

Downloadable raw PET data of a single brain amyloid scan (^{18}F -florbetapir), with all the necessary input components for independent image reconstruction, can be obtained from the research data repository **Zenodo** (click the DOI link to download the data) [8]:

The downloaded zip file contains a full dynamic list-mode PET data acquired on a **Siemens Biograph mMR** for 60 minutes, using amyloid tracer ^{18}F -florbetapir, provided by **Avid Radiopharmaceuticals, Inc.**, a wholly owned subsidiary of **Lilly**. The file also includes normalisation files and the μ -map based on MR Ultrashort TE (UTE) sequence [9, 10], all three parts needed for an independent image reconstruction using **NiftyPET**.

14.1 Citing the data

When using this data set for research or publications, please cite the following two publications: [2, 8]:

- Markiewicz, P. J., Cash, D., & Schott, J. M. (2018, November 5). Single amyloid PET scan on the Siemens Biograph mMR. London: Zenodo. <https://doi.org/10.5281/ZENODO.1472951>
- Lane, C. A., Parker, T. D., Cash, D. M., Macpherson, K., Donnachie, E., Murray-Smith, H., ... Schott, J. M. (2017). Study protocol: Insight 46 - a neuroscience sub-study of the MRC National Survey of Health and Development. *BMC Neurology*, 17(1), 75. <https://doi.org/10.1186/s12883-017-0846-x>

If the data is reconstructed and/or analysed using *NiftyPET*, additionally please cite []:

- Markiewicz, P. J., Ehrhardt, M. J., Erlandsson, K., Noonan, P. J., Barnes, A., Schott, J. M., ... Ourselin, S. (2018). NiftyPET: a High-throughput Software Platform for High Quantitative Accuracy and Precision PET Imaging and Analysis. *Neuroinformatics*, 16(1), 95–115. <https://doi.org/10.1007/s12021-017-9352-y>

RAW ACR PHANTOM PET DATA

The PET data of two 30 minute acquisitions of the American College of Radiology (ACR) Jaszczak Deluxe Flangeless ECT phantom (with a modified faceplate for PET) were acquired at the [King's College London & Guy's and St Thomas' PET Centre](#). The raw list PET data, including synthetic and MR-based (UTE) -maps, as well as templates for generating sampling volumes of interest, phantom structural and PET NAC registration templates are freely available at **Zenodo** repository (click the DOI link to download the data) [11]:

15.1 Citing the data

When using this data set for research or publications, please cite the following: [11]:

- Markiewicz, P. J.; Krokos, G; MacKewn J; Hammers A (2021, Dec 6). ACR PET phantom raw data and templates for advanced analysis. London: Zenodo. <https://doi.org/10.5281/zenodo.5760092>



ACKNOWLEDGEMENTS

This project is being developed at University College London (UCL) at the department of **Medical Physics and Biomedical Engineering** and the Centre for Medical Image Computing (CMIC). Initially, it was supported and funded by the Engineering and Physical Sciences Research Council (EPSRC) of the United Kingdom (UK). Currently, the project is being further developed under the following funding streams:

1. The **Innovative Medicines Initiative 2** Joint Undertaking under grant agreement No 115952. This Joint Undertaking receives support from the European Union's **Horizon 2020** research and innovation programme and **EFPIA**.
2. The **Dementias Platform UK MR-PET Partnership**, supported by the Medical Research Council (MRC) in the UK.

I gratefully acknowledge the support of **NVIDIA Corporation** with the donation of the Tesla K20 and Titan X Pascal GPUs used for this research and work.



CITING NIFTYPET

When using *NiftyPET*, please cite this article:

Markiewicz, P. J., Ehrhardt, M. J., Erlandsson, K., Noonan, P. J., Barnes, A., Schott, J. M., ... Ourselin, S. (2018). NiftyPET: a High-throughput Software Platform for High Quantitative Accuracy and Precision PET Imaging and Analysis. *Neuroinformatics*, 16(1), 95–115. <https://doi.org/10.1007/s12021-017-9352-y>

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