HOF Processing

Image analysis guide

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CNDA and HOF

CNDA: online research imaging database

- stores anonymized DICOM images
- images are organized into projects, experiments and scans

HOF: Preprocessing environment for tumor studies

-- a set of scripts

-- generates DWI and DSC based parametric maps

-- co-registers and resamples raw and derived images

-- can work with CNDA to download raw data and upload processed results.

Terminology

- DICOM study is CNDA experiment
- DICOM series is CNDA and HOF scan
- DICOM series number is CNDA scan ID
- DICOM series description is (roughly) CNDA scan type
- CNDA Experiment label – used by HOF to identify the study
- HOF scan type: a generic class of sequences, e.g. MPRAGE is used for isotropic voxel high-resolution T1, DWI for all diffusion sequences, DSC for all DSC-based sequences.
- Each HOF scan type has category and quality.

What HOF does

- Downloads an MRI study from CNDA
- Organizes all downloaded DICOM series into a study directory
- Resolves HOF type for each downloaded image and converts from DICOM to 4dfp (explained later)
- Picks the “best” T1 high-resolution image and “best” atlas image to be used as registration targets

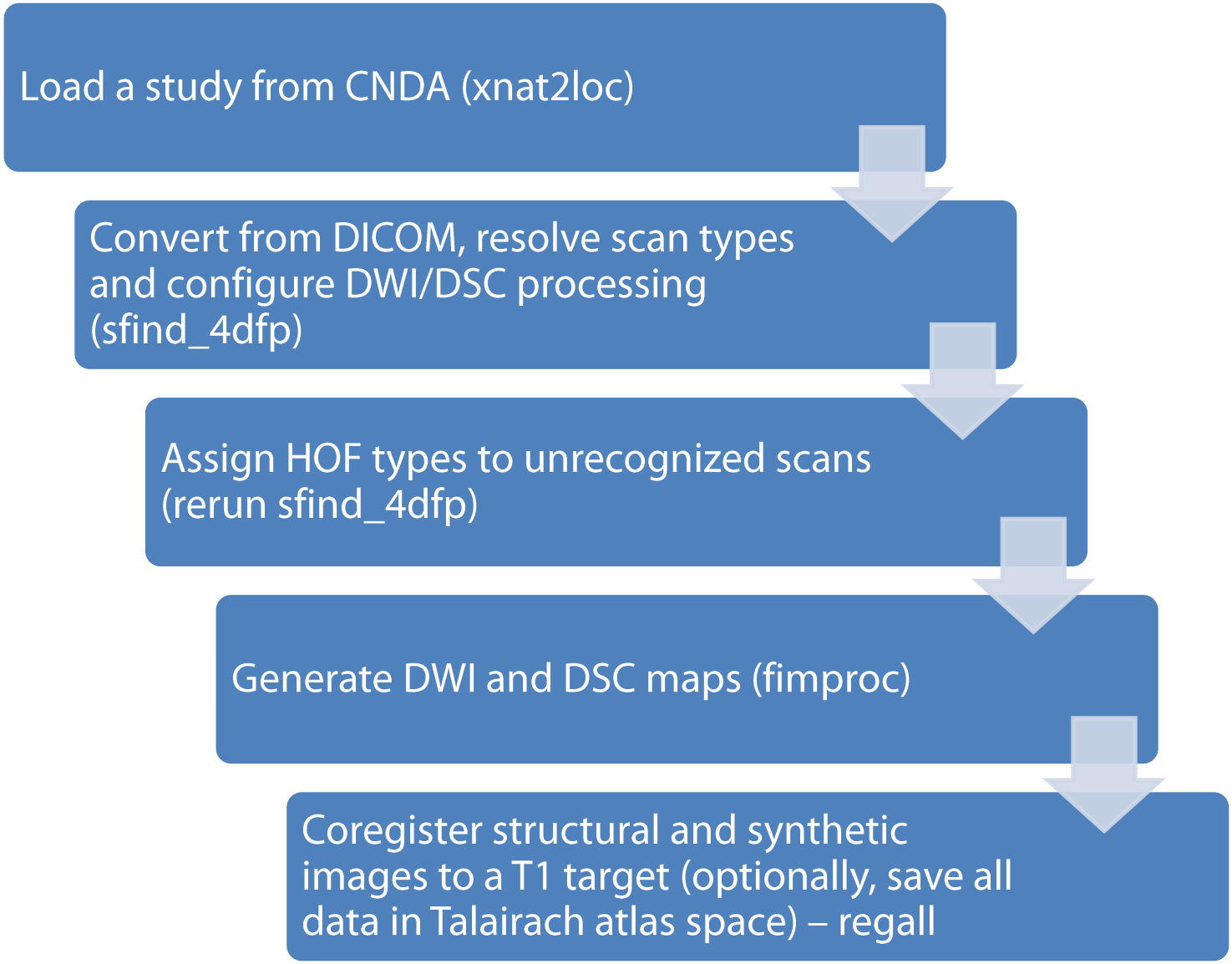
What HOF does (cont.)

- Automatically configures DWI and DSC processing parameters
- Generates FA, MD, CBF, CBV, MTT parametric (derived) maps from DWI and DSC sequences.
- Co-registers (linearly) recognized raw and derived images to the “best” high resolution T1 image. Optionally produces registration in Talairach space.
- Generates a pdf QC report to assess the quality of co-registration

Image Data Formats

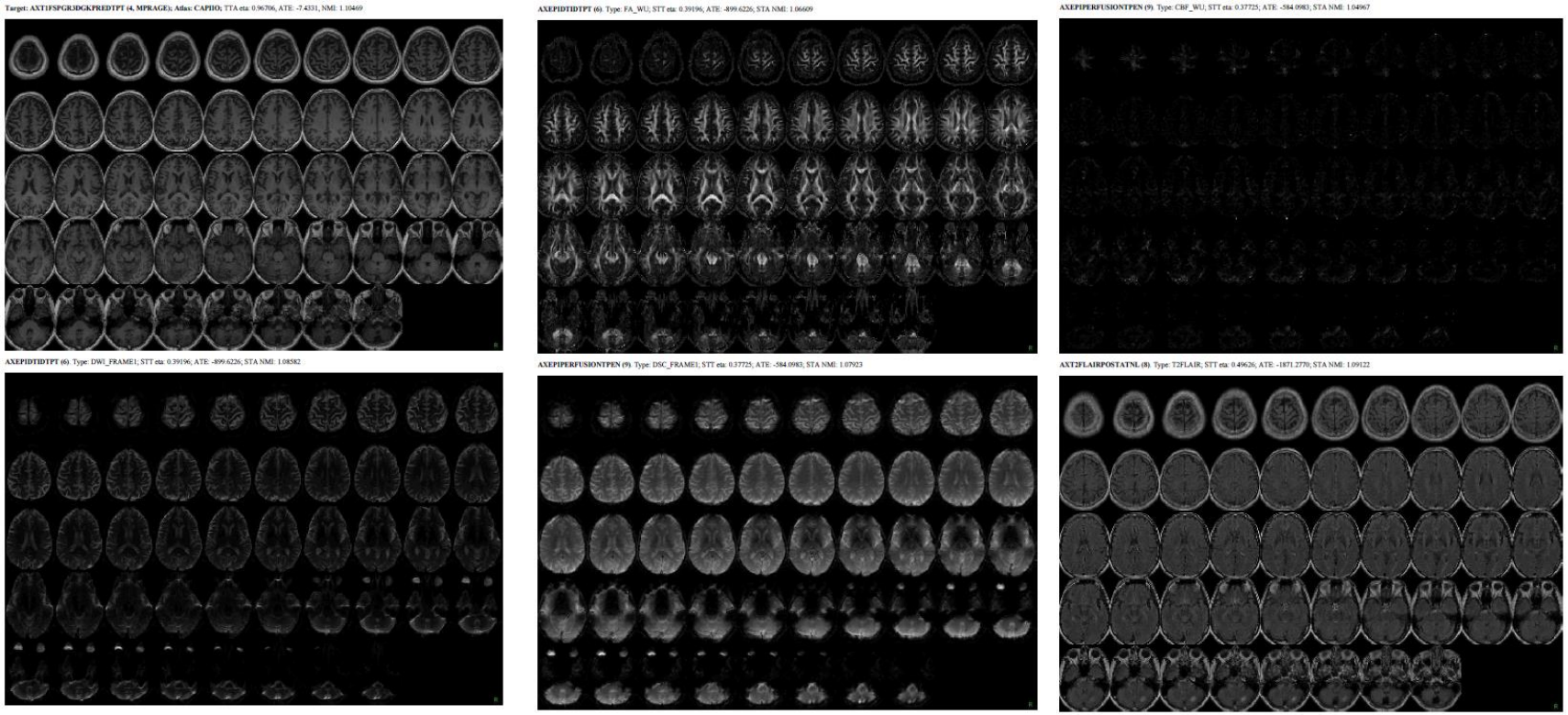
- Raw imaging studies are stored in DICOM (Anonymized)
- Image processing is done in 4dfp format.
- 4dfp format: WUSTL-homegrown.
  - Essentially, Analyze (.hdr+.img pair) with additional tracking processing history (.rec) and human readable header file (.ifh)
  - y-flipped compared to Analyze
  - All WashU processing happens in 4dfp format
- DICOM<->4dfp, 4dfp<->NIFTI and 4dfp<->Analyze tools exist.

HOF preprocessing overview



Quality review

- condr_qc: generate a PDF report listing mosaic view of all coregistered scans



HOF Detailed steps

- Locate the study in CNDA

- Download from CNDA (xnat2loc)

```
cd /home/shared /NRG/CONDR_METS/<my_username>
xnat2loc MS002_SR_20121204_PreOp -sr https://cnda.wustl.edu -u mmilch -
pa ***** -pr CONDR_METS -subj MS002
```

- Resolve HOF scan ID's and convert images to 4dfp

```
sfind_4dfp . -g
```

NOTE: ' . ' has to be specified when running from the study directory

File naming conventions

- Image in its original orientation and resolution:

  <Experiment label>_<scan number>_<HOF ID>.4dfp.*

- Co-registered and resampled image:
  - <Raw1>_on_<Atlas>, Atlas is one of available WashU atlases (CAPIIO, TRIO_Y_NDC, stealth, …) in Talairach space (normally, 1x1x1mm voxels)
  - <Raw1>_on_<Raw2> where Raw2 is session target

Detecting scan types

- Known scan types (DICOM series description <-> HOF library) are resolved with sfind_4dfp.

- What if scan types are unknown?
  - specify explicitly, based on DICOM.studies.txt list.
  (for a complete list of recognized ID's, refer to scan_types.txt).

Adding scan types

- Find missing scans (compare with CNDA session page):

```
ls *.img
```

- List all available DICOM scans:

```
cat DICOM.studies.txt
```

- List all available HOF scan ID's:

```
slist li
```

- Create a file listing missing scans with HOF ID's:

```
nano scanlist.params
MPRAGE=(4 10 11)
T2FLAIR=8
COR_T2=3
Ctrl+X
```

Adding scan types. DWI and DSC processing

- Re-run sfind_4dfp to re-generate runtime parameters:

```
sfind_4dfp . -o -g -tl scanlist.params
```

- Generate derived maps for DWI and DSC.

```
fimproc .
```

Note ' . ' for current directory.

Execution time of fimproc can be up to 1 hour.

Spatial coregistration

- Target scan: T1 of high resolion
  - suggested automatically by the program for optimal results
  - can be overridden (not recommended)

- Run coregistration of raw and derived images in the study:

```
regall .
```

- Generate QC report for quick evaluation of quality:

```
condr_qc .
```

HOF directory structure

- <root dir> - all configuration files and 4dfp version of raw scans are stored here.
  - DICOM.studies.txt – list of all downloaded DICOM studies
  - <Study label>_diff.params – configuration file for DWI and DSC processing
  - sfind_4dfp.txt – HOF configuration file for all processing (generated by sfind_4dfp)
- DICOM/ - all original DICOM files in one dir;
- studyxx/ - DICOM files for each scan

HOF directory structure (cont'd)

- atlas/ - atlas registrations generated by DSC and DWI processing files
- atltest/ - atlas and target optimization processing files
- perf/ - DSC processing files
- perf/ - DSC processing files
- DWI – DWI processing files
- reg – image resampling and coregistering is performed here
- out – all coregistered images in atlas space
- QC – QC files, including QC pdf.

What HOF doesn't presently do

- Recognize ALL downloaded DICOM images.
- Always coregister highly distorted brains (e.g. with significant anatomy variability or highly distorted by tumor)
- Always coregister scans with high voxel anisotropy (e.g. 1x1x5mm), small FOV, extreme EPI distortions

Final notes

- sfind_4dfp, fimproc, regall, condr_qc can be rerun at each step when some scans are added or other settings are modified
- ROI evaluation and generation tools exist for HOF