ASL/CBF Pipeline

Structure & Objectives

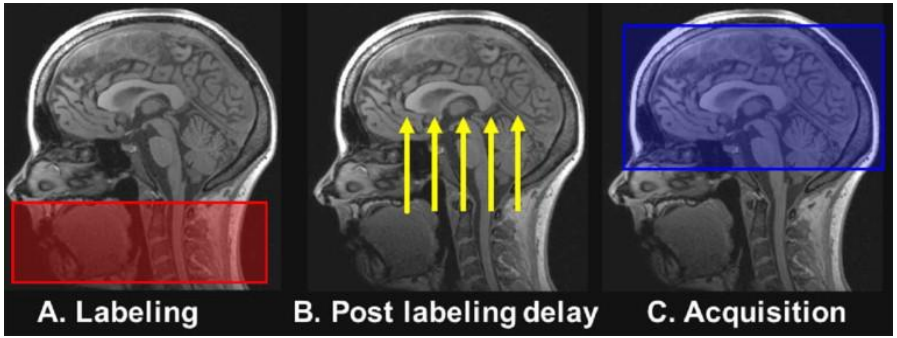
Lauren Beard

Outline

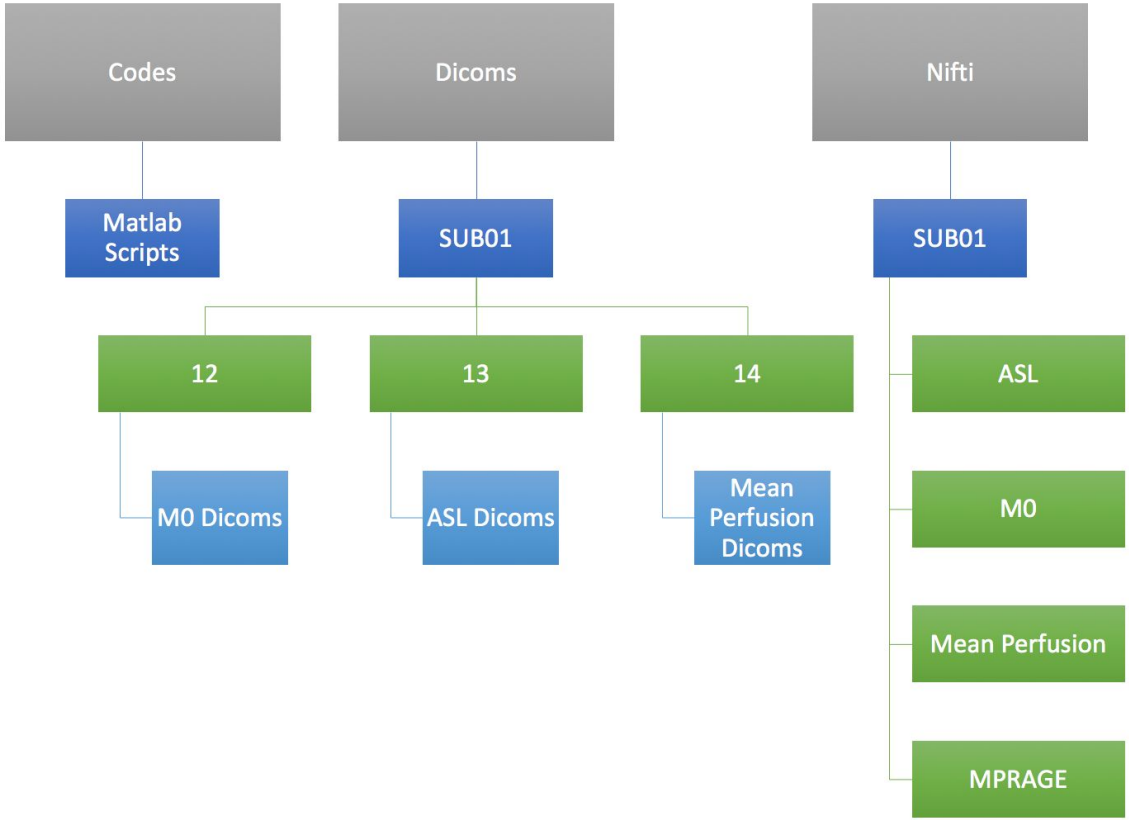
- Overview of ASL MRI
- Directory structure
- Overview of pipeline procedure
- Breakdown of pipeline processes
- Implementation
- Objectives

Arterial Spin Labeling (ASL)

- Definition: MRI technique used for **quantifying CBF** using magnetically labeled arterial spins as an endogenous tracer
- Method:
  - Two brain images are acquired: one with a magnetic inversion at the neck to label the inflowing arterial blood, and one without the inversion
  - The two images are subtracted to cancel out the static brain tissue signal and reveal a perfusion-weighted image
- Multiple types:
  - PASL: pulsed ASL
  - CASL: continuous ASL
  - **pCASL: pseudo-CASL**



Directory Structure

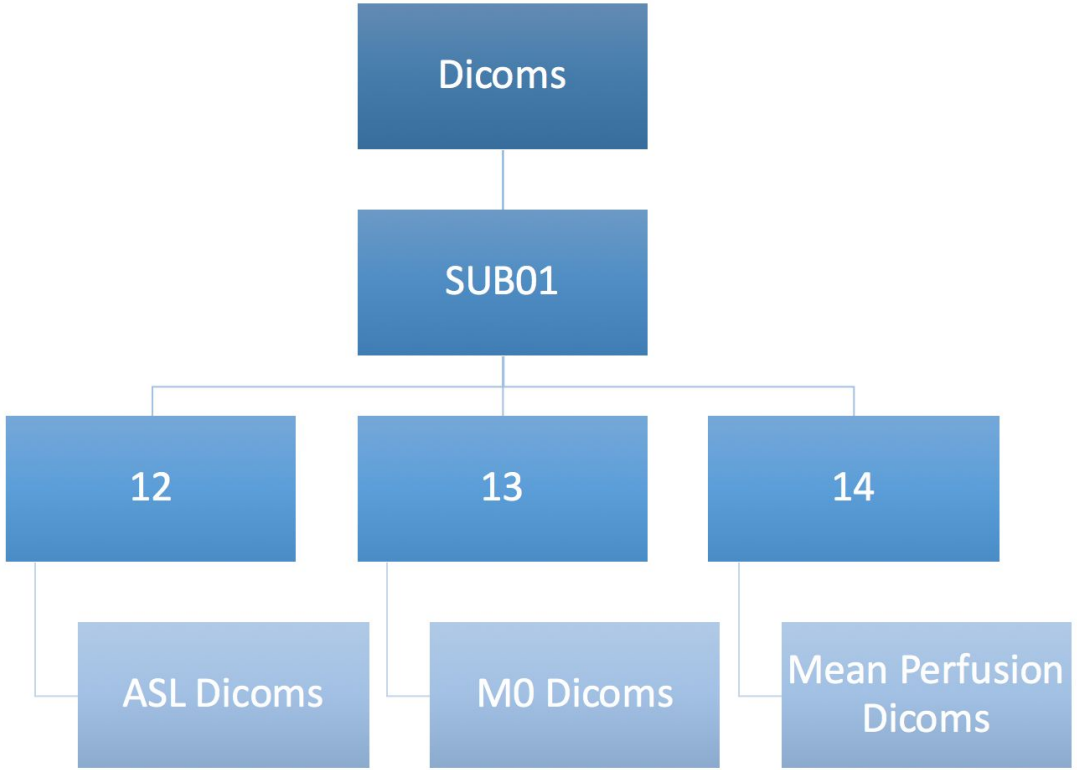


Pipeline Steps

1. Convert dicom to nifti
2. Set parameters
3. Organize data
4. Segment brain
5. Create Mask
6. Realign
7. Coregister ASL to MPRAGE
8. Compute CBF

Dicom to Nifti

- Creates flexible path variables
- Creates nifti files from dicoms: ASL, M0, Perfusion
  - Read header information from dicom files



Set parameters

- Stores standard parameter values in a matrix
- Set paths, prefixes, and number of subjects
- Values:

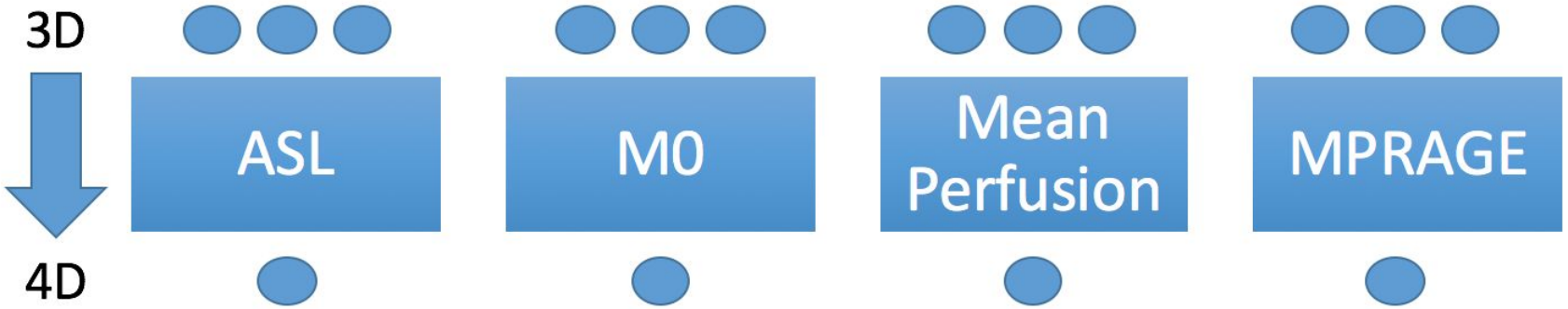
FWHM: 5 mm ● Smoothing, typically 4-8 in ASL lit.	Alpha: 0.72 ● Labeling efficiency, corrects for background suppression pulses
Lambda: 0.9 mL/g ● Blood to brain partition coefficient for gray matter	M0 scale: 10 ● M0: magnetization of arterial blood
$T_{1,blood}$: 1.65 seconds ● Longitudinal relaxation time of arterial blood	Post labeling delay (PLD): 1.5 ms

- Used to compute CBF Factor:

$$CBF = \frac{6000 \cdot \lambda \cdot (SI_{control} - SI_{label}) \cdot e^{\frac{PLD}{T_{1,blood}}}}{2 \cdot \alpha \cdot T_{1,blood} \cdot SI_{PD} \cdot (1 - e^{-\frac{\tau}{T_{1,blood}}})} [ml/100g/min]$$

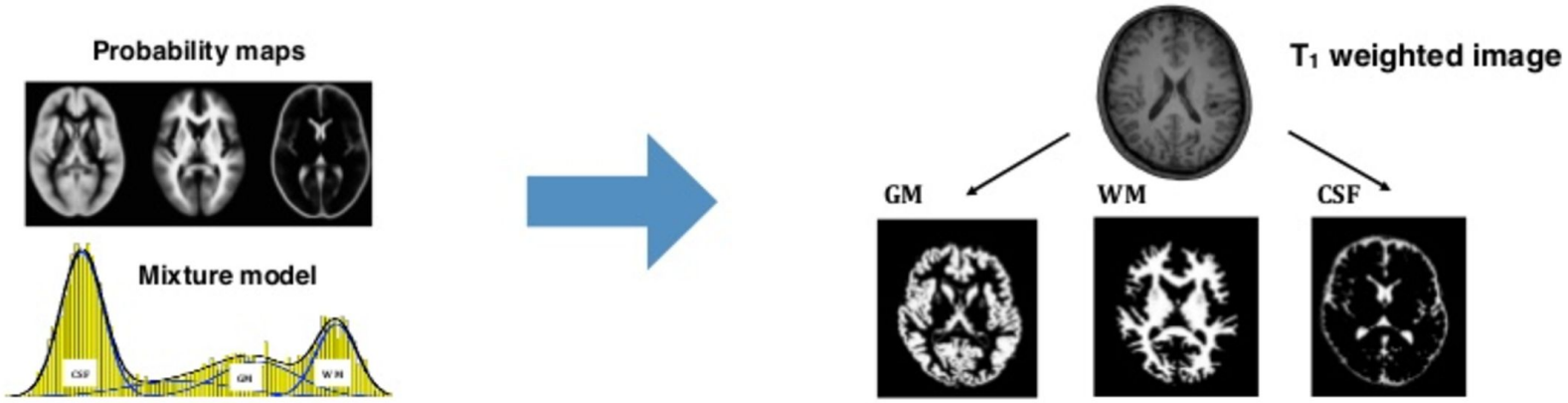
Organize data

- Load in all subject nifti files
- Concatenate 3D ASL, M0 and input T1 images into single 4D volumes
- Creates zip file of raw nifti files



Segment

- Segment and normalize the T1 mprage images
  - Based on the six SPM TPM (tissue probability map) volumes in the 4D *TPM.nii* NIfTI file
- Submit spm segmenting jobs to the cluster
- Also creates a segmented .mat file for the mprage



Create Mask

- Checks for pre-existing map in mprage directory
- Smooths data (4 mm)
- Creates M0 mask
- Fills 3D holes in the mask
  - Throw out voxels for which data is not available in all subjects and for those voxels that are below a certain threshold
    - Threshold = 0.1* (not stringent)
  - Fill in order to allow for voxel analysis across subjects

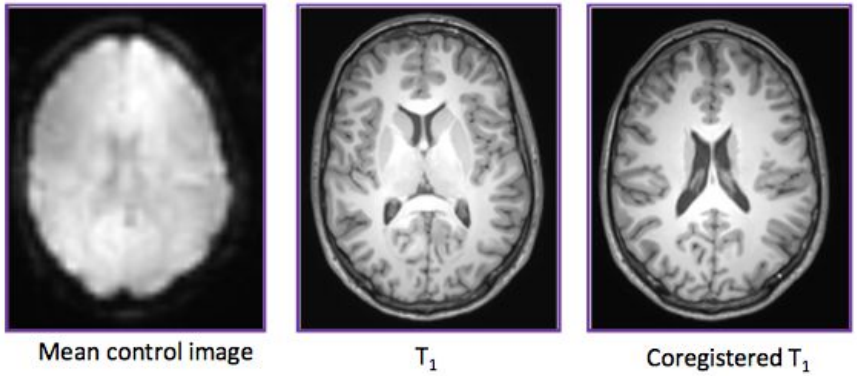
Realignment

- Remove the artificial motion component caused by systematic label/control signal modulations
- Realigns the ASL images to the reference volume
- Coregistration is to the first image, and resampling of images is into the space of the first image
    - Output: realigned images, .mat file for 4D images, set of realignment parameters
- Sets realignment defaults: must pass to create resliced images

Quality: 1 ● Highest, slower realignment	FWHM: 5 ● Applied before estimating realignment parameters
Separation: 4 mm ● Distance between two points sampled in reference space	Interpolation: 2 ● Highest, B-spline degree

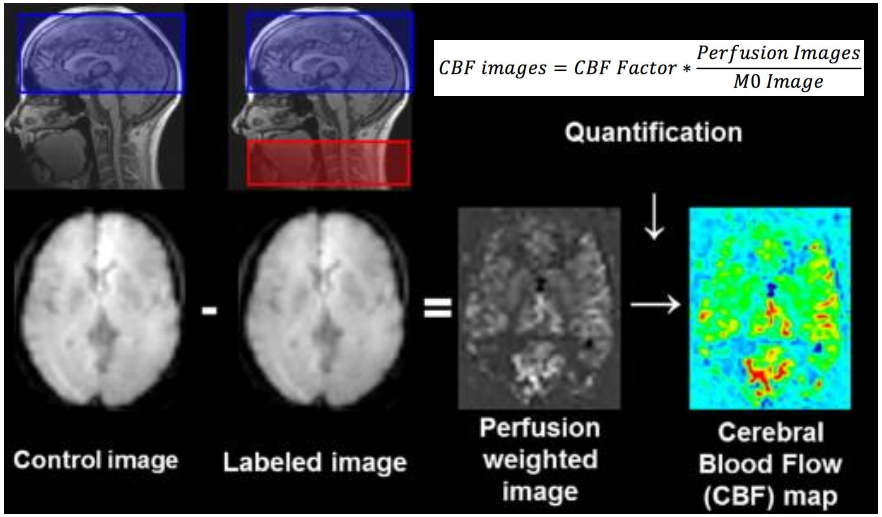
Coregistration

- T1 images and ASL: very different intensities
- Coregister the realigned ASL image to the subject's T1 image
  - Target image: T1
  - Source image: mean ASL image

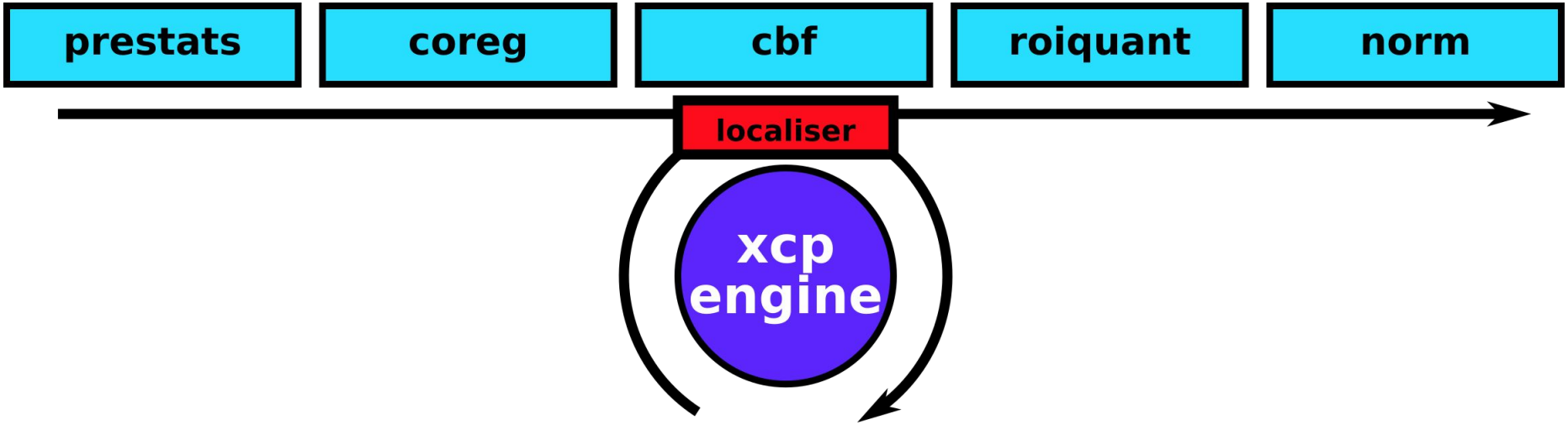


CBF Computation

- Smooths the M0 image (5 mm)
- Creates perfusion images and mean perfusion image
  - Control image - tagged image
- Compute CBF factor and CBF images



Implementation



Objectives

- Primary goal: compute CBF values
- Additional goals:
  - Restructure the pipeline to allow for greater flexibility
  - Re-invent SPM scripts
  - Adapt our data for CBF computation