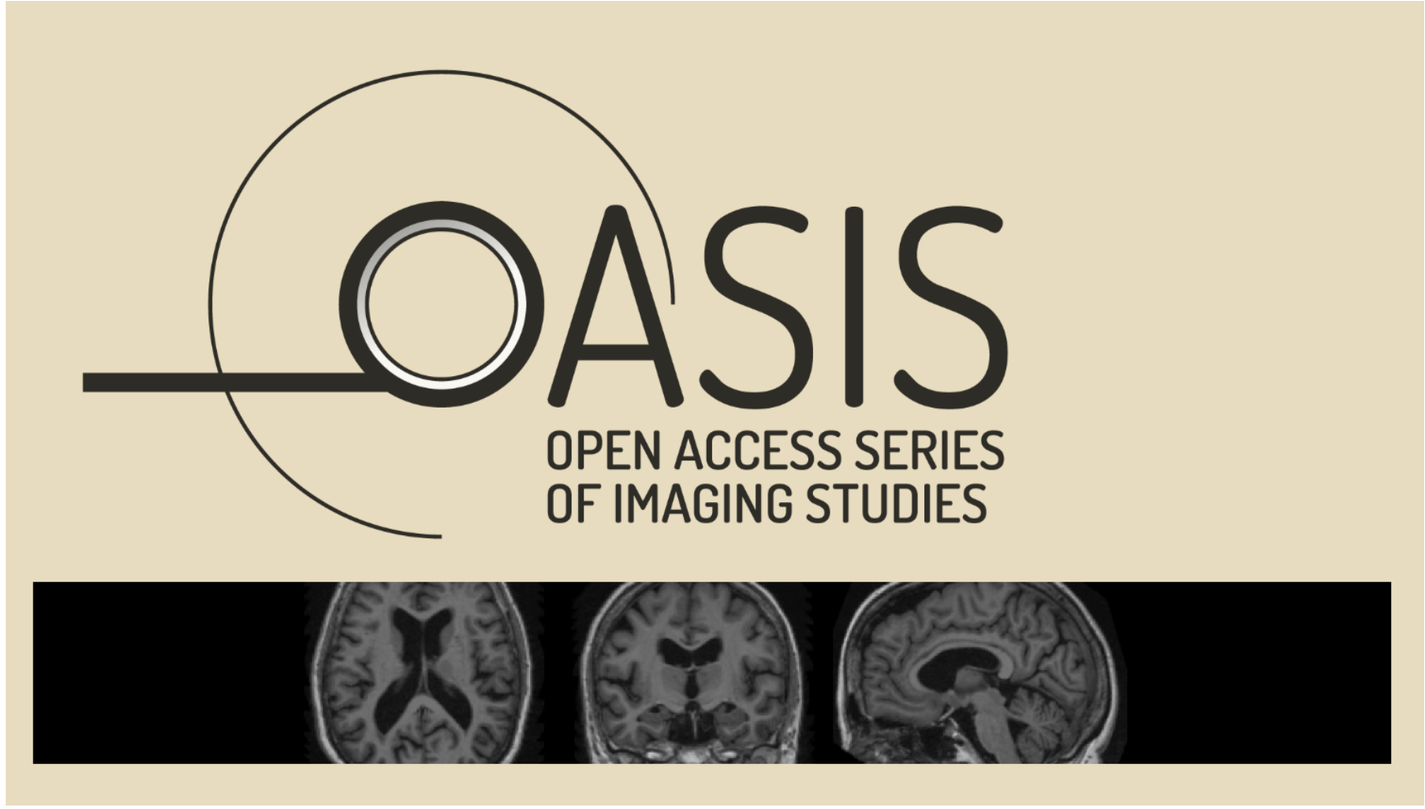
BIOMEDICAL IMAGE ANALYSIS IN PYTHON

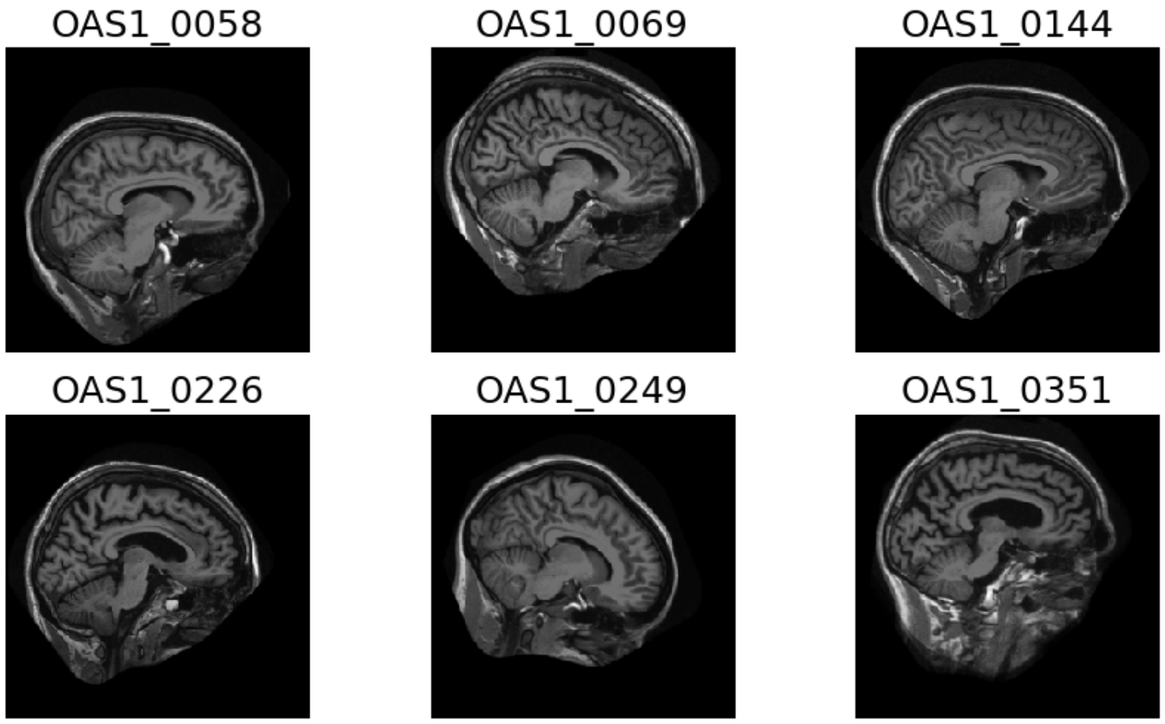
Spatial Transformation

Stephen Bailey
Instructor

OASIS Database

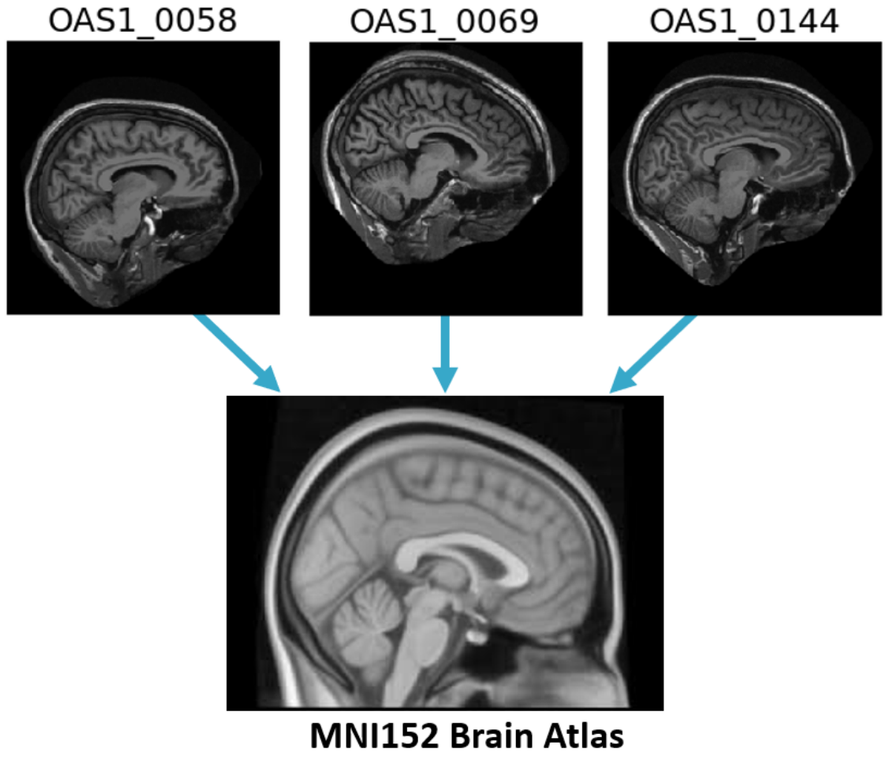


Significant variability

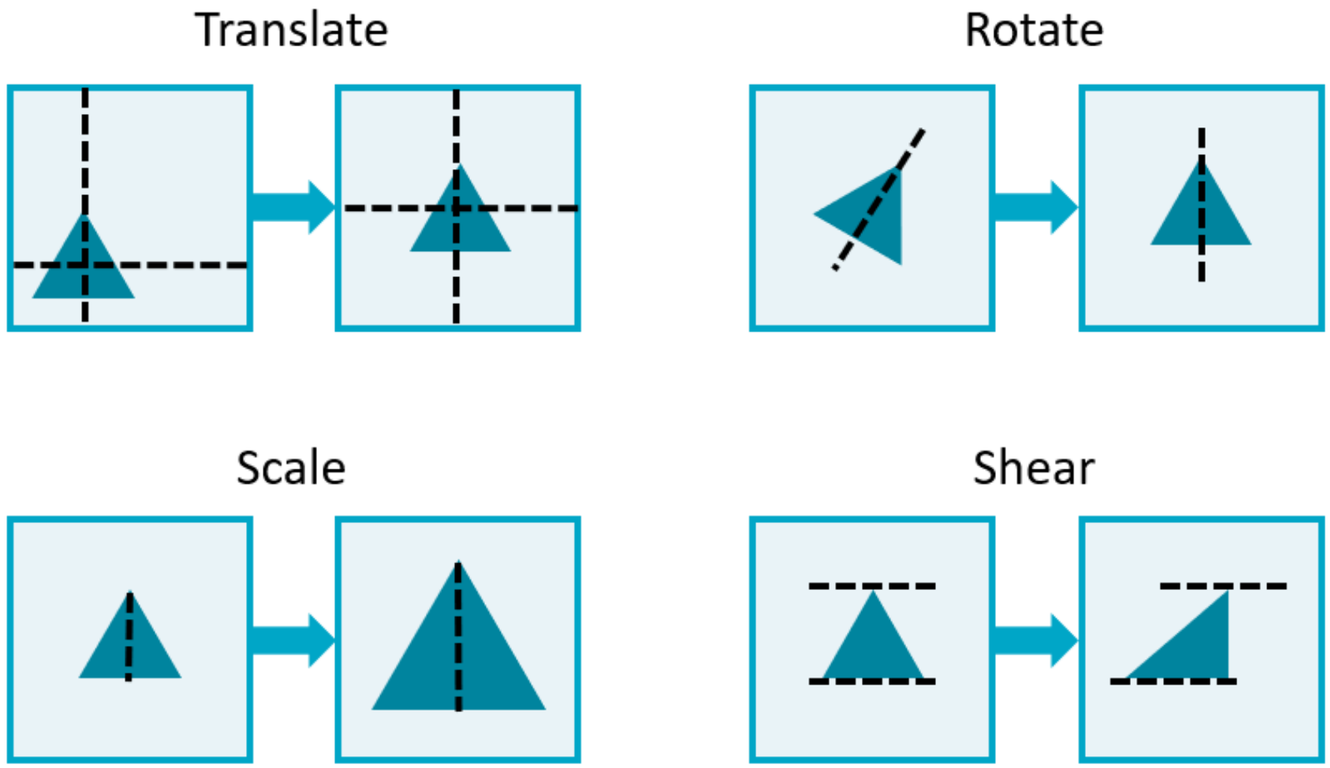


Registration

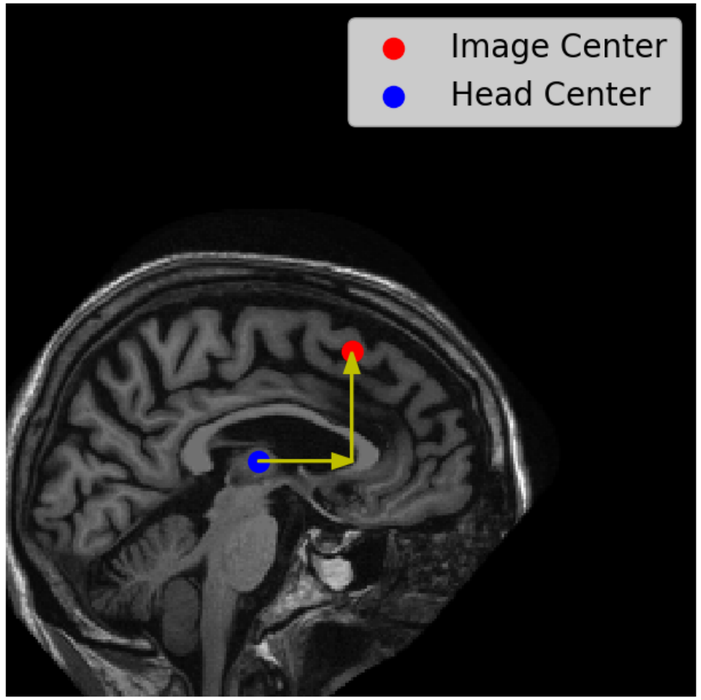
- Align images to template
- Minimize spatial variability
- Templates:
  - may represent multiple subjects
  - may be an "average" image
- Entails many spatial transformations



Affine transformations preserve points, lines, and planes



Translation




```
import imageio
import scipy.ndimage as ndi

im=imageio.imread('OAS1036-2d.dcm')
im.shape
    (256, 256)

com = ndi.center_of_mass(im)

d0 = 128 - com[0]
d1 = 128 - com[1]

xfm = ndi.shift(im, shift=[d0, d1])
```

Rotation

```
ndi.rotate(im,
           angle=25,
           axes=(0,1))
```

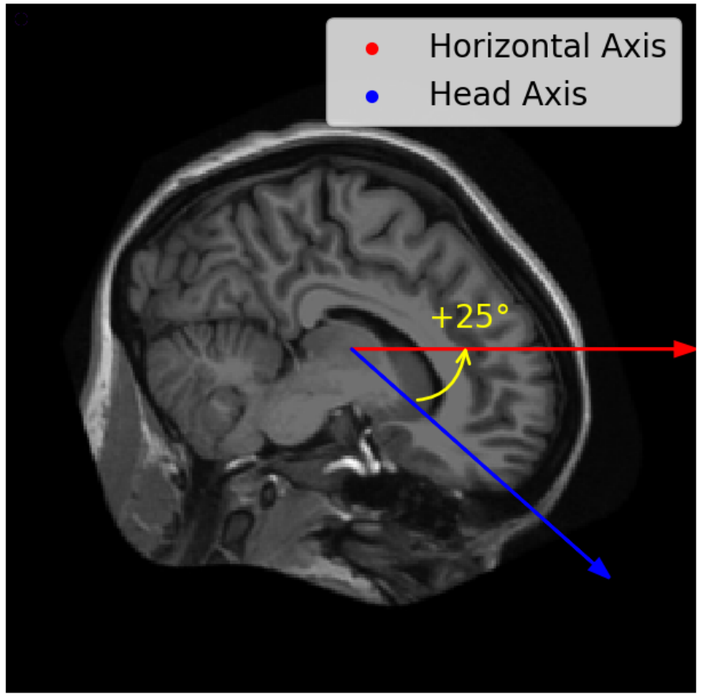
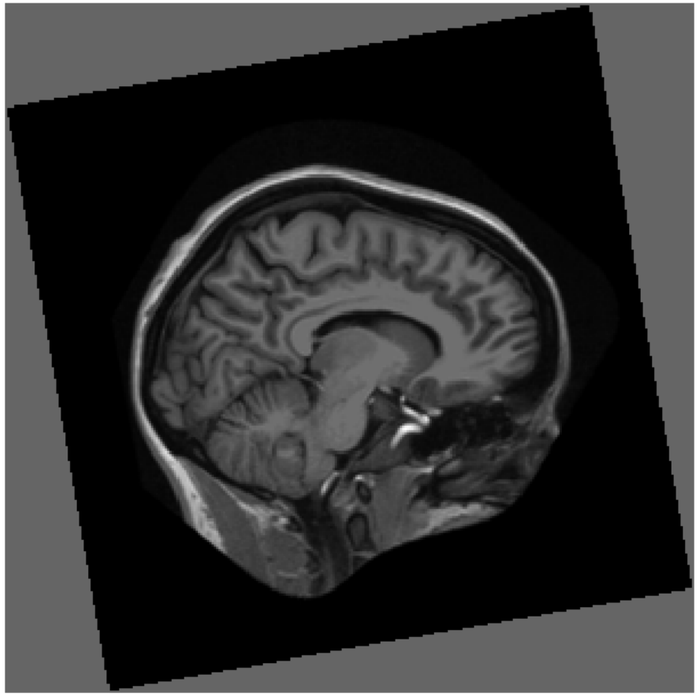
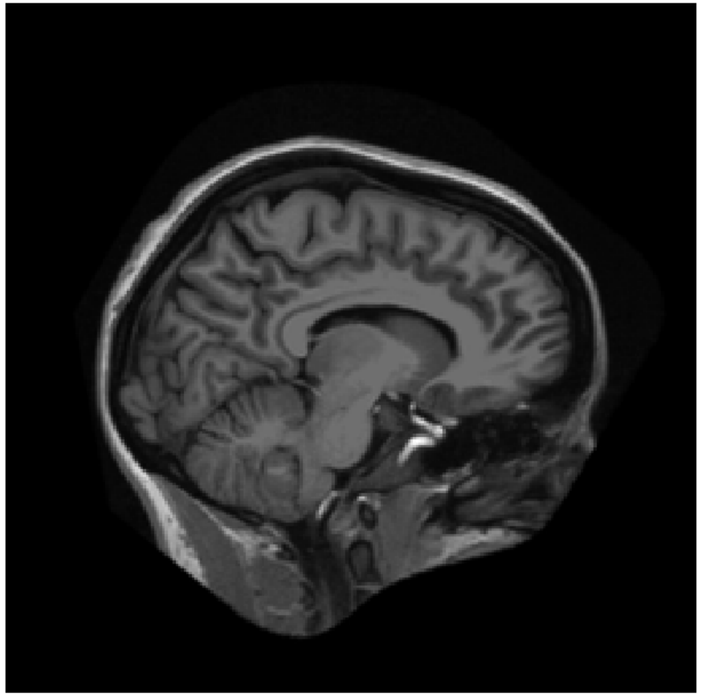


Image rotation

```
xfm = ndi.rotate(im, angle=25)

xfm.shape
    (297, 297)
```

```
xfm = ndi.rotate(im, angle=25,
                 reshape=False)
xfm.shape
    (256, 256)
```





Transformation matrix

Transformation matrix: applied to one image for registration.

Elements of the matrix encode "instructions" for different affine transformations.

Translation

$$\begin{bmatrix} 1 & 0 & T_x \\ 0 & 1 & T_y \\ 0 & 0 & 1 \end{bmatrix}$$

Rotation

$$\begin{bmatrix} \cos(\Theta) & -\sin(\Theta) & 0 \\ \sin(\Theta) & \cos(\Theta) & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

Scale

$$\begin{bmatrix} S_x & 0 & 0 \\ 0 & S_y & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

Shear

$$\begin{bmatrix} 1 & Sh_x & 0 \\ Sh_y & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

Applying a transformation matrix

```
# Identity matrix
mat = [[1, 0, 0],
       [0, 1, 0],
       [0, 0, 1]]

xfm = ndi.affine_transform(im, mat)
```

```
# Translate and rescale
mat = [[0.8, 0,   -20],
       [0,   0.8, -10],
       [0,   0,   1]]

xfm = ndi.affine_transform(im, mat)
```

Translate

$$\begin{bmatrix} 1 & 0 & T_x \\ 0 & 1 & T_y \\ 0 & 0 & 1 \end{bmatrix}$$

Rotate

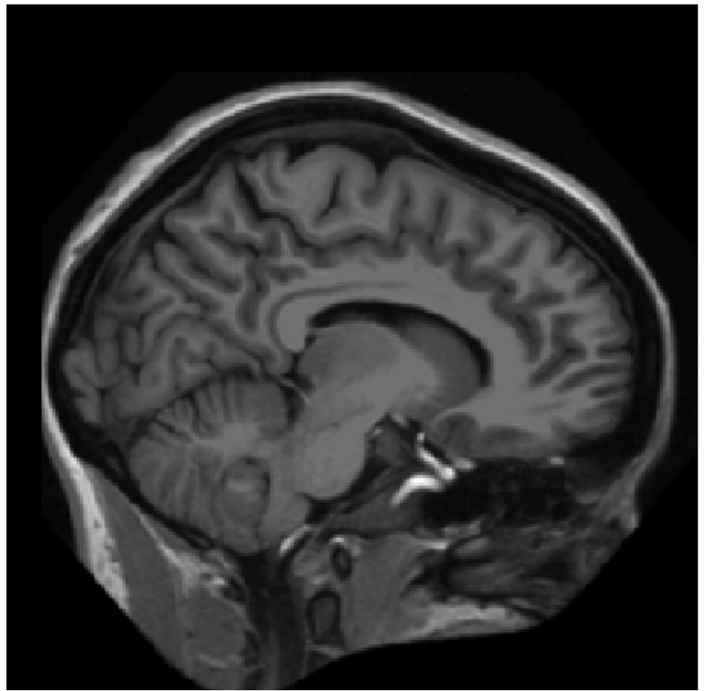
$$\begin{bmatrix} \cos(\Theta) & -\sin(\Theta) & 0 \\ \sin(\Theta) & \cos(\Theta) & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

Scale

$$\begin{bmatrix} S_x & 0 & 0 \\ 0 & S_y & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

Shear

$$\begin{bmatrix} 1 & Sh_x & 0 \\ Sh_y & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$



BIOMEDICAL IMAGE ANALYSIS IN PYTHON

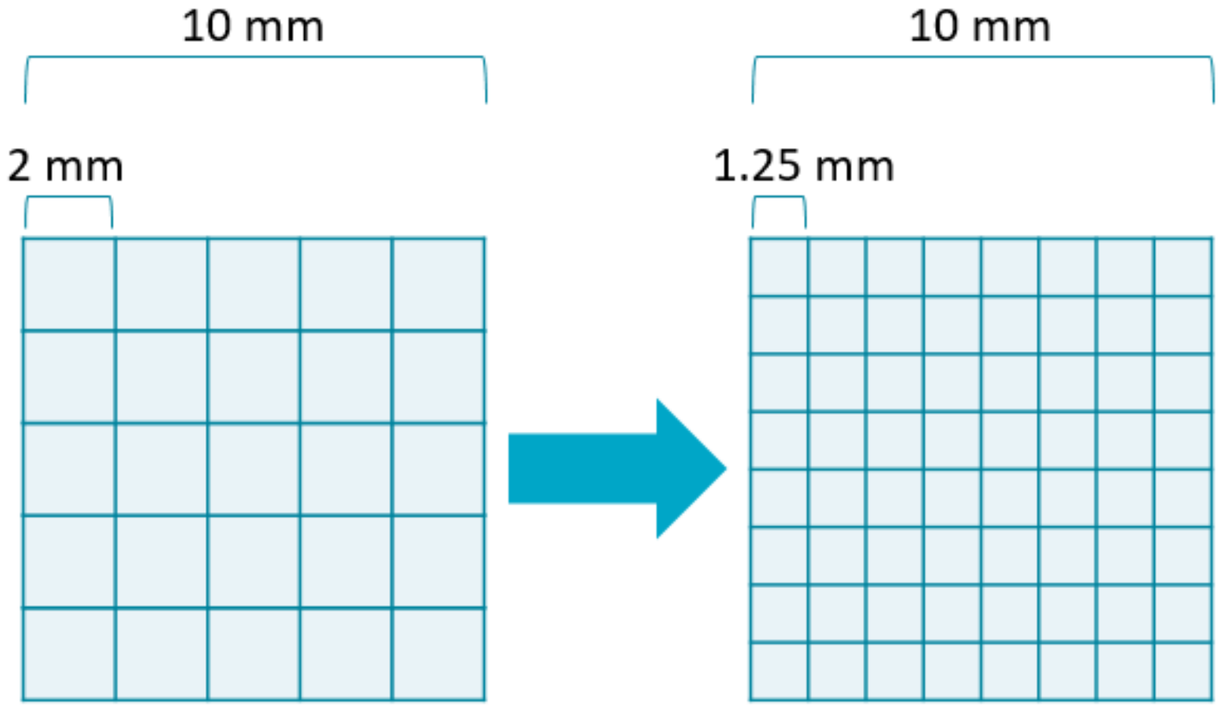
Let's practice!

BIOMEDICAL IMAGE ANALYSIS IN PYTHON

Resampling and Interpolation

Stephen Bailey
Instructor

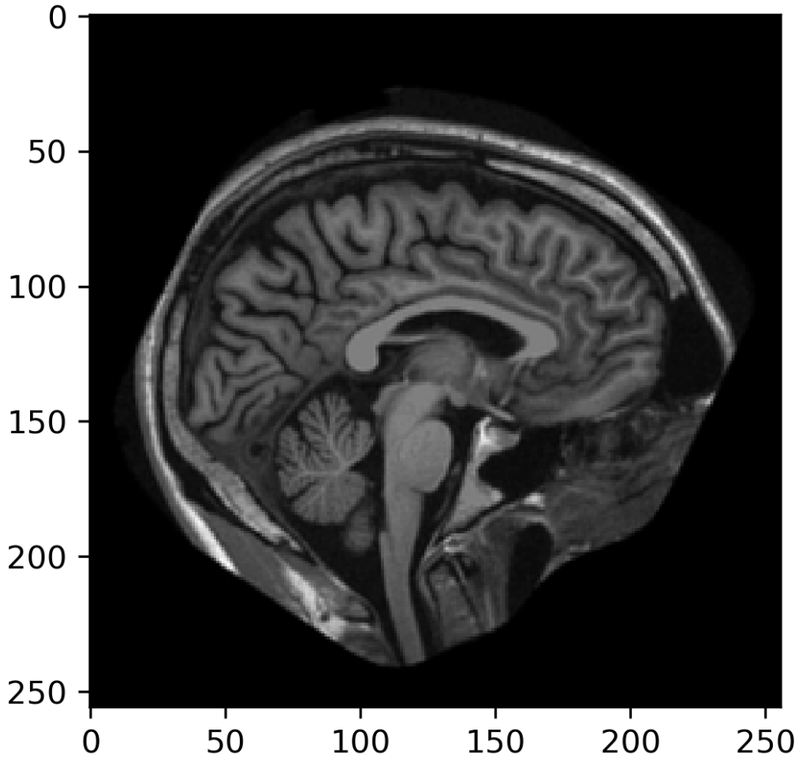
Resampling changes the array shape

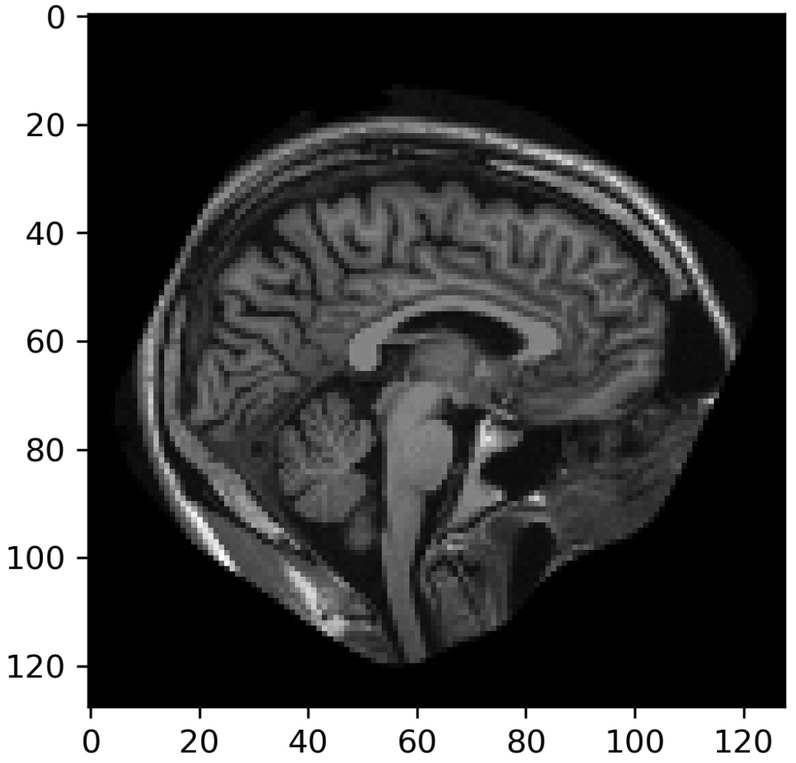


Downsampling

```
vol = imageio.volread('OAS1_0255')

vol.shape
    (256, 256, 256)
```

```
vol_dn = ndi.zoom(vol, zoom=0.5)

vol_dn.shape
    (128, 128, 128)
```

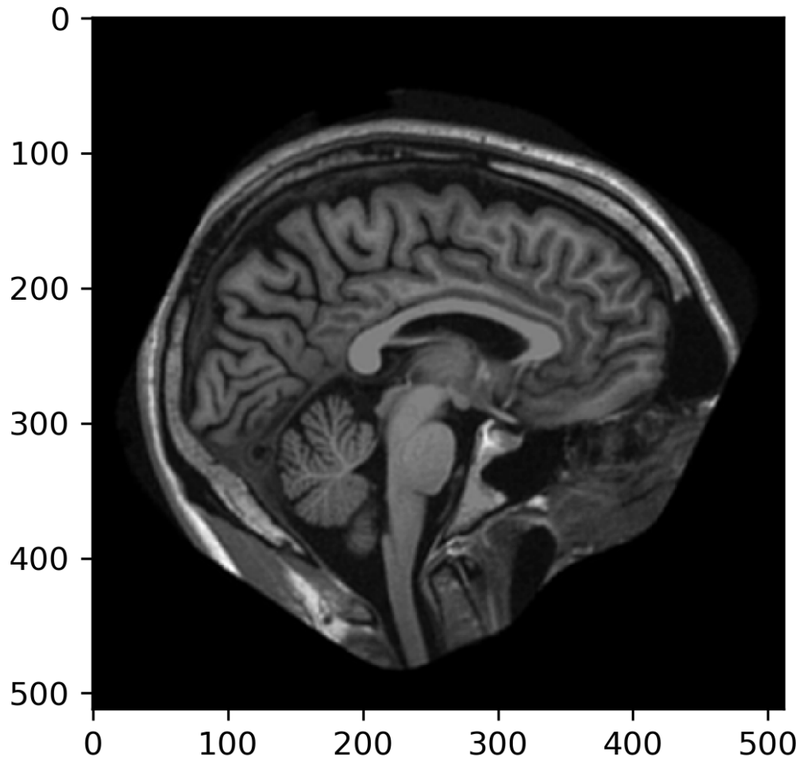




Upsampling

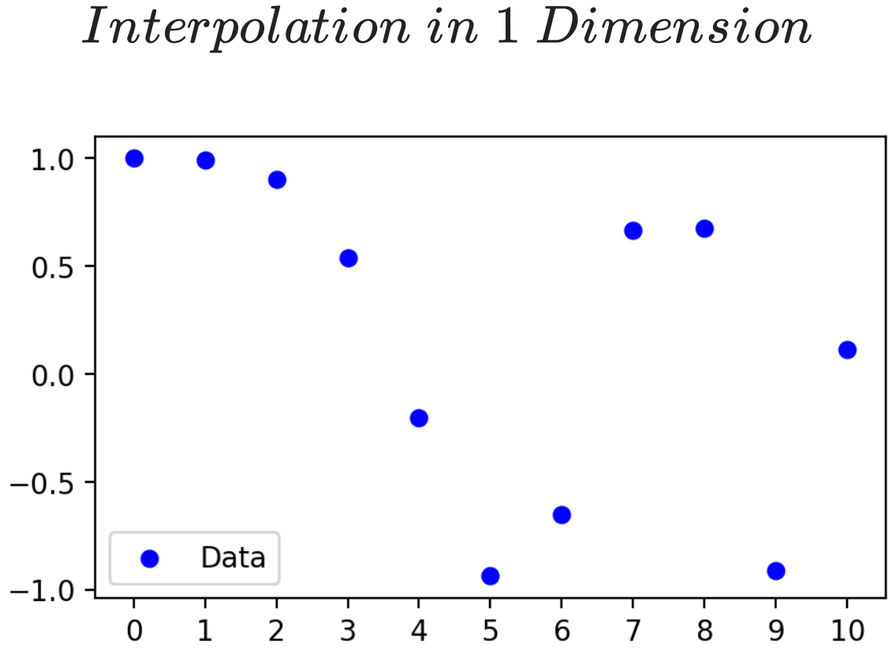
- Resampling to a larger grid
- Not the same as collecting higher-resolution data
- Useful for standardizing sampling rates that are unequal

```
vol_up = ndi.zoom(vol, zoom=2)

vol_up.shape
    (512, 512, 512)
```



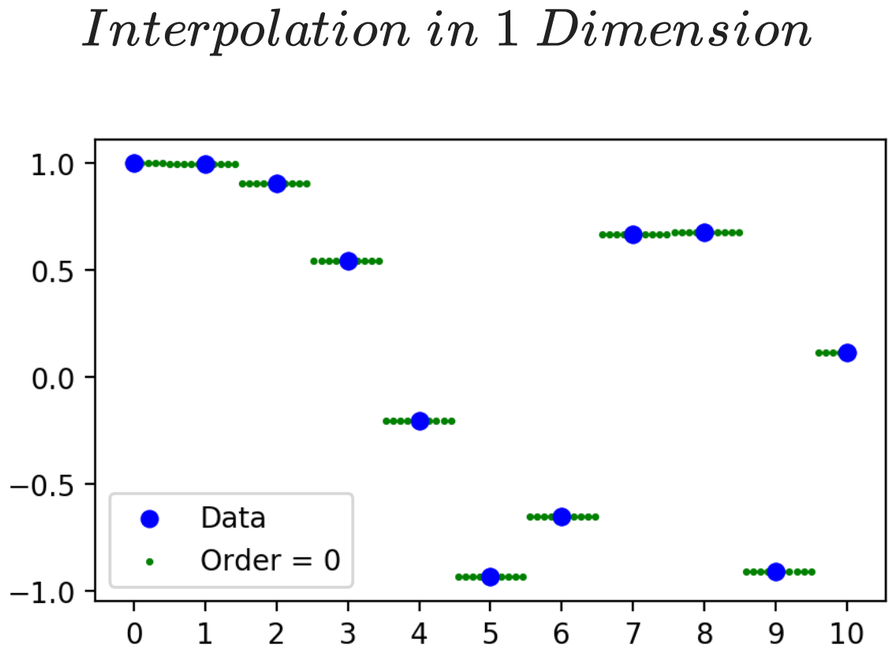
Interpolation

- "Stitches together" grid points to model the space between points.



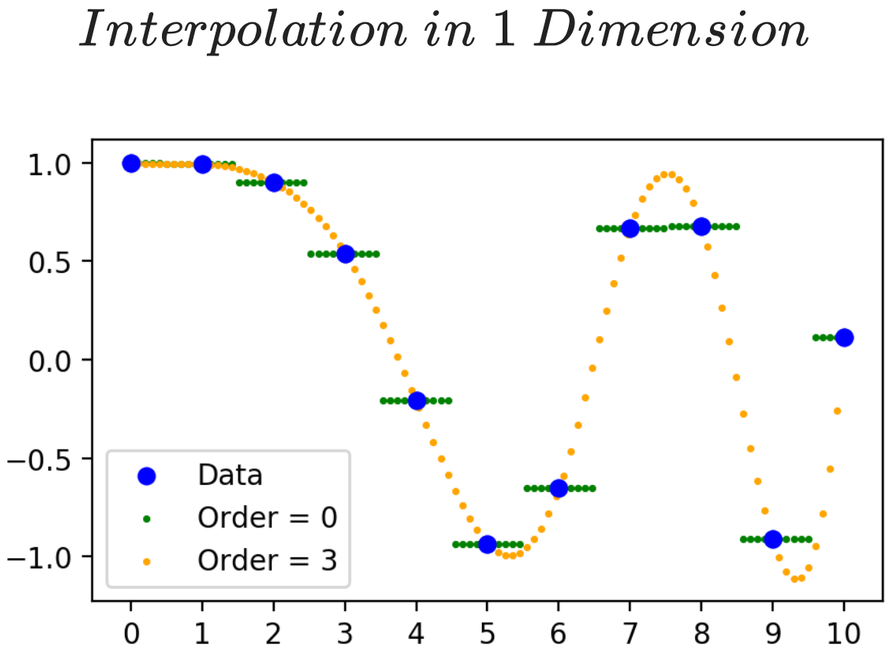
Interpolation

- "Stitches together" grid points to model the space between points.
- **Nearest-neighbor**: uses the closest measured value.



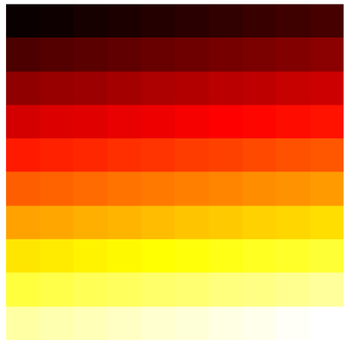
Interpolation

- "Stitches together" grid points to model the space between points.
- **Nearest-neighbor**: uses the closest measured value.
  - `order = 0`
- **B-spline interpolation**: models space between points with spline functions of a specified order.
  - `order` is between `1` and `5`

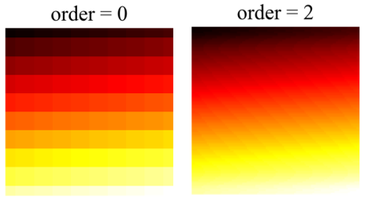


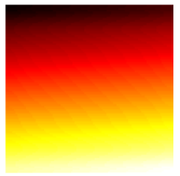
Interpolation in 2D

```
im=np.arange(100).reshape([10,10])
```



```
zm1=ndi.zoom(im, zoom=10, order=0)
zm2=ndi.zoom(im, zoom=10, order=2)
zm3=ndi.zoom(im, zoom=10, order=4)
```





BIOMEDICAL IMAGE ANALYSIS IN PYTHON

Let's practice!

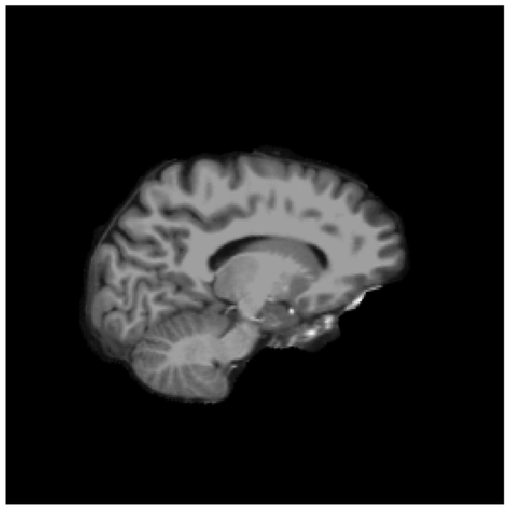
BIOMEDICAL IMAGE ANALYSIS IN PYTHON

Comparing Images

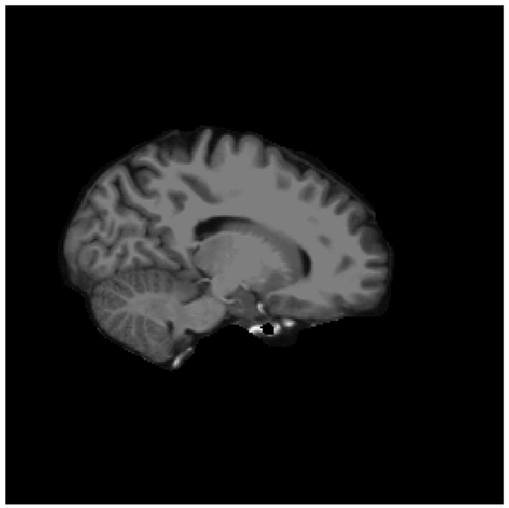
Stephen Bailey
Instructor

Comparing images

Visit 1



Visit 2



Mask Overlay

Summary metrics

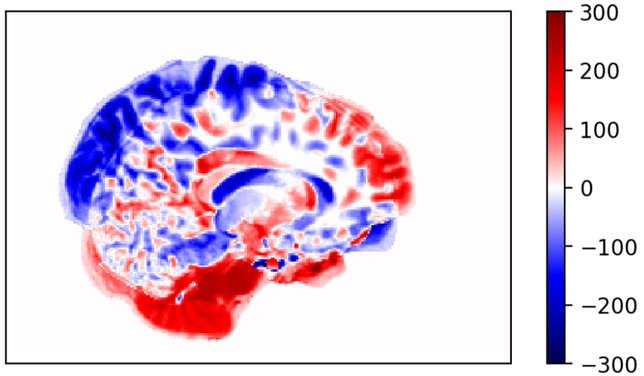
Goal: *define* a metric of similarity between two images.

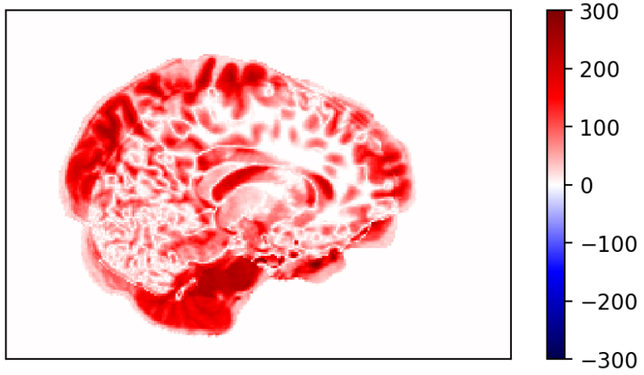
Cost functions produce metrics to be minimized.

Objective functions produce metrics to be maximized.

Mean absolute error

```
import imageio
import numpy as np

i1=imageio.imread('OAS1035-v1.dcm')
i2=imageio.imread('OAS1035-v2.dcm')

err = i1 - i2

plt.imshow(err)

abs_err = np.abs(err)

plt.imshow(abs_err)

mae = np.mean(abs_err)

mae
    29.8570
```



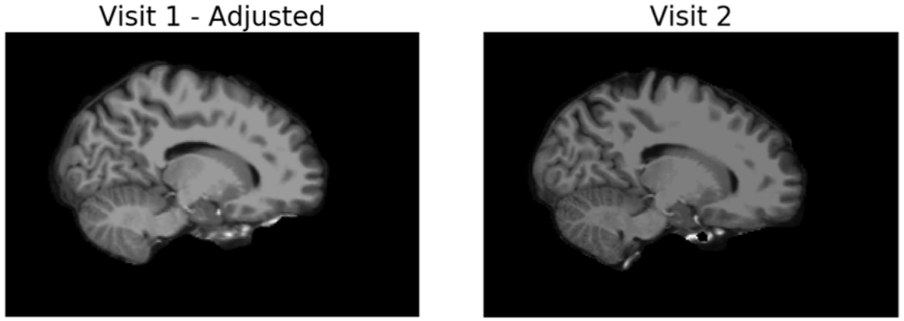


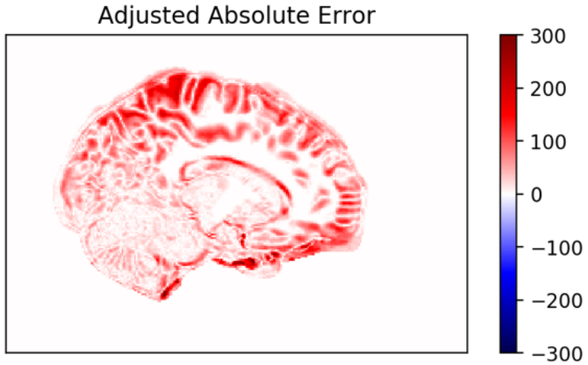
Mean absolute error

Goal: *minimize* the cost function

```
# Improve im1 alignment to im2
xfm=ndi.shift(im1, shift=(-8, -8))
xfm=ndi.rotate(xfm, -18,
                reshape=False)

# Calculate cost
abs_err = np.abs(im1 - im2)
mean_abs_err = np.mean(abs_err)
```

```
mean_abs_err
    13.0376
```

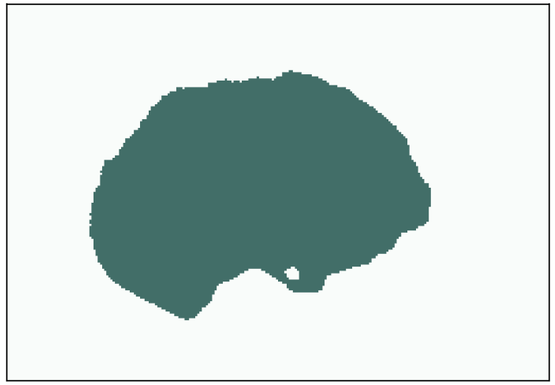




Intersection of the Union

$$IOU = \frac{I_1 \cap I_2}{I_1 \cup I_2}$$

```
mask1 = im1 > 0
mask2 = im2 > 0

intsxn = mask1 & mask2
plt.imshow(intsxn)

union = mask1 | mask2
plt.imshow(union)

iou = intsxn.sum() / union.sum()

iou
    0.68392
```



BIOMEDICAL IMAGE ANALYSIS IN PYTHON

Let's practice!

BIOMEDICAL IMAGE ANALYSIS IN PYTHON

Normalizing Measurements

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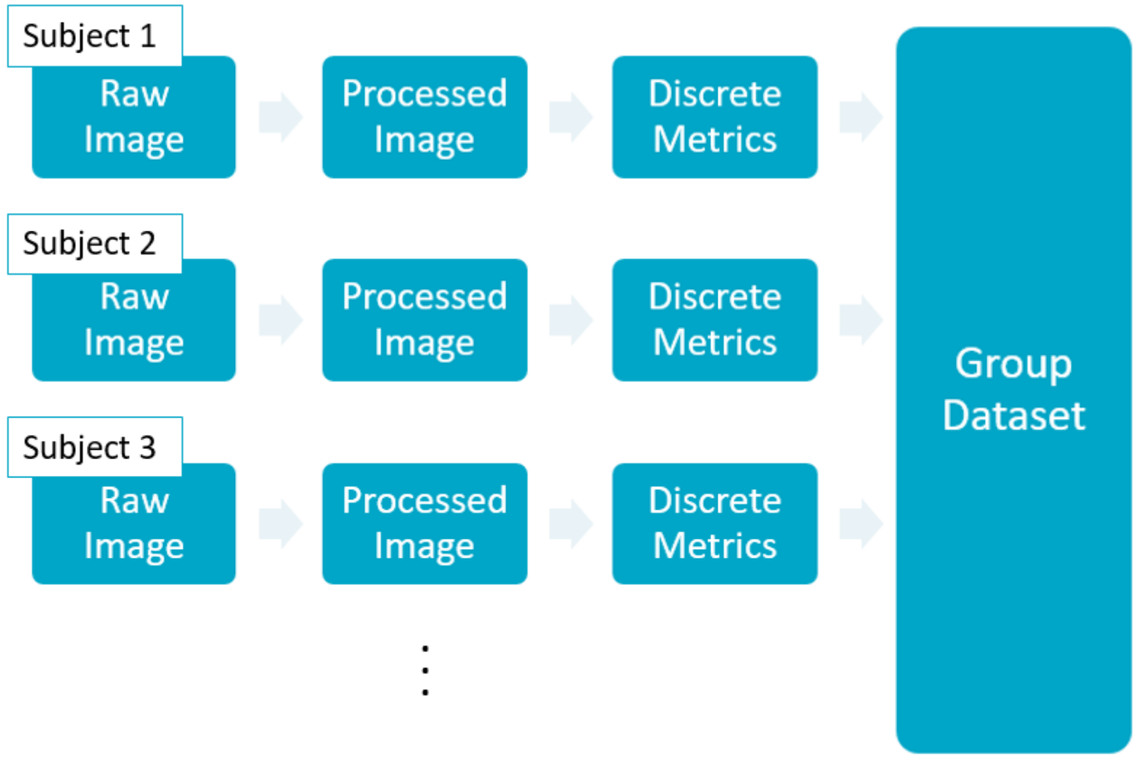
Instructor

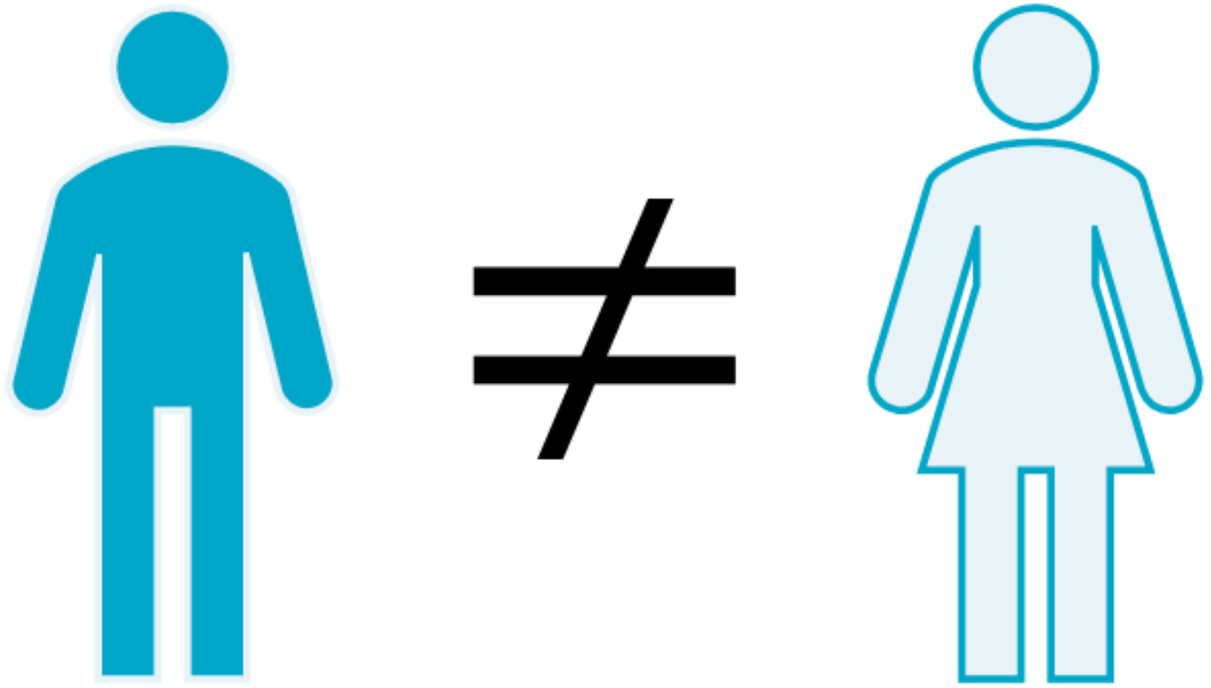
Analysis workflow



OASIS Population

```
df.shape
    (400, 5)

df.sample(5)
                age sex  alzheimers  brain_vol    skull_vol
    ID
    OAS1_0272   75   F        True    851.451  1411.125695
    OAS1_0112   69   F       False    894.801  1434.146892
    OAS1_0213   48   F       False    925.859  1412.781004
    OAS1_0311   22   F       False    980.163  1363.413762
    OAS1_0201   85   F       False    904.104  1420.631447
```

Hypothesis testing



Hypothesis testing

Null hypothesis: two populations' mean brain volumes (μ_m, μ_w) are equal.

$$H_{null} : \mu_w = \mu_m$$
$$H_{alt} : \mu_w \neq \mu_m$$

$$t = \frac{\bar{X} - \mu}{s/\sqrt{n}}$$

Implemented in `scipy.stats.ttest_ind()`

Hypothesis testing

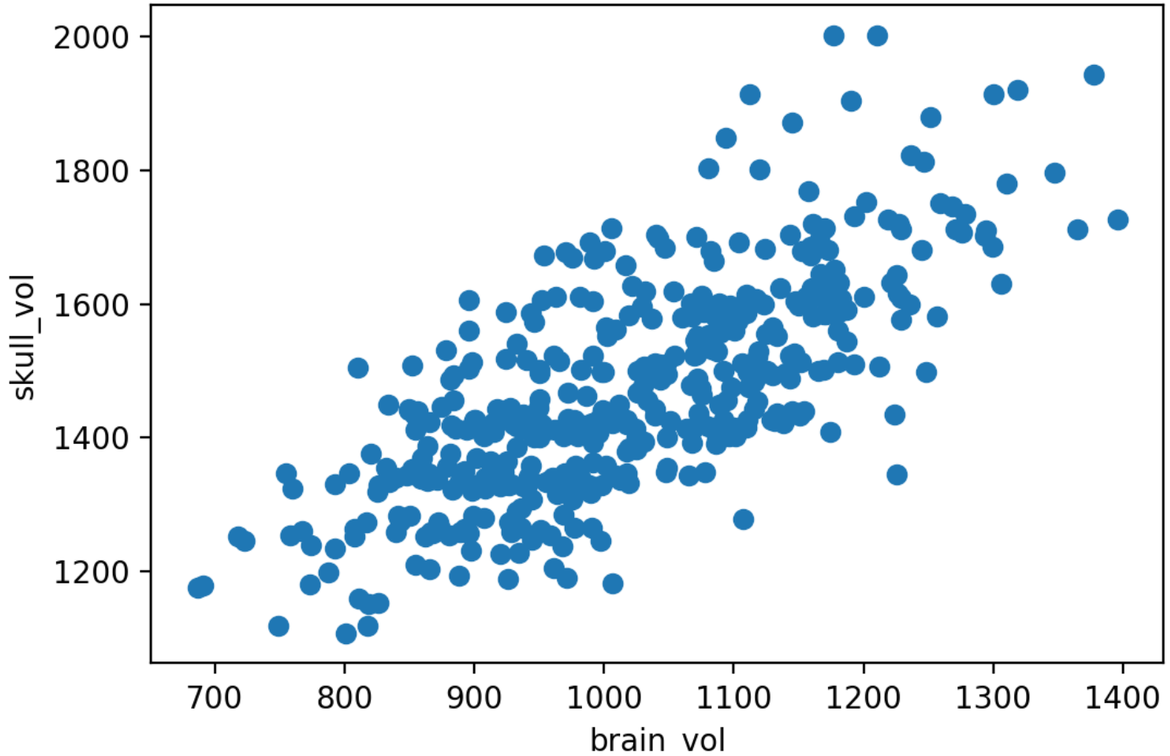
```
brain_m = df.loc[df.sex == 'M', 'brain_vol']

brain_f = df.loc[df.sex == 'F', 'brain_vol']

from scipy.stats import ttest_ind

results = ttest_ind(brain_m, brain_f)
```

```
results.statistic
    10.20986

results.pvalue
    5.03913e-22
```

A large t-statistic and low p-value suggests that there is a significant difference!

Correlated measurements

```
df[['brain_vol', 'skull_vol']].corr()

                'brain_vol' 'skull_vol'
    'brain_vol'       1.000       0.736
    'skull_vol'       0.736       1.000
```



Normalization

```
df['brain_norm'] = df.brain_vol / df.skull_vol

brain_norm_m = df.loc[df.sex == 'M', 'brain_norm']
brain_norm_f = df.loc[df.sex == 'F', 'brain_norm']

results = ttest_ind(brain_norm_m, brain_norm_f)
```

```
results.statistic
    -0.94011

results.pvalue
    0.34769
```

Size, not gender likely drove original results.

Many potential confounds in imaging

Image acquisition

- Contrast
- Resolution
- Field of view

Subject / object

- Age
- Gender
- Pathology

Context

- Hospital
- Radiologist
- Equipment

Data Quality

- Format
- Artifacts

Congratulations!

Exploration

- Loading images
- N-D data
- Subplots

Masks and Filters

- Intensity distributions
- Convolutions
- Edge detection

Measurement

- Labelling
- Multi-object measurement
- Morphology

Image Comparison

- Transformations
- Resampling
- Cost functions
- Normalization

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Good luck!