

# Spatial transformations

BIOMEDICAL IMAGE ANALYSIS IN PYTHON



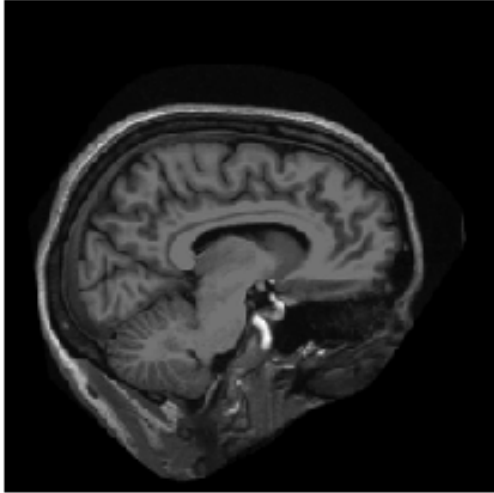
**Stephen Bailey**  
Instructor

# OASIS Database

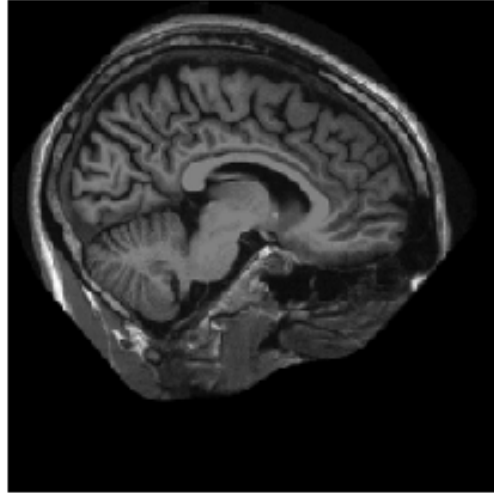


# Significant variability

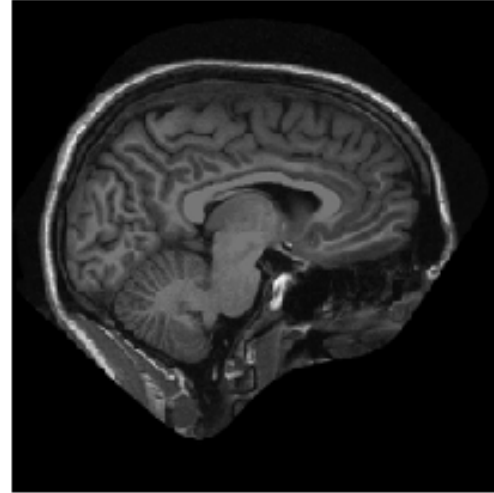
OAS1\_0058



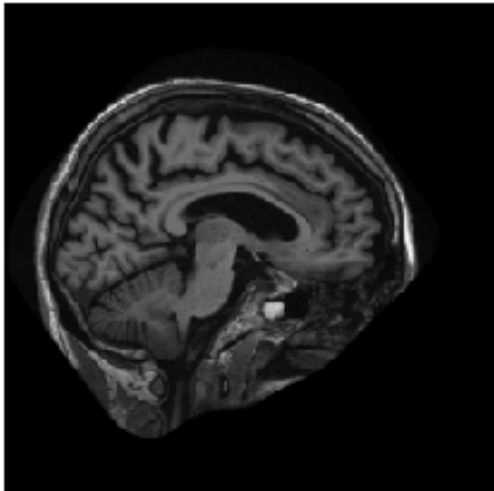
OAS1\_0069



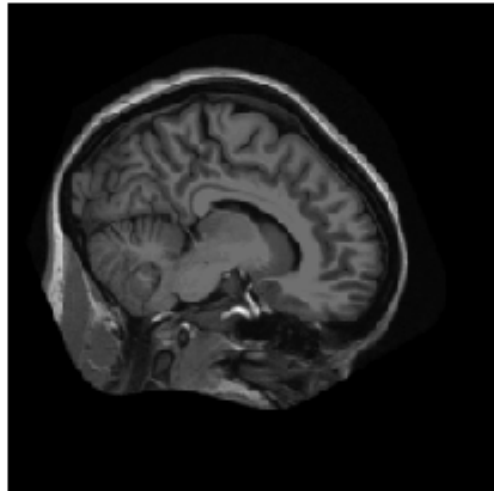
OAS1\_0144



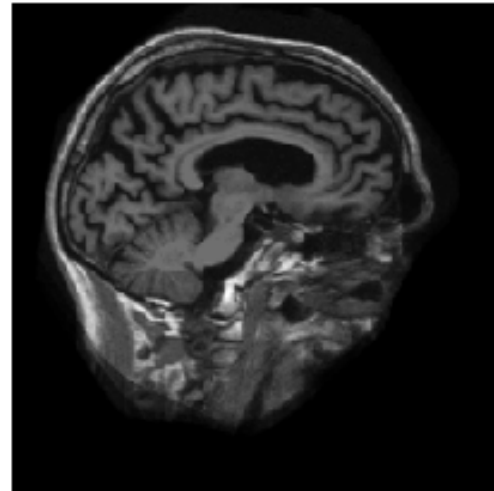
OAS1\_0226



OAS1\_0249

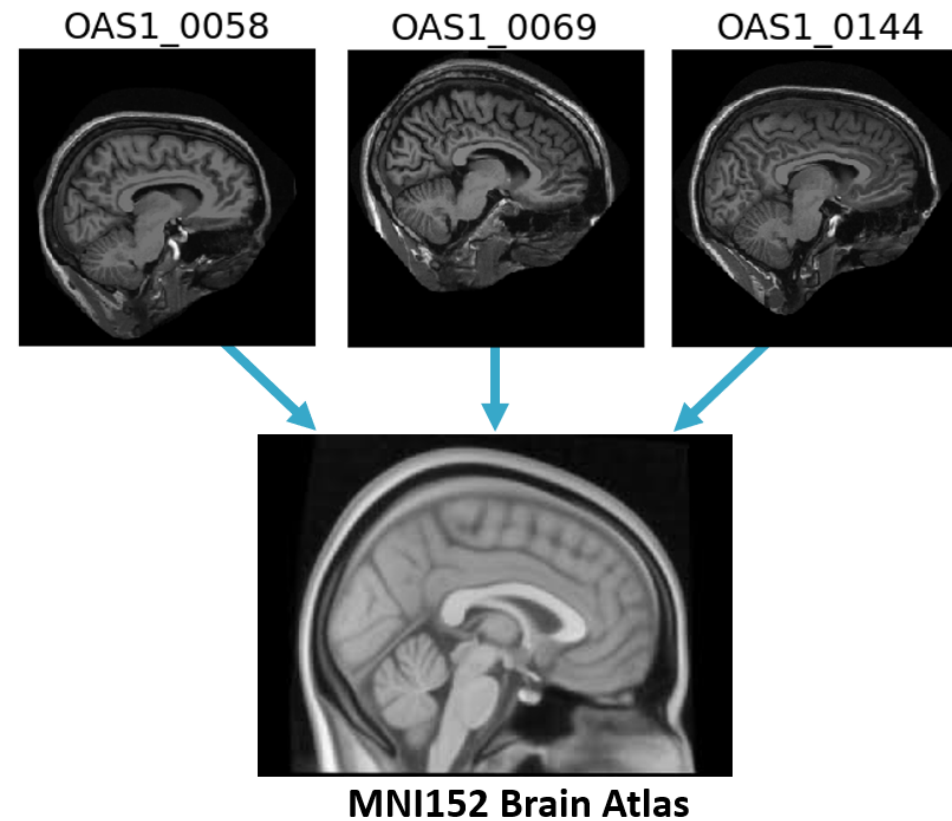


OAS1\_0351



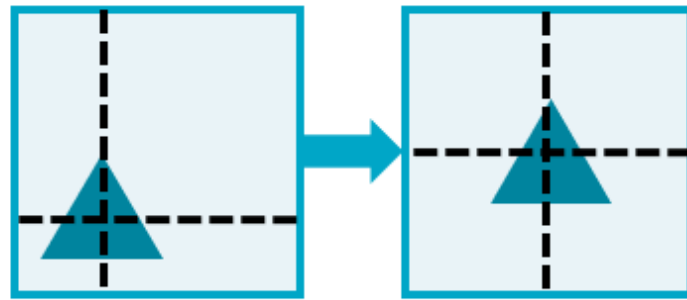
# Registration

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

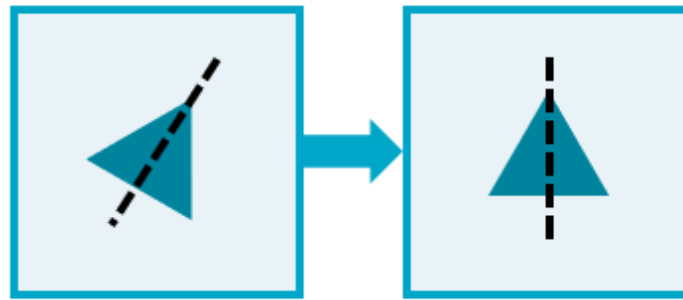


# Affine transformations preserve points, lines, and planes

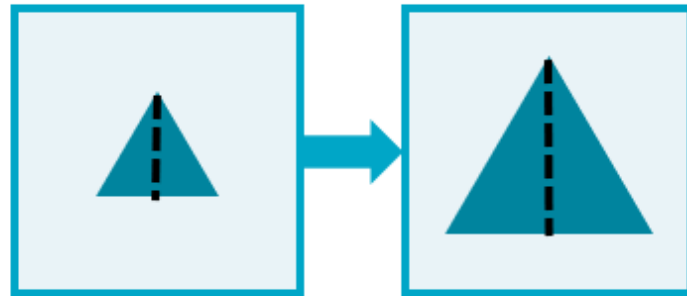
Translate



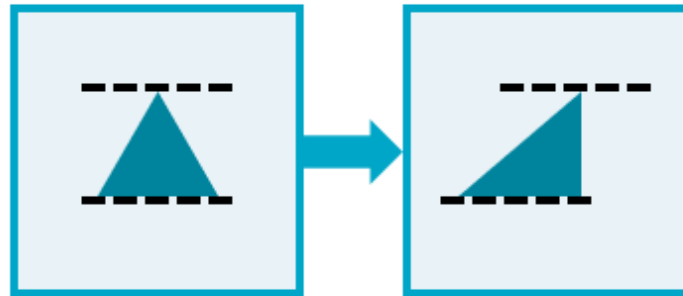
Rotate



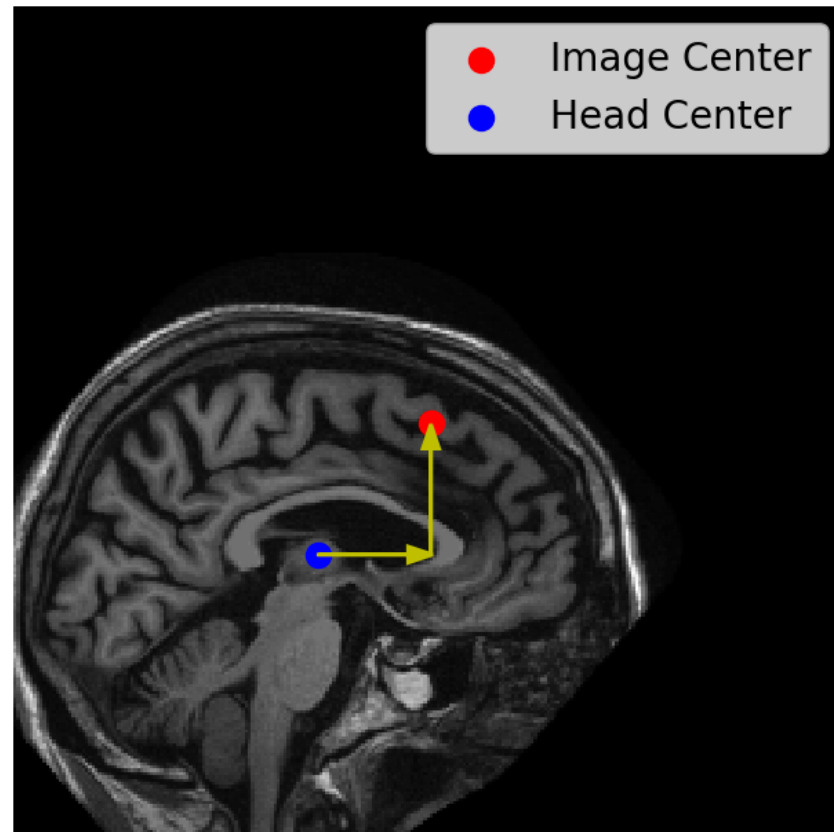
Scale



Shear



# Translation



```
import imageio
import scipy.ndimage as ndi
```

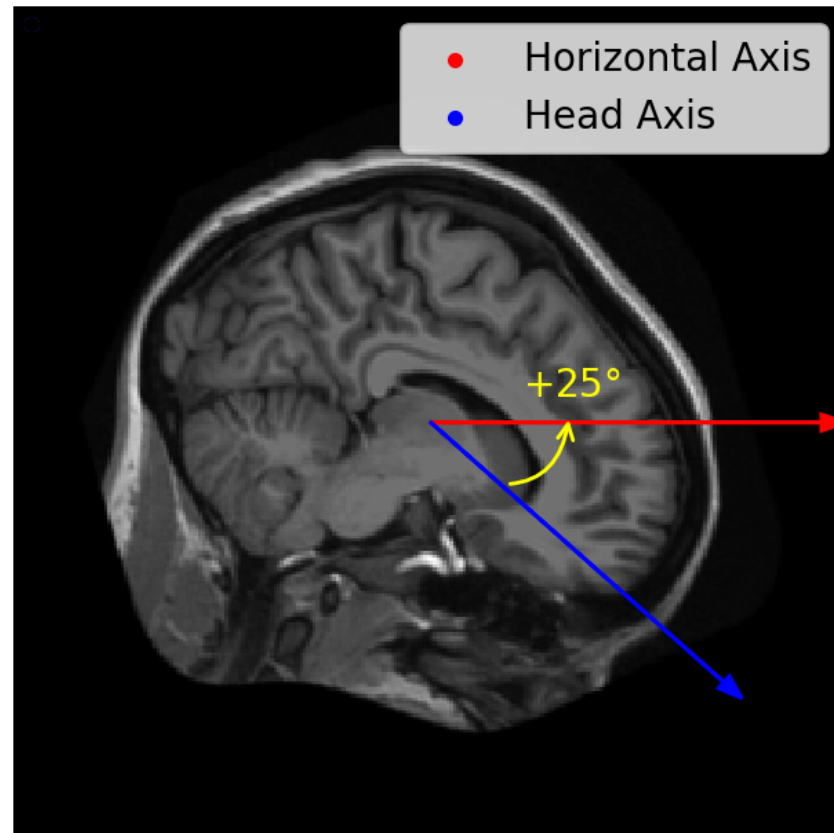
```
im=imageio.imread('0AS1036-2d.dcm')
im.shape
```

```
(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))
```

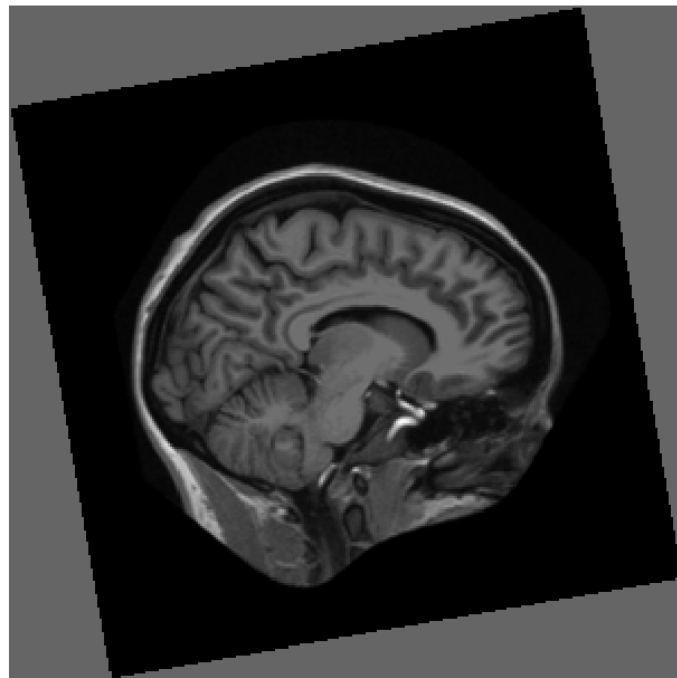


# Image rotation

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

```
xfm.shape
```

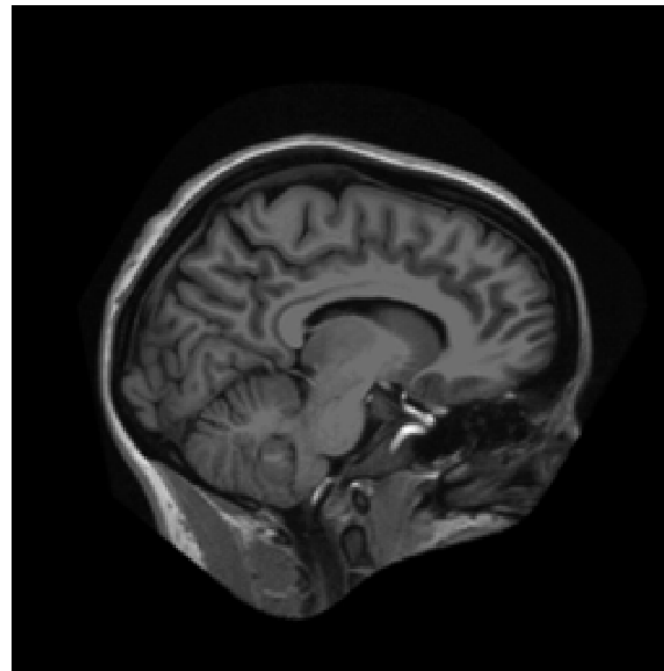
```
(297, 297)
```



```
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

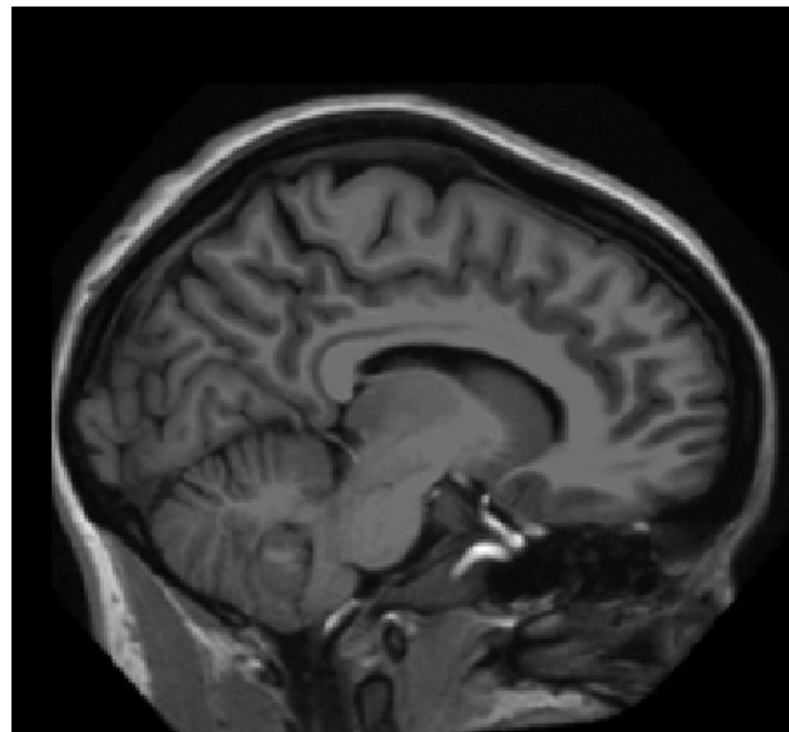
$$\begin{bmatrix} \cos(\theta) & -\sin(\theta) & 0 \\ \sin(\theta) & \cos(\theta) & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

Scale

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

Shear

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



# Let's practice!

BIOMEDICAL IMAGE ANALYSIS IN PYTHON

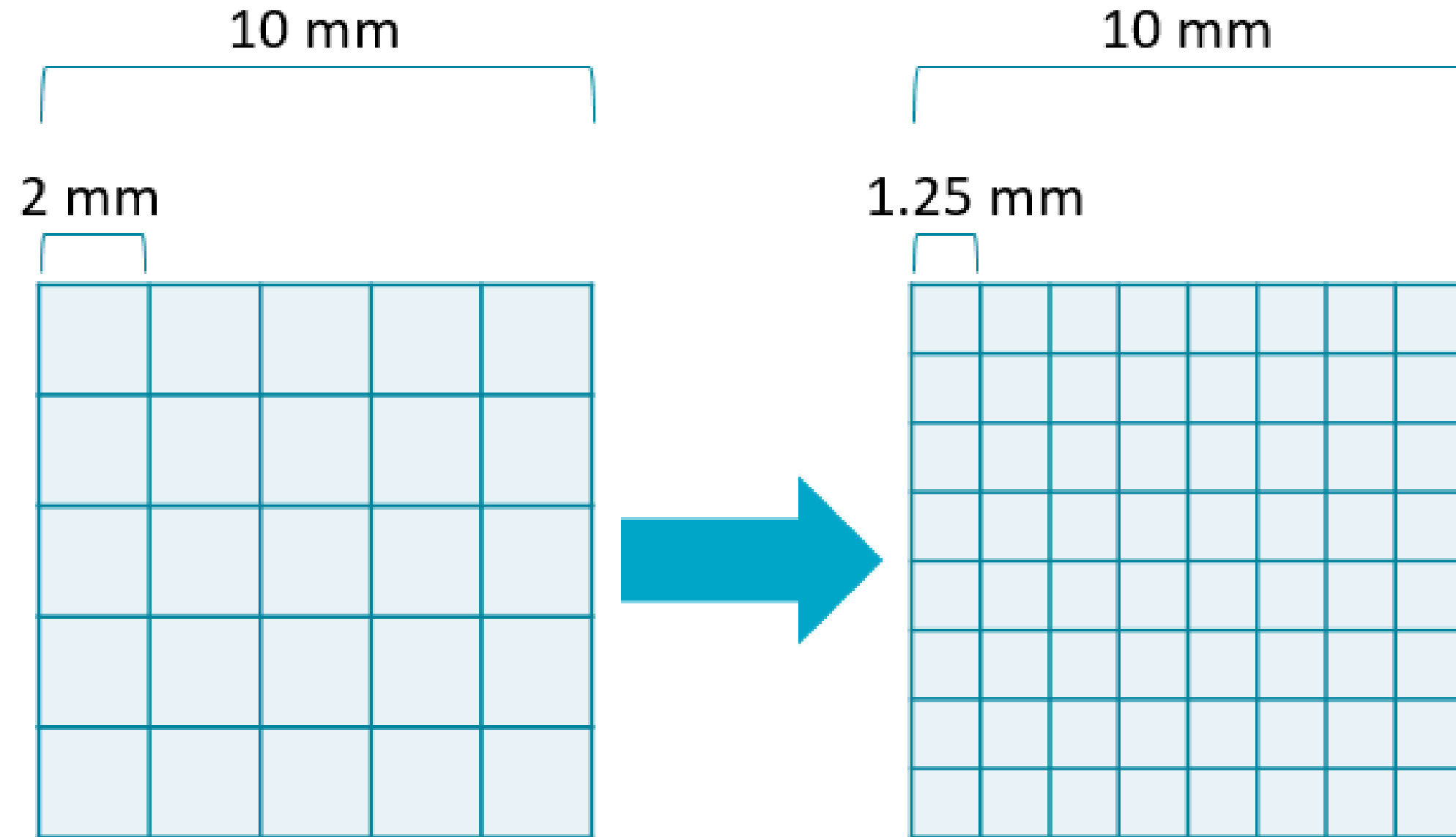
# Resampling and interpolation

BIOMEDICAL IMAGE ANALYSIS IN PYTHON



**Stephen Bailey**  
Instructor

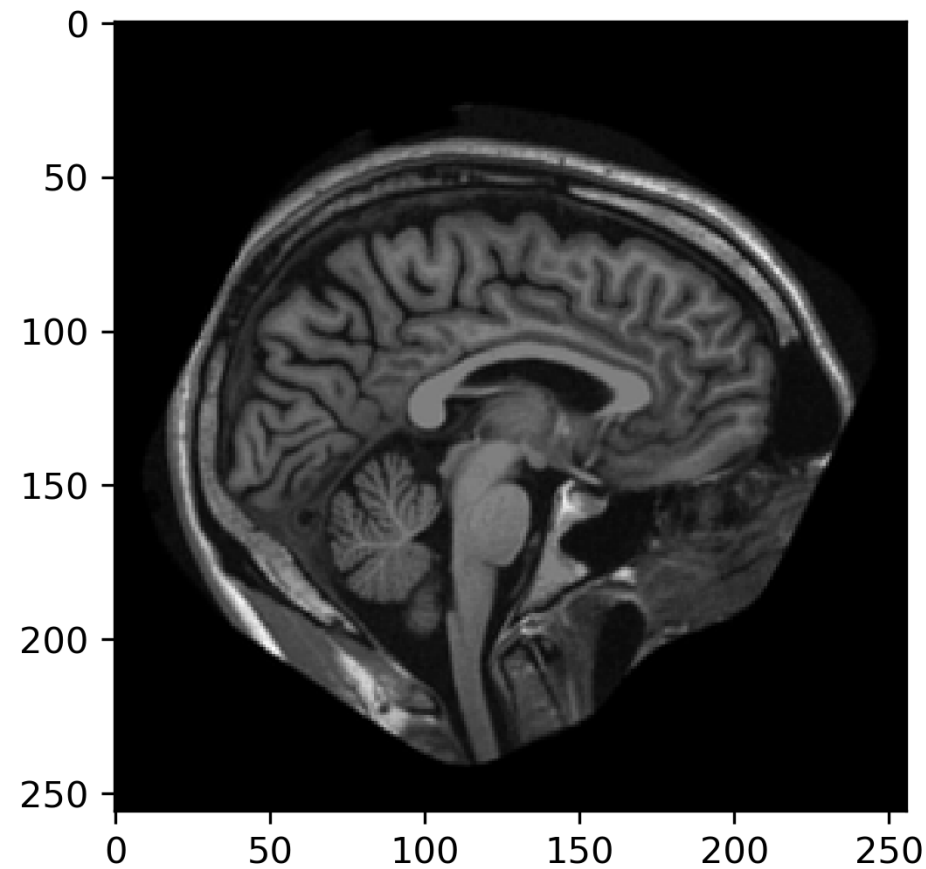
# Resampling changes the array shape



# Downsampling

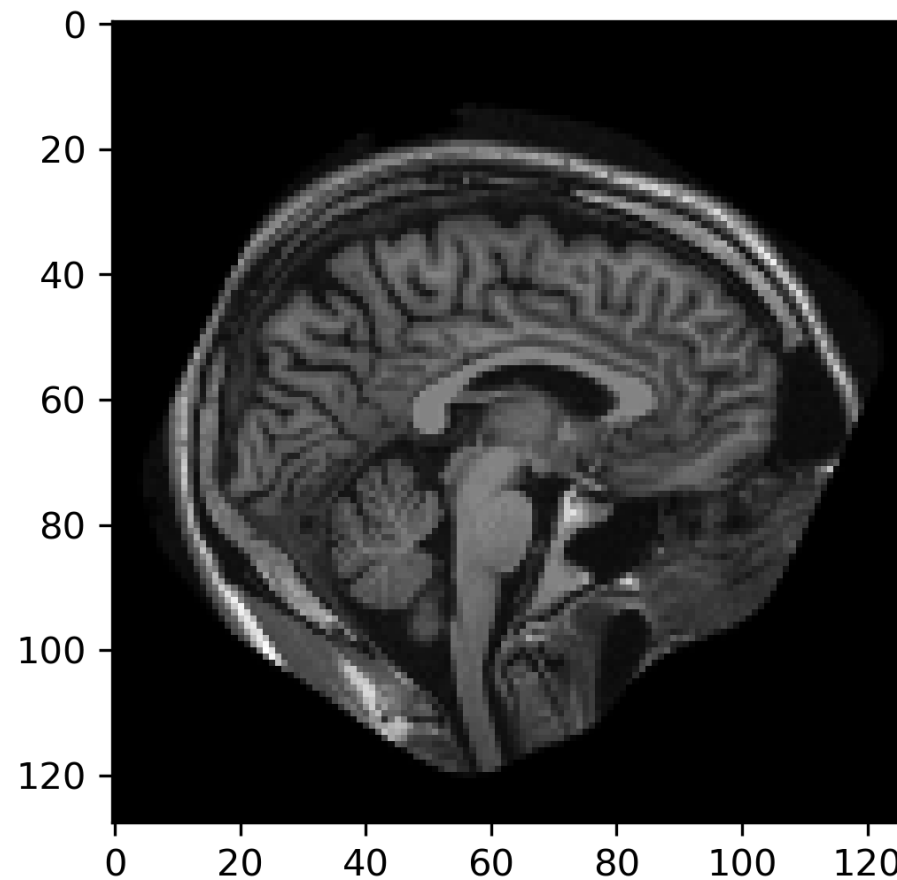
```
vol = imageio.volread('OAS1_0255')  
vol.shape
```

(256, 256, 256)



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

(128, 128, 128)

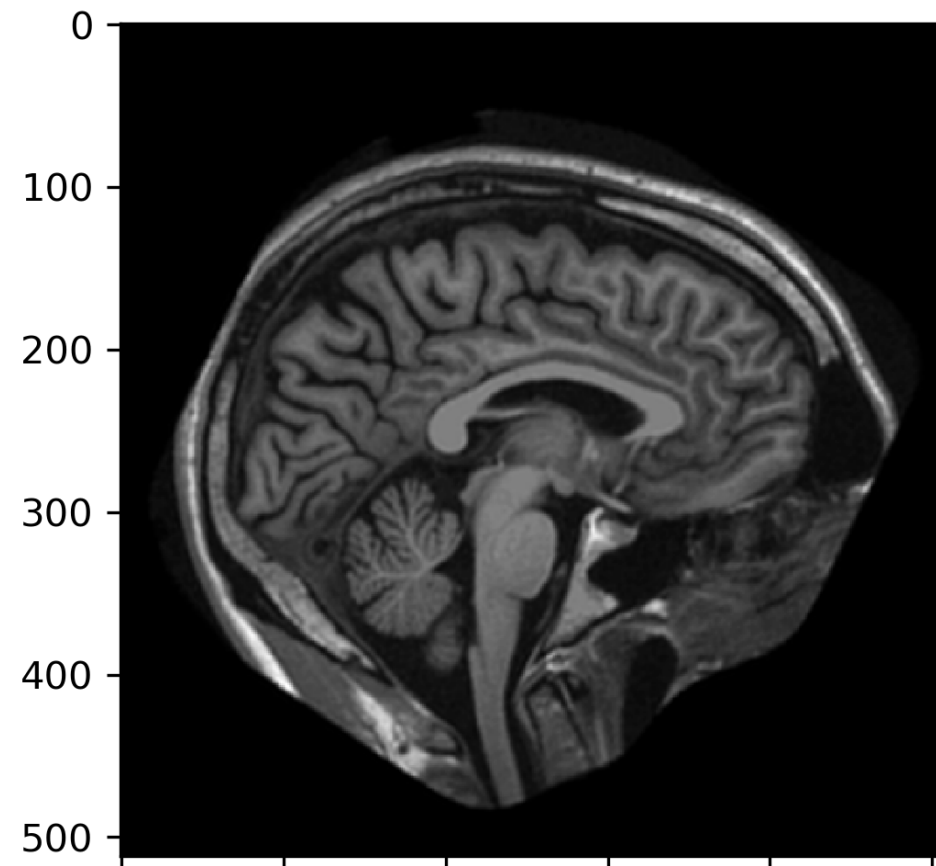


# Upsampling

- 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
```

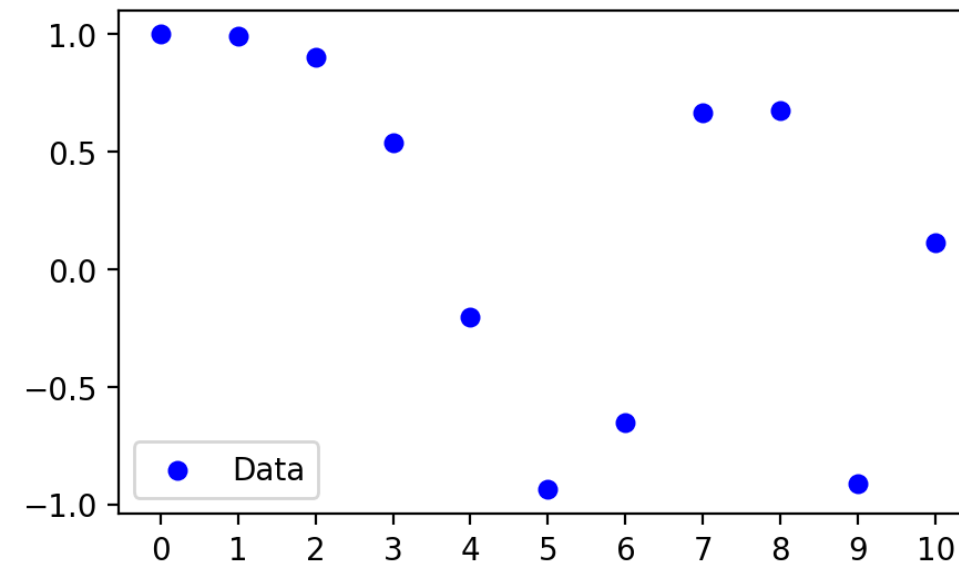
```
(512, 512, 512)
```



# Interpolation

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

*Interpolation in 1  $D$*

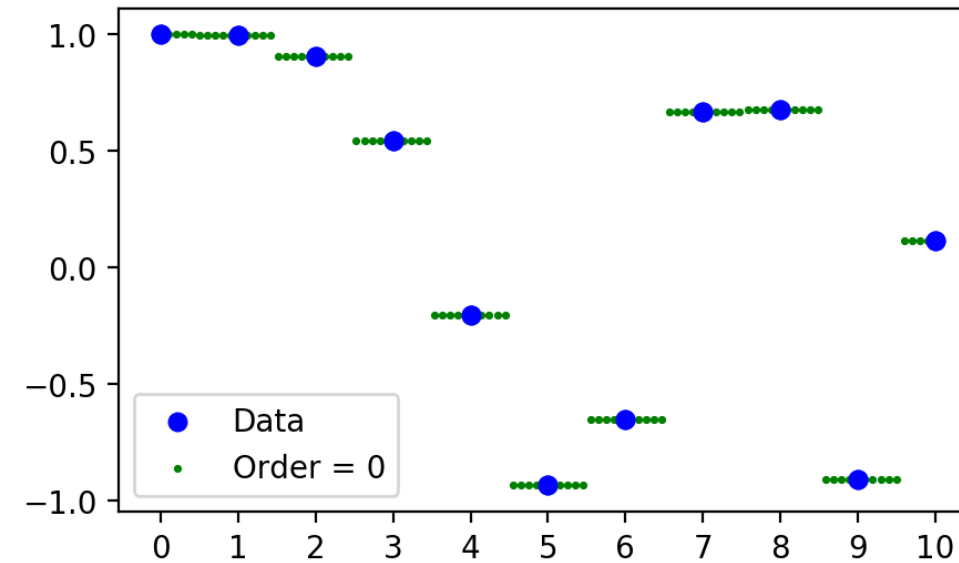




# Interpolation

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

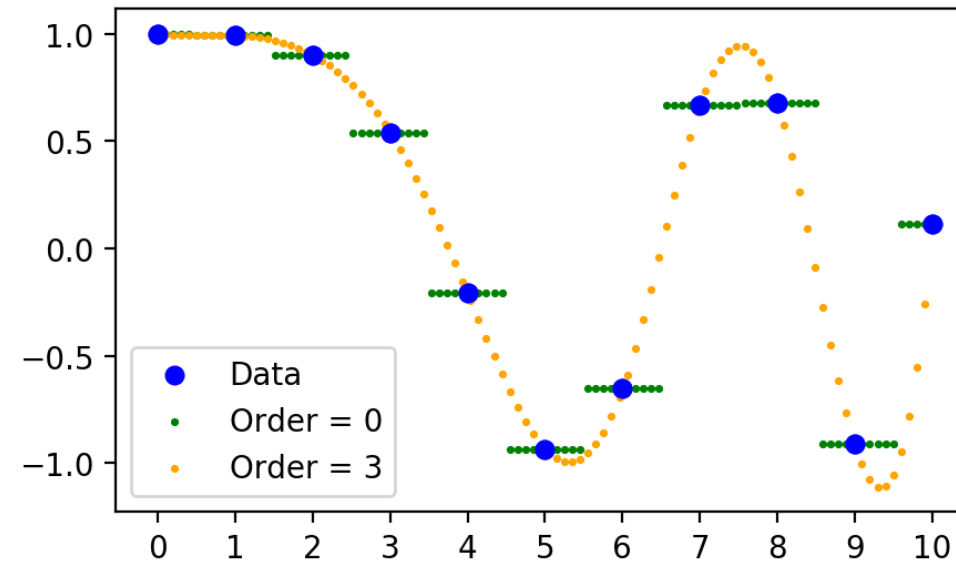
*Interpolation in 1  $D$*



# 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 1 D*



# 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)
```

order = 0



order = 2

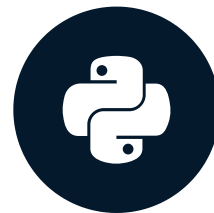


# Let's practice!

BIOMEDICAL IMAGE ANALYSIS IN PYTHON

# Comparing images

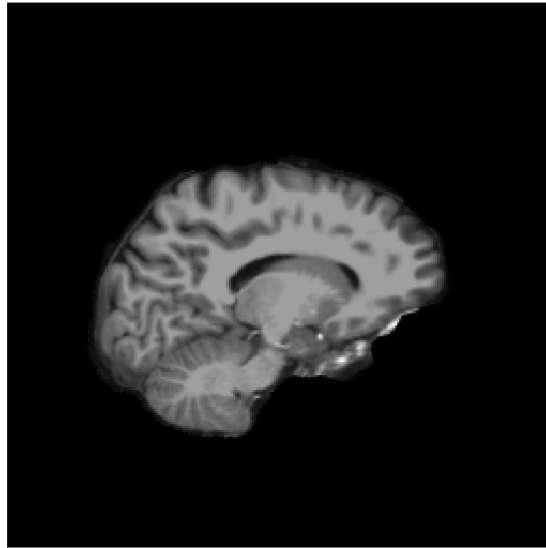
BIOMEDICAL IMAGE ANALYSIS IN PYTHON



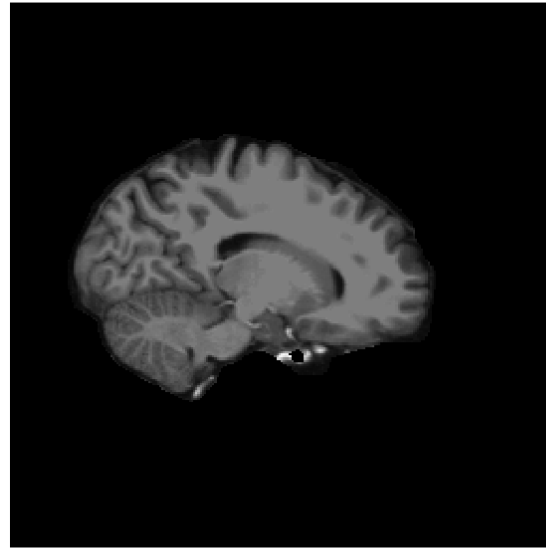
**Stephen Bailey**  
Instructor

# Comparing images

Visit 1



Visit 2



Mask Overlay



# Summary metrics

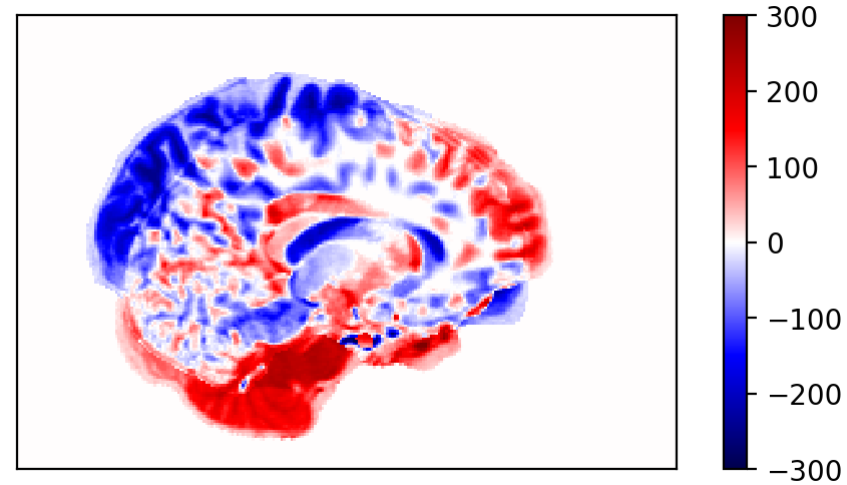
Goal: *define* a metric of similarity between two images.

**Cost functions** produce metrics to be minimized.

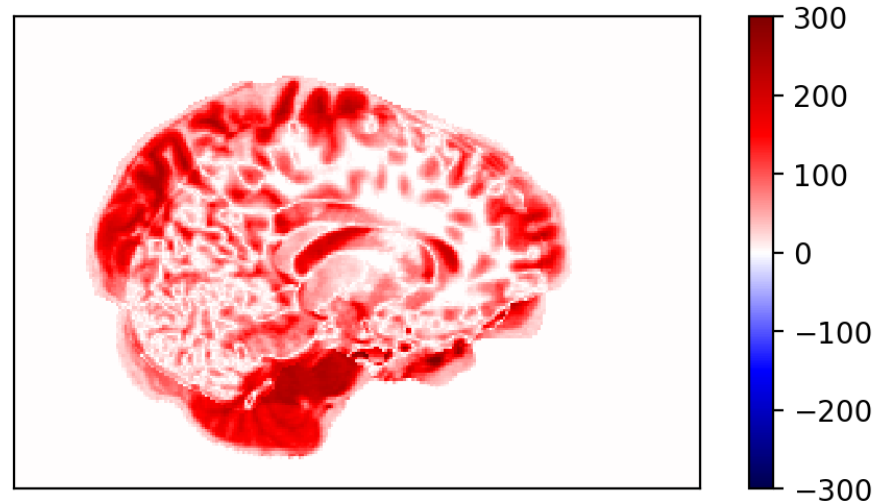
**Objective functions** produce metrics to be maximized.

# Mean absolute error

```
import imageio
import numpy as np
i1=imageio.imread('0AS1035-v1.dcm')
i2=imageio.imread('0AS1035-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



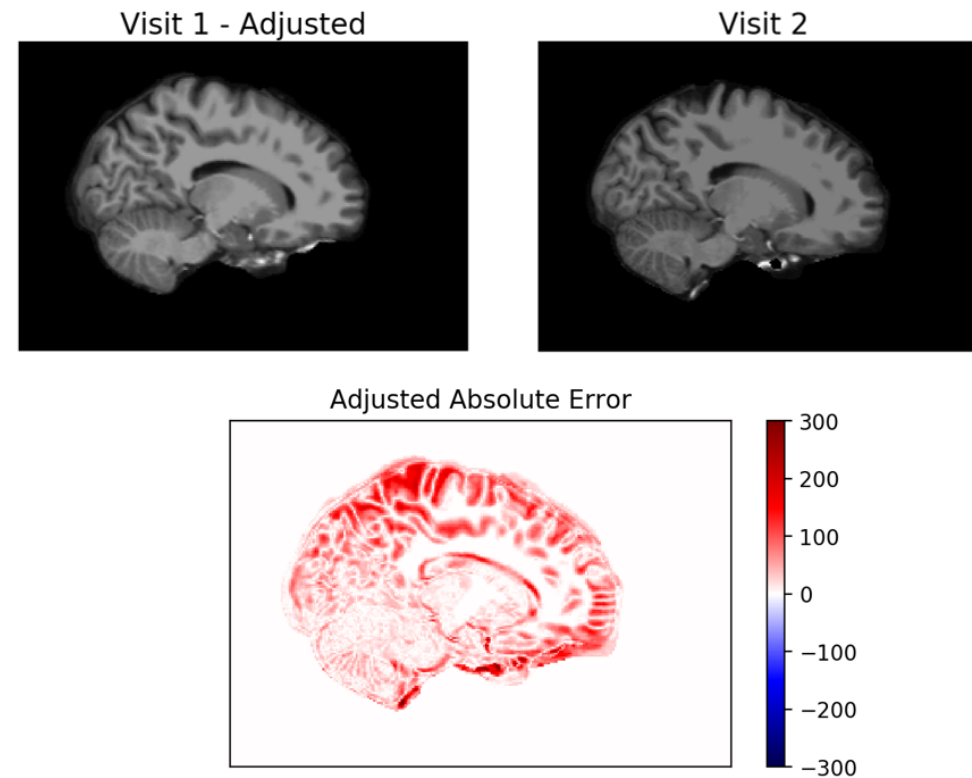
# Mean absolute error

Goal: *minimize* the cost function

```
# Improve im1 alignment to im2
xfm=ndi.shift(im1, shift=(-8, -8, -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
```

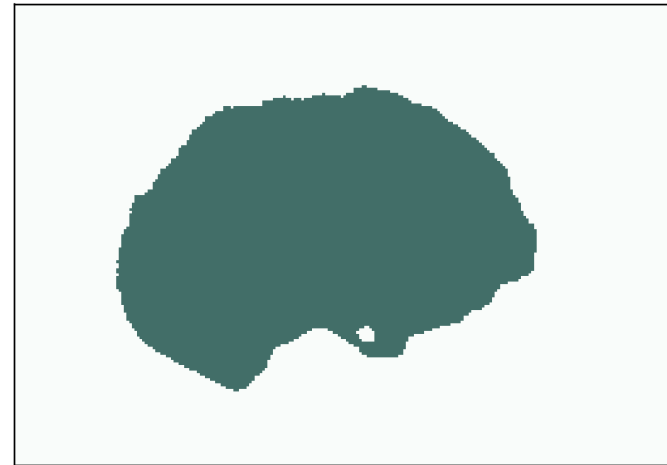
13.0376



# Intersection of the union

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

```
mask1 = im1 > 0  
mask2 = im2 > 0  
intsn = mask1 & mask2  
plt.imshow(intsn)
```



```
union = mask1 | mask2  
plt.imshow(union)  
iou = intsn.sum() / union.sum()  
iou
```



0.68392

# Let's practice!

BIOMEDICAL IMAGE ANALYSIS IN PYTHON

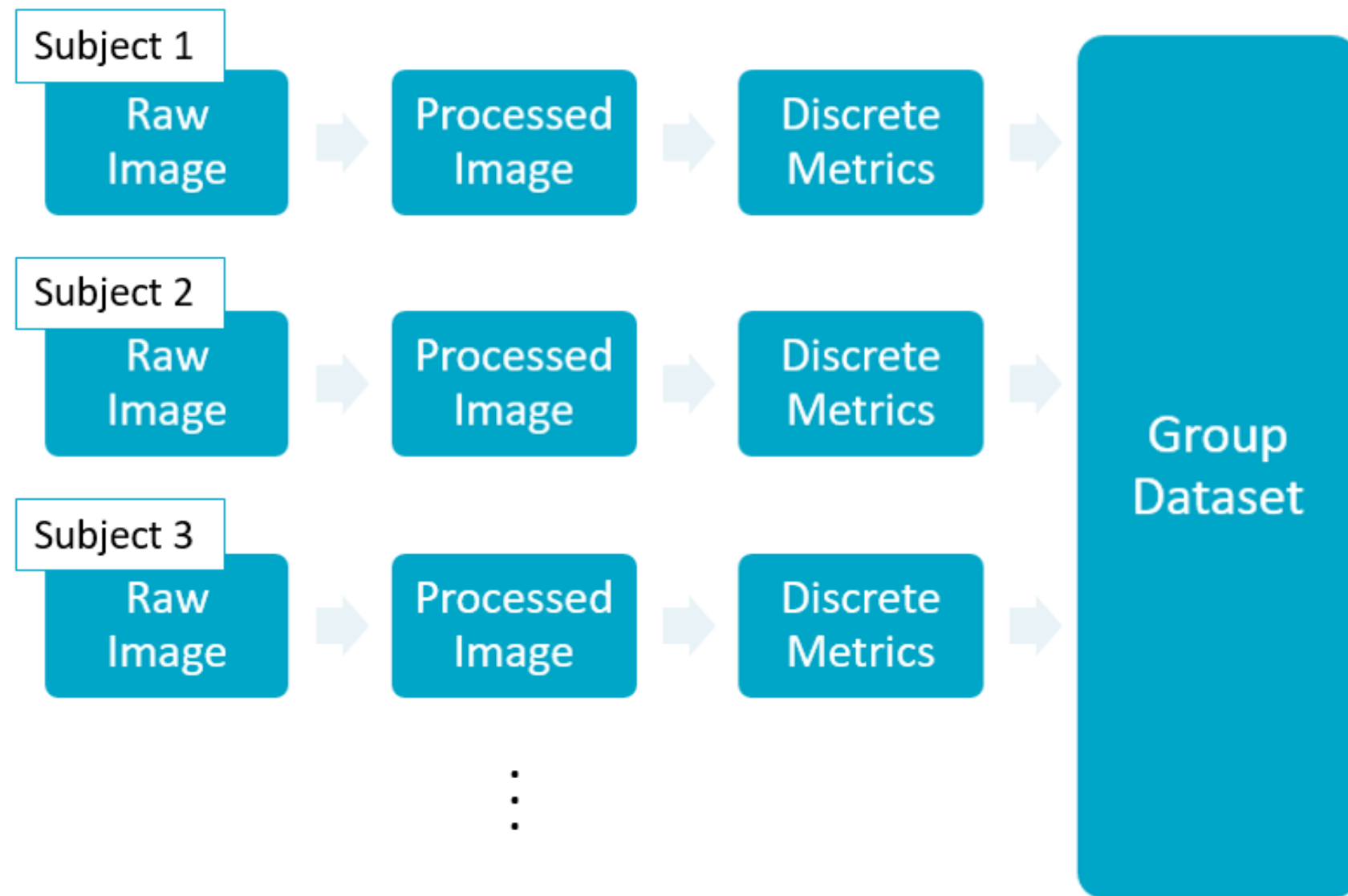
# Normalizing measurements

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**Stephen Bailey**  
Instructor

# Analysis workflow



# OASIS population

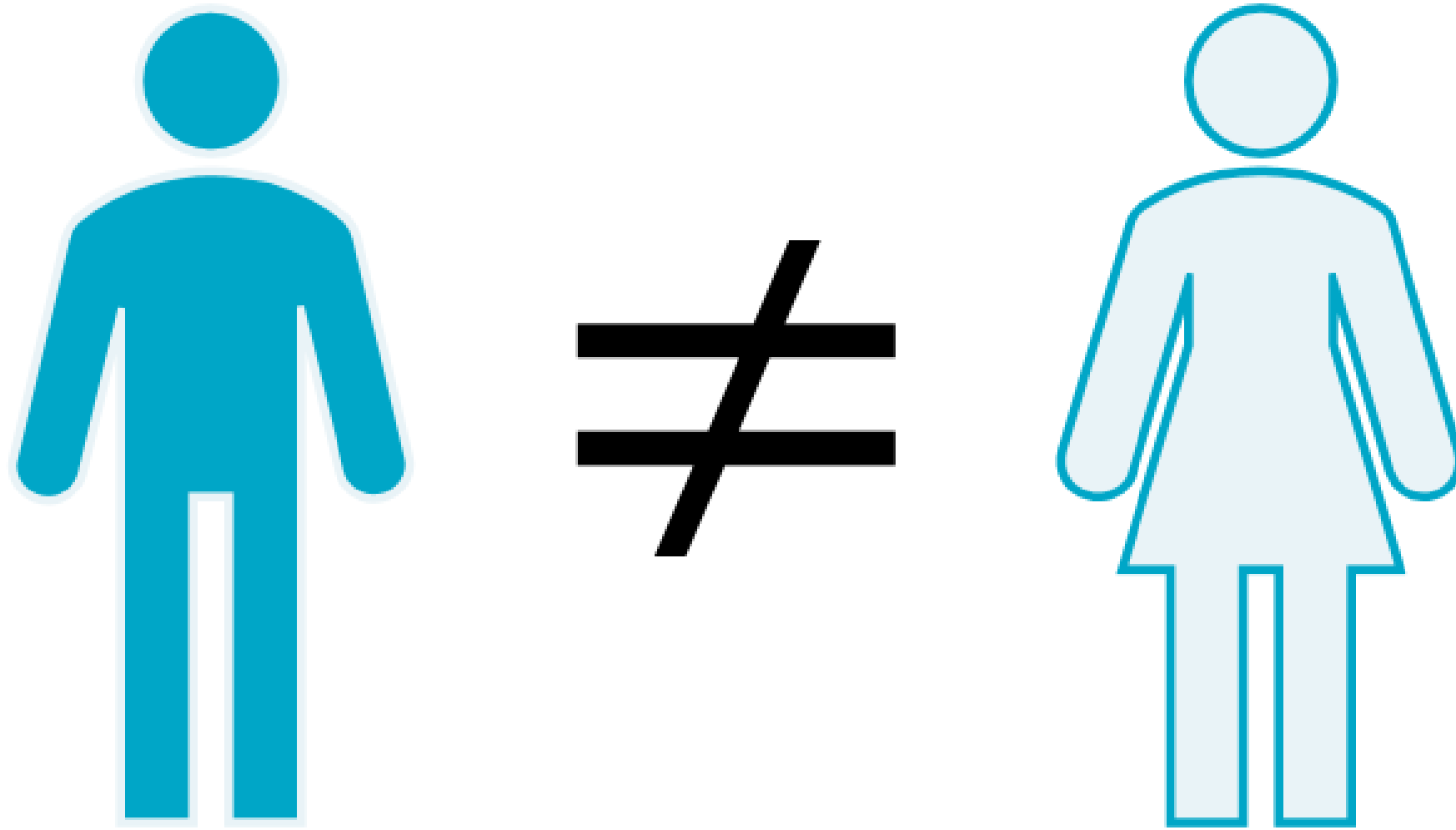
```
df.shape
```

```
(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 ( $\mu_m, \mu_w$ ) 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  
results.pvalue
```

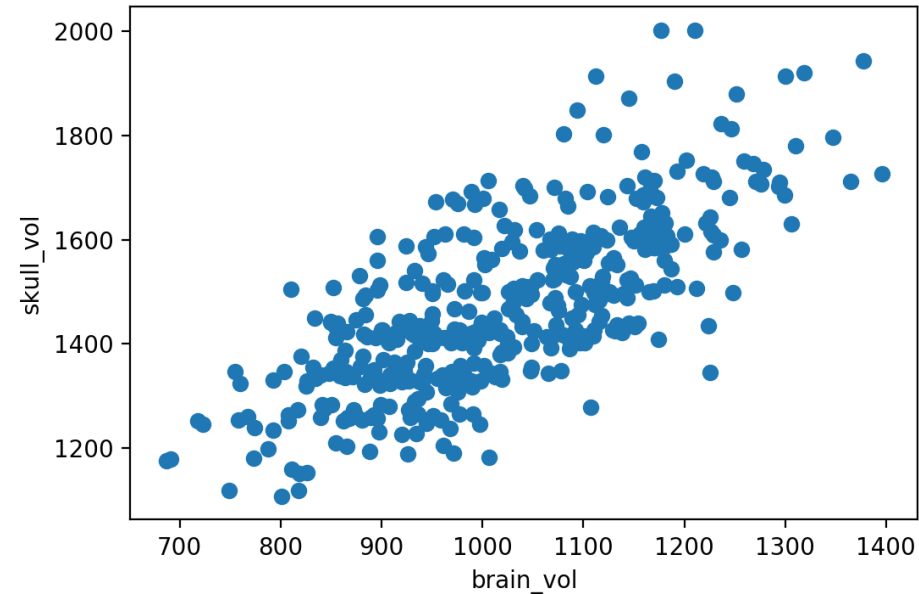
```
10.20986  
5.03913e-22
```

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  
results.pvalue
```

```
-0.94011  
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

# Good luck!

BIOMEDICAL IMAGE ANALYSIS IN PYTHON