



Institut et hôpital neurologiques de Montréal
Montreal Neurological Institute and Hospital

Deep Learning with MRI

Neurotech MTL

About Us

Thomas Funck: Having originally studied philosophy and cognitive science as an undergraduate at McGill, Thomas is now a Ph.D. candidate in neuroscience at the MNI. He uses multi-modal brain imaging, signal processing, and computational simulation to study the cellular architecture of the living brain.

Twitter : @tffunck



Andrew Doyle:

During his MSc with Tal Arbel, Andrew developed machine learning algorithms to detect lesions in multiple sclerosis. He is now continuing his work in the MCIN lab at the MNI, with a special interest in using AI to automate quality control for brain imaging.

Twitter : @crocodoye

Robert Fratila: Robert is a Co-Founder and CTO of aifred health. He is very passionate about combining medicine and AI throughout his work and research. His work as a software developer at the Montreal Neurological Institute, integrating state-of-the-art machine learning models in healthcare, specifically brain imaging, has given him lots of experience in finding efficient solutions to complex problems.

LinkedIn : robertfratila



Installation

- Google Colab (super easy)
 - Create / Log-in to Google account
 - Go to <https://colab.research.google.com>
 - Download and load: <https://tinyurl.com/yd8dd5x3>
- Docker (very easy):
 - Install docker on your OS
 - <https://docs.docker.com/install/#cloud>
 - `docker pull tffunck/neurotech:latest`
 - `docker run -it --rm tffunck/neurotech:latest`
- DIY (pretty easy):
 - `wget https://bootstrap.pypa.io/get-pip.py`
 - Or go to the link and download manually
 - `python3 get-pip.py`
 - `pip3 install pandas numpy scipy h5py tensorflow keras`
 - `git clone https://github.com/tffunck/minc_keras`
- Data
 - Unzip : `minc_keras/data/ouput.gz.bz2`

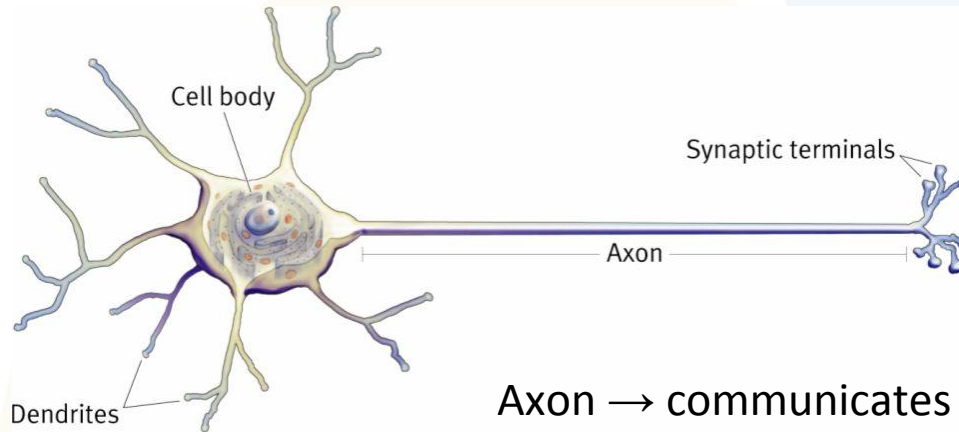
Outline

1. Brain imaging and neuroanatomy
2. Machine Learning
3. Deep Learning
4. Keras Example



Super simple neuroanatomy

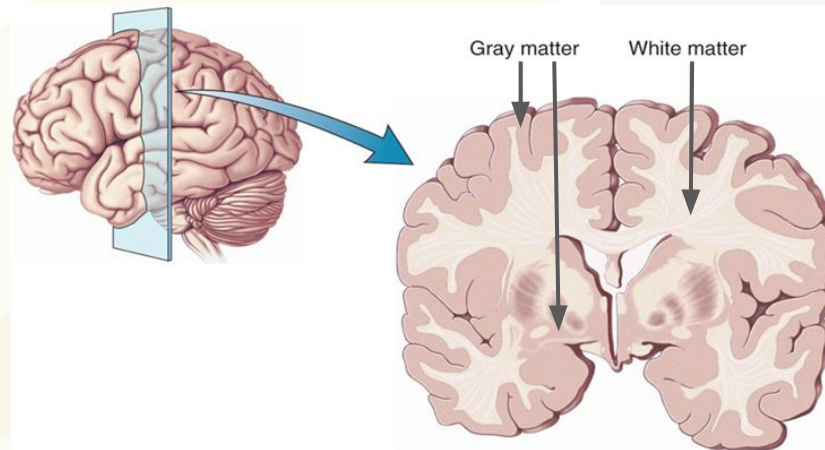
Cell body and dendrites → integrate information



Axon → communicates information downstream



Super simple neuroanatomy

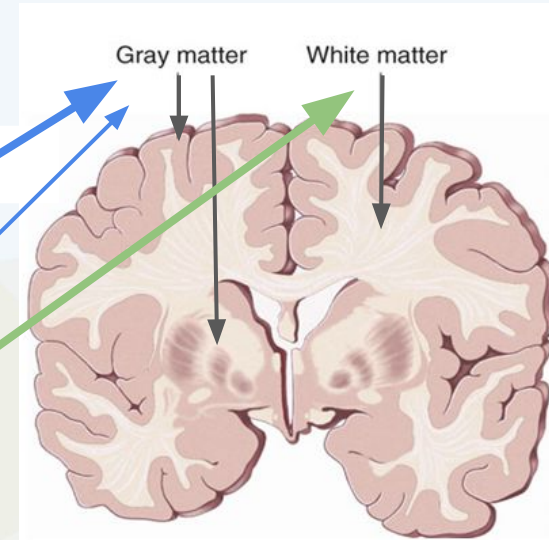
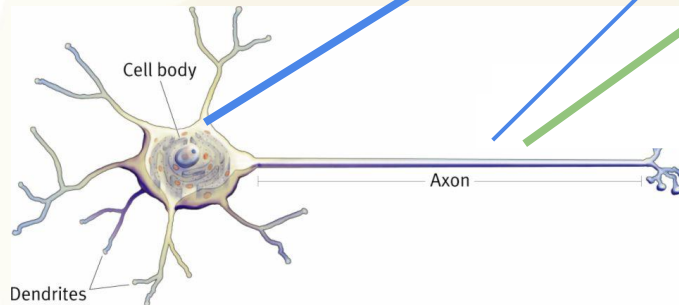


Super simple neuroanatomy

Grey Matter (GM) : cell bodies + short range axons

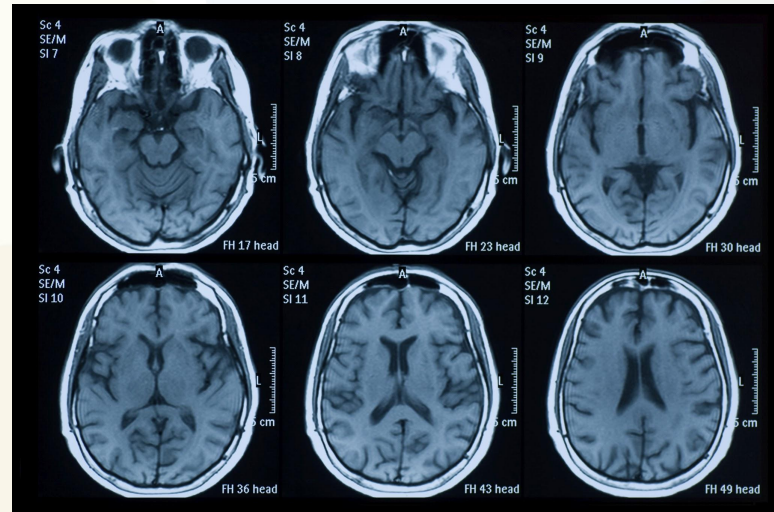
White Matter (WM) : long range axons

Cerebrospinal Fluid (CSF) : liquid that your brain floats in



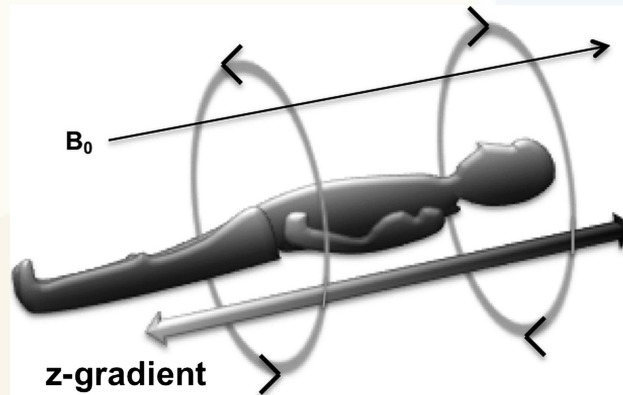
Magnetic Resonance Imaging (MRI)

- Uses powerful magnets to create images of biological tissue (e.g., brains)



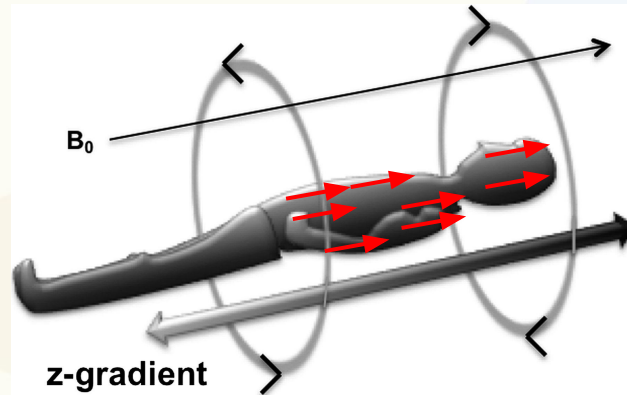
Magnetic Resonance Imaging (MRI)

1. MRI scanners first create a magnetic field along the axis of the scanner



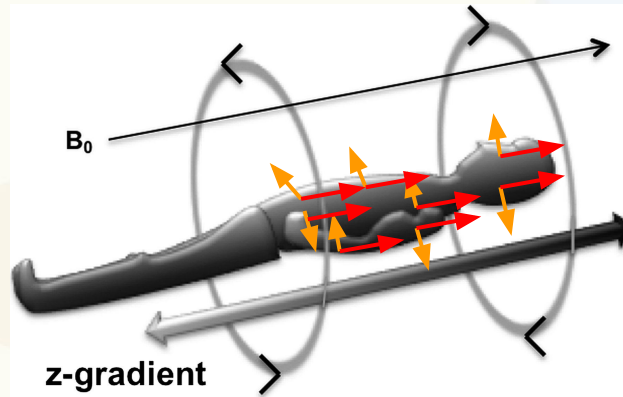
Magnetic Resonance Imaging (MRI)

1. MRI machines first create a magnetic field along the axis of the scanner
2. Aligns hydrogen (H) atoms in the body to the magnetic field



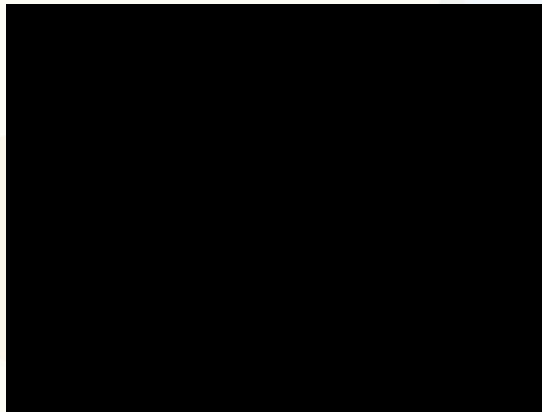
Magnetic Resonance Imaging (MRI)

1. MRI machines first create a magnetic field along the axis of the scanner
2. Aligns hydrogen (H) atoms in the body to the magnetic field
3. MRI emits magnetic pulse that knocks H atoms out of alignment



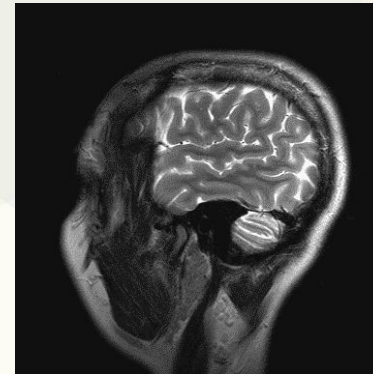
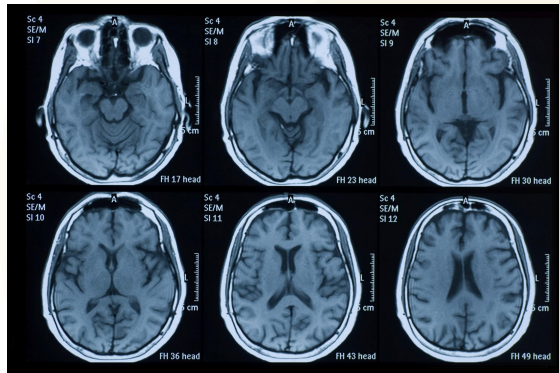
Magnetic Resonance Imaging (MRI)

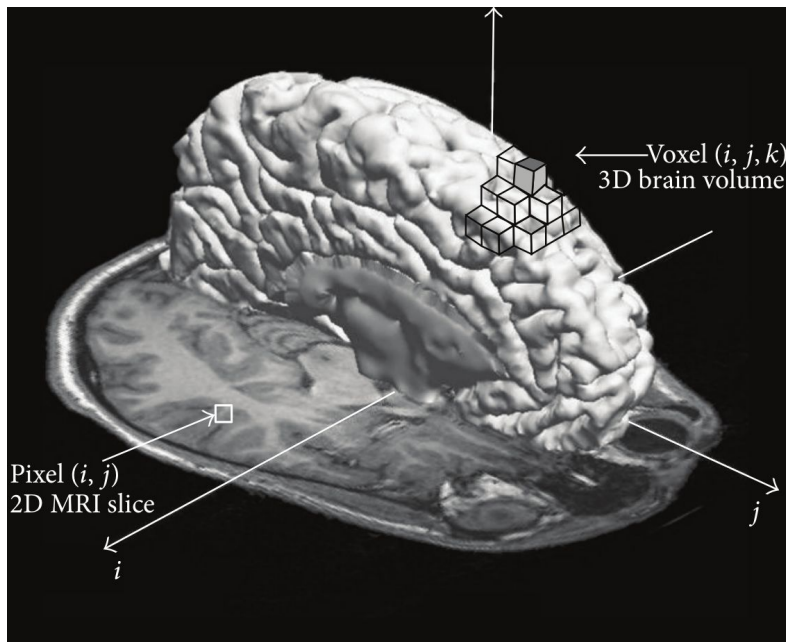
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2. Aligns hydrogen (H) atoms in the body to the magnetic field
3. MRI emits magnetic pulse that knocks H atoms out of alignment
4. Time it takes for H atoms to regain alignment depends on biological tissue



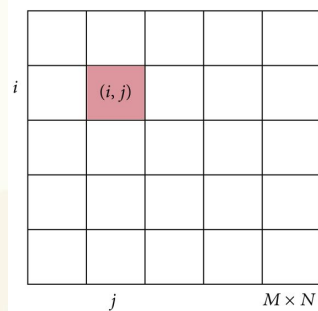
Magnetic Resonance Imaging (MRI)

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2. Aligns hydrogen (H) atoms in the body to the magnetic field
3. MRI emits magnetic pulse that knocks H atoms out of alignment
4. Time it takes for H atoms to regain alignment depends on biological tissue
5. MRI image is based on this realignment time and this reflects type of tissue
 - a. Realignment speed : WM (bright) > GM (medium) > CSF (dark)

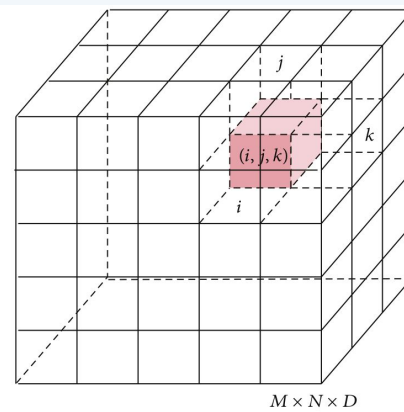




Pixel (2D image)

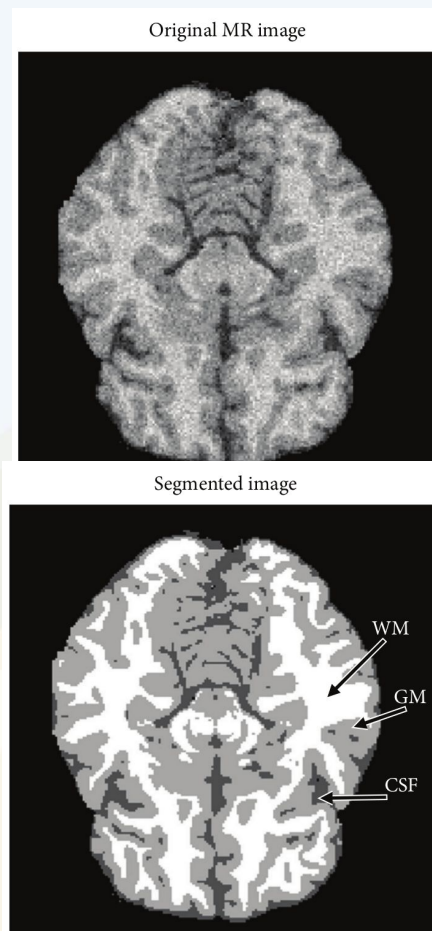


Voxel (3D volume)



MRI Segmentation

- Lots of ways to analyze MRI
 - Brain size
 - Cortical thickness
 - GM/WM intensity ratio
- Segmenting MRI very useful
 - Segmenting into GM and WM is common processing step
 - Helps to quantify brain metrics measured in these regions
- ML can be used to perform segmentation!



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- 2. Machine Learning**
3. Deep Learning
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Introduction to Deep Learning

- Layers of artificial neurons learn increasingly abstract representations of your data
- Can capture very complex interactions between features using non-linear activations

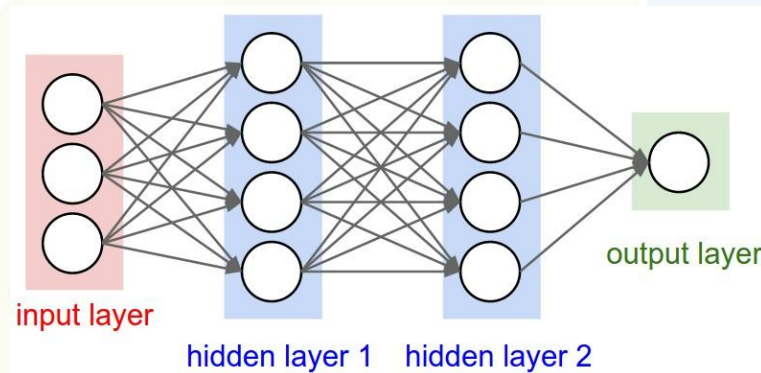


Image: <http://cs231n.github.io/convolutional-networks/>

Components of neural networks

- Each layer has a set of artificial neurons/nodes
- Traditionally activated with rectified linear units (i.e. ReLU)
- Regularization done through dropout

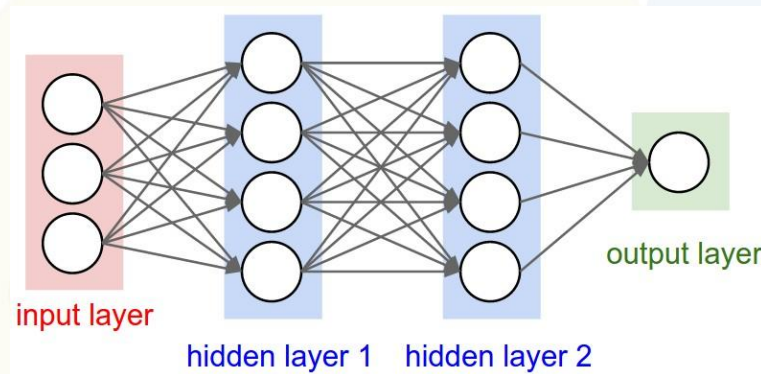
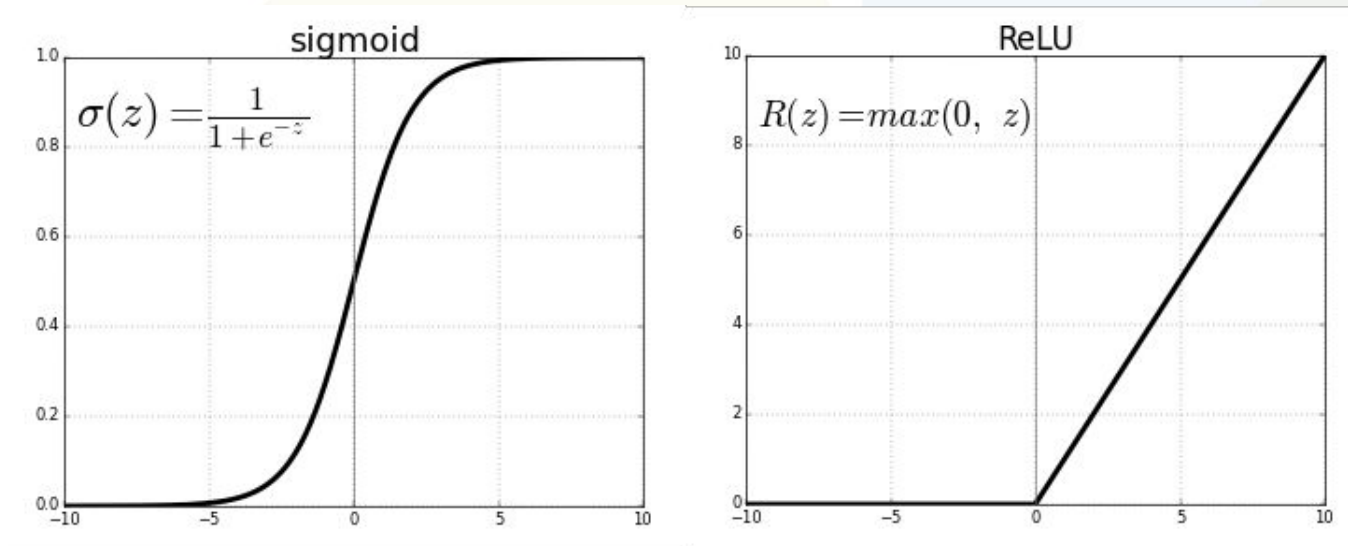


Image: <http://cs231n.github.io/convolutional-networks/>

Components of neural networks

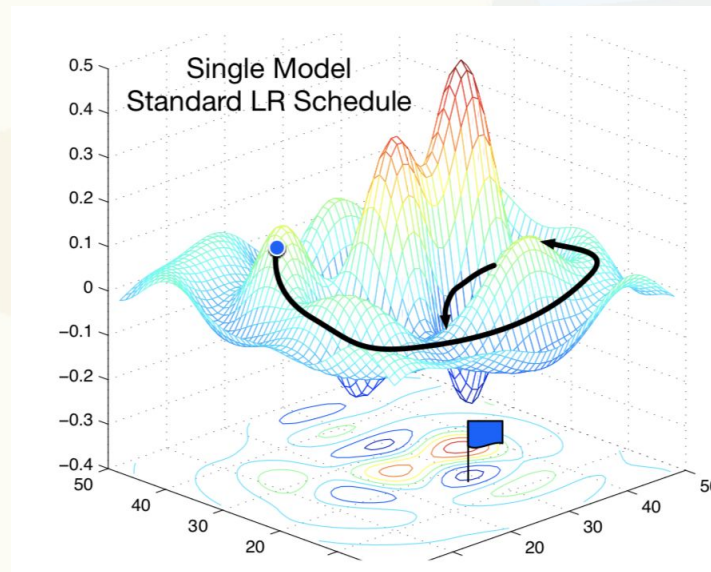
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https://cdn-images-1.medium.com/max/1600/1*XxxiA0jJvPrHEJHD4z893g.png

Training neural networks

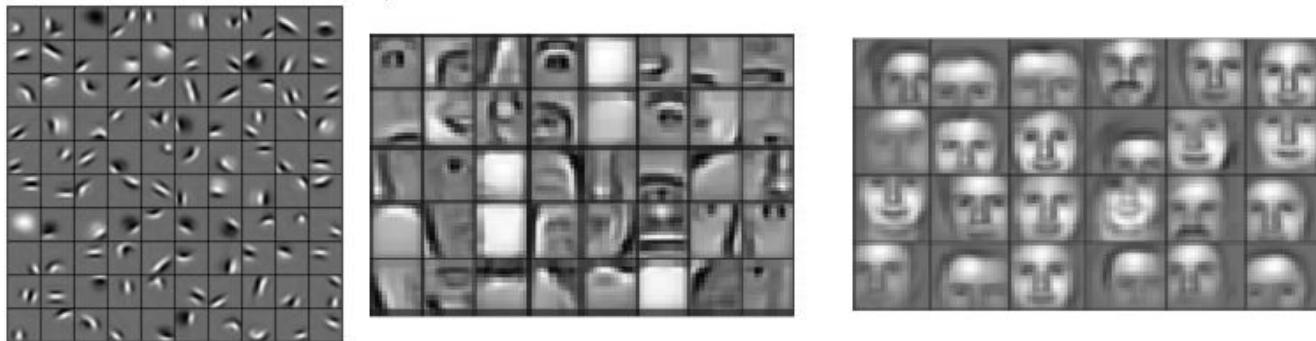
- Stochastic gradient descent
 - Pick a training sample
 - Feed it through the network
 - Determine the error of said prediction
 - Compute the share of correction for all hidden nodes and update the weights
- Many algorithms for updating the weights such as:
 - Gradient Descent
 - RMSProp
 - Adam



https://cdn-images-1.medium.com/max/2000/1*T5WWecP_EaQWk1yDX15h_w.png

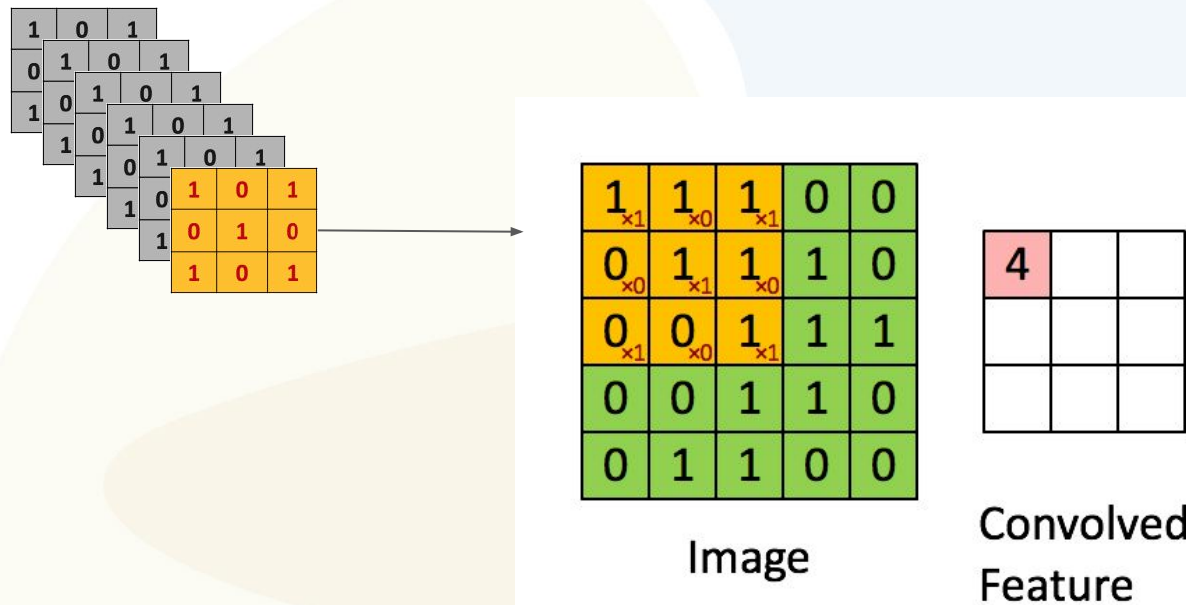
Convolutional neural networks

- Typically used in imaging data
- Many feature filters scan over the image to pick out specific features (e.g. edges, curves, eyes, nose, face)
- These filters learn to recognize features that make the performance of the prediction increase



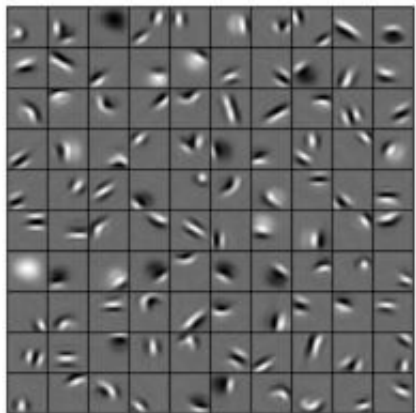
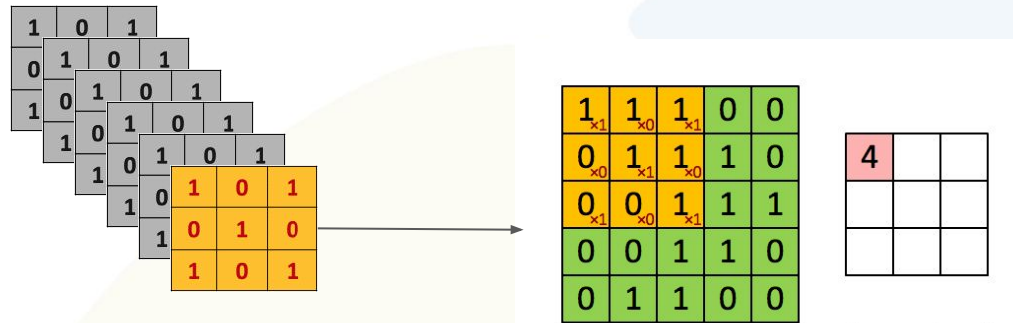
<https://devblogs.nvidia.com/parallelforall/deep-learning-nutshell-core-concepts/>

Learning features through kernels



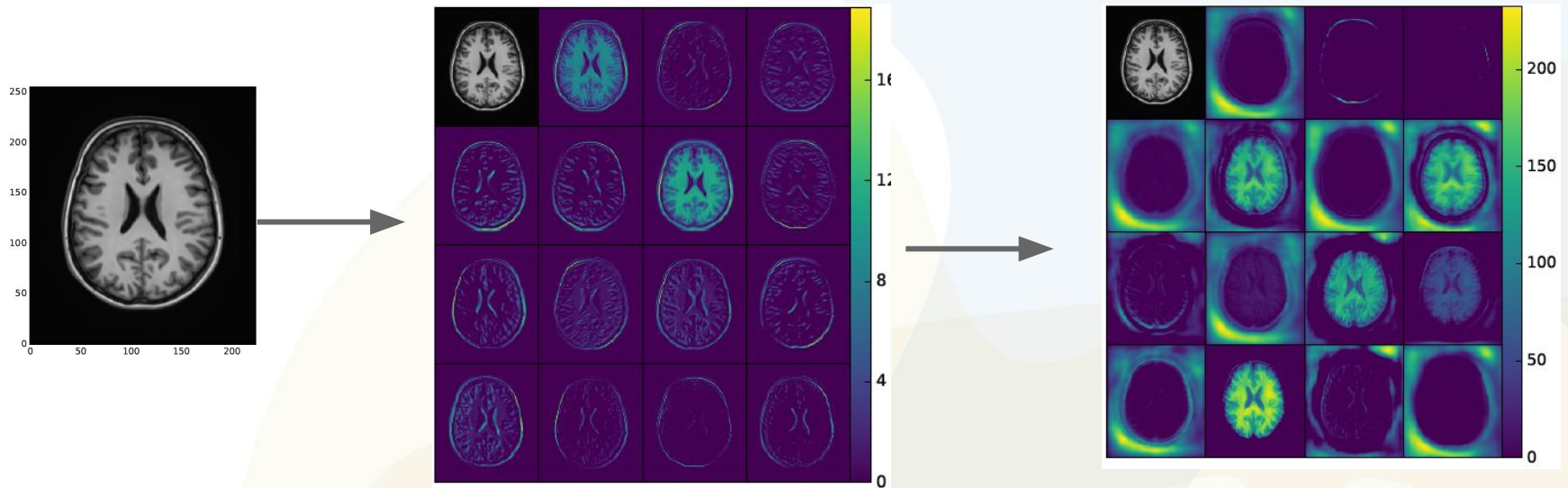
http://deeplearning.stanford.edu/wiki/index.php/Feature_extraction_using_convolution

Learning features through kernels



http://deeplearning.stanford.edu/wiki/index.php/Feature_extraction_using_convolution

Learning brain segmentation



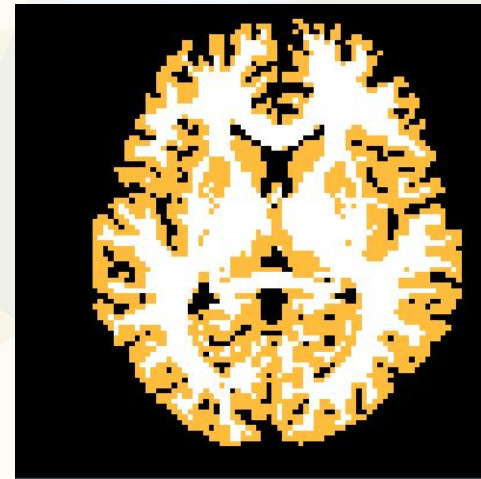
Fratila, R., Fonov, V., Collins, L.D., Arnold, D.L., Brown, R. (2017). DeepDiscovery: Rapid and Efficient Deep Learning for NeuroImaging. NeuroImage (submitted).

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1000 Functional Connectomes Project

- 261 MRI (skull stripped)
 - http://fcon_1000.projects.nitrc.org/fcpClassic/FcpTable.html
- Data stored in MINC (.mnc)
 - MINC is a medical imaging format based on HDF5
- GM/WM segmentation with FSL-5.0-fast



Build a Conv Net with Keras



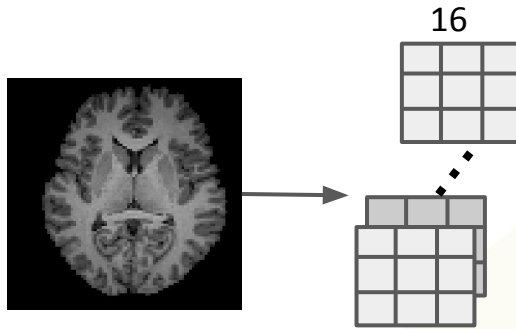
```
#Setup the input (IN) based on image dimensions <image_dim>
IN = Input(shape=(image_dim[1], image_dim[2],1))

#Create 4 convolutional layers with 3x3 kernels and 16, 32, 64, 128 kernels per layer
CONV1 = Conv2D(16, kernel_size=[3,3],activation='relu',padding='same')(IN)
CONV2 = Conv2D(32, kernel_size=[3,3],activation='relu',padding='same')(CONV1)
CONV3 = Conv2D(64, kernel_size=[3,3],activation='relu',padding='same')(CONV2)
CONV4 = Conv2D(128, kernel_size=[3,3],activation='relu',padding='same')(CONV3)

#Setup output layer (OUT)
OUT = Conv2D(1, kernel_size=1, padding='same', activation='softmax')(CONV4)

#Create model
model = keras.models.Model(inputs=[IN], outputs=OUT)
```

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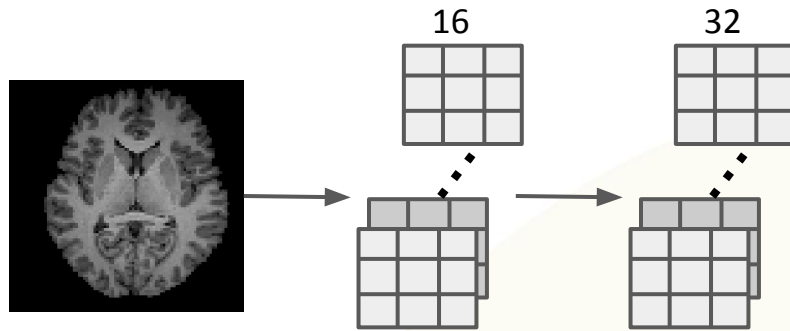
```
#Setup output layer (OUT)
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OUT = Conv2D(3, kernel_size=1, padding='same', activation='softmax')(CONV4)
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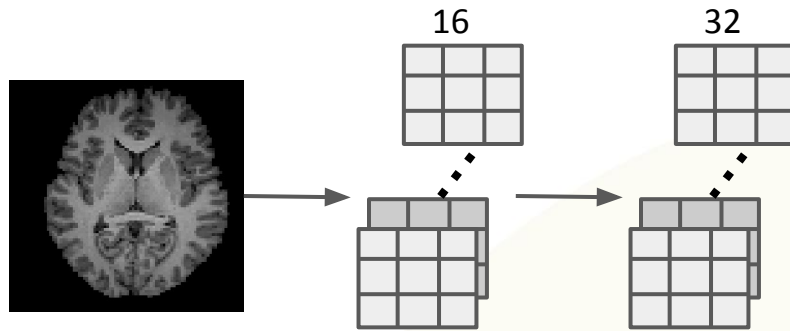
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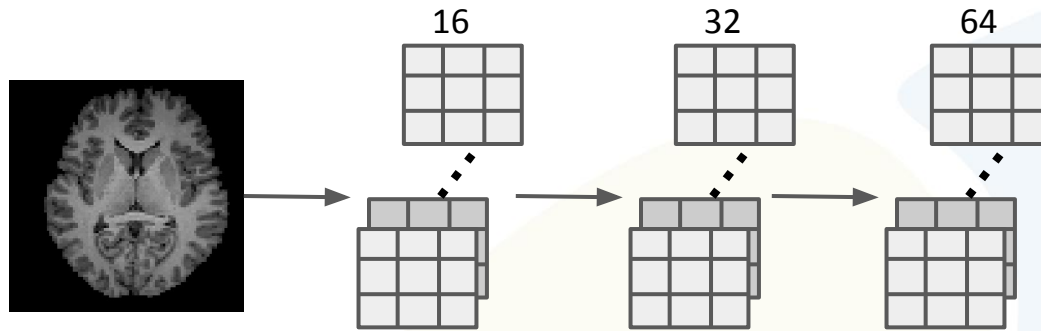
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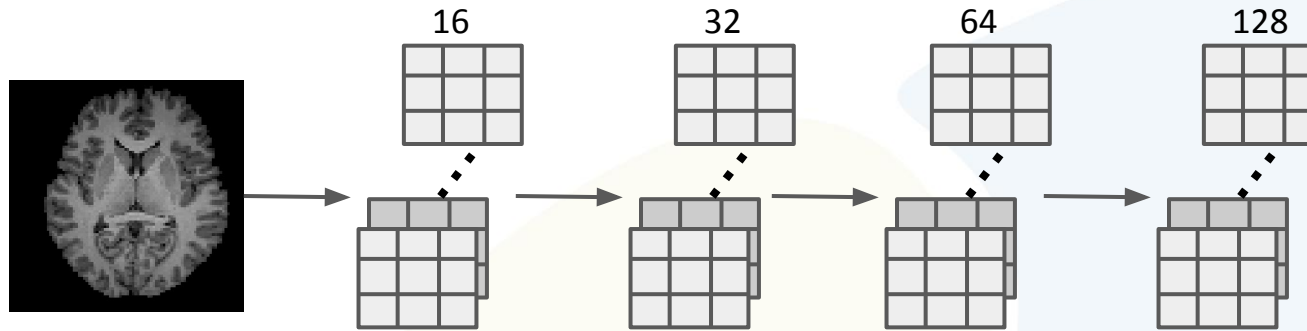
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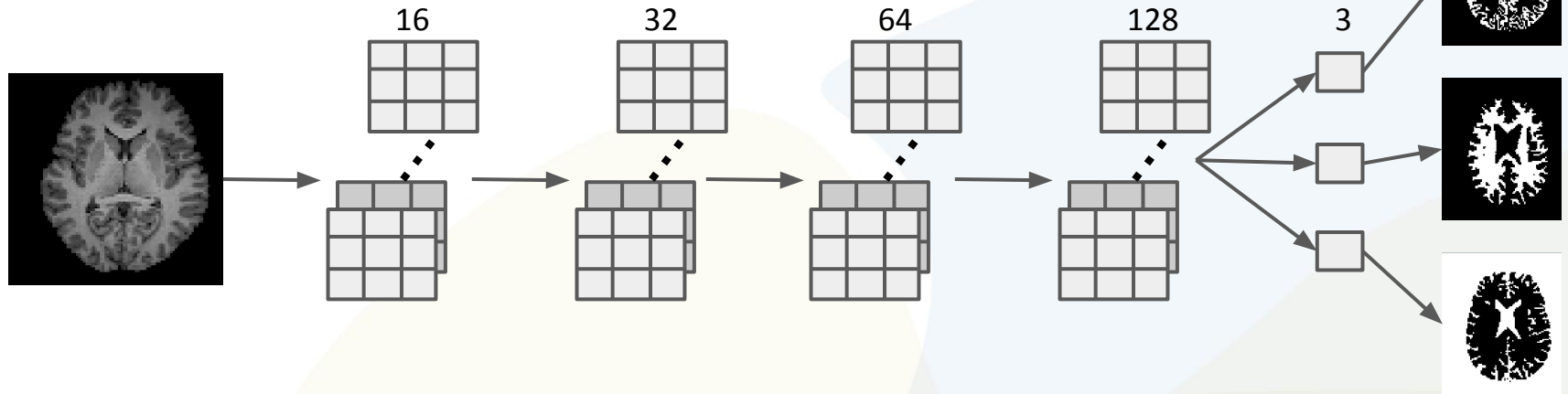
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```

```
#Create model  
model = keras.models.Model(inputs=[IN], outputs=OUT)
```

Setup & Fit Model

make_and_run_model.py

```
def compile_and_run(X_train, Y_train, X_validate, Y_validate, epochs):  
    #setup optimizer  
    ada = keras.optimizers.Adam(0.0001)  
  
    #setup define loss function  
    loss_function = 'categorical_crossentropy'  
  
    #compile the model  
    model.compile(loss = loss_function, optimizer=ada,metrics=[categorical_accuracy] )  
  
    #fit model  
    model.fit([X_train],Y_train,batch_size,validation_data=([X_validate],Y_validate),epochs=epochs)  
  
    #save model  
    model.save(model_name)
```

Base Model

models/neurotech_models.py

```
def base_model(image_dim, nK, kernel_size, drop_out):  
    # nK = number of kernels per layer  
    # kernel_size = size of the kernels  
    # dropout = dropout rate for each layer  
  
    #Setup the input (IN) and output (OUT) layers based on image dimensions  
    IN = OUT = Input(shape=(image_dim[1], image_dim[2],1))  
  
    n_layers=int(len(nK)) # number of layer  
    kDim=[kernel_size] * n_layers #list of kernel size equal in length to n_layers  
  
    for i in range(n_layers): # for each layer...  
        OUT=Conv2D(nK[i],kernel_size=[kDim[i],kDim[i]],activation='relu',padding='same')(OUT)  
        OUT = Dropout(drop_out)(OUT)  
  
    OUT = Conv2D(1, kernel_size=1, padding='same', activation='sigmoid')(OUT)  
    model = keras.models.Model(inputs=[IN], outputs=OUT)  
    return(model)
```



model_0_0

models/neurotech_models.py

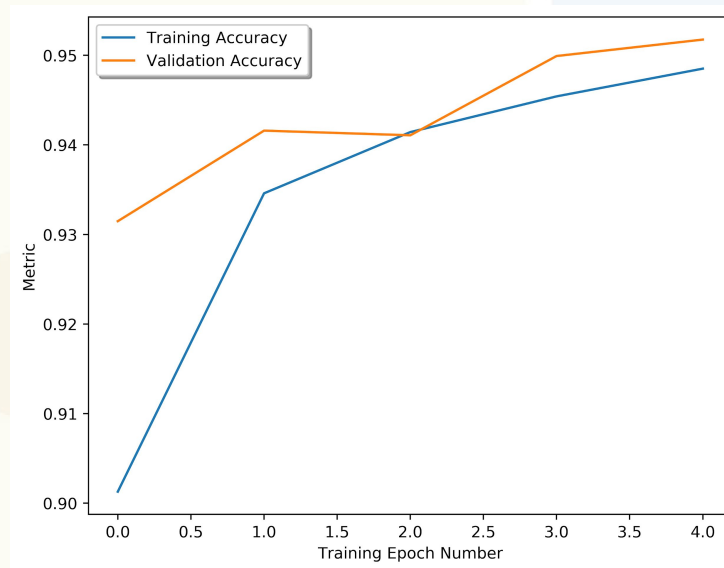
```
def model_0_0(image_dim):  
    # Create a convolutional network with  
    # [3,3] x 16  
    # [3,3] x 16  
    # [3,3] x 32  
    # [3,3] x 32  
    # [3,3] x 64  
    # [3,3] x 64  
    nK=[16,16,32,32,64,64]  
    kernel_size = 3  
    drop_out=0  
    return base_model( image_dim, nK, kernel_size, drop_out)
```

How to run a model with *minc_keras.py*

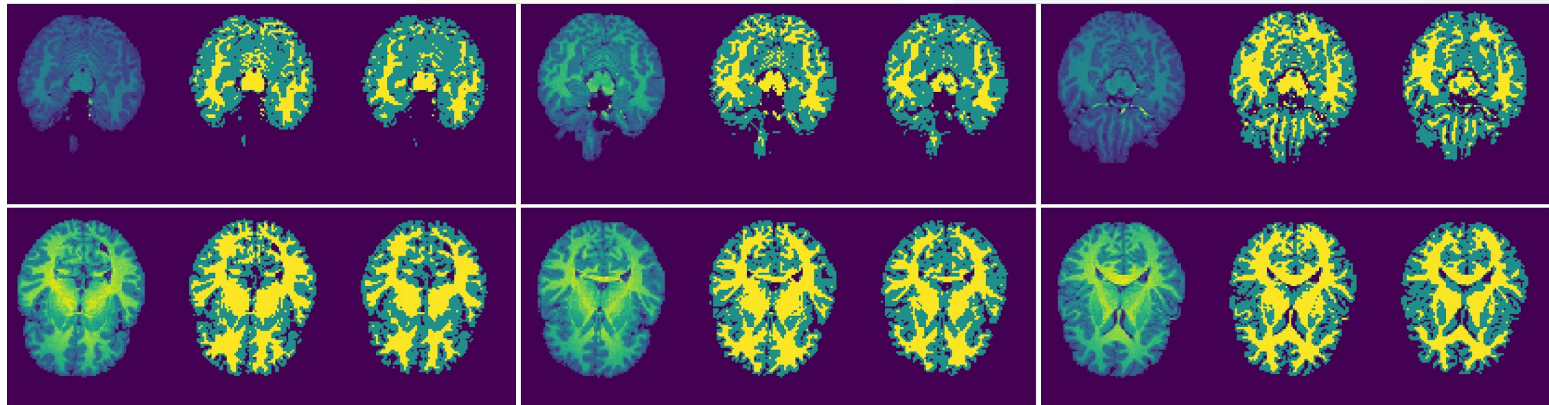
```
python3 minc_keras/minc_keras.py
--source output/          # source dir where input data is stored
--target .                 # output dir where results will be placed
--epochs 5                 # number of epochs to use to fit model
--model-type "model_0_0"   # name of model you want to use
--input-str "*T1w_anat*"   # string that identifies the input MRI images
--label-str "*seg*"        # string that identifies the labeled GM/WM images
--predict 1                # comma-separated list of subjects for prediction
--ratios 0.7 0.15          # ratio to use in training/validation/test splits
--activation-hidden "relu" # activation function for hidden layer
--activation-output "softmax" # activation function for output layer
```

Results for model_0_0

- Parameters = 71,987
- Test Accuracy= 0.951



Results for model_0_0



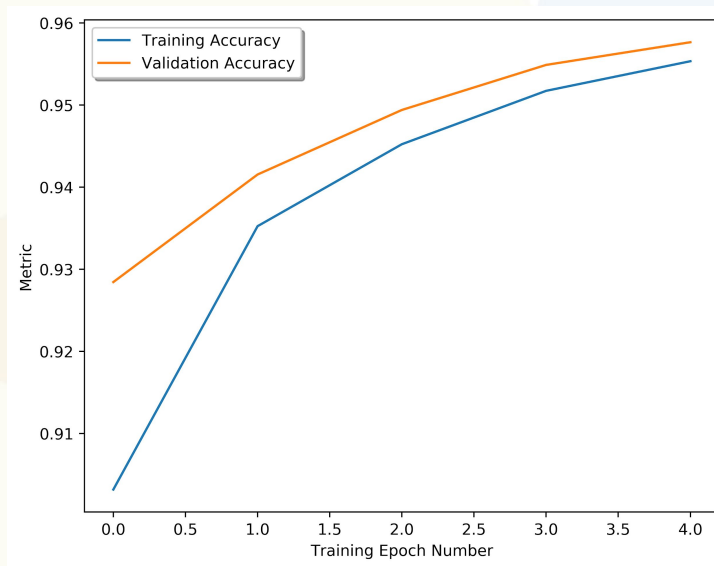
model_1_0

models/neurotech_models.py

```
def model_1_0(image_dim):  
    # Create a convolutional network with  
    # [3,3] x 16  
    # [3,3] x 16  
    # [3,3] x 32  
    # [3,3] x 32  
    # [3,3] x 32  
    # [3,3] x 64  
    # [3,3] x 64  
    # [3,3] x 64  
    # [3,3] x 128  
    nK=[16,16,32,32,32,64,64,64,128]  
    kernel_size = 3  
    drop_out=0  
    return base_model( image_dim, nK, kernel_size, drop_out)  
  
python3 minc_keras/minc_keras.py --source output/ --target . --epochs 5 --model-type model_1_0  
--input-str "*T1w_anat*" --label-str "*seg*" --predict 1 --ratios .1 .1
```

Results for model_1_0

- Parameters = 192,211
 - model_0_0: 71,987
- Test Accuracy = 0.957
 - model_0_0: 0.951



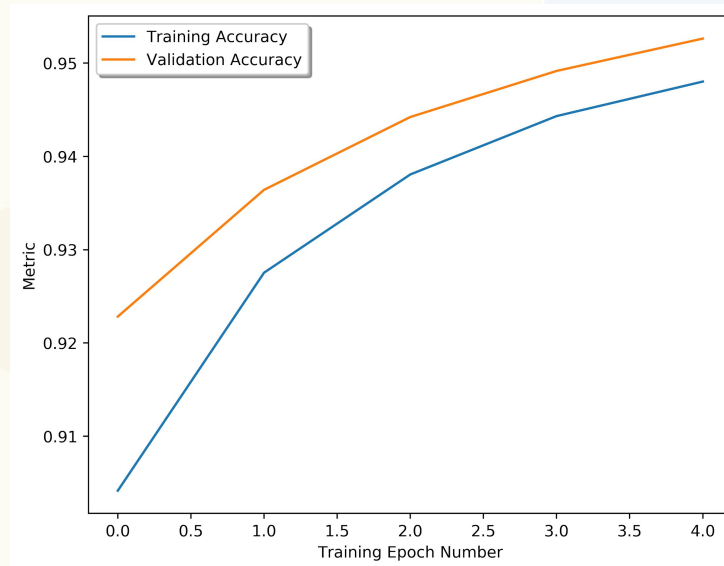
model_2_0

models/neurotech_models.py

```
def model_2_0(image_dim):  
    # Create a convolutional network with  
    # [5,5] x 16  
    # [5,5] x 16  
    # [5,5] x 32  
    # [5,5] x 32  
    # [5,5] x 64  
    # [5,5] x 64  
    nK=[16,16,32,32,64,64]  
    kernel_size = 5  
    drop_out=0  
    return base_model( image_dim, nK, kernel_size, drop_out)  
  
python3 minc_keras/minc_keras.py --source output/ --target . --epochs 5 --model-type model_2_0  
--input-str "*T1w_anat*" --label-str "*seg*" --predict 1 --ratios .1 .1
```

Results for model_2_0

- Parameters = 199,219
 - model_0_0: 71,987
- Metric Accuracy = 0.952
 - model_0_0: 0.951



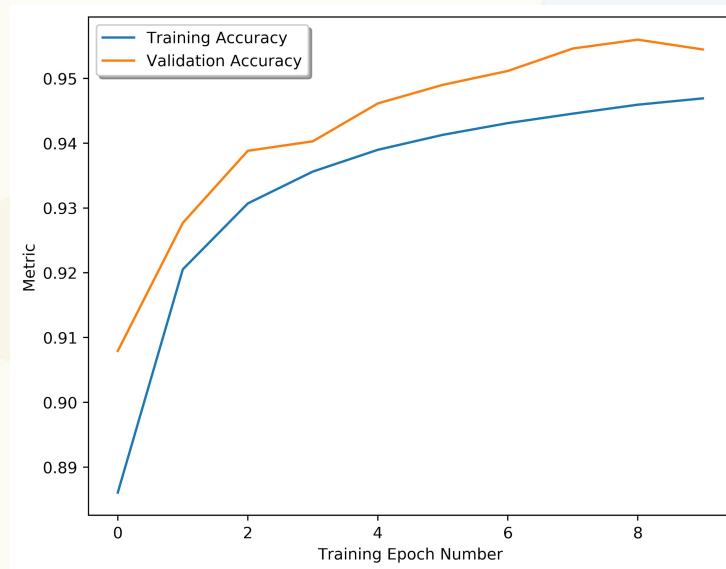
model_4_0

models/neurotech_models.py

```
def model_1_0(image_dim):  
    # Create a convolutional network with  
    # [5,5] x 16  
    # [5,5] x 16  
    # [5,5] x 32  
    # [5,5] x 32  
    # [5,5] x 64  
    # [5,5] x 64  
    nK=[16,16,32,32,64,64]  
    kernel_size = 5  
    drop_out=0.25  
    return base_model( image_dim, nK, kernel_size, drop_out)  
  
python3 minc_keras/minc_keras.py --source output/ --target . --epochs 5 --model-type model_4_0  
--input-str "*T1w_anat*" --label-str "*seg*" --predict 1 --ratios .1 .1
```

Results for model_4_0

- Parameters = 532,435
 - model_0_0: 71,987
- Test Accuracy: 0.954
 - model_0_0: 0.951



Free coding

1. Can you find a model that does better than 95% without overfitting?
 - a. What happens when you change the activation functions?

2. You can change the training/validation/test ratio to increase samples for training
 - a. e.g., `--train 0.3 0.3` (30% training, 30% validation, 60% split)
 - b. a large training set will slow down the training, but reduce overfitting

3. Ask volunteers and organizers for help!

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- Paul Lemaitre, PhD
 - Slides + writing code for minc_keras

