Chance, Machine Learning Algorithms, MVPA, Brains on Trial

Commentary on this assignment:

This assignment revisits concepts from probability and hypothesis testing in assessing accuracy of machine learning algorithms. Then you'll investigate a specific ML algorithm (separate submission). Then you'll apply machine learning to a more complex problem than the 4 brain regions, which will allow you to apply methods to avoid overfitting. Finally, you'll read or watch a video about the use of neuroscience in the courtroom and in lie detection, which raises important questions about how our legal system works.

I provided very rough time estimates just to give you a sense of scale. I expect that there will be lots of variability in how much time people spend on this assignment overall and how much time people spend in each section. I trust you to make the good decisions for your learning goals and the course goals around challenging yourself, engaging your curiosity, and contributing to class.

This document is a bit long, so I've included a linked table of contents and pictures of puppies (puppies only available in this version: https://docs.google.com/document/d/1CmVUOSBBxdDdp-JU8pCzN5pKm6gdCE1sWJtiQXHqv4E/edit?usp=sharing).

The data you need are here: https://drive.google.com/file/d/12cJmNYllwkhTGyHa9NAWpZWJVqPw4hib/view?usp=sharing

Table of Contents

Understanding “chance” in relation to classification [30 mins]

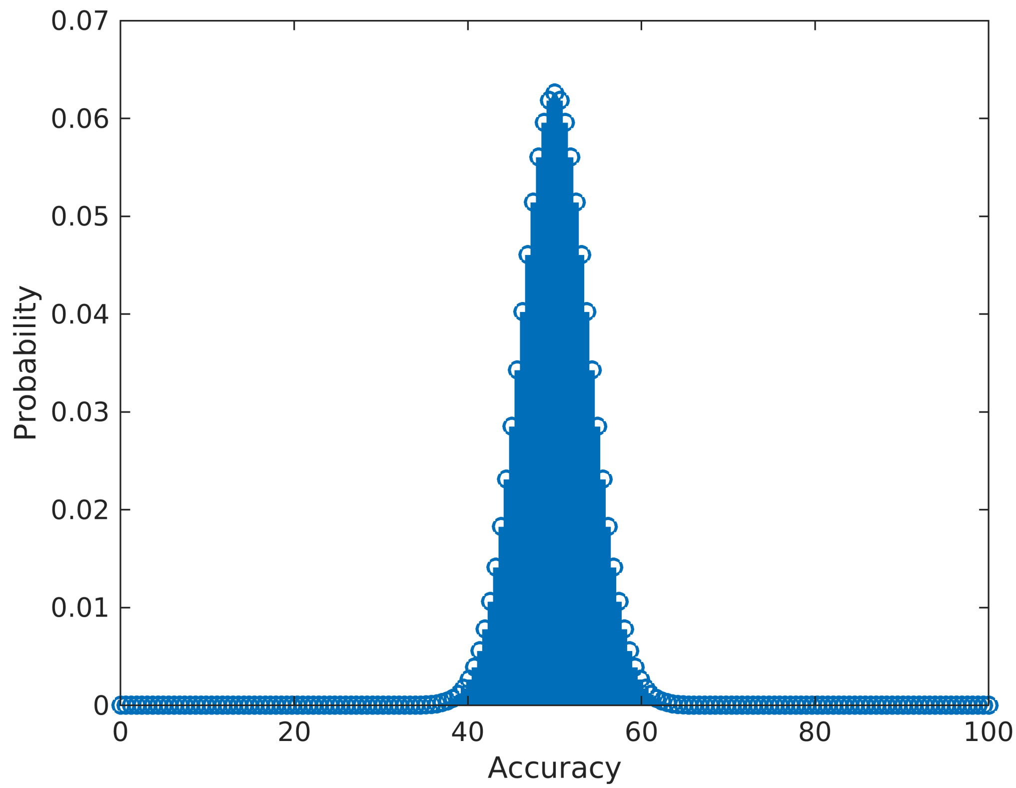
In this section, we’re going to explore probability in relation to classification accuracy. We’ll use the example from our faces vs houses fMRI data. In the training data, we have 162 total examples and in the test data we have 54 total rows of data. Each is evenly split between faces and houses.

If my algorithm just flips a coin each time (“operates at chance level”, p(face)=0.5):

Exercise 1a: What is the most probable accuracy?

I think it should be close to 50, but since we have a discrete sample set, the accuracy might not be exactly 50 if there is an odd number of samples

```
n = 162;
test_n = 54;
b = makedist("Binomial", 'N', n, 'p', 0.5);
x = 0:n; % number of correct predictions
stem(100.*(x./n), b.pdf(x), 'LineWidth', 2);
xlabel('Accuracy');
ylabel('Probability');
```



Exercise 1b: What is the expected value of the accuracy?

Here are some resources about expected values that might be helpful:

https://ocw.mit.edu/courses/mathematics/18-05-introduction-to-probability-and-statistics-spring-2014/readings/MIT18_05S14_Reading4b.pdf

https://www.stat.purdue.edu/~zhanghao/STAT511/handout/Stt511%20Sec3.3.pdf

Expecting around 50, but it can be a non-discrete integer because it is a weighted average

```
expectedValueAccuracy = b.mean/n
```

```
expectedValueAccuracy = 0.5000
```

Exercise 2a: For the training data, what is the probability of getting an accuracy of 50% or worse?

```
p = binocdf(n*0.5, n, 0.5) % inclusive of 50%
```

```
p = 0.5313
```

Exercise 2b: For the training data, what is the probability of getting an accuracy of 50% or worse?

```
% for testing data
p = binocdf(test_n*0.5, test_n, 0.5) % inclusive of 50% and fewer options so each optic
```

```
p = 0.5540
```

I want to set a threshold to reject the hypothesis that my algorithm is operating a chance level. Let's say that I feel comfortable being wrong 10% of the time when my algorithm is operating at chance.

Exercise 3a: What should I choose as my accuracy threshold for the training data?

null_hypothesis: my algorithm is operating at chance level

alternative_hypothesis: my algorithm is not operating at chance level

alpha = 0.1

```
b = makedist("Binomial", 'N', n, 'p', 0.5);
100 * icdf(b, 0.9)/n % if 90% were correct, find number correct
```

```
ans = 54.9383
```

Exercise 3b: What accuracy threshold should I use for my test data?

```
b = makedist("Binomial", 'N', test_n, 'p', 0.5);
100 * icdf(b, 0.9)/test_n % if 90% were correct, find number correct
```

```
ans = 59.2593
```

Exercise 3c: Are these the same or different? Why?

Different because there are a different number of trials in train and test. If there are more trials, we can be more confident in our result and tighten the range.

Now, let's suppose I have an algorithm that is 70% accurate in reality.

Exercise 4: What is the probability that it will perform at chance or worse on the test data?

```
p = 0.7;
binocdf(0.5*test_n, test_n, p)
```

```
ans = 0.0016
```

In the questions above, we have been considering a situation where we have an equal number of face and house examples in our data. Now let's think about a situation where that is not the case. Our training data still has 162 total examples, but now 130 of them are faces.

Exercise 5: What classification accuracy would we get on the train data if our algorithm just guessed face every time?

```
100 * 130/162
```

```
ans = 80.2469
```

Challenge exercise: If our algorithm is still just a coin flipper, what is the expected value of the accuracy on our training data?

```
p = 0.5;
tp = 130 * p; % number of tp guessed correctly by random chance
tn = (162 - 130) * p; % number of tn guessed correctly by random chance
(tp + tn)./162
```

```
ans = 0.5000
```

Used a bayesian tree to draw prior and posterior

.3 /   \ .7

.5 / \ .5   .5 / \ .5

Use external resources to investigate, understand, and explain an algorithm [90 mins]

Exercise 6: Explain algorithm (separate submission)

Choose one machine learning algorithm that you want to learn more about. Create a short explanation of this algorithm using whatever media you prefer (text, video, slides, whiteboard, audio, stone carving).

Please share any good resources that you find in this mutual document.

https://docs.google.com/document/d/1AC4ULXd8sHEbw2M3u-tdkT0lvJylNvOjN7ojFg1NOQw/edit?usp=sharing

If you are new to machine learning, I recommend “K nearest neighbors” or “linear support vector machines” as good starting algorithms.

How to submit this part: This part of the assignment has a separate submission. This will serve as one of our learning check-offs. Please submit this on time if possible, since we’ll probably be doing a peer review between Monday and Wednesday.

Multi-voxel pattern analysis on fMRI data [90 mins]

This is the fMRI data from one person (subject 2 in this study: Haxby, J.V., Gobbini, M.I., Furey, M.L., Ishai, A., Schouten, J.L., Pietrini, P. (2001). Distributed and overlapping representations of faces and objects in ventral temporal cortex. Science, 293(5539):2425-30). There are 162 examples in the training set (these correspond to times where a person saw a house or a face). The labels tell you whether they were looking at a face or a house (same as last assignment). The data are linked at the top of this document.

Think of the voxel values as the potential features. In the train_fmri3d data, the voxels are in a 3 dimensional array (that is 40 x 64 x 64), plus a 4th dimension that is the 162 examples. However, for the classifier, you need to reshape the data to a 2 dimensional array.

```
fmri2d= squeeze(reshape(train_fmri3d,1,1,[],162))'
```

```
fmri2d = 162×163840 single matrix
     0     0     0     0     0     0     0     0     0     0     0     0     0 ...
     0     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0     0
```

⋮

fmri2d has the dimensions of examples x voxels. However, we know that a bunch of these values are outside of the brain (since train_fmri3d is just a cube shape, and fun fact… our brains are not cube shaped).

If we wanted to make a variable that contained every voxel in the brain (but excluded those not in the brain), we can use our brain mask. The brain mask has 1s for voxels in the brain and 0s for voxels not in the brain. We need to reshape this to align with the shape of fmri2d.

```
brainmask2d=single(reshape(mask,1,[]))
```

```
brainmask2d = 1×163840 single row vector
     0     0     0     0     0     0     0     0     0     0     0     0     0 ···
```

Create a variable called brainvals that has the dimensions of (examples x voxels in the brain). Exercise 7: What are the actual dimensions of this variable (numbers)?

```
brainvals = fmri2d.*repmat(brainmask2d, [162 1])
```

```
brainvals = 162×163840 single matrix
     0     0     0     0     0     0     0     0     0     0     0     0     0 ···
     0     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0     0
     ⋮
```

```
brainvals = brainvals( :, any(brainvals))
```

```
brainvals = 162×39912 single matrix
   45.1284  -26.6410  -42.3341  -15.2561   59.0485  -11.6695  -17.1604  -20.3824 ···
   41.1242  -16.6047  -36.3399   -8.2558   63.0427  -18.6882  -23.0782   -6.3803
   39.1200  -22.5684  -26.3456   -1.2556   62.0368  -20.7068  -20.9959  -12.3783
   39.1159  -15.5321  -31.3513  -10.2553   68.0310  -15.7255  -26.9137  -17.3762
   36.1117  -24.4957  -27.3571   -4.2551   75.0251   -7.7441  -22.8314  -15.3742
   48.1075  -27.4594  -32.3628   -6.2549   77.0193  -10.7627  -21.7491  -19.3722
   42.1034  -24.4231  -22.3686    0.7454   65.0134  -16.7814  -20.6669  -14.3701
   45.0992  -17.3868  -27.3743  -10.2544   68.0076  -15.8000  -23.5846  -11.3681
   40.0950  -21.3505  -19.3801  -10.2542   64.0017  -14.8186  -17.5024  -18.3660
   31.9532  -48.1158  -42.5753  -56.2460   36.8028  -23.4524  -26.7056  -42.2967
     ⋮
```

162 x 39912

Dang, that's a lot of voxels! We could throw all of these voxels into our classifier, with each voxel serving as a feature. I would strongly recommend against this, why?

Think. Then highlight text below for answer

This may lead to overfitting our classifier. We have 162 examples and more than 30k variables.

Also, this will take forever to run and load.

Exercise (BIG ONE): Run multivoxel pattern analysis (machine learning on voxels).

Run classification of faces vs houses using some subset of voxels. Be sure to use cross-validation to help prevent overfitting.

For this part of the assignment, I'm asking you to piece together and extend some of the code that you've seen already. You can look at the brainViewer.mlx for more example code for selecting a subset of voxels from the data. You can look at fmriToFeaturesClassification for tips on how to implement the classifier using only code (though you'll still need to look up how to do cross validation). You are also welcome to use the classificationLearner app if you prefer.

You should explore different aspects of the feature space and document what you try and what you observed. Some things you might try:

- downsample the brain data to a smaller number of voxels randomly
- downsample the brain data to a smaller number of voxels by strategically selecting a brain region (you may still want to downsample within a region if it is big)
- use a dimensionality reduction technique such as PCA or ICA
- create new features that represent and summarize information about groups of voxels (this is like what we did by taking the average activity in each of the 4 regions, but you can get more creative if you want to)

Challenge: Choose some parameter to manipulate (e.g., # of nearest neighbors in KNN algorithm, or how many voxels to include). Generate a plot to represent the relationship between this parameter and a measure of how well your classifier performs (e.g., accuracy). Important tips (feel free to add some here or ask questions)

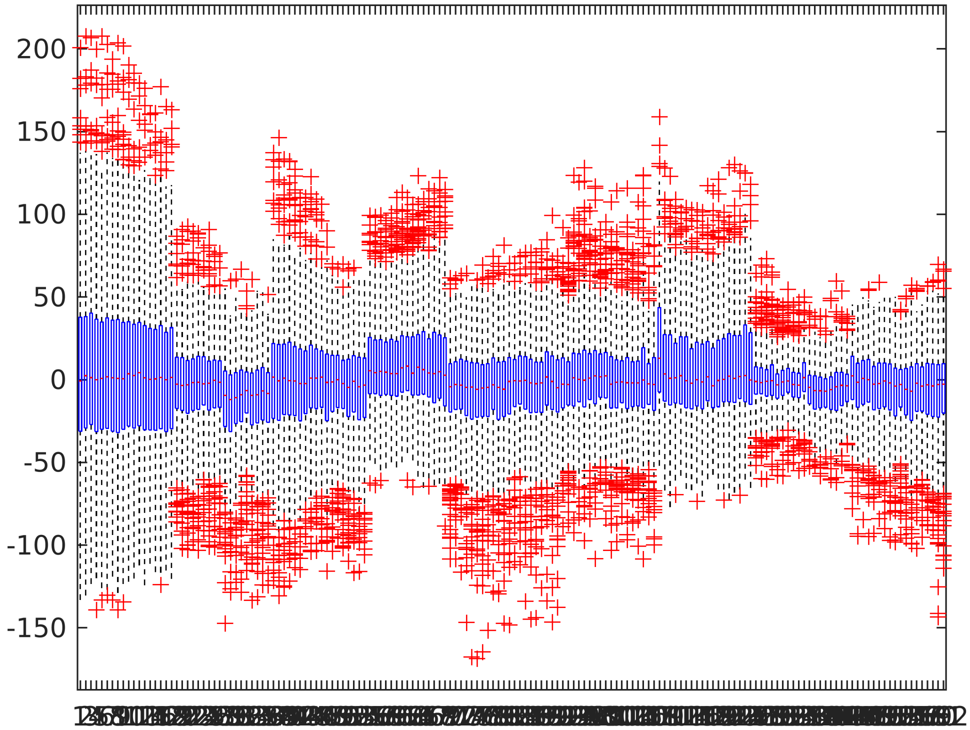
- As I mentioned in class, the ventral temporal lobe plays an important role in visual processing. One of the 4 regions that we explored before is the ventral temporal lobe.
- If you are using the Classification Learner, only use a table that has a reduced number of features already, otherwise, it will take forever to load the data. (My computer took several minutes to load a table that was 162 x 39913). For computational reasons, you'll probably want max out at around 1000 (but this depends on your computer.)
- Matlab is probably looking for your "predictors" (features) to be in a table. If you need to convert an array to a table, check out: array2table(brainvals).

- If you are using Matlab 2019, you'll need to take one additional step if you want to use the classificationLearner app. You must put the "responses" and the "predictors" in the same table.
- You can do this by following this general format: train_all = [table(train_labels) train_4regions]; In your version, you'll have a different variable than train_4regions.
- Or you can use something like this if you have an array:
- train_table2d = array2table(train_fmri2d); %
- train_table2d.labels = train_labels;
- Other tips from students (you can add a comment here).

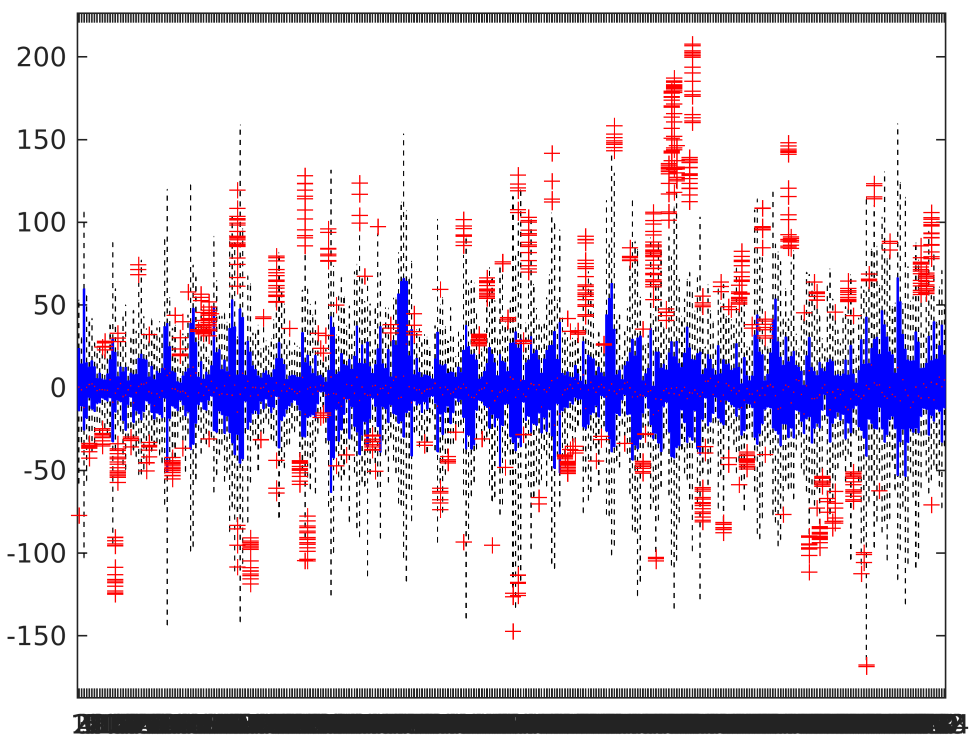
```
n = 162;
region1 = fmri2d.*repmat(single(reshape(mask_region1,1,[])), [n 1]);
region1 = region1( :, any(region1))
```

```
region1 = 162×334 single matrix
   44.8421   29.0900   88.2853  -23.1248   -0.8906    4.6762   25.0965   -6.1110 ···
   40.9222   27.1457  106.1361  -10.0830    7.1035    4.7111   23.0804    0.8875
   43.0023   30.2014   97.9869  -24.0412   -4.9025    0.7461   20.0644   -5.1141
   41.0824   25.2571   97.8377  -16.9994   -0.9084   -0.2190   20.0483   -5.1156
   40.1625   26.3128   99.6885  -12.9575    6.0856    4.8159   23.0322   -6.1171
   40.2426   24.3685   96.5393  -18.9157    2.0796    2.8509   19.0162   -8.1186
   49.3227   26.4242   82.3901  -20.8739    0.0737    1.8858   22.0001   -2.1201
   46.4028   27.4799   90.2409  -20.8321   -2.9323    0.9207   17.9841   -4.1216
   41.4829   22.5356   86.0917  -21.7903    0.0618    3.9556   20.9680   -5.1231
   42.2065   26.4295   70.0187  -19.3685    0.8591    1.1433   18.4219   -2.1741
      ⋮
```

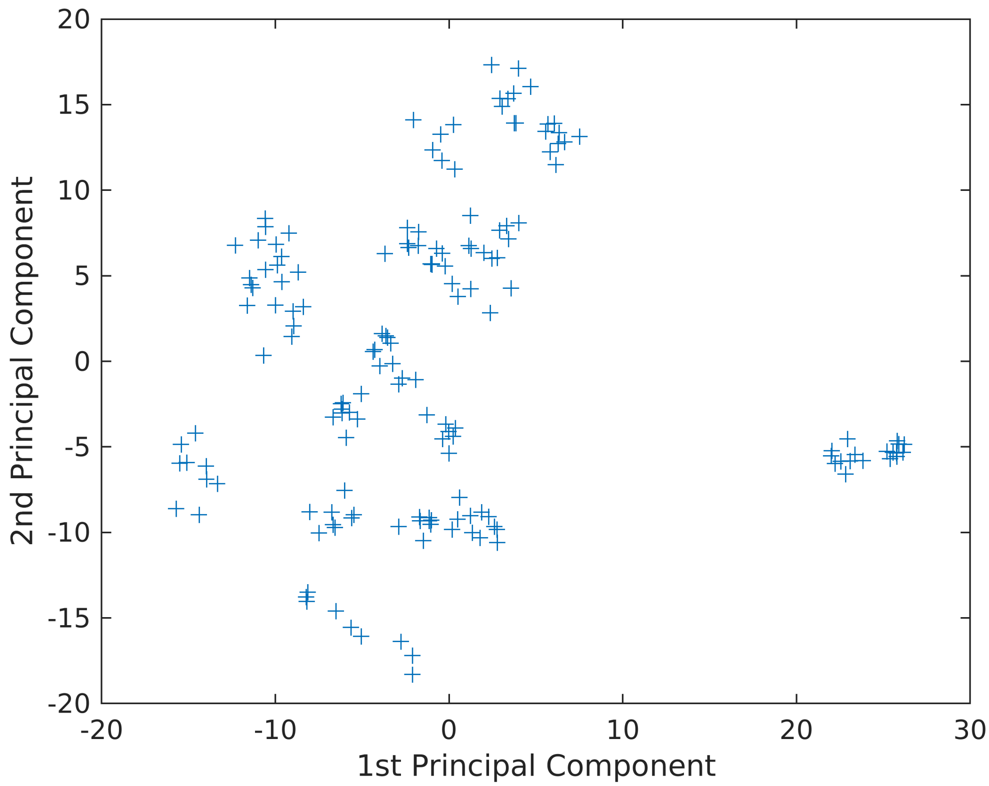
```
% boxplot by sample
boxplot(region1')
```



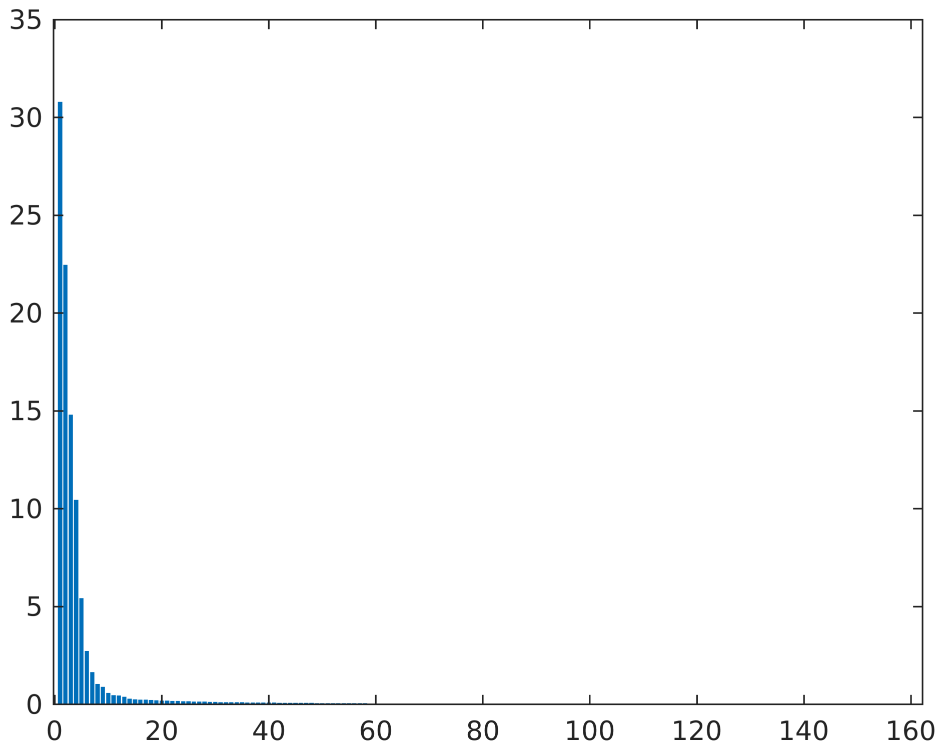

```
% boxplot by feature
boxplot(region1)
```



```
%corr(region1,region1);
[wcoeff,score,latent,~,explained] = pca(region1,'VariableWeights','variance');
figure()
plot(score(:,1),score(:,2),'+')
xlabel('1st Principal Component')
ylabel('2nd Principal Component')
```




```
figure()
bar(explained)
```




```
region1 = fmri2d.*repmat(single(reshape(mask_region1,1,[])), [n 1]);
region1 = region1( :, any(region1));
region2 = fmri2d.*repmat(single(reshape(mask_region2,1,[])), [n 1]);
region2 = region2( :, any(region2));
region3 = fmri2d.*repmat(single(reshape(mask_region3,1,[])), [n 1]);
region3 = region3( :, any(region3));
region4 = fmri2d.*repmat(single(reshape(mask_region4,1,[])), [n 1]);
region4 = region4( :, any(region4));

[wcoeff1,score1,latent1,~,explained1] = pca(region1);
[wcoeff2,score2,latent2,~,explained2] = pca(region2);
```

```
Warning: Columns of X are linearly dependent to within machine precision.
Using only the first 155 components to compute TSQUARED.
```

```
[wcoeff3,score3,latent3,~,explained3] = pca(region3);
[wcoeff4,score4,latent4,~,explained4] = pca(region4);

explained1 % first 7
```

```
explained1 = 161×1 single column vector
   36.2376
   23.9686
   15.8495
   10.7287
    4.2774
    1.8731
    1.1529
    0.7581
```

```
    0.5554
    0.4024
     ⋮
```

```
explained2 % first 8
```

```
explained2 = 161×1 single column vector
   43.1001
   19.9416
    9.8243
    7.8444
    3.7835
    2.1081
    1.6599
    1.2185
    0.7526
    0.5982
     ⋮
```

```
explained3 % first 9
```

```
explained3 = 161×1 single column vector
   30.9446
   19.2588
   14.2063
    5.7947
    4.4339
    3.8011
    2.8119
    1.3967
    1.0155
    0.9470
     ⋮
```

```
explained4 % first 8
```

```
explained4 = 31×1 single column vector
   52.1313
   15.8923
   10.1483
    7.3441
    3.6160
    2.2814
    1.6386
    1.3586
    0.9103
    0.7898
     ⋮
```

```
region1_10 = score1(:, 1:10)
```

```
region1_10 = 162×10 single matrix
  882.2699 -249.0720  -17.4099   99.1775   28.8254  -62.8130  -19.3104   36.6531 ···
  870.9958 -238.3671    0.1133  148.2624   38.4298  -62.0343  -25.2092   43.2560
  884.9216 -229.5898   22.2092  141.0955   41.0693  -65.1118  -37.8074   31.4339
  873.9255 -247.0448  -16.7304  142.4166   22.6208  -67.9866  -21.6513   26.2031
  855.6765 -251.0692  -18.9221  132.2741   39.1652  -76.4831  -13.2179   27.8672
```

```
  876.3199 -230.3638    3.4694  128.8664   34.3494  -67.4803  -25.3893   27.2125
  866.0078 -256.0186    6.7014  100.1808   11.7942  -53.0865  -13.0122   30.2270
  877.5620 -243.5495  -17.7944  103.2499   27.9399  -76.0061  -16.4831   19.0183
  857.6501 -264.7130  -24.1600  118.0704   13.0859  -61.9725  -11.5007   23.3495
  809.6169 -261.3054   67.0503   88.7841   25.6060  -41.0882   -6.1224   11.0350
      ⋮
```

```
region2_10 = score2(:, 1:10)
```

```
region2_10 = 162×10 single matrix
  500.3787  -17.8039   53.0067  -63.0664   -6.9085  -30.1563   36.5739  -11.0019 ···
  476.8148  -18.8309   38.2953  -64.6518  -12.3547   -7.2812   24.9917    1.2449
  474.8785  -14.6288   43.4600  -61.0633  -21.0159  -10.7514   29.6061   -0.8047
  491.4526  -25.5925   48.6052  -56.0446  -13.0624   -5.6371   27.1252   -6.8921
  474.1767  -13.9762   48.3750  -63.4748  -13.0364   -5.8352   31.7320    7.9991
  487.9001  -23.4758   43.8801  -59.3961  -15.3894  -26.1054   30.9382  -18.9955
  490.4452  -26.3618   42.5140  -63.7428    3.0023  -41.1618   27.9324  -19.6379
  486.4983  -28.6231   48.3556  -61.0351    3.5750  -55.3451   30.2215  -16.7835
  504.4672  -30.7581   48.3434  -55.0466   -9.9613  -31.1667   20.1318  -13.8631
  440.9283  -11.7494   18.2610  -34.5127   16.9274  -35.4605   -2.2187  -16.8447
      ⋮
```

```
region3_10 = score3(:, 1:10)
```

```
region3_10 = 162×10 single matrix
 -602.9750    4.3032 -267.0129   -3.7728  -27.3058  -29.2039   46.4935   51.0825 ···
 -606.9026   16.3646 -247.8228   39.7788  -34.4314  -10.7661   16.0021    4.3593
 -597.9197   -5.4570 -248.6415   19.6119  -34.7483  -12.5068   44.4269   22.7052
 -600.8988  -15.2894 -242.4704    3.1686  -50.0556  -32.8292   36.7889   22.3156
 -610.7221    8.3663 -244.7362   10.9536  -52.8146  -28.6015   41.1013    8.9603
 -605.3700  -13.4790 -243.7588   11.9757  -54.5816  -40.2087   64.9597    3.9702
 -569.9920    2.7016 -245.7481    5.8671  -11.7410  -29.9437   26.8847   18.8572
 -587.5948   -5.5146 -248.1978   27.1901  -25.3469  -60.6531   52.7184  -30.1970
 -583.7650  -48.5553 -213.8648   24.3634  -29.9500  -65.3586   76.7826   -1.7185
 -477.6545  -20.4015 -156.0078   -1.0636   58.3452  -51.4016  -21.7912   35.6059
      ⋮
```

```
region4_10 = score4(:, 1:10)
```

```
region4_10 = 162×10 single matrix
 -200.7725  -88.9944   66.3656   30.2970    7.5523    2.0962   -5.4538   -5.7794 ···
 -142.5894  -25.5757  128.2361   46.4931   -6.5584  -10.7303  -28.3200    9.1455
 -169.1275  -21.1523  101.0748   87.2609  -56.4232   12.0617    2.9201    9.8378
 -190.8640  -79.1459   77.3002   28.7072   -4.2127   -0.5531    6.3055   -0.1726
 -185.5584  -79.0591   91.0915   35.9461   -4.6241   -1.3296    8.1930   -6.1525
 -185.4122  -76.7435   78.5448   24.6691   -6.5634    6.8628   -1.1384   -0.2712
 -197.2589  -59.4490   74.7602   43.4277   -8.1264   -1.1025  -22.3357    6.4737
 -207.4717  -75.2307   78.9758   28.4065  -20.0961   -1.3167    1.7366  -11.4634
 -212.6579  -75.7360   71.7959   24.7281   -7.0967   -1.8303   10.4450   -1.5655
 -230.9032  -86.6549   53.2212   31.3413   -8.3701    1.6614  -15.4309   10.1136
      ⋮
```

```
chosen_features = [region1_10 region2_10 region3_10 region4_10]
```

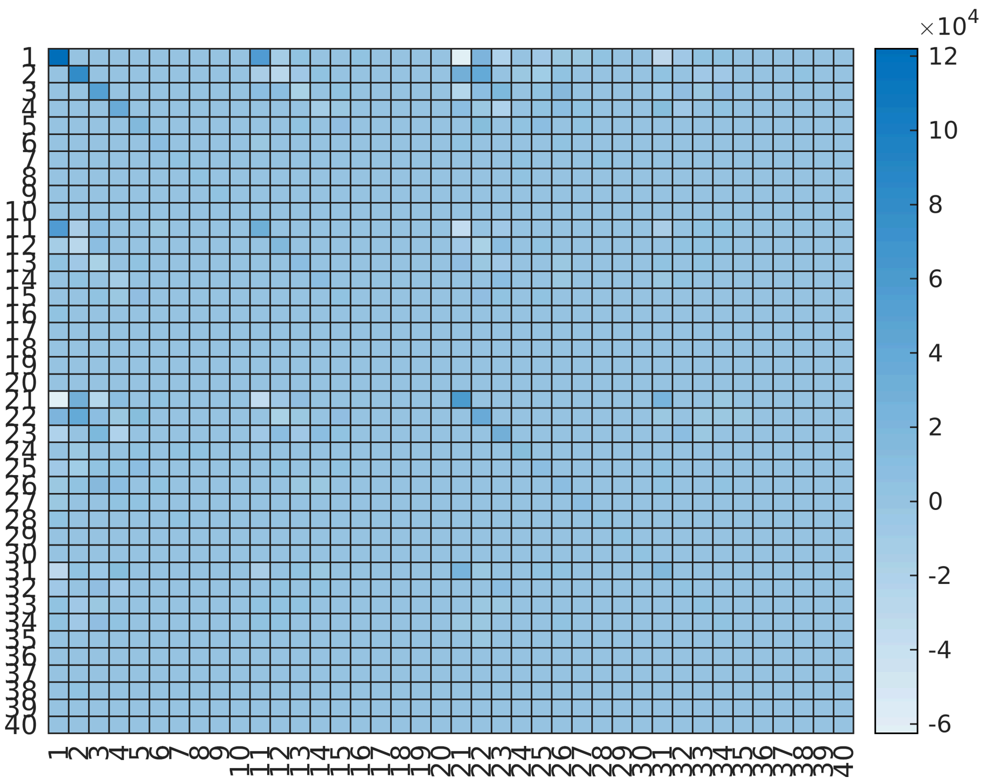
```
chosen_features = 162×40 single matrix
  882.2699 -249.0720  -17.4099   99.1775   28.8254  -62.8130  -19.3104   36.6531 ···
  870.9958 -238.3671    0.1133  148.2624   38.4298  -62.0343  -25.2092   43.2560
```

```
    884.9216 -229.5898   22.2092  141.0955   41.0693  -65.1118  -37.8074   31.4339
    873.9255 -247.0448  -16.7304  142.4166   22.6208  -67.9866  -21.6513   26.2031
    855.6765 -251.0692  -18.9221  132.2741   39.1652  -76.4831  -13.2179   27.8672
    876.3199 -230.3638    3.4694  128.8664   34.3494  -67.4803  -25.3893   27.2125
    866.0078 -256.0186    6.7014  100.1808   11.7942  -53.0865  -13.0122   30.2270
    877.5620 -243.5495  -17.7944  103.2499   27.9399  -76.0061  -16.4831   19.0183
    857.6501 -264.7130  -24.1600  118.0704   13.0859  -61.9725  -11.5007   23.3495
    809.6169 -261.3054   67.0503   88.7841   25.6060  -41.0882   -6.1224   11.0350
       ⋮
```

```
covmat = cov(chosen_features)
```

```
covmat = 40×40 single matrix                         Rows 27:36 | Columns 1:15
10^5 ×
   -0.0276   -0.0107    0.0130    0.0268    0.0363    0.0037    0.0034    0.0002
    0.0228   -0.0080   -0.0071   -0.0048   -0.0031    0.0075    0.0177   -0.0047
    0.0054    0.0144    0.0054    0.0026   -0.0097   -0.0159    0.0093    0.0036
    0.0097   -0.0108   -0.0100   -0.0027    0.0098    0.0106    0.0036    0.0020
   -0.3138    0.0361   -0.0614    0.1048    0.0101    0.0108    0.0049    0.0071
   -0.0736   -0.0181    0.0517   -0.0632   -0.0173    0.0116   -0.0071   -0.0021
    0.0437   -0.0746   -0.0543    0.0153   -0.0018   -0.0030   -0.0115    0.0004
    0.0163   -0.0638    0.0482    0.0387   -0.0093   -0.0024    0.0020   -0.0006
   -0.0061   -0.0192   -0.0226    0.0013   -0.0210    0.0054    0.0038   -0.0029
   -0.0104   -0.0005   -0.0028   -0.0094   -0.0153   -0.0013   -0.0014    0.0054
```

```
figure();
heatmap(covmat)
```



After doing PCA and choosing the top 10 features from each region (after the first 10 features the explained variance < 1), I got a reduced feature set of 40 features.

Model	Accuracy
Fine Tree	88.9%
Medium Tree	88.9%
Coarse Tree	89.5%
Fine KNN	98.1% <-- pretty good training accuracy
Medium KNN	88.9%

Brains on Trial [120 minutes]

Watch this video or read this paper and think about the prompts below.

- Brains on Trial 1 (60 minutes): https://www.youtube.com/watch?v=o0eSqIAmKxU
- Neuroimaging and lie detection paper: https://drive.google.com/open?id=1V9YiLcl82VtDBnQLG_0-LT87tdW2D5tM

Other suggested resources if you want more of this:

- Brains on Trial: Part 2: https://www.youtube.com/watch?v=_cBK_fgTZvk
- Law, Responsibility, and the Brain paper: https://drive.google.com/file/d/1P-AoQPkPbp2EjC6u9LD-IXqgPjoRrChR/view?usp=sharing

Prompt to start thinking about prior to class discussion:

How would you **go about determining** if a future, more accurate, version of brain-based lie detection technology should be permissible in the American justice system and in what situations?

What information would you want? (How realistic is it to obtain this information?) What groups would you need to consider? What measurements of tool effectiveness would you want to see (and under what conditions)? What social and societal implications should you consider?

You should write notes on the video and the prompt. You can either submit them (I would enjoy reading them), or write a note that you did this (what an appropriately themed use of the honor code!).

Gati's Notes

- A jury is like a pooled decision maker
- I would want the data tested and fine-tuned to each individual
- **I would want all the jurors and judge to know the short-comings of the technology** (how do you make sure they listen and understand?)
- I would want masking techniques and adversarial patterns to be less effective