# Lab: Model Selection for Neural Data

Machine learning is a key tool for neuroscientists to understand how sensory and motor signals are encoded in the brain. In addition to improving our scientific understanding of neural phenomena, understanding neural encoding is critical for brain machine interfaces. In this lab, you will use model selection for performing some simple analysis on real neural signals.

Before doing this lab, you should review the ideas in the polynomial model selection demo (./polyfit.ipynb). In addition to the concepts in that demo, you will learn to:

- Load MATLAB data
- Formulate models of different complexities using heuristic model selection
- Fit a linear model for the different model orders
- Select the optimal model via cross-validation

The last stage of the lab uses LASSO estimation for model selection. If you are doing this part of the lab, you should review the concepts in LASSO demonstration (./prostate.ipynb) on the prostate cancer dataset.

## Loading the data

The data in this lab comes from neural recordings described in:

Stevenson, Ian H., et al. "Statistical assessment of the stability of neural movement representations." Journal of neurophysiology 106.2 (2011): 764-774 (http://jn.physiology.org/content/106/2/764.short)

Neurons are the basic information processing units in the brain. Neurons communicate with one another via *spikes* or *action potentials* which are brief events where voltage in the neuron rapidly rises then falls. These spikes trigger the electro-chemical signals between one neuron and another. In this experiment, the spikes were recorded from 196 neurons in the primary motor cortex (M1) of a monkey using an electrode array implanted onto the surface of a monkey's brain. During the recording, the monkey performed several reaching tasks and the position and velocity of the hand was recorded as well.

The goal of the experiment is to try to *read the monkey's brain*: That is, predict the hand motion from the neural signals from the motor cortex.

We first load the basic packages.

In [52]:
```
import numpy as np
import matplotlib
import matplotlib.pyplot as plt
%matplotlib inline
```

The full data is available on the CRCNS website [http://crcns.org/data-sets/movements/dream (http://crcns.org/data-sets/movements/dream)](http://crcns.org/data-sets/movements/dream). This website has a large number of great datasets and can be used for projects as well. To make this lab easier, I have pre-processed the data slightly and placed it in the file `StevensonV2.mat`, which is a MATLAB file. You will need to have this file downloaded in the directory you are working on.

Since MATLAB is widely-used, `python` provides method for loading MATLAB `mat` files. We can use these commands to load the data as follows.

In [53]:
```
import scipy.io
mat_dict = scipy.io.loadmat('StevensonV2.mat')
```

The returned structure, `mat_dict`, is a dictionary with each of the MATLAB variables that were saved in the `.mat` file. Use the `.keys()` method to list all the variables.

In [54]:
```
#TODO
print(*mat_dict.keys(), sep="\n")
```

```
__header__
__version__
__globals__
Publication
timeBase
spikes
time
handVel
handPos
target
startBins
targets
startBinned
```

We extract two variables, `spikes` and `handVel`, from the dictionary `mat_dict`, which represent the recorded spikes per neuron and the hand velocity. We take the transpose of the spikes data so that it is in the form time bins $\times$ number of neurons. For the `handVel` data, we take the first component which is the motion in the $x$-direction.

In [55]:
```
X0 = mat_dict['spikes'].T
y0 = mat_dict['handVel'][0,:]
```

The `spikes` matrix will be a `nt x nneuron` matrix where `nt` is the number of time bins and `nneuron` is the number of neurons. Each entry `spikes[k,j]` is the number of spikes in time bin `k` from neuron `j`. Use the `shape` method to find `nt` and `nneuron` and print the values.

In [56]:
```
# TODO
print(("There are {} bins(samples) of each of the {} neurons(features) "+
       "which attempt to predict \nthe {} hand velocities.\n").format(*X0.shape, *y0.shape))

print("This yields a {} x {} data matrix with a {} x 1 target vector.\n"
          .format(*X0.shape, *y0.shape))

nt, nneuron = X0.shape

print("So nt = {} and nneuron = {}.".format(nt, nneuron))
```

```
There are 15536 bins(samples) of each of the 196 neurons(features) which attempt to predict
the 15536 hand velocities.

This yields a 15536 x 196 data matrix with a 15536 x 1 target vector.

So nt = 15536 and nneuron = 196.
```

Now extract the `time` variable from the `mat_dict` dictionary. Reshape this to a 1D array with `nt` components. Each entry `time[k]` is the starting time of the time bin `k`. Find the sampling time `tsamp` which is the time between measurements, and `ttotal` which is the total duration of the recording.

In [57]:
```
# TODO
time = mat_dict['time'].squeeze()

# unnessesarily complicated way to show that timesteps are basically equ
al in length
tsamp_arr = time[1:nt] - time[:nt-1]
tsamp = np.mean(tsamp_arr)

SE = np.std(tsamp_arr)/np.sqrt(nt-2)

print(("min\t\tmean\t\tmax\t\tstd\t\tSE\n" + "{:.5f}\t\t" * 5)
          .format(np.min(tsamp_arr), np.mean(tsamp_arr),
                  np.max(tsamp_arr), np.std(tsamp_arr),
                  SE))

print("\ntsamp = {0:} ± {1:.5}\n=> tsamp is basically {0:} s".format(tsa
mp, SE))

# get total time
ttotal = time[-1] - time[0]
print("\nttotal =", ttotal, "s")
```

```
min             mean            max             std             SE
0.04950         0.05000         0.05050         0.00007         0.00000


tsamp = 0.05 ± 5.987e-07
=> tsamp is basically 0.05 s

ttotal = 776.75 s
```

## Linear fitting on all the neurons

First divide the data into training and test with approximately half the samples in each. Let `Xtr` and `ytr` denote the training data and `Xts` and `yts` denote the test data.

In [58]:
```
from sklearn import preprocessing

n_train = int(nt/2)
n_test = nt-n_train

Xs = preprocessing.scale(X0)
XY0 = np.hstack((Xs, y0[:, None]))
np.random.shuffle(XY0)

Xshuf = XY0[:, :X0.shape[1]]
yshuf = XY0[:, X0.shape[1]]

Xtr = Xshuf[:n_train]
ytr = yshuf[:n_train]
Xts = Xshuf[n_train:]
yts = yshuf[n_train:]

print("Xtr={}\nytr={}\nXts={}\nyts={}".format(Xtr.shape, ytr.shape,
Xts.shape, yts.shape))
print("Train:\tmean={:.4}\tstd={:.4}".format(np.mean(Xtr), np.std(Xtr)))
print("Test:\tmean={:.4}\tstd={:.4}".format(np.mean(Xts), np.std(Xts)))
```

```
Xtr=(7768, 196)
ytr=(7768,)
Xts=(7768, 196)
yts=(7768,)
Train:  mean=-0.001513  std=1.001
Test:   mean=0.001513   std=0.9935

/usr/local/lib/python3.6/site-packages/sklearn/utils/validation.py:429:
DataConversionWarning: Data with input dtype uint8 was converted to flo
at64 by the scale function.
  warnings.warn(msg, _DataConversionWarning)
```

Now, we begin by trying to fit a simple linear model using *all* the neurons as predictors. To this end, use the `sklearn.linear_model` package to create a regression object, and fit the linear model to the training data.

In [59]:
```
# import sklearn.linear_model
from sklearn import linear_model

# TODO
model = linear_model.LinearRegression()
model.fit(Xtr, ytr)
```

Out[59]:
```
LinearRegression(copy_X=True, fit_intercept=True, n_jobs=1, normalize=F
alse)
```

Measure and print the normalized RSS on the test data.

In [60]:
```
from sklearn.metrics import r2_score

# TODO
y_hat_tr = model.predict(Xtr)
RSSn_tr = (np.mean((y_hat_tr - ytr)**2))/(np.std(ytr)**2)
rsq_tr = r2_score(ytr, y_hat_tr)


print(("R^2 = {:.4}").format(rsq_tr))
print(("The normalized RSStr = {:.4}").format(RSSn_tr))


y_hat_ts = model.predict(Xts)
RSSn_ts = (np.mean((y_hat_ts - yts)**2))/(np.std(yts)**2)
rsq_ts = r2_score(yts, y_hat_ts)

print(("\nR^2 = {:.4}").format(rsq_ts))
print(("The normalized RSSts = {:.4}").format(RSSn_ts))
```

```
R^2 = 0.5272
The normalized RSStr = 0.4728

R^2 = -2.747e+20
The normalized RSSts = 2.747e+20
```

You should see that the test error is enormous -- the model does not generalize to the test data at all.

## Linear Fitting with Heuristic Model Selection

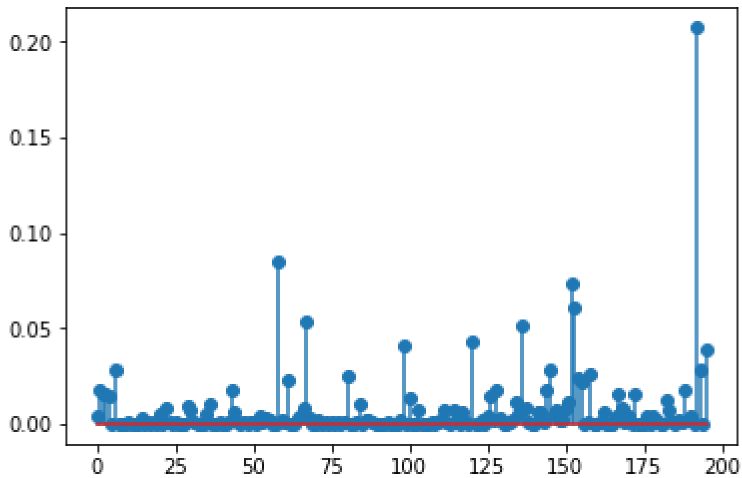
The above shows that we need a way to reduce the model complexity. One simple idea is to select only the neurons that individually have a high correlation with the output.

Write code which computes the coefficient of determination, $R_k^2$, for each neuron $k$. Plot the $R_k^2$ values.

You can use a for loop over each neuron, but if you want to make efficient code try to avoid the for loop and use python broadcasting (../Basics/numpy_axes_broadcasting.ipynb).

In [61]:
```
# TODO
# Rsq = ...
# plt.stem(...)
model = linear_model.LinearRegression()
rsq = np.zeros(Xtr.shape[1])
for i in range(Xtr.shape[1]):
    x = Xtr[:, i].reshape(-1, 1)
    model.fit(x, ytr)
    y_hat = model.predict(x)
    rsq[i] = r2_score(ytr, y_hat)

plt.stem(rsq)
```

Out[61]: <Container object of 3 artists>




We see that many neurons have low correlation and can probably be discarded from the model.

Use the `np.argsort()` command to find the indices of the `d=100` neurons with the highest $R_k^2$ value. Put the `d` indices into an array `Isel`. Print the indices of the neurons with the 10 highest correlations.

In [62]:
```
d = 100  # Number of neurons to use

# TODO
# Isel = ...
# print("The neurons with the ten highest R^2 values = ...)

Isel = np.argsort(-rsq)
# rsq[Isel[:d]]

print("The neurons with the ten highest R^2 values are:\n"+
            "\tidx  |  R^2\n\t"+"-"*15+"\n"+
            ("\n".join("\t{:3d}  |  {:.4f}"
            .format(*neuron) for neuron in zip(Isel[:10],
rsq[Isel[:10]]))))
```

```
The neurons with the ten highest R^2 values are:
        idx  |  R^2
        ---------------
        192  |  0.2076
         58  |  0.0853
        152  |  0.0736
        153  |  0.0613
         67  |  0.0536
        136  |  0.0512
        120  |  0.0431
         98  |  0.0406
        195  |  0.0392
        193  |  0.0286
```

Fit a model using only the `d` neurons selected in the previous step and print both the test RSS per sample and the normalized test RSS.

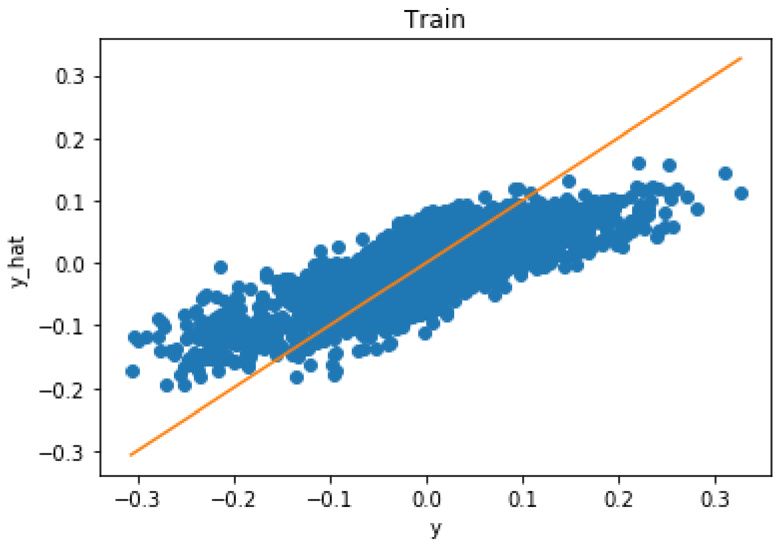
In [63]:
```
# TODO
X_tr_sel = Xtr[:,Isel[:d]]
X_ts_sel = Xts[:,Isel[:d]]

model.fit(X_tr_sel, ytr )

y_hat_tr = model.predict(X_tr_sel)
y_hat_ts = model.predict(X_ts_sel)


RSSper_samp_tr = np.mean((y_hat_tr - ytr) ** 2)
RSSnorm_tr = np.mean((y_hat_tr - ytr) ** 2) / (np.std(ytr)**2)

RSSper_samp_ts = np.mean((y_hat_ts - yts) ** 2)
RSSnorm_ts = np.mean((y_hat_ts - yts) ** 2) / (np.std(yts)**2)


rsq_tr = r2_score(ytr, y_hat_tr)
rsq_ts = r2_score(yts, y_hat_ts)



print("TRAIN: R^2= {:.4}, RSSper_samp={:.4}, RSSnorm={:.4}"
          .format(rsq_tr, RSSper_samp_tr, RSSnorm_tr))

print("TEST:  R^2={:.4}, RSSper_samp={:.4}, RSSnorm={:.4}"
          .format(rsq_ts, RSSper_samp_ts, RSSnorm_ts))
```

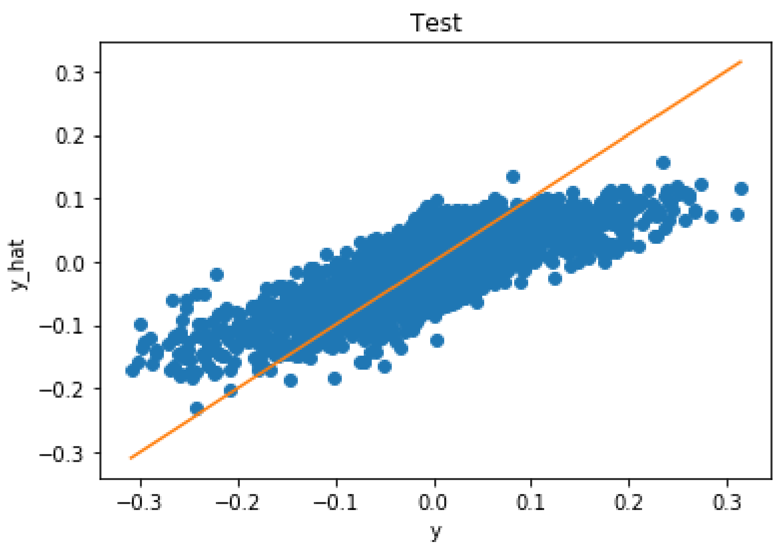
```
TRAIN: R^2= 0.5096, RSSper_samp=0.001489, RSSnorm=0.4904
TEST:  R^2=0.5195, RSSper_samp=0.001529, RSSnorm=0.4805
```

Create a scatter plot of the predicted vs. actual hand motion on the test data. On the same plot, plot the line where `yts_hat = yts`.

In [64]:
```
# TODO
plt.plot(ytr, y_hat_tr, 'o')
ax = plt.gca()
lims = [
    np.min([np.min(y_hat_tr), np.min(ytr)]),  # min of both axes
    np.max([np.max(y_hat_tr), np.max(ytr)]),  # max of both axes
]
plt.plot(lims, lims)
plt.title("Train")
plt.xlabel("y")
plt.ylabel("y_hat")


plt.figure()
ax = plt.gca()
lims = [
    np.min([np.min(y_hat_ts), np.min(yts)]),  # min of both axes
    np.max([np.max(y_hat_ts), np.max(yts)]),  # max of both axes
]
plt.plot(yts, y_hat_ts, 'o')
plt.plot(lims, lims)
plt.title("Test")
plt.xlabel("y")
plt.ylabel("y_hat")
# limits = [-6, 6]
# plt.plot(limits, limits)
# axes = plt.gca()
# axes.set_xlim(limits)
# axes.set_ylim(limits)
```

```
Out[64]: <matplotlib.text.Text at 0x1185cf320>
```




# Using K-fold cross validation for the optimal number of neurons

In the above, we fixed `d=100`. We can use cross validation to try to determine the best number of neurons to use. Try model orders with `d=10,20,...,190`. For each value of `d`, use K-fold validation with 10 folds to estimate the test RSS. For a data set this size, each fold will take a few seconds to compute, so it may be useful to print the progress.

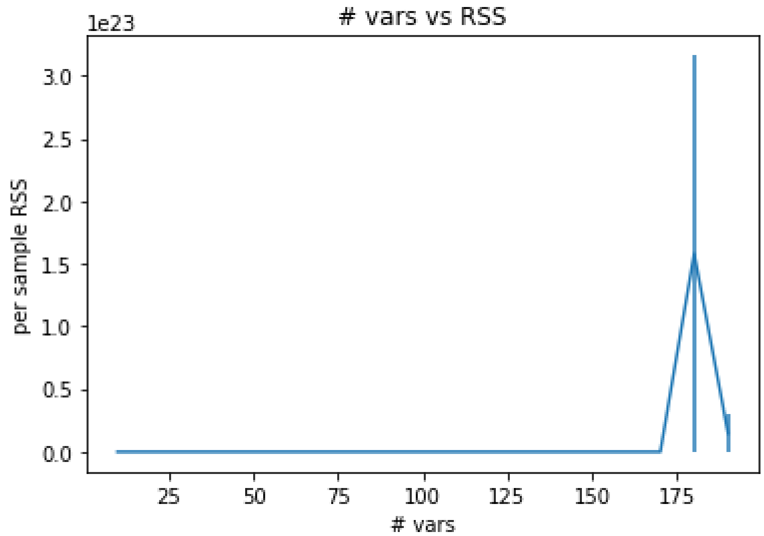
In [65]:
```
import sklearn.model_selection


# Create a k-fold object
nfold = 10
kf = sklearn.model_selection.KFold(n_splits=nfold,shuffle=True)

# Model orders to be tested
dtest = np.arange(10,200,10)
nd = len(dtest)

# TODO.
model  = linear_model.LinearRegression()

# Loop over the folds
RSSts = np.zeros((nd,nfold))
for isplit, Ind in enumerate(kf.split(Xtr)):

    # Get the training data in the split
    Itr, Its = Ind
    x_cv_tr = Xtr[Itr]
    y_cv_tr = ytr[Itr]
    x_cv_ts = Xtr[Its]
    y_cv_ts = ytr[Its]

    for it, d in enumerate(dtest):

        # Fit data on training data

        model.fit(x_cv_tr[Isel[:d]], y_cv_tr[Isel[:d]])

        # Measure RSS on test data
        y_hat = model.predict(x_cv_ts)
        RSSts[it,isplit] = np.mean((y_hat-y_cv_ts)**2)

#     print(("{:.2f} "*19).format(*RSSts[:,isplit]))
#     print("fold#","{}:".format(isplit), ("{:.2}\t"*19).format(*RSSts
[:,isplit]))
```

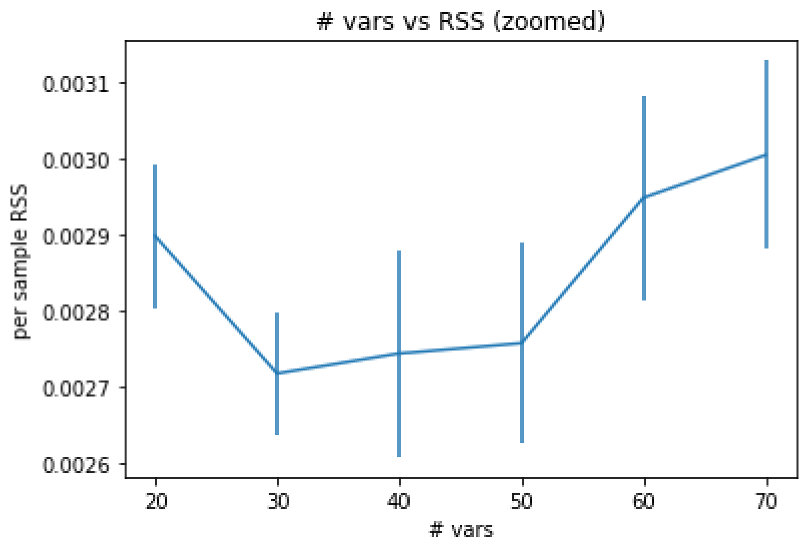
Compute the RSS test mean and standard error and plot them as a function of the model order `d` using the `plt.errorbar()` method.

In [72]:
```
# TODO
# print(RSSts.shape)
means = np.mean(RSSts, axis=1)
stdErrs = np.std(RSSts, axis=1)/np.sqrt(nfold-1)
idx = np.argsort(means)
print("# vars\tRSS/sample\tstdErr")
print("\n".join(["{:3d}\t{:.3}\t\t{:.3}".format(*row) for row in zip(dte
st[idx], means[idx], stdErrs[idx])]))

targetRSS = means[idx][0]+stdErrs[idx][0]
print("\n\nTarget RSS = min(RSS)+SE = {:.4}+{:.4} =
{:.4}".format(means[idx][0], stdErrs[idx][0], targetRSS))
print("So we need to find # vars such that the corrisponding RSS is less
 than {:.4}\n".format(targetRSS))

print("\n".join(["{:3d}\t{:.3}\t{}".format(*row) for row in zip(dtest, m
eans, means<targetRSS)]))


# plt.plot(dtest, means)
# plt.plot(dtest, means, 'o')
plt.errorbar(dtest, means, yerr=stdErrs)
plt.title("# vars vs RSS")
plt.xlabel("# vars")
plt.ylabel("per sample RSS")

plt.figure()
plt.title("# vars vs RSS (zoomed)")

# l, r = 0, 5
# plt.errorbar(dtest[l:r], means[l:r], yerr=stdErrs[l:r])
# plt.xlabel("# vars")
# plt.ylabel("per sample RSS")

l, r = 1, 7
# plt.figure()
plt.errorbar(dtest[l:r], means[l:r], yerr=stdErrs[l:r])
plt.xlabel("# vars")
plt.ylabel("per sample RSS")

# l, r = 10, 15
# plt.figure()
# plt.errorbar(dtest[l:r], means[l:r], yerr=stdErrs[l:r])
# plt.xlabel("# vars")
# plt.ylabel("per sample RSS")

# l, r = 15, 20
# plt.figure()
# plt.errorbar(dtest[l:r], means[l:r], yerr=stdErrs[l:r])
# plt.xlabel("# vars")
# plt.ylabel("per sample RSS")
```

```
# vars  RSS/sample      stdErr
 30     0.00272         7.99e-05
 40     0.00274         0.000135
 50     0.00276         0.000131
 20     0.0029          9.36e-05
 60     0.00295         0.000134
 70     0.003           0.000123
 10     0.0031          0.000115
 80     0.00321         0.000145
 90     0.00358         0.000193
100     0.00423         0.000291
110     0.00529         0.000423
120     0.00673         0.000458
130     0.00889         0.000598
140     0.0132          0.00136
150     0.0309          0.00562
170     0.0379          0.0112
160     0.288           0.0816
190     1.47e+22                1.47e+22
180     1.58e+23                1.58e+23


Target RSS = min(RSS)+SE = 0.002718+7.992e-05 = 0.002798
So we need to find # vars such that the corrisponding RSS is less than
 0.002798

 10     0.0031  False
 20     0.0029  False
 30     0.00272 True
 40     0.00274 True
 50     0.00276 True
 60     0.00295 False
 70     0.003   False
 80     0.00321 False
 90     0.00358 False
100     0.00423 False
110     0.00529 False
120     0.00673 False
130     0.00889 False
140     0.0132  False
150     0.0309  False
160     0.288   False
170     0.0379  False
180     1.58e+23        False
190     1.47e+22        False
```

Out[72]: <matplotlib.text.Text at 0x115c882e8>




Find the optimal order using the one standard error rule. Print the optimal value of `d` and the mean test RSS per sample at the optimal `d`.

In [73]:
```
# TODO
RSSmeans = np.mean(RSSts, axis=1)
stdErrs = np.std(RSSts, axis=1)/np.sqrt(nfold-1)
minidx = np.argmin(means)
target = RSSmeans[minidx]+stdErrs[minidx]
d = np.min(dtest[RSSmeans < target])

model = linear_model.LinearRegression()
print(Xtr[:, Isel[:10]].shape)

model.fit(Xtr[:, Isel[:10]], ytr)
y_hat_tr = model.predict(Xtr[:, Isel[:10]])

RSS_tr = np.mean((ytr-y_hat_tr)**2)
Rsq_tr = r2_score(ytr, y_hat_tr)

RSS_ts = np.mean((yts-y_hat_ts)**2)
Rsq_ts = r2_score(yts, y_hat_ts)

print("The optimal value of d is {}.".format(d))
print("The train and test RSS/sample vales are {:.4} and {:.4} respectiv
ely.".format(RSS_tr, RSS_ts))
```

```
(7768, 10)
The optimal value of d is 30.
The train and test RSS/sample vales are 0.001862 and 0.001529 respectiv
ely.
```

In [74]:
```
model = linear_model.LinearRegression()
X_subset_tr = Xtr[:, Isel[:d]]
X_subset_ts = Xts[:, Isel[:d]]

model.fit(X_subset_tr, ytr)
print(X_subset_tr.shape)

y_hat_tr = model.predict(X_subset_tr)
y_hat_ts = model.predict(X_subset_ts)

Rsq_tr = r2_score(ytr, y_hat_tr)
Rsq_ts = r2_score(yts, y_hat_ts)

print("Train R^2 = {}".format(Rsq_tr))
print("Test R^2 = {}".format(Rsq_ts))
# print(("{} R^2 = {}\n"*2).format(["Train", Rsq_tr, "Test", Rsq_ts]))
```

```
(7768, 30)
Train R^2 = 0.4394042849266767
Test R^2 = 0.4558766373353268
```

## Using LASSO regression

Instead of using the above heuristic to select the variables, we can use LASSO regression.

First use the `preprocessing.scale` method to standardize the data matrix `X0`. Store the standardized values in `Xs`. You do not need to standardize the response. For this data, the `scale` routine may throw a warning that you are converting data types. That is fine.

In [75]:
```
from sklearn import preprocessing

# TODO
Xs = preprocessing.scale(X0)
```

```
/usr/local/lib/python3.6/site-packages/sklearn/utils/validation.py:429:
DataConversionWarning: Data with input dtype uint8 was converted to flo
at64 by the scale function.
  warnings.warn(msg, _DataConversionWarning)
```

Now, use the LASSO method to fit a model. Use cross validation to select the regularization level `alpha`. Use `alpha` values logarithmically spaced from `1e-5` to `0.1`, and use 10 fold cross validation.

In [76]:
```
# TODO
alphas = np.logspace(-5, -1)
# print(alphas)

nfolds = 10

model = linear_model.LassoCV(alphas=alphas, cv=nfolds, verbose=True)
model.fit(Xs, y0)

bestAlpha = model.alpha_
print("Optimal alpha = {}.".format(bestAlpha))
```

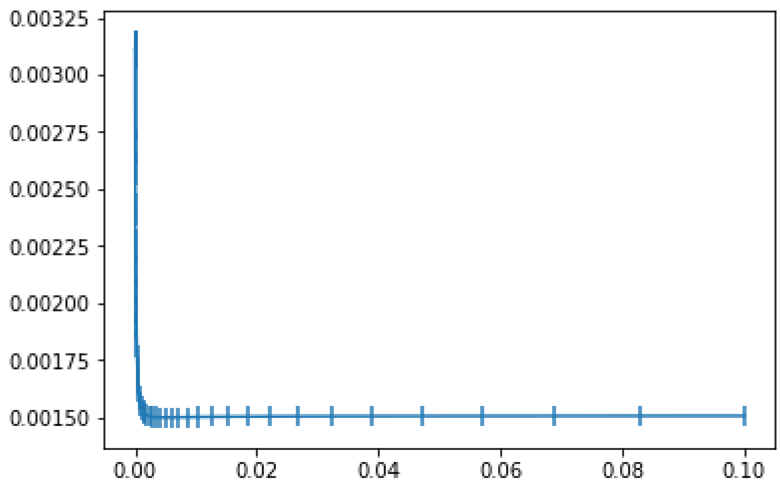
```
.........................................................................

Optimal alpha = 0.00020235896477251554.

..................................................[Parallel(n_jobs=1)]:
Done  10 out of  10 | elapsed:    0.9s finished
```

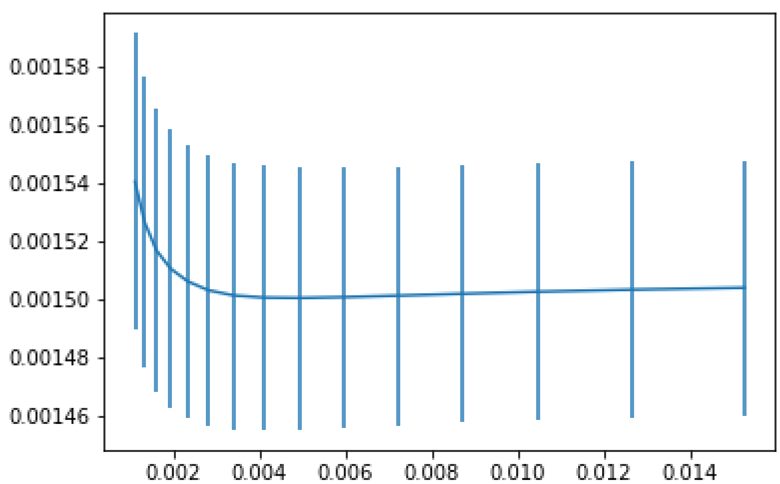
Plot the mean test RSS and test RSS standard error with the `plt.errorbar` plot.

In [77]:
```
# TODO

mean_RSS_each_fold_and_alpha = model.mse_path_
print(mean_RSS_each_fold_and_alpha.shape)

mean_RSS_each_alpha = np.mean(mean_RSS_each_fold_and_alpha, axis=1)
std_err_each_alpha  = np.std (mean_RSS_each_fold_and_alpha, axis=1) /
np.sqrt(nfolds-1)


plt.errorbar(alphas, mean_RSS_each_alpha, yerr=std_err_each_alpha)

plt.figure()
a, b = 25, 40
plt.errorbar(alphas[a:b], mean_RSS_each_alpha[a:b], yerr=std_err_each_al
pha[a:b])
```

```
(50, 10)
```

Out[77]: <Container object of 3 artists>




Find the optimal `alpha` and mean test RSS using the one standard error rule.

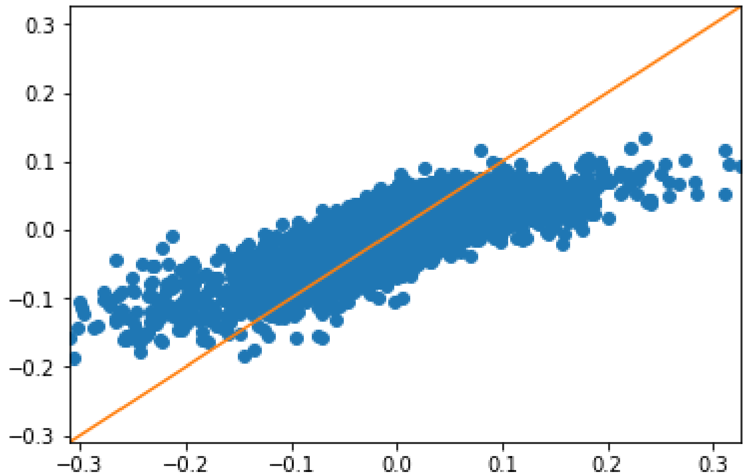
In [78]:
```
# TODO
mean_RSS_each_fold_and_alpha = model.mse_path_
mean_RSS_each_alpha = np.mean(mean_RSS_each_fold_and_alpha, axis=1)
std_err_each_alpha  = np.std (mean_RSS_each_fold_and_alpha, axis=1) /
np.sqrt(nfolds-1)

# print(*["{:03.3}\t\t{:05.6f}\n".format(*row) for row in zip(alphas, me
an_RSS_each_alpha)])

minidx = np.argmin(mean_RSS_each_alpha)
# print(minidx)
# print(mean_RSS_each_alpha[33])
# print(mean_RSS_each_alpha <= mean_RSS_each_alpha[33])

target = mean_RSS_each_alpha[minidx]+std_err_each_alpha[minidx]
opt_alpha_idx = np.argmax(alphas[mean_RSS_each_alpha < target])    # cho
ose the biggest alpha => simpler model

opt_alpha = alphas[opt_alpha_idx]
opt_alpha_RSS = mean_RSS_each_alpha[opt_alpha_idx]

print("The optimal value of d is using the one standard error rule is al
pha={:.5f} with RSS={:.4f}."
          .format(opt_alpha, mean_RSS_each_alpha[opt_alpha_idx]))

print("As opposed to alpha = {:.5f} with RSS={:.4f} without using the ru
le."
          .format(model.alpha_, mean_RSS_each_alpha[minidx]))
```

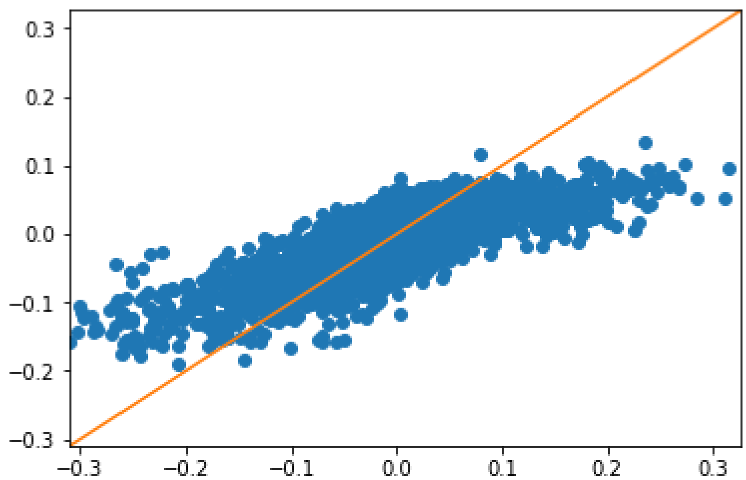
```
The optimal value of d is using the one standard error rule is alpha=0.
00091 with RSS=0.0016.
As opposed to alpha = 0.00020 with RSS=0.0015 without using the rule.
```

Using the optimal alpha, recompute the predicted response variable on the whole data. Plot the predicted vs. actual values.

In [79]:
```
# TODO
new_model = linear_model.Lasso(alpha=opt_alpha)
# new_model = linear_model.Lasso(alpha=0.01)

n = len(Xs) // 2
Xtr = Xs[n:]
ytr = y0[n:]

Xtr = Xs[:n]
ytr = y0[:n]


new_model.fit(Xtr, ytr)
y_hat_tr = new_model.predict(Xtr)



limits = [np.min([np.min(y_hat_tr), np.min(ytr)]), np.max([np.max(y_hat_
tr), np.max(ytr)])]
plt.figure()
plt.plot(ytr,y_hat_tr, 'o')
plt.plot(limits, limits)
axes = plt.gca()
axes.set_xlim(limits)
axes.set_ylim(limits)

y_hat_ts = new_model.predict(Xts)

plt.figure()
plt.plot(yts, y_hat_ts, 'o')
plt.plot(limits, limits)
axes = plt.gca()
axes.set_xlim(limits)
axes.set_ylim(limits)

print("R^2 Train = ", r2_score(ytr, y_hat_tr))
print("R^2 Test = ", r2_score(yts, y_hat_ts))

print(np.sum(new_model.coef_ != 0), "features have been selected.")
```

```
R^2 Train =  0.507501380223
R^2 Test =  0.514930508264
82 features have been selected.
```





## More Fun

You can play around with this and many other neural data sets. Two things that one can do to further improve the quality of fit are:

- Use more time lags in the data. Instead of predicting the hand motion from the spikes in the previous time, use the spikes in the last few delays.
- Add a nonlinearity. You should see that the predicted hand motion differs from the actual for high values of the actual. You can improve the fit by adding a nonlinearity on the output. A polynomial fit would work well here.

You do not need to do these, but you can try them if you like.

```
In [ ]:
```