1. Convolutions

0.1

-0.1

In this exercise, you will implement a convolution function which you will then use to convolve stimulus vectors with a hemodynamic response function to create response vectors.

(a) [0.5pts] You will start by creating an HRF and plotting it. Use the function <code>create_hrf</code> which we used in class (use the import below) to create a hemodynamic response function for <code>TR=2</code>, and a <code>time_length=32</code> seconds. Call it <code>hrf</code>. This should lead to an hrf array of length 16 (make sure it has this length, and double-check the <code>oversampling</code> parameter if it doesn't.). Create a figure of size (20, 4) called <code>fig_hrf</code> and plot the HRF into it. Make the x-axis correspond to the correct time in seconds of each point of the HRF, and label the x-axis as <code>time</code> (<code>seconds</code>). Label the y-axis as <code>hemodynamic</code> response <code>level</code>.

```
In [6]:
         ## HRF import
         from nistats.hemodynamic_models import glover_hrf as create_hrf
In [7]:
         hrf = create_hrf(tr=2, time_length=32, oversampling=1)
In [8]:
         fig_hrf = plt.figure(figsize=(20, 4))
         time = np.arange(0, 32, 2)
         plt.plot(time, hrf)
         plt.xlabel("time (seconds)")
         plt.ylabel("hemodynamic response level")
        <matplotlib.text.Text at 0x7fe0a024f748>
Out[8]:
          0.4
          0.3
          0.2
```

(b) [1pt] Next you need to create a stimulus time series to convolve with the hrf we just created. To do this, you first need to load the relevant condition labels: Load the category labels for the motor localizer out of the file

15 time (seconds) /home/jovyan/motorloc_experimental_conditions.npy . Call the array category_labels . As in the lecture, use np.unique to find the unique labels in this array. Call the output unique_labels . The label 'rest' indicates that no action was performed. This condition should be excluded from further analysis. Make an array unique_labels_no_rest containing all unique_labels except rest . You can do this by masking.

```
In [9]: ## motor localizer filename
motorloc_filename = '/home/jovyan/motorloc_experimental_conditions.npy'

In [10]: category_labels = np.load(motorloc_filename)
    unique_labels = np.unique(category_labels)
    unique_labels_no_rest = unique_labels[unique_labels != 'rest']
    print(unique_labels)
    print(unique_labels_no_rest)

['move eyes' 'move foot' 'move hand' 'move mouth' 'rest' 'speak']
['move eyes' 'move foot' 'move hand' 'move mouth' 'speak']
```

(c) [0.5pts] Now you'll make a stimulus vector: Make a stimulus vector called stim_vec_move_eyes such that it has the value True whenever category_labels contains 'move eyes' as an entry and False at all other times. Create a figure named fig_stim_vec_move_eyes, of size (20, 2), and plot stim_vec_move_eyes with the correct time on the x axis (remember: each entry in category_labels corresponds to one TR of 2s). Make the xlabel say time (seconds).

```
In [11]: stim_vec_move_eyes = category_labels == 'move eyes'
    fig_stim_vec_move_eyes = plt.figure(figsize=(20, 2))
    plt.plot(np.arange(len(stim_vec_move_eyes)) * 2, stim_vec_move_eyes)
    plt.xlabel("time (seconds)")

Out[11]: 

Out[11]:
```

(d) [1pt] Now you will perform convolution on the stimulus vector and hrf to create a response vector. You will implement convolution slightly differently than we did in class. Instead of making the response vector the same size as the stimulus vector, you will do what np.convolve does, and make the response vector long enough to contain the HRF convolved with the last value in the stimulus vector. To do this you will:

Start by determining the length of the response vector: The length of the response vector will be the sum of the lengths of stim_vec_move_eyes and hrf minus 1. Set conv_length to this value.

Then create a vector of zeros, named resp vec move eyes that has length conv length.

Now iterate over the input (stimulus) vector to create the output (response) vector, doing the following: Step through the stimulus vector <code>stim_vec_move_eyes</code>, one element at a time. Multiply each element by the hrf and add that product to the response vector starting at the current position and ranging the length of the <code>hrf</code>.

In detail: Write a for loop that iterates a loop variable i over the range from 0 to the length of resp_vec_move_eyes , in which you:

• extract the current value of stim_vec_move_eyes using the for loop variable i, and call it cur_stim

- multiply hrf by cur_stim and call it cur_response
- Use slicing to select the subarray of resp_vec_move_eyes that starts at index i and ends at i plus the length of the hrf. Use += to add cur response to that part of the vector you just sliced.

Once you are done with the for loop, create a figure named fig_convolution, of size (20, 2) and plot resp_vec_move_eyes into it.

Note: You should see a line plot with the same number of activation bumps as fig_stim_vec_move_eyes. If you don't, make absolutely sure you are using += , and not = or + . The += operator performs an increment of the left hand side by the right hand side.

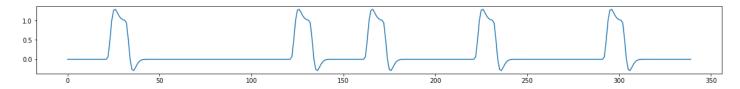
```
In [12]:
    conv_length = len(stim_vec_move_eyes) + len(hrf) - 1
    resp_vec_move_eyes = np.zeros(conv_length)

for i in range(0, len(stim_vec_move_eyes)):
        cur_stim = stim_vec_move_eyes[i]
        cur_response = cur_stim * hrf
        resp_vec_move_eyes[i:i + len(cur_response)] += cur_response

fig_convolution= plt.figure(figsize=(20, 2))
    plt.plot(resp_vec_move_eyes)
```

Out[12]: [<matplotlib.lines.Line2D at 0x7fe0a013c860>]

print(same1)



(e) [1pt] Now you'll put the convolution code you just created into a reusable function.

Create the function def convolution(stimulus_vector, impulse_response), which implements convolution in the exact same way as in part (d). This amounts to taking the code you wrote above and changing the names to be more general. In the next exercise you will be able to check whether you succeeded in a general manner.

Now use the convolution function you just wrote, and convolve the stimulus vector stim_vec_move_eyes with hrf . Store the resulting response vector into resp_vec_move_eyes2 .

Finally, verify that your function does exactly what you did in part **(d)** by using <code>np.allclose()</code> to compare <code>resp_vec_move_eyes</code> and <code>resp_vec_move_eyes2</code>. Store the result of <code>np.allclose</code> into <code>same1</code> and print it.

```
def convolution(stimulus_vector, impulse_response):
    out_length = len(stimulus_vector) + len(impulse_response) - 1
    output_array = np.zeros(out_length)
    for i in range(len(stimulus_vector)):
        output_array[i:i + len(impulse_response)] += stimulus_vector[i] * impulse_response
    return output_array
```

```
In [14]: resp_vec_move_eyes2 = convolution(stim_vec_move_eyes, hrf)
In [15]: same1 = np.allclose(resp_vec_move_eyes, resp_vec_move_eyes2)
```

True

(f) [0.5 pts] In order to check whether your function works in general, you will now compare the results of using both convolution and np.convolve to conduct a convolution of a random stimulus vector with a random impulse response to obtain a response vector. To do so:

Make a vector called random_stimulus_vector of length 100 and a vector called random impulse response of length 10 using np.random.randn for both vectors.

Use the function convolution to convolve the two and store the output in my_convolution_output.

Then convolve the two vectors using <code>np.convolve</code> and store the outputs in <code>np convolution output</code>.

Finally, compare these two outputs using np.allclose and store the output in same2. Print same2.

Note: This exercise is a check to see whether your implementation is correct. If the two outputs are not exactly the same, then there is an error in your code.

```
In [16]:
```

```
random_stimulus_vector = np.random.randn(100)
random_impulse_response = np.random.randn(10)
my_convolution_output = convolution(random_stimulus_vector, random_impulse_response)
np_convolution_output = np.convolve(random_stimulus_vector, random_impulse_response)
same2 = np.allclose(my_convolution_output, np_convolution_output)
print(same2)
```

True

2. In this exercise, you will create the stimulus vectors and the response vectors for each *motor localizer* category. The **motor localizer** is a block design experiment during which the participant is asked to perform small movements with different body parts, such as hands, feet, eyes, and mouth. Internal speech (forming sentences but not saying them) is also recorded. Up to now you have mostly worked with the visual category localizer, where images of different categories were shown in a block design. The motor localizer is the corresponding experiment for finding motor regions.

You will create a stimulus design matrix from the stimulus vectors and a response design matrix from the response vectors.

(a) [0.5pts] In class you learned that it is sometimes useful to pre-allocate an array in memory and then populate it with data. This is especially true for very large arrays. You will practice this here to create a response design matrix.

To preallocate an array you need to know its size in advance. In this case the response design matrix will have as many rows as category_labels has entries (use len() to obtain its length) and as many columns as unique_labels_no_rest has entries. Create an array of zeros with this many rows and columns and call it motor response design.

```
In [17]:
```

```
motor_response_design = np.zeros((len(category_labels), len(unique_labels_no_rest)))
```

(b) [0.5 pts] In this part you will create the stimulus vectors for all the motor categories and arrange them in a stimulus design matrix. To do so:

Create an empty list called stimulus vectors to keep the stimulus vectors you create.

Then, in a for loop that iterates over the unique labels (without "rest"), call the current label cur label.

Use the == operator to create the stimulus vector pertaining to the current label by comparing category_labels to cur_label , and call it stimulus_vector . Append stimulus_vector to stimulus vectors .

After the for loop, use np.stack to stack the stimulus vectors into columns of a 2D array. Call it motor stimulus design.

```
In [18]:
    stimulus_vectors = []
    for i in range(len(unique_labels_no_rest)):
        cur_label = unique_labels_no_rest[i]
        stimulus_vector = category_labels == cur_label
        stimulus_vectors.append(stimulus_vector)

motor_stimulus_design = np.stack(stimulus_vectors, axis=1)
```

(c) [1pt] In this part you will populate the response design matrix with stimulus vectors for all the motor categories. To do so:

Create a for loop with index i that iterates over the number of unique labels without rest.

Select the i th stimulus vector from motor stimulus design and store it in stimulus vector.

Then create the corresponding response vector by convolving stimulus_vector with hrf. You can use your own function convolution to do this or np.convolve. Store the output in response vector.

Because the output of the convolution is longer than the stimulus vector, and thus longer than a column of motor_design , you need to shorten it. Use slicing to make response_vector have the same length as stimulus_vector by selecting that amount of entries from the beginning of response_vector (throw away the end), and call it response vector shortened .

Finally, store response vector shortened into the i th column of motor design.

```
for i in range(len(unique_labels_no_rest)):
    stimulus_vector = motor_stimulus_design[:, i]
    response_vector = convolution(stimulus_vector, hrf)
    response_vector_shortened = response_vector[:len(stimulus_vector)]
    motor_response_design[:, i] = response_vector_shortened
```

(d) [0.5 pts] Next let's visualize both design matrices you just created.

Create a figure named fig_matrices of size (20, 10).

Using plt.subplot, plot the response design matrix on the left and the stimulus design matrix on the right, using plt.imshow with aspect='auto'.

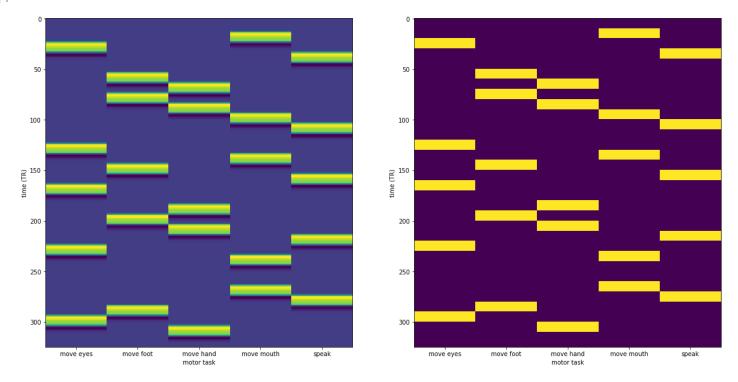
Make the xticks correspond to the unique categories without rest for both matrices.

Label the y axis as time(TR) and the x axis as motor task.

```
fig_matrices = plt.figure(figsize=(20, 10))
plt.subplot(1, 2, 1)
plt.imshow(motor_response_design, aspect='auto')
plt.xticks(np.arange(5), unique_labels_no_rest)
plt.xlabel('motor task')
plt.ylabel('time (TR)')
plt.subplot(1, 2, 2)
```

```
plt.imshow(motor_stimulus_design, aspect='auto')
plt.xticks(np.arange(5), unique_labels_no_rest)
plt.xlabel('motor task')
plt.ylabel('time (TR)')
```

Out[21]: <matplotlib.text.Text at 0x7fe09a4f3be0>



(e) [0.5 pts] In order to perform a close-up comparison of stimulus vs response vectors and the lag induces by the hemodynamic response, you will now plot one stimulus vector and one response vector into the same plot. To do this:

First, create a figure named fig_move_foot of size (20, 2).

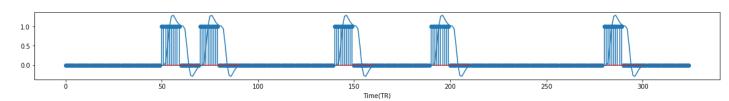
Then plot the stimulus vector corresponding to <code>move_foot</code> into this figure using <code>plt.stem</code> (you can obtain it by selecting the appropriate column of <code>stimulus_matrix</code>).

Next, plot the response vector of move_foot into the same figure using plt.plot (obtain it by selecting the appropriate column of motor_design).

Finally, label the x axis as time(TR)

```
fig_move_foot = plt.figure(figsize=(20, 2))
plt.stem(stimulus_matrix[:, 1])
plt.plot(motor_design[:, 1])
plt.xlabel("Time(TR)")
```

Out[19]: <matplotlib.text.Text at 0x7f4972767630>

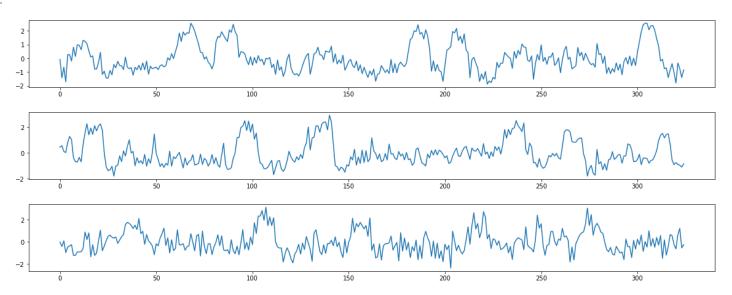


- **3.** In this exercise you will look at some real voxel time courses and assess which task they might be responding to.
- (a) [1 pt] Load the file /home/jovyan/mystery_voxels.npy and store it in mystery_voxels.It

contains a matrix with 3 columns, where each column contains a voxel time series. Plot the time series from each column in separate figures named fig_voxel_0, fig_voxel_1, fig_voxel_2, all of figsize= (20, 2).

```
In [20]: mystery_voxels = np.load("/home/jovyan/mystery_voxels.npy")
    fig_voxel_0 = plt.figure(figsize=(20, 2))
    plt.plot(mystery_voxels[:, 0])
    fig_voxel_1 = plt.figure(figsize=(20, 2))
    plt.plot(mystery_voxels[:, 1])
    fig_voxel_2 = plt.figure(figsize=(20, 2))
    plt.plot(mystery_voxels[:, 2])
```

Out[20]: [<matplotlib.lines.Line2D at 0x7f4972368860>]

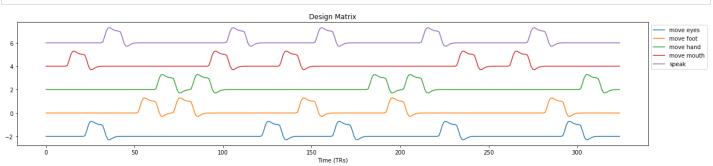


(b) [0.5 pts] Use plot_design_matrix_line from the lecture (included below) to plot the columns of the design matrix as lines into a figure named fig design lines of size (20, 4).

```
In [21]: # From lecture

def plot_design_matrix_line(design_mat, labels):
    num_stim_types = design_mat.shape[1]
    for cur_stim_type in np.arange(num_stim_types):
        cur_y_offset = (cur_stim_type - 1) * 2
        plt.plot(design_mat[:, cur_stim_type] + cur_y_offset, label = labels[cur_stim_type]
    plt.title('Design Matrix')
    plt.xlabel('Time (TRs)')
    _ = plt.legend(bbox_to_anchor=(1, 1))
```

```
In [25]: fig_design_lines = plt.figure(figsize=(20, 4))
    plot_design_matrix_line(motor_design, unique_labels_no_rest)
```



(c) [0.5 pts] Figure out which column of motor_design matches best visually to each one of these plots. Make three more figures named fig_voxel_XX_resp where X is from [0,1,2], and plot the 3 voxel time series and the response vector time series that you think best matches each of the 3 mystery voxel time series. Use the figure title to indicate which task label this corresponds to (e.g. "move_eyes" or "move_mouth").

```
fig_voxel_0 = plt.figure(figsize=(20, 2))
plt.plot(mystery_voxels[:, 0])
plt.plot(motor_design[:, 2])
plt.title('move hand')

fig_voxel_1 = plt.figure(figsize=(20, 2))
plt.plot(mystery_voxels[:, 1])
plt.plot(motor_design[:, 3])
plt.title('move mouth')

fig_voxel_2 = plt.figure(figsize=(20, 2))
plt.plot(mystery_voxels[:, 2])
plt.plot(motor_design[:, 4])
plt.title('speak')
```

Out[23]: <matplotlib.text.Text at 0x7f4972142978>

