fmrisim demo script

Overview

Example script to demonstrate fmrisim functionality. This generates data for a two condition, event-related design in which each condition evokes different activity within the same voxels. It then runs simple univariate and multivariate analyses on the data.

If you would like a script that can be executed from the command line and scaffolds the simulation process, refer to the `fmrisim_real_time_generator.py` script in the `brainiak/utils` folder.

Annotated bibliography

1. Ellis, C. T., Baldassano, C., Schapiro, A. C., Cai, M. B., Cohen, J. D. (2020). Facilitating open-science with realistic fMRI simulation: validation and application. *PeerJ* 8:e8564 `link` *Describes and validates the fmrisim method. Applies it to a dataset to test alternative design parameters and evaluate how these parameters influence the effect size*

2. Ellis, C. T., Lesnick, M., Henselman-Petrusek, G., Keller, B., & Cohen, J. D. (2019). Feasibility of topological data analysis for event-related fMRI, Network Neuroscience, 1-12 `link` *Example of using fmrisim to evaluate the plausibility of an analysis procedure under different signal parameters and design constraints*

3. Kumar, S., Ellis, C., O'Connell, T. P., Chun, M. M., & Turk-Browne, N. B. (in press). Searching through functional space reveals distributed visual, auditory, and semantic coding in the human brain. *PLoS Computational Biology* `link` *Example of using fmrisim to test different possible neural bases for an observed effect in real data*

4. Welvaert, M., et al. (2011) neuRosim: An R package for generating fMRI data. *Journal of Statistical Software* 44, 1-18 `link` *A package in R for simulating fMRI data that was an inspiration for fmrisim*

Table of Contents

Authors: Cameron Ellis (Yale) 2018

1. Set parameters.

It is necessary to set various parameters that describe how the signal and the noise will be generated.

1.1 Import necessary Python packages

In [1]:
```
%matplotlib notebook

from pathlib import Path
from brainiak.utils import fmrisim
import nibabel
import numpy as np
import matplotlib.pyplot as plt
import scipy.ndimage as ndimage
import scipy.spatial.distance as sp_distance
import sklearn.manifold as manifold
import scipy.stats as stats
import sklearn.model_selection
import sklearn.svm
```

1.2 Load participant data

Any 4 dimensional fMRI data that is readible by nibabel can be used as input to this pipeline. For this example, data is taken from the open access repository DataSpace: http://arks.princeton.edu/ark:/88435/dsp01dn39x4181. This file is unzipped and placed in the home directory with the name Corr_MVPA

In [2]:
```
home = str(Path.home())
nii = nibabel.load(home + '/Corr_MVPA/Participant_01_rest_run01.nii')
volume = nii.get_data()
```

1.3 Specify participant dimensions and resolution

The size of the volume and the resolution of the voxels must be specified (or extracted from the real data as is the case below).

In [3]:
```
dim = volume.shape  # What is the size of the volume
dimsize = nii.header.get_zooms()  # Get voxel dimensions from the nifti header
tr = dimsize[3]
if tr > 100:  # If high then these values are likely in ms and so fix it
    tr /= 1000
print('Volume dimensions:', dim)
print('TR duration: %0.2fs' % tr)
```

```
Volume dimensions: (64, 64, 27, 294)
TR duration: 1.50s
```

1.4 Generate an activity template and a mask

Functions in fmrisim require a continuous map that describes the appropriate average MR value for each voxel in the brain and a mask which specifies voxels in the brain versus voxels outside of the brain. One way to generate both of these volumes is the mask_brain function. At a minimum, this takes as an input the fMRI volume to be simulated. To create the template this volume is averaged over time and bounded to a range from 0 to 1. In other words, voxels with a high value in the template have high activity over time. To create a mask, the template is thresholded. This threshold can be set manually or instead an appropriate value can be determined by looking for the minima between the two first peaks in the histogram of voxel values. If you would prefer, you could use the compute_epi_mask function in nilearn which uses a similar method.

In [4]:
```
mask, template = fmrisim.mask_brain(volume=volume,
                                    mask_self=True,
                                    )
```

1.5 Determine noise parameters

A critical step in the fmrisim toolbox is determining the noise parameters of the volume to be created. Many noise parameters are available for specification and if any are not set then they will default to reasonable values. As mentioned before, it is instead possible to provide raw fMRI data that will be used to estimate these noise parameters. The goal of the noise estimation is to calculate general descriptive statistics about the noise in the brain that are thought to be important. The simulations are then useful for understanding how signals will survive analyses when embedded in realistic neural noise.

Now the disclaimers: the values here are only an estimate and will depend on noise properties combining in the ways assumed. In addition, because of the non-linearity and stochasticity of this simulation, this estimation is not fully invertible: if you generate a dataset with a set of noise parameters it will have similar but not the same noise parameters as a result. Moreover, complex interactions between brain regions that likely better describe brain noise are not modelled here: this toolbox pays no attention to regions of the brain or their interactions. Finally, for best results use raw fMRI because if the data has been preprocessed then assumptions this algorithm makes are likely to be erroneous. For instance, if the brain has been masked then this will eliminate variance in non-brain voxels which will mean that calculations of noise dependent on those voxels as a reference will fail.

To ameliorate some of these concerns, it is possible to fit the spatial and temporal noise properties of the data. This iterates over the noise generation process and tunes parameters in order to match those that are provided. This is time consuming (especially for fitting the temporal noise) but is helpful in matching the specified noise properties.

This toolbox separates noise in two: spatial noise and temporal noise. To estimate spatial noise both the smoothness and the amount of non-brain noise of the data must be quantified. For smoothness, the Full Width Half Max (FWHM) of the volume is averaged for the X, Y and Z dimension and then averaged across a sample of time points. To calculate the Signal to Noise Ratio (SNR) the mean activity in brain voxels for the middle time point is divided by the standard deviation in activity across non-brain voxels for that time point. For temporal noise an auto-regressive and moving average (ARMA) process is estimated, along with the overall size of temporal variability. A sample of brain voxels is used to estimate the first AR component and the first MA component of each voxel's activity over time using the statsmodels package. The Signal to Fluctuation Noise Ratio (SFNR) is calculated by dividing the average activity of voxels in the brain with that voxel's noise (Friedman & Glover, 2006). That noise is calculated by taking the standard deviation of that voxel over time after it has been detrended with a second order polynomial. The SFNR then controls the amount of functional variability. Other types of noise can be generated, such as physiological noise, but are not estimated by this function.

In [5]:
```python
# Calculate the noise parameters from the data. Set it up to be matched.
noise_dict = {'voxel_size': [dimsize[0], dimsize[1], dimsize[2]], 'matched': 1}
noise_dict = fmrisim.calc_noise(volume=volume,
                                mask=mask,
                                template=template,
                                noise_dict=noise_dict,
                                )
```

In [6]:
```python
print('Noise parameters of the data were estimated as follows:')
print('SNR: ' + str(noise_dict['snr']))
print('SFNR: ' + str(noise_dict['sfnr']))
print('FWHM: ' + str(noise_dict['fwhm']))
```

```
Noise parameters of the data were estimated as follows:
SNR: 23.175648200023815
SFNR: 70.7171164884859
FWHM: 5.661164924881941
```

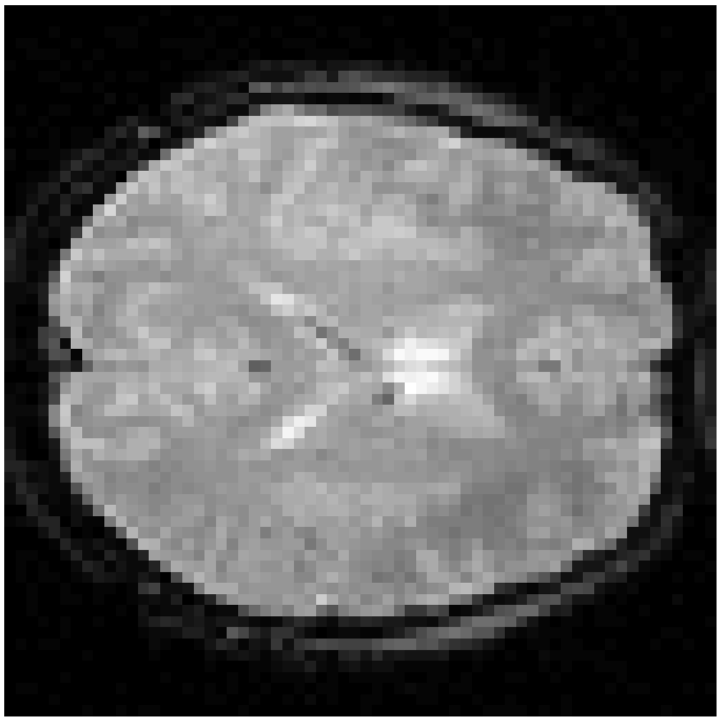
2. Generate noise

fmrisim can generate realistic fMRI noise when supplied with the appropriate inputs. A single function receives these inputs and deals with generating the noise. The necessary code to run this is in the next cell. For clarity, we walk through the steps of how this simulation is performed.

In [7]:
```
# Calculate the noise given the parameters
noise = fmrisim.generate_noise(dimensions=dim[0:3],
                               tr_duration=int(tr),
                               stimfunction_tr=[0] * dim[3],
                               mask=mask,
                               template=template,
                               noise_dict=noise_dict,
                               )
```

```
/Users/cellis/anaconda/envs/brainiak_test/lib/python3.6/site-packages/scipy/stat
s/stats.py:2279: RuntimeWarning: divide by zero encountered in true_divide
  np.expand_dims(sstd, axis=axis))
/Users/cellis/anaconda/envs/brainiak_test/lib/python3.6/site-packages/scipy/stat
s/stats.py:2279: RuntimeWarning: invalid value encountered in true_divide
  np.expand_dims(sstd, axis=axis))
```

In [8]:
```
# Plot a slice through the noise brain
plt.figure()
plt.title('Axial slice from template used for generating noise')
plt.imshow(noise[:, :, int(dim[2] / 2), 0], cmap=plt.cm.gray)
plt.axis('off')
txt="This template is generated by averaging the real functional data in time"
plt.figtext(0.5, 0.01, txt, wrap=True, horizontalalignment='center', fontsize=12
```



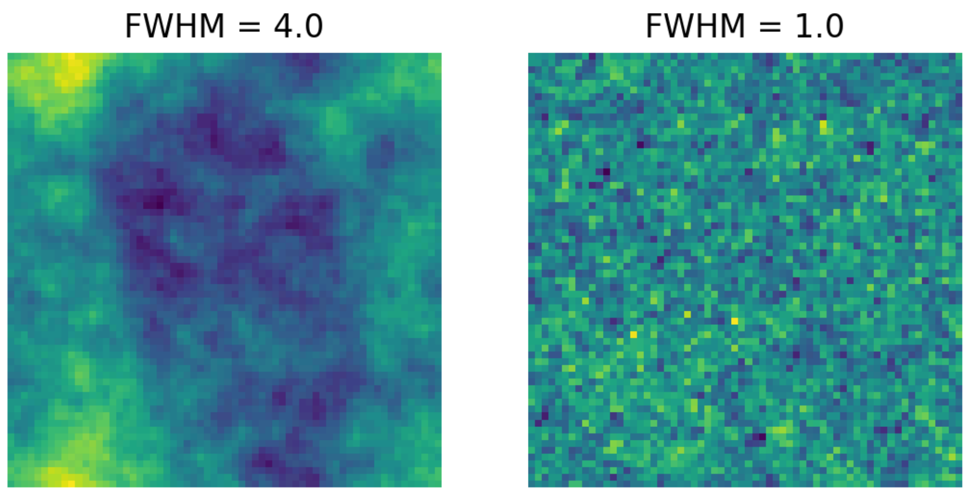
This template is generated by averaging the real functional data in time

2.1 Create temporal noise

The temporal noise of fMRI data is comprised of multiple components: drift, autoregression, task related motion and physiological noise. To estimate drift, cosine basis functions are combined, with longer runs being comprised of more basis functions (Welvaert, et al., 2011). This drift is then multiplied by a three-dimensional volume of Gaussian random fields of a specific FWHM. Autoregression noise is estimated by initializing with a brain shaped volume of gaussian random fields and then multiplying then creating an ARMA time course by adding additional volumes of noise. Physiological noise is modeled by sine waves comprised of heart rate (1.17Hz) and respiration rate (0.2Hz) (Biswal, et al., 1996) with random phase. This time course is also multiplied by brain shaped spatial noise. Finally, task related noise is simulated by adding Gaussian or Rician noise to time points where there are events (according to the event time course) and in turn this is multiplied by a brain shaped spatial noise volume. These four noise components are then mixed together in proportion to the size of their corresponding sigma values. This aggregated volume is then Z scored and the SFNR is used to estimate the appropriate standard deviation of these values across time.

In [9]:
```
# Plot spatial noise
low_spatial = fmrisim._generate_noise_spatial(dim[0:3],
                                              fwhm=4.0,
                                              )

high_spatial = fmrisim._generate_noise_spatial(dim[0:3],
                                               fwhm=1.0,
                                               )
```

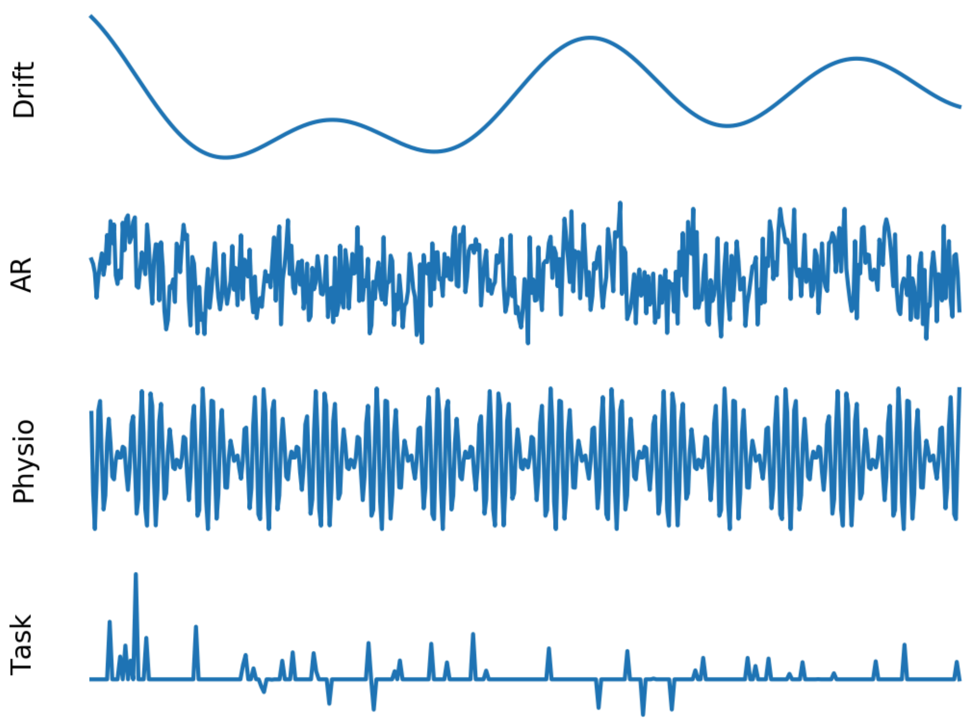
```
plt.figure()
plt.subplot(1,2,1)
plt.title('FWHM = 4.0')
plt.imshow(low_spatial[:, :, 12])
plt.axis('off')

plt.subplot(1,2,2)
plt.title('FWHM = 1.0')
plt.imshow(high_spatial[:, :, 12])
plt.axis('off')

txt="Slices through the volume for different amounts of spatial noise. FWHM star
plt.figtext(0.5, 0.01, txt, wrap=True, horizontalalignment='center', fontsize=12
```



Slices through the volume for different amounts of spatial noise. FWHM stands for full width half maximum, referencing the width of the Gaussian distribution used to simulate the data

In [10]:
```
# Create the different types of noise
total_time = 500
timepoints = list(range(0, total_time, int(tr)))

drift = fmrisim._generate_noise_temporal_drift(total_time,
                                               int(tr),
                                               )


mini_dim = np.array([2, 2, 2])
autoreg = fmrisim._generate_noise_temporal_autoregression(timepoints,
                                                          noise_dict,
                                                          mini_dim,
                                                          np.ones(mini_dim),
                                                          )


phys = fmrisim._generate_noise_temporal_phys(timepoints,
                                                   )

stimfunc = np.zeros((int(total_time / tr), 1))
stimfunc[np.random.randint(0, int(total_time / tr), 50)] = 1
task = fmrisim._generate_noise_temporal_task(stimfunc,
                                                   )
```

In [11]:
```
# Plot the different noise types
plt.figure()
plt.title('Noise types')

def clean_axis(ax):
    # Remove the borders and ticks of the plots (but different than plt.axis('of
    ax.spines["top"].set_visible(False)
    ax.spines["bottom"].set_visible(False)
    ax.spines["left"].set_visible(False)
    ax.spines["right"].set_visible(False)
    plt.xticks([])
    plt.yticks([])

ax = plt.subplot(4, 1, 1)
plt.plot(drift)
clean_axis(ax)
plt.ylabel('Drift')

ax = plt.subplot(4, 1, 2)
plt.plot(autoreg[0, 0, 0, :])
clean_axis(ax)
plt.ylabel('AR')

ax = plt.subplot(4, 1, 3)
plt.plot(phys)
clean_axis(ax)
plt.ylabel('Physio')

ax = plt.subplot(4, 1, 4)
plt.plot(task)
clean_axis(ax)
plt.ylabel('Task')

txt="Time course of different noise properties that are usable in fmrisim."
plt.figtext(0.5, 0.01, txt, wrap=True, horizontalalignment='center', fontsize=12
```



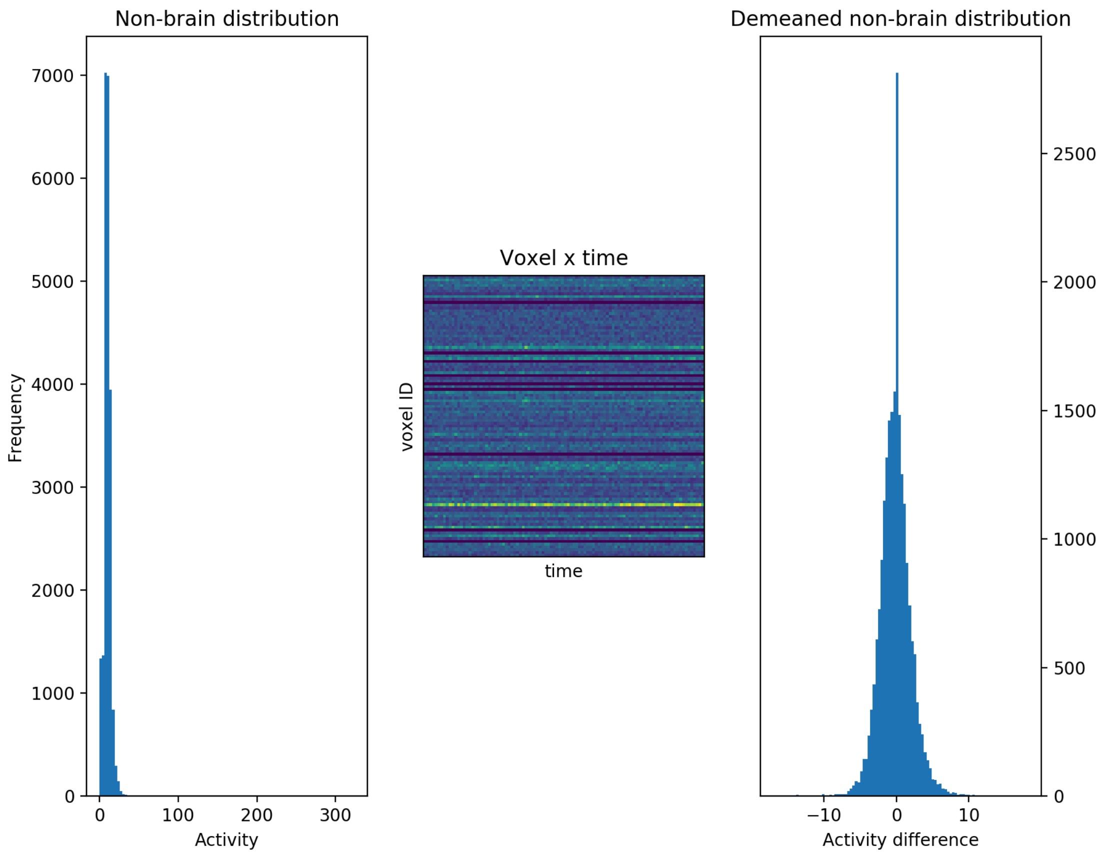
Time course of different noise properties that are usable in fmrisim.

2.2 Create system noise

Machine/system noise causes fluctuations in all voxels in the acquisition. When SNR is low, Rician noise is a good estimate of background noise data (Gudbjartsson, & Patz, 1995). However if you look at the distribution of non-brain voxel values averaged across time (i.e., the template) then you see that this is also rician, suggesting that most of the rician noise is a result of the structure in the background of the brain (e.g. the baseline MR of the head coil or skull). If you subtract this baseline then the noise becomes approximately gaussian, especially in the regions far from the brain (which is what the `calc_noise` algorithm considers when calculating SNR). Hence the machine noise here is gaussian added to an inherently rician baseline.

Below we take the distribution of voxel intensity for voxels that are more than 5 units away from the brain voxels. We then plot those voxels as a histogram at the first timepoint. Next we take a sample of voxels and display the distribution of intensity for these voxels over time, the lines indicating that the values are relatively stable. The last plot shows the distribution of values for the non-brain voxels after their baseline is removed which is a kurtotic gaussian (the peak reflects zero values).

In [12]:
```
# Dilate the mask so as to only take voxels far from the brain (performed in cal
mask_dilated = ndimage.morphology.binary_dilation(mask, iterations=10)

# Remove all non brain voxels
system_all = volume[mask_dilated == 0]  # Pull out all the non brain voxels in t
system_baseline = volume - (template.reshape(dim[0], dim[1], dim[2], 1) * noise_
system_baseline = system_baseline[mask_dilated == 0]

# Plot the distribution of voxels
plt.figure(figsize=(10,8))
plt.subplot(1, 3, 1)
plt.hist(system_all[:,0].flatten(),100)
plt.title('Non-brain distribution')
plt.xlabel('Activity')
plt.ylabel('Frequency')

# Identify a subset of voxels to plot
idxs = list(range(system_all.shape[0]))
np.random.shuffle(idxs)

temporal = system_all[idxs[:100], :100]
plt.subplot(1, 3, 2)
plt.imshow(temporal)
plt.xticks([], [])
plt.yticks([], [])
plt.ylabel('voxel ID')
plt.xlabel('time')
plt.title('Voxel x time')

# Plot the difference
ax=plt.subplot(1, 3, 3)
plt.hist(system_baseline[:,0].flatten(),100)
ax.yaxis.tick_right()
ax.yaxis.set_label_position("right")
plt.title('Demeaned non-brain distribution')
plt.xlabel('Activity difference')

txt="Histogram of non-brain voxel intensity. Left shows the raw intensity histog
plt.figtext(0.5, 0.01, txt, wrap=True, horizontalalignment='center', fontsize=1
```



Histogram of non-brain voxel intensity. Left shows the raw intensity histogram, middle shows the voxel by time matrix (showing that there is variance in mean but not much in time) and then right shows the demeaned voxel intensity for the first time point.

2.3 Combine noise and template

The template volume is used to estimate the appropriate baseline distribution of MR values. This estimate is then combined with the temporal noise and the system noise to make an estimate of the noise.

2.4 Fit the data to the noise parameters

The generate_noise function does its best to estimate the appropriate noise parameters using assumptions about noise sources; however, because of the complexity of these different noise types, it is often wrong. To compensate, fitting is performed in which parameters involved in the noise generation process are changed and the noise metrics are recalculated to see whether those changes helped the fit. Due to their importance, the parameters that can be fit are SNR, SFNR and AR.

The fitting of SNR/SFNR involves reweighting spatial and temporal metrics of noise. This analysis is relatively quick because this reweighting does not require that any timecourses are recreated, only that they are reweighted. At least 10 iterations are recommended because the initial guesses tend to underestimate SFNR and SNR (although the size of this error depends on the data). In the case of fitting the AR, the MA rho is adjusted until the AR is appropriate and in doing so the timecourse needs to be recreated for each iteration. In the noise_dict, one of the keys is 'matched' which is a binary value determining whether any fitting will be done

In terms of timing, for a medium size dataset (64x64x27x300 voxels) it takes approximately 2 minutes to generate the data when fitting on a Mac 2014 laptop.

In [13]:
```
# Compute the noise parameters for the simulated noise
noise_dict_sim = {'voxel_size': [dimsize[0], dimsize[1], dimsize[2]], 'matched':
noise_dict_sim = fmrisim.calc_noise(volume=noise,
                                    mask=mask,
                                    template=template,
                                    noise_dict=noise_dict_sim,
                                    )
```

In [14]:
```
print('Compare noise parameters for the real and simulated noise:')
print('SNR: %0.2f vs %0.2f' % (noise_dict['snr'], noise_dict_sim['snr']))
print('SFNR: %0.2f vs %0.2f' % (noise_dict['sfnr'], noise_dict_sim['sfnr']))
print('FWHM: %0.2f vs %0.2f' % (noise_dict['fwhm'], noise_dict_sim['fwhm']))
print('AR: %0.2f vs %0.2f' % (noise_dict['auto_reg_rho'][0], noise_dict_sim['aut
```

```
Compare noise parameters for the real and simulated noise:
SNR: 23.18 vs 22.53
SFNR: 70.72 vs 69.19
FWHM: 5.66 vs 5.69
AR: 0.86 vs 0.84
```

3. Generate signal

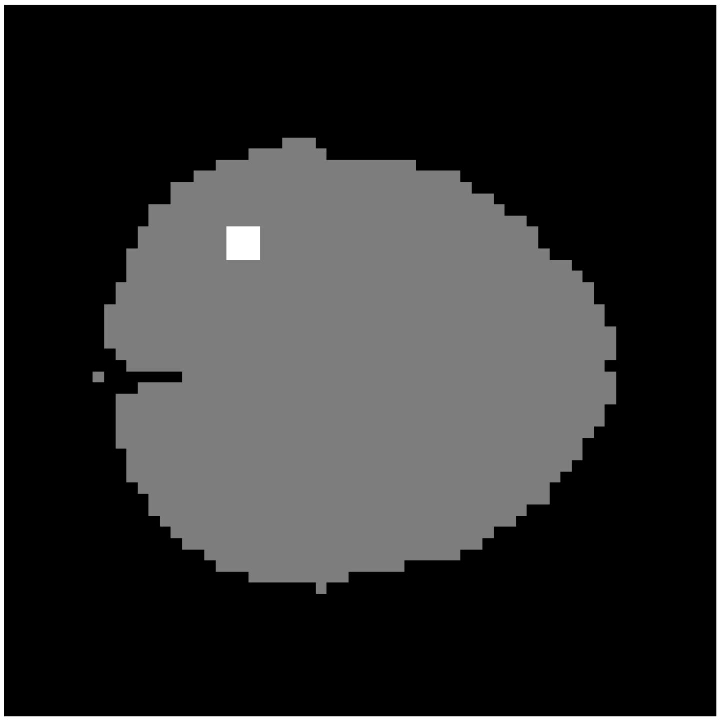
fmrisim can be used to generate signal in a number of different ways depending on the type of effect being simulated. Several tools are supplied to help with different types of signal that may be required; however, custom scripts may be necessary for unique effects. Below an experiment will be simulated in which two conditions, A and B, evoke different patterns of activity in the same set of voxels in the brain. This pattern does not manifest as a uniform change in activity across voxels but instead each condition evokes a consistent pattern across voxels. These conditions are randomly intermixed trial by trial. This code could be easily changed to instead compare univariate changes evoked by stimuli in different brain regions.

3.1 Specify which voxels in the brain contain signal

fmrisim provides tools to specify certain voxels in the brain that contain signal. The generate_signal function can produce regions of activity in a brain of different shapes, such as cubes, loops and spheres. Alternatively a volume could be loaded in that specifies the signal voxels (e.g. for ROIs from nilearn). The value of each voxel can be specified here, or set to be a random value.

In [15]:
```
# Create the region of activity where signal will appear
coordinates = np.array([[21, 21, 21]])  # Where in the brain is the signal
feature_size = 3  # How big, in voxels, is the size of the ROI
signal_volume = fmrisim.generate_signal(dimensions=dim[0:3],
                                        feature_type=['cube'],
                                        feature_coordinates=coordinates,
                                        feature_size=[feature_size],
                                        signal_magnitude=[1],
                                        )
```

In [16]:
```
plt.figure()
plt.imshow(signal_volume[:, :, 21], cmap=plt.cm.gray)
plt.imshow(mask[:, :, 21], cmap=plt.cm.gray, alpha=.5)
plt.axis('off')

txt="Mask of volume showing all voxels in gray. In white is the cube where signa
plt.figtext(0.5, 0.01, txt, wrap=True, horizontalalignment='center', fontsize=12
```



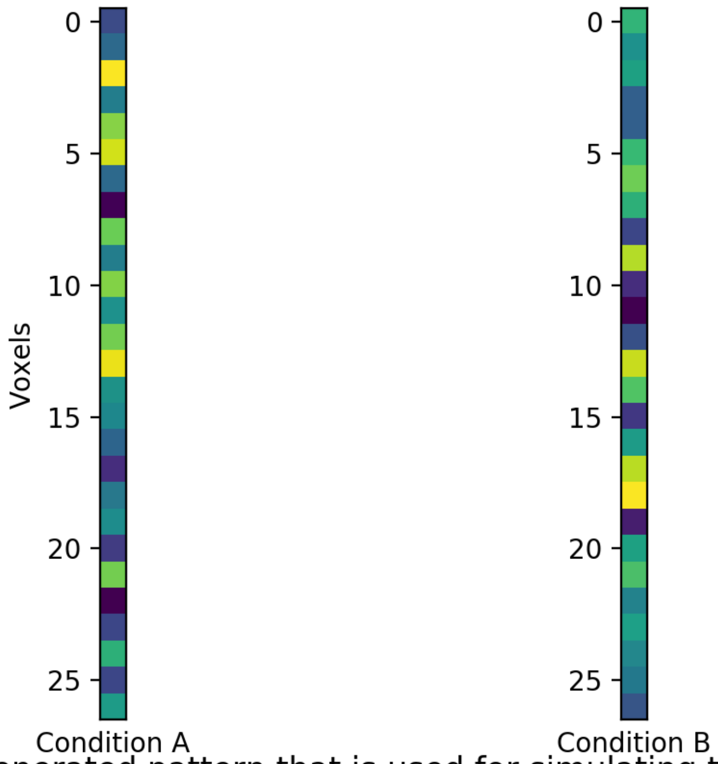
Mask of volume showing all voxels in gray. In white is the cube where signal is inserted

3.2 Characterize signal for voxels

Specify the pattern of activity across a given number of voxels that characterizes each condition. This pattern can simply be random, as is done here, or can be structured, like the position of voxels in high-dimensional representation space.

In [17]:
```
# Create a pattern for each voxel in our signal ROI
voxels = feature_size ** 3

# Pull the conical voxel activity from a uniform distribution
pattern_A = np.random.rand(voxels).reshape((voxels, 1))
pattern_B = np.random.rand(voxels).reshape((voxels, 1))
```

In [18]:
```
# Plot pattern of activity for each condition
plt.figure()
plt.subplot(1,2,1)
plt.imshow(pattern_A)
plt.ylabel('Voxels')
plt.tick_params(which='both', left='off', labelleft='off', bottom='off', labelbo
plt.xticks([])
plt.xlabel('Condition A')
plt.subplot(1,2,2)
plt.imshow(pattern_B)
plt.tick_params(which='both', left='off', labelleft='off', bottom='off', labelbo
plt.xticks([])
plt.xlabel('Condition B')

txt="Randomly generated pattern that is used for simulating the response evoked
plt.figtext(0.5, 0.01, txt, wrap=True, horizontalalignment='center', fontsize=12
```



Randomly generated pattern that is used for simulating the response evoked by two different events

3.3 Generate event time course

generate_stimfunction can be used to specify the time points at which task stimulus events occur. The timing of events can be specified by describing the onset and duration of each event. Alternatively, it is possible to provide a path to a 3 column timing file, used by fMRI software packages like FSL, which specifies event onset, duration and weight.

In [19]:
```
# Set up stimulus event time course parameters
event_duration = 2  # How long is each event
isi = 7  # What is the time between each event
burn_in = 1  # How long before the first event

total_time = int(dim[3] * tr) + burn_in  # How long is the total event time cour
events = int((total_time - ((event_duration + isi) * 2))  / ((event_duration + i
onsets_all = np.linspace(burn_in, events * (event_duration + isi), events)  # Sp
np.random.shuffle(onsets_all)  # Shuffle their order
onsets_A = onsets_all[:int(events / 2)]  # Assign the first half of shuffled eve
onsets_B = onsets_all[int(events / 2):]  # Assign the second half of shuffled ev
temporal_res = 10.0 # How many timepoints per second of the stim function are to
```

In [20]:
```
# Create a time course of events
stimfunc_A = fmrisim.generate_stimfunction(onsets=onsets_A,
                                           event_durations=[event_duration],
                                           total_time=total_time,
                                           temporal_resolution=temporal_res,
                                           )

stimfunc_B = fmrisim.generate_stimfunction(onsets=onsets_B,
                                           event_durations=[event_duration],
                                           total_time=total_time,
                                           temporal_resolution=temporal_res,
                                           )
```

3.4 Export stimulus time course for analysis

If a time course of events is generated, as is the case here, it may be useful to store this in a certain format for future analyses. The `export_3_column` function can be used to export the time course to be a three column (event onset, duration and weight) timing file that might readable to FSL. Alternatively, the export_epoch_file function can be used to export numpy files that are necessary inputs for MVPA and FCMA in BrainIAK.

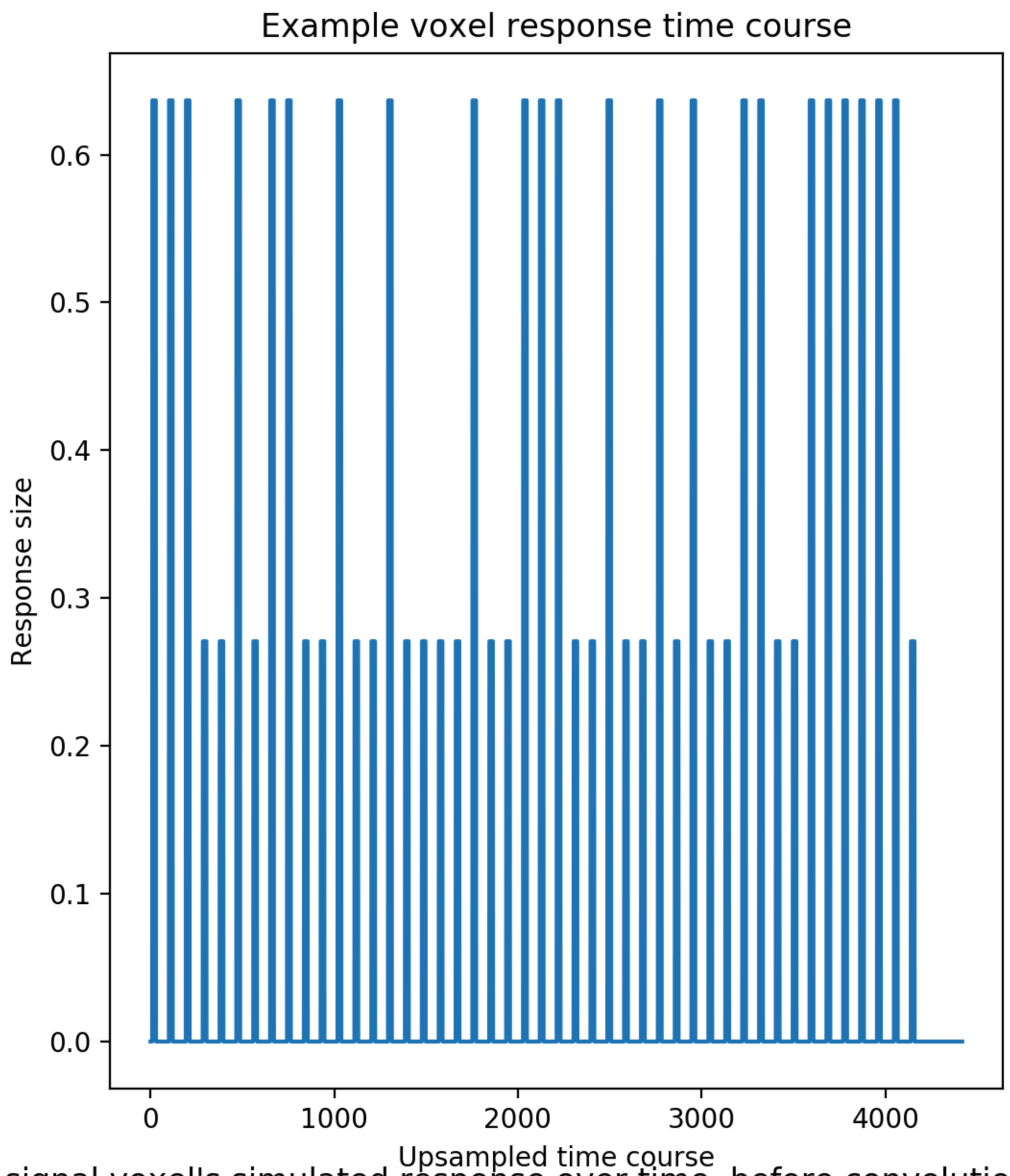
In [21]:
```
fmrisim.export_epoch_file(stimfunction=[np.hstack((stimfunc_A, stimfunc_B))],
                          filename=home + '/epoch_file.npy',
                          tr_duration=tr,
                          temporal_resolution=temporal_res,
                          )

fmrisim.export_3_column(stimfunction=stimfunc_A,
                        filename=home + '/Condition_A.txt',
                        temporal_resolution=temporal_res,
                        )

fmrisim.export_3_column(stimfunction=stimfunc_B,
                        filename=home + '/Condition_B.txt',
                        temporal_resolution=temporal_res,
                        )
```

3.5 Estimate the voxel weight for each event

According to the logic of this example, each voxel carrying signal will respond a different amount for condition A and B. To simulate this we multiply a voxel's response to each condition by the time course of events and then combine these to make a single time course. This time course describes each voxel's response to signal over time.

In [22]:
```
# Multiply each pattern by each voxel time course
weights_A = np.matlib.repmat(stimfunc_A, 1, voxels).transpose() * pattern_A
weights_B = np.matlib.repmat(stimfunc_B, 1, voxels).transpose() * pattern_B

# Sum these time courses together
stimfunc_weighted = weights_A + weights_B
stimfunc_weighted = stimfunc_weighted.transpose()
```

In [23]:
```
plt.figure(figsize=(6,7))
plt.plot(stimfunc_weighted[:, 0])
plt.title('Example voxel response time course')
plt.xlabel('Upsampled time course')
plt.ylabel('Response size')

txt="A signal voxel's simulated response over time, before convolution. The two
plt.figtext(0.5, 0.01, txt, wrap=True, horizontalalignment='center', fontsize=12
```



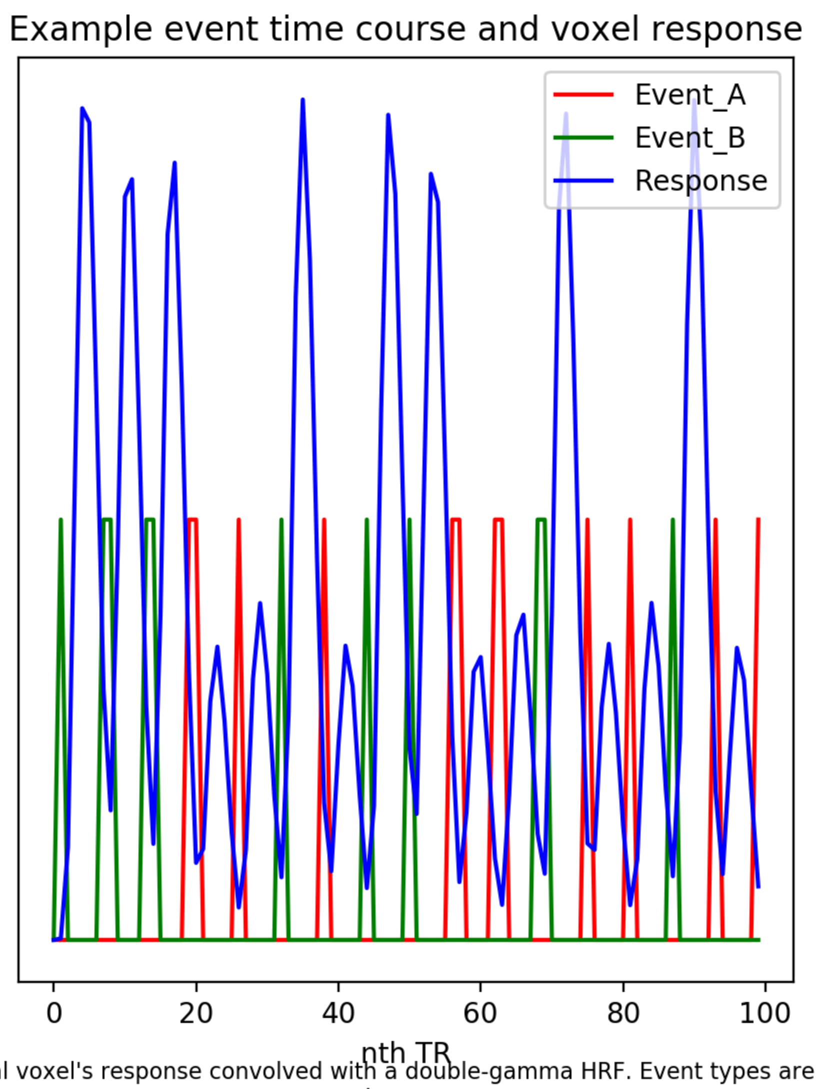
A signal voxel's simulated response over time, before convolution. The two heights of the bars refer to different event types

3.6 Convolve each voxel's time course with the Hemodynamic Response Function

With the time course of stimulus events it is necessary to estimate the brain's response to those events, which can be estimated by convolving it with using a Hemodynamic Response Function (HRF). By default, `convolve_hrf` assumes a double gamma HRF appropriately models a brain's response to events, as modeled by fMRI (Friston, et al., 1998). To do this convolution, each voxel's time course is convolved to make a function of the signal activity. Hence this produces an estimate of the voxel’s activity, after considering the temporal blurring of the HRF. This can take a single vector of events or multiple time courses.

In [24]:
```
signal_func = fmrisim.convolve_hrf(stimfunction=stimfunc_weighted,
                                   tr_duration=tr,
                                   temporal_resolution=temporal_res,
                                   scale_function=1,
                                   )
```

In [25]:
```
# Prepare the data to be plotted
response = signal_func[0:100,0] * 2
downsample_A = stimfunc_A[0:int(100*temporal_res * tr):int(temporal_res * tr), 0
downsample_B = stimfunc_B[0:int(100*temporal_res * tr):int(temporal_res * tr), 0

# Display signal
plt.figure(figsize=(5,6))
plt.title('Example event time course and voxel response')
Event_A = plt.plot(downsample_A, 'r', label='Event_A')
Event_B = plt.plot(downsample_B, 'g', label='Event_B')
Response = plt.plot(response, 'b', label='Response')
plt.legend(loc=1)
plt.yticks([],'')
plt.xlabel('nth TR')

txt="A signal voxel's response convolved with a double-gamma HRF. Event types ar
plt.figtext(0.5, 0.01, txt, wrap=True, horizontalalignment='center', fontsize=8)
```



A signal voxel's response convolved with a double-gamma HRF. Event types are also shown.

3.7 Establish signal magnitude

When specifying the signal we must determine the amount of activity change each voxel undergoes. fmrisim contains a tool to allow you to choose between a variety of different metrics that you could use to scale the signal. For instance, we can calculate percent signal change (referred to as PSC) by taking the average activity of a voxel in the noise volume and multiplying the maximal activation of the signal by a percentage of this number. This metric doesn't take into account the variance in the noise but other metrics in this tool do. One metric that does take account of variance, and is used below, is the signal amplitude divided by the temporal variability. The choices that are available for computing the signal scale are based on Welvaert and Rosseel (2013).

In [26]:
```
# Specify the parameters for signal
signal_method = 'CNR_Amp/Noise-SD'
signal_magnitude = [0.5]

# Where in the brain are there stimulus evoked voxels
signal_idxs = np.where(signal_volume == 1)
```

```
# Pull out the voxels corresponding to the noise volume
noise_func = noise[signal_idxs[0], signal_idxs[1], signal_idxs[2], :].T
```

In [27]:
```
# Compute the signal appropriate scaled
signal_func_scaled = fmrisim.compute_signal_change(signal_func,
                                                   noise_func,
                                                   noise_dict,
                                                   magnitude=signal_magnitude,
                                                   method=signal_method,
                                                   )
```

3.8 Multiply the convolved response with the signal voxels

If you have a time course of simulated response for one or more voxels and a three dimensional volume representing voxels that ought to respond to these events then apply_signal will combine these appropriately. This function multiplies each signal voxel in the brain by the convolved event time course.

In [28]:
```
signal = fmrisim.apply_signal(signal_func_scaled,
                              signal_volume,
                              )
```

3.9 Combine signal and noise

Since the brain signal is expected to be small and sparse relative to the noise, it is assumed sufficient to simply add the volume containing signal with the volume modeling noise to make the simulated brain.

In [29]:
```
brain = signal + noise
```

4. Analyse data

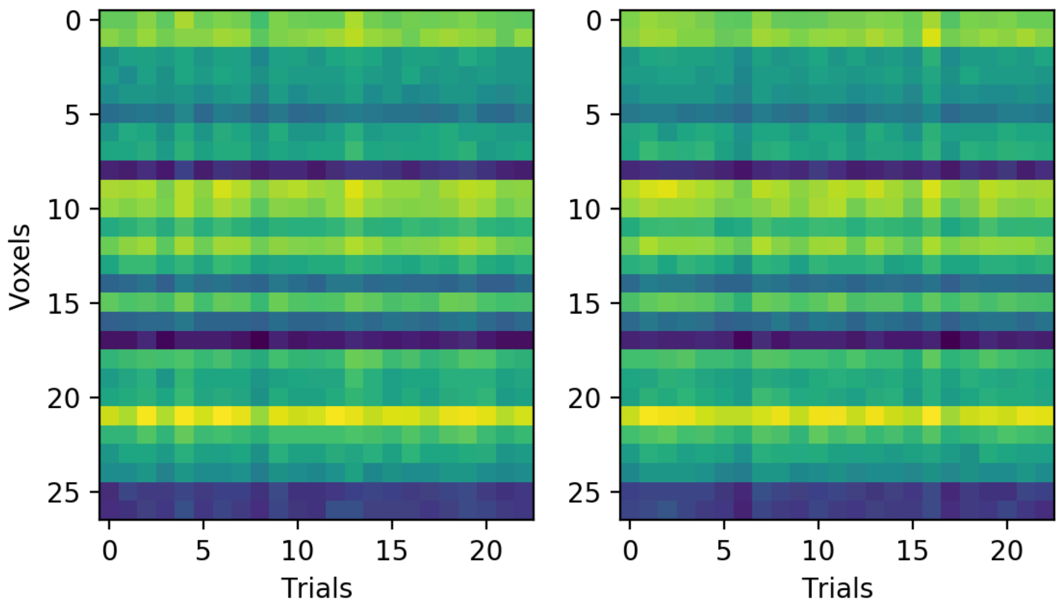
Several tools are available for multivariate analysis in BrainIAK. These greatly speed up computation and are critical in some cases, such as a whole brain searchlight. However, for this example data we will only look at data in the ROI that we know contains signal and so do not need these advanced tools optimized for whole-brain analyses.

4.1 Pull out data for each trial

Identify which voxels are in the signal ROI by using the coordinates provided earlier. To identify the relevant timepoints, assume that the peak of the neural response occurs 4 - 6s after each event onset. Take the TR corresponding to this peak response as the TR for that trial. In longer event/block designs you might instead average over each event.

In [30]:
```
hrf_lag = 4  # Assumed time from stimulus onset to HRF peak

# Get the lower and upper bounds of the ROI
lb = (coordinates - ((feature_size - 1) / 2)).astype('int')[0]
ub = (coordinates + ((feature_size - 1) / 2) + 1).astype('int')[0]

# Pull out voxels in the ROI for the specified timepoints
trials_A = brain[lb[0]:ub[0], lb[1]:ub[1], lb[2]:ub[2], ((onsets_A + hrf_lag) /
trials_B = brain[lb[0]:ub[0], lb[1]:ub[1], lb[2]:ub[2], ((onsets_B + hrf_lag) /
# Reshape data for easy handling
trials_A = trials_A.reshape((voxels, trials_A.shape[3]))
trials_B = trials_B.reshape((voxels, trials_B.shape[3]))
```

In [31]:
```
# Plot the pattern of activity for our signal voxels at each timepoint
plt.figure()
plt.subplot(1,2,1)
plt.imshow(trials_A)
plt.ylabel('Voxels')
plt.xlabel('Trials')
plt.subplot(1,2,2)
plt.imshow(trials_B)
plt.xlabel('Trials')

txt="Time course of activity for each signal voxel when combining signal and noi
plt.figtext(0.5, 0.01, txt, wrap=True, horizontalalignment='center', fontsize=12
```



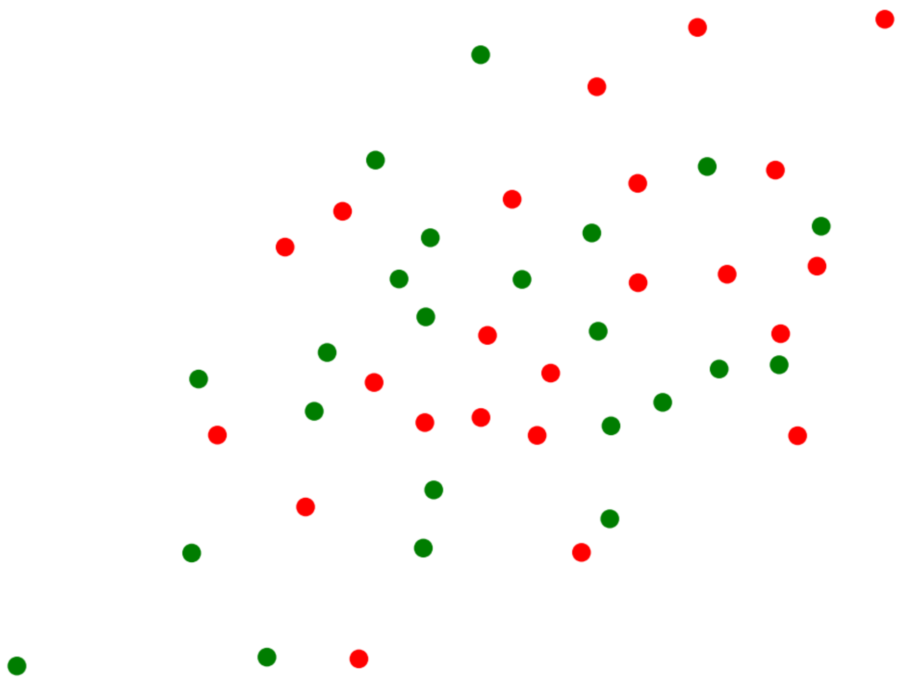
Time course of activity for each signal voxel when combining signal and noise

4.2 Represent the data

Treat each voxel as a dimension and each trial as a point in this voxel space. It is then possible to display the different conditions and determine whether these are separable in this lower dimensionality (note that the conditions may be separable in higher dimensionality but unsupervised techniques like Multidimensional Scaling used below, might not show such a difference)

In [32]:
```
# Calculate the distance matrix between trial types
distance_matrix = sp_distance.squareform(sp_distance.pdist(np.vstack([trials_A.t
mds = manifold.MDS(n_components=2, dissimilarity='precomputed')  # Fit the mds c
coords = mds.fit(distance_matrix).embedding_  # Find the mds coordinates

# Plot the data
plt.figure()
plt.scatter(coords[:, 0], coords[:, 1], c=['red'] * trials_A.shape[1] + ['green'
plt.axis('off')
plt.title('Low Dimensional Representation of conditions A and B')

txt="Low dimensional representation of the two conditions. Different colors refe
plt.figtext(0.5, 0.01, txt, wrap=True, horizontalalignment='center', fontsize=12
```

Low Dimensional Representation of conditions A and B



Low dimensional representation of the two conditions. Different colors refer to different conditions

4.3 Test for univariate effect

Do a t test to compare the means of the voxels between these two conditions to determine if there is a difference

In [33]:
```
mean_difference = (np.mean(trials_A,0) - np.mean(trials_B,0))
ttest = stats.ttest_1samp(mean_difference, 0)

print('Mean difference between condition A and B: %0.2f\np value: %0.3f' % (mear
```

```
Mean difference between condition A and B: 3.14
p value: 0.229
```

4.4 Test for a multivariate effect

Use SVM from scikit-learn to estimate the classification accuracy between the conditions

```
In [34]: # Get the inputs to the SVM
         input_mat = np.vstack([trials_A.transpose(), trials_B.transpose()])
         input_labels = trials_A.shape[1] * [1] + trials_B.shape[1] * [0]

         # Set up the classifier
         X_train, X_test, y_train, y_test = sklearn.model_selection.train_test_split(
             input_mat, input_labels, test_size=0.2, random_state=0)

         clf = sklearn.svm.SVC(kernel='linear', C=1, gamma='auto').fit(X_train, y_train)

         score = clf.score(X_test, y_test)
         print('Classification accuracy between condition A and B: %0.3f' % score)
```

```
Classification accuracy between condition A and B: 0.700
```

Summary

Using fmrisim we were able to take in raw data and create a simulation with matched noise properties. This simulated data was used for designing an example experiment time course for a two condition event-related design, such as a localizer task.

fmrisim can be used to optimize experimental design parameters (e.g., what is the best ISI given the time constraints of the experiment) and to pre-register an experiment preprocessing pipeline.

More resources and examples of fmrisim usage can be found here: `brainiak/utils` , also please checkout thereferences below for published examples of fmrisim.

References

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