CRCNS.org vim-2 data description

Version 0.61 (Feb 17, 2015)

This document describes the Gallant Lab Natural Movie 4T fMRI Data set (data set "vim-2" at CRCNS.org). The data set contains BOLD fMRI responses to a set of natural movies. The data were originally published in Nishimoto et al, 2011 (see below for full reference).

-- BOLD data --

The functional data were collected for three subjects, in three sessions over three separate days for each subject (please see the Nishimoto et al. 2011 for scanning and preprocessing parameters). Peak BOLD responses to each timepoint in the stimuli were estimated from the preprocessed data. The responses are provided in the VoxelResponses_subject1.mat, VoxelResponses_subject2.mat, and VoxelResponses_subject3.mat files. The files are stored in Matlab version 7.3 format, which is hf5 format compatible and can be read directly into numpy/python using the PyTables library. The files have been compressed in tar.gz format.

Variables in each file:

- rt: training responses: 7200 (timepoints) x 73728 (voxels) matrix. The voxel dimension is a linearized vector from the 64x64x18 scanning volume.
- rv: validation responses: 540 (timepoints) x 73728 (voxels) matrix.
- rva: validation responses (not averaged): 540 (timepoints) x 10 (trials) x 73728 (voxels) matrix
- roi: structure containing volume matrices (64x64x18) with indices corresponding to each region of interest in each hemisphere. The name of each roi variable corresponds to the name of the ROI plus hemisphere, e.g. "roi.v1lh" contains the indices for region V1 in the left hemisphere.
- ei: structure containing experiment information:
 - ei.datasize: size of the data volume ([64, 64, 18])
 - ei.TRsec: repetition time in seconds (1)
 - ei.imhz: frame rate of movie stimulus presentation in Hz (15)
 - ei.valrepnum: number of validation stimulus trials (10)

-- Stimuli --

All stimuli are stored in the "Stimuli.mat" file, in Matlab version 7.3 format, compressed in tar.gz format. Variables are:

- st: training stimuli: 128x128x3x108000 matrix (108000 128x128 rgb frames). Presented at 15 Hz over 7200 timepoints = 120 minutes.
- sv: validation stimuli: 128x128x3x8100 matrix (8100 128x128 rgb frames). Presented at 15 Hz over 540 timepoints = 9 minutes, repeated 10 times.

The order of the stimuli in the "st" and "sv" variables matches the order of the stimuli in the "rt" and "rv" variables in the response files.

-- Anatomy --

File **anatomy.zip** contains the subjects anatomy in files S1_anatomy.nii, S2_anatomy.nii, and S3_anatomy.nii. These are all standard anatomical files that can be read by any standard MRI software. They were collected on the 4T Varian scanner at UC Berkeley, using an MP-RAGE T1-weighted anatomy sequence, 1mm isotropic voxels, axial slices.

-- How to get started --

First, the files should be uncompressed using the tar function in Unix.

The files provided are in Matlab format, so use the standard "load" function to load the files.

To load the files in Python, you'll need the pyTables library, as well as numpy.

Here is an example of using Python to load the left hemisphere V1 voxel responses for the first subject in the training data set:

```
import tables, numpy
f = tables.openFile('VoxelResponses_subject1.mat')
f.listNodes # Show all variables available
data = f.getNode('/rt')[:]
roi = f.getNode('/roi/v1lh')[:].flatten()
v1lh_idx = numpy.nonzero(roi==1)[0]
v1lh resp = data[v1lh idx]
```

-- References --

Nishimoto, S., Vu, A. T., Naselaris, T., Benjamini, Y., Yu, B., & Gallant, J. L. (2011). Reconstructing visual experiences from brain activity evoked by natural movies. Current Biology, 21(19), 1641-1646.

-- Conditions for usage of the data in publications -

If you publish any work using the data, please cite the paper listed above and also cite the data set using the reference below.

Shinji Nishimoto, An T. Vu, Thomas Naselaris, Yuval Benjamini, Bin Yu, Jack L. Gallant (2014): Gallant Lab Natural Movie 4T fMRI Data. CRCNS.org. http://dx.doi.org/10.6080/K00Z715X

-- Document change history -

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2015-02-17; v0.60 -> v0.61, last line of example Python modified; v1lh_resp = data[:,v1lh_idx] changed to: v1lh_resp = data[v1lh_idx] (':,' removed).
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