yakview

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1   Introduction

yakview is a program for displaying the results of selective averaging and statistical analysis of fMRI data on a slice-by-slice basis. Specifically, it can be used to view images with multiple planes, overlays, and time-courses of hemodynamic estimates for multiple conditions in a point-and-click environment. Requires matlab 5.2 or higher.

Note: in previous versions (prior to 3/1/2000), yakview would, by default, assume that significances were stored as the natural log of the significance values. It now defaults to log10 of the significance values.

2   Usage

Typing yakview at the command-line without any options will give the following message:

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USAGE: -i imgstem -sn slicenum -p sigstem -th threshold -f pformat -h hdrstem
   -i imgstem: stem of image to view
   -sn slice number
 Options:
   -p sigstem:        stem of stat map to overlay
   -thmin threshold: min threshold for stat overlay (2)
   -thmax threshold: max threshold for stat overlay (7)
   -h hdrstem: stem of hemodynamic averages
   -r rawstem: stem of raw data to plot
   -nskip n  : skip when displaying raw timecourses
   -off offsetstem: stem of offset volume (default is hdrstem-offset)
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3   Command-line Arguments

Note: there are two basic ways to invoke yakview. The first is to specify the entire name of a slice (including slice number and extension). The second is to provide the stem and the slice number as separate arguments.

-i instem: stem of the input volume for a single in *bfile format*. This can actually be either a stem or a full file name. If it is a stem, then it must be accompanied by the *-sn* flag to indicate the slice number to use.

-sn slicenumber: the slice number of the stem(s) to view. This must be omitted if full file names are specified in the *-i*, *-h*, and *-p* flags. All the flags must specify either a full file name or a stem; no mixing is allowed.

-h hdrstem: name of file in which the selective averages (ie, hemodynamic responses) are stored. This can actually be either a stem or a full file name. If it is a stem, then it must be accompanied

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by the *-sn* flag to indicate the slice number to use. It is expected that there will also be a data file called "hdrstem.dat".

-r rawstem: name of raw data file. Hitting "r" inside the yakview window will bring up a plot of the raw data at the active voxel.

-p sigstem: name of the file in which the overlay data are stored (in bfile format). This can actually be either a stem or a full file name. If it is a stem, then it must be accompanied by the *-sn* flag to indicate the slice number to use. The actual values in the volume have no inherent meaning to yakview. The color given to overlay voxels is dependent upon the values of the minium and maximum threshold (see -thmin and -thmax).

-f format: obsolete.

-thmin threshold: specifies the minimum value that an overlay voxel must achieve in order to be displayed as a color. This is currently the only way to set the display threshold.

-thmax threshold: specifies the maximum value to map in the color scale. Voxels beyond this maximum will be displayed in the color of maximum threshold.

-nskip n: specifies the number of initial data points to skip when displaying raw time courses.

-off offsetstem: specifies the stem of an offset (or baseline) file. This volume indicates the factor (at each voxel) to use when computing percent signal change (and so it is only relevant with the -h option). If *offsetstem* is unspecified, yakview will look for a volume with stem *instem-offset* (which is automatically produced with selxavg).

4 General Usage

In its most sophisticated invocation, yakview can be used to overlay a significance map onto a co-planar structural image and to view the hemodynamic responses at a voxel in a separate window by clicking on the voxel in the image. Manipulation of the data in both the image window and the HDR window relies heavily on keypress commands. A help menu can be displayed for either window by clicking in the window and then pressing the "h" key.

4.1 The Image Window

Upon invocation, only the image window is displayed. It will show the underlying structural in gray scale and super-threshold statistics in color. Initially, only the voxels with statistics with a positive sign are displayed. Hitting the "t" key once will cause only those with negative sign to be displayed. Hitting the "t" key again will display the absolute value. Hitting the "t" key again will bring the sign back to positive only. Yakview keypress commands are:

4.2 The Hemodynamic Response Window

To bring up the hemodyanmic response window (aka *HDRView*), click in the image window and then press the "g" key. Note that the hemodynamic response *cannot* be viewed if the raw data was fit to an ideal response. HDRView keypress commands are:

+	step to the next image plane
-	step to the previous image plane
b	bone scale (instead of grey)
c	toggle crosshair
h	display help menu
i	invert underlay image
g	view hemodynamic averages
m	toggle marker
p	pink scale (instead of grey)
q	exit yakview
r	view raw time courses
t	change overlay sign to view (+,-,+/-)
z	toggle zoom state

d	toggle subtraction of condition 0
e	toggle display standard error bars
h	display help menu
n	toggle display of condition n (n=0,1,...)
p	toggle dipslay of percent signal change
q	close HDRView
s	toggle display standard deviation bars
v	save graph as ascii file
z	subtract prestim avg for all conditions