Psymat version 0.35 - Psychophysical matching and comparison

- **www.juno3d.com/software/**

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Overview and workflow

Psymat is software that allows experimenters to present stimuli for a psychophysical matching or paired comparisons.

Matching

For matching, stimuli are presented on one side of the display and a pre-generated image from a potentially large pool of matches on the opposite side of the display. Because the number of options can be quite large, the steps involved are more similar to the method of adjustment than a multiple alternative forced-choice task.

The target stimuli are presented in a randomly permutated order. The observer uses the arrow keys on a standard keyboard to move through the psychophysical space of potential matches. The spacebar is then depressed to record their selected match and the data are recorded to a default output file (*data.txt*). The experimenter renames each file once the texting session is completed and the program terminates.

For convenience, the program initially reads in an AVI file containing all the images or image sequences for separate conditions. The number of images or image sequences is indicated in a config.txt file that is also read at the time of program execution. Separate AVI files containing pools of images are used to organise one or more matching spaces.
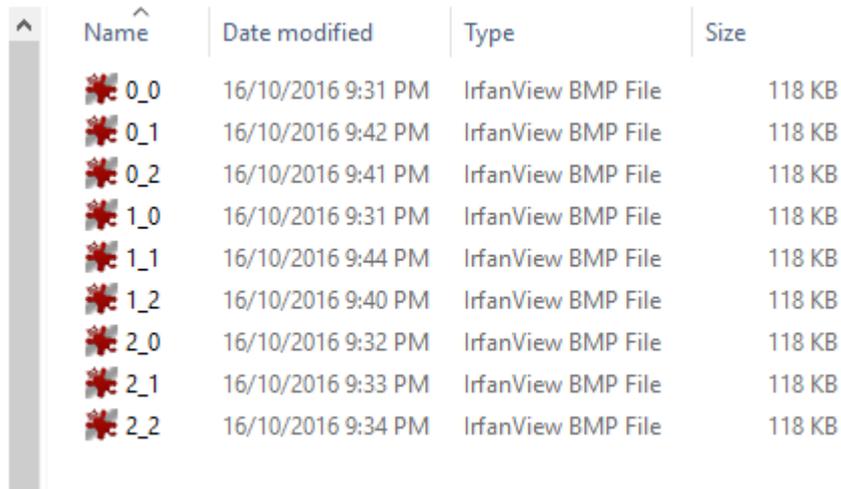
Paired comparisons

The sequences contained in the AVI are presented either side of the display and the observer uses the LEFT/RIGHT arrow keys to indicate their preference. There are N x (N-1) trials in a single block of repeats. This counterbalances presentation across the display. Preferences are stored in the same *data.txt* file.

Creating the stimulus sequencing AVI

Stimulus images (or image sequences) are generated using software of choice (e.g., Blender 3d). Moving sequences are supported, but the same number of frames are required for all conditions. Each image or image sequence is stitched together into a continuous AVI. The number of images/sequences is specified in the config.txt file. The AVI must have the filename *stimuli.avi* and be located in the [*./Data*] directory.

Creating psychophysical spaces (for matching tasks)

Matching spaces are matrices of images that form two-dimension multi-parametric spaces. The image frames should be organised into a hierarchical formal of blocks, as exemplified in the directory below:

Stitching the image above in order will form a 3x3 psychophysical space to move through. Two sets of sample images are provided in the [./sample] directory of the program folder. Once stitched together into a continuous AVI, the images in these movies are indexed using the config.txt file.
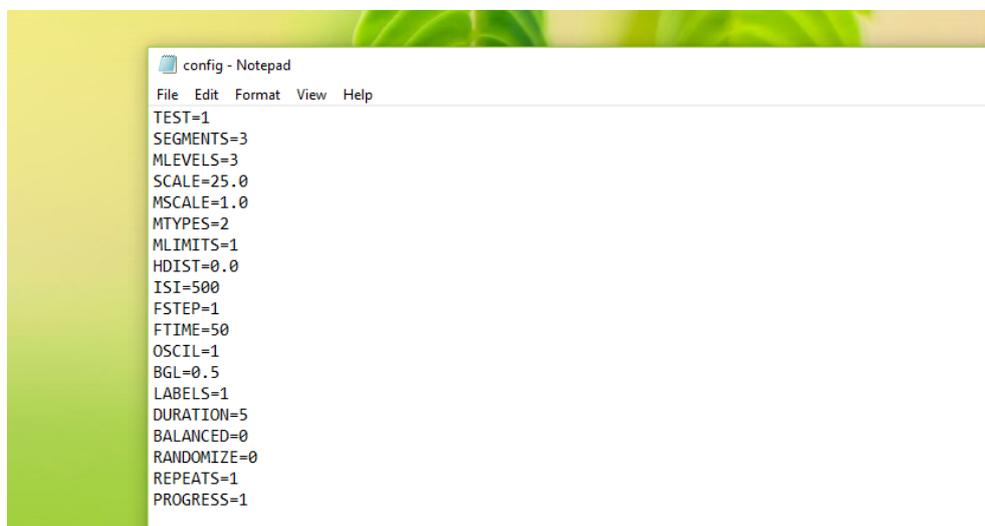
Up to two AVIs can be used for matching spaces (for Matching tasks only). They are indexed using filenames:

match0.avi

match1.avi

Configuration

Setup is performed using the config.txt file. A screenshot of the default setting (and their properties) is shown below:

Detailed description of the config.txt entries:

TEST: Designates whether the experiment to run is a matching (=0) or paired-comparisons task (=1). Matching task by default.

SEGMENTS: The number of images/image-sequences in the stimuli.avi file (Here set to 3).

MLEVELS: The number of levels horizontally and vertically in the psychophysical matching spaces. This is assumed to be the same for all *match*.avi* files. Here set to 3x3.

SCALE: The size of the billboard used to present the stimulus image/movie.

MSCALE: The proportion in size that the match images are presented on the opposite side of the display (a value of 1.0 means the same size as the stimulus).

MTYPES: The number of types of matching spaces to use. In other words, the number of *match*.avi* files that need to be read. This option may only take on a value or 1 or 2. This is ignored for a paired comparisons.

MLIMITS: Used for matching tasks. A value of 1 (no gridlines) or 2 (gridlines) will cause the contents of *limits.txt* file to be read, which contains user-defined invalid ratings (0 = disabled). A pictorial grid displays the current position relative to invalid and valid settings during presentation. Details on *limits.txt* syntax are provided below.

HDIST: Horizontal offset that can be used for increasing or decreasing the displacement between stimulus and match images.

ISI: Delay in milliseconds between stimulus trials. This applies between successive matches to the same stimulus condition.

FSTEP: The number of images to advance on each frame presentation.

FTIME: The number of milliseconds each frame is presented before advancing through the AVI by a single FSTEP. Set to 0 for static presentations.

OSCIL: Indicates what to do when an FSTEP moves beyond the image sequence limits. This can be a value of 0 or 1. A value of 0 indicates that the index should be adjusted immediately to the start of the image sequence. A value of 1 indicates that the index should be decremented through the space until the other end is reached.

BGL: Greyscale luminance of the background (range is 0.0 to 1.0).

LABELS: Boolean 0 or 1 to indicate whether text labels for match0 and match1 are displayed onscreen during each trial. Labels are provided separately in the *config_labels.txt* file described below.

DURATION: Presentation time for paired-comparisons tasks.

BALANCED: Sets counterbalancing for paired comparisons. A value of 1 will perform a normal counterbalanced presentation of n*(n-1) comparisons. A value of 0 will only perform half the number of trials (i.e., each pair is only presented once). Hence, unbalanced presentation mode will only require n*(n-1)/2 comparisons.

RANDOMIZE: Type of randomization to use when presenting paired-comparisons. (0 = none; 1 = same random start position for both pairs; 2 = different random start positions for both pairs).

REPEATS: The number of times to repeat a full block of randomly permutated stimulus presentations. One set of repeats equates to a total of exactly SEGMENTS x (SEGMENTS – 1) trials (Note that if MTYPES is 2, then there would be twice as many settings; one for each psychophysical matching space).

PROGRESS: An optional progress indicator will present a line of text at the top of the display to show the current trial as a fraction of the total number of trials. The current block number relative to the total number of repeat blocks will also be shown (0=OFF and 1=ON).

Configuration labels

The *config_labels.txt* file contains two lines of text. Each line will be displayed onscreen during each of the two trials match0 and match1. The first line of text for match0 and the second for match1. These lines of text can be modified to provide simple instructions to observers. Note that the maximum character length for each line is 24. The lines are only displayed when LABELS is set to 1 in the *config.txt* file (only the first label entry is displayed for a paired comparisons task).

Range limiting of settings for matching tasks

The format for the *limits.txt* file entries is exemplified in the included sample file. Each entry should refer to a 2D coordinate in *x,y* format that is terminated by a newline character. A single line entry of *0,0* (without spaces) would prevent the user from navigating to the upper-left most rating. This feature can be used to prevent the user from selecting (and displaying) specific image segments contained in a pre-created AVI file for psychophysical matching tasks.

Output data files

Output files names *data.txt* are tabulated in ASCII format and should be easily recognisable by standard analysis software (e.g., R).

For all matching tasks, the data are organized under labels as follows:

Tr (Trial), **St** (Stimulus), **Mt** (Match type), **Mx** (Match setting X), **My** (Match setting Y)

For paired comparisons tasks, the data are organized under labels as follows:

Tr (Trial), **Img0** (Left image), **Img1** (Right image), **Sel** (Selection/Preference: 0 or 1)