This a description of the data files accompanying “A Spectral Chronometer for Interval Timing in Drosophila”, J Kropf, C.B. Talbot and G. Miesenböck.

**behaviour\_data.mat**

Matlab file with data from the behaviour experiments (figure 4). Contains three structs: “Heat” contains data acquired from flies trained with warm air stimulation; “DAN” contains data acquired from the flies carrying the *MB504B-GAL4* driver and trained with optical stimulation; “ChrCtrl” contains data acquired from flies carrying the undriven *UAS-CsChrimson* transgene and presented with the same optical training protocol as those in the “DAN” group.

Each struct contains a single three-element cell array, “raw”, corresponding to the test presentations of the three odors. Elements 1 and 2 correspond to the aversive reinforcement during training at 3 and 7 s respectively and element 3 corresponds to the non-reinforced odor. The cell arrays contain a 2-dimensional array, with rows indexing time-points and columns containing responses from different flies. The metric is the frame-to-frame magnitude of the ball rotation ( in equation (1), units in radians). The flies are sorted according to the initiation time of the most vigorous movement bout. The data here represents the raw ball movement, i.e. including the non-locomotion events (e.g. grooming and flicking the ball). The flies that fail to have any locomotion, as defined in the methods, are given a movement initiation time of zero, and so appear in the first columns and have been sorted according to the integrated ball movement over the 10-s odor exposure.

**KC\_data.mat**

Matlab file containing the spike times of the Kenyon Cell electrophysiology measurements. The file contains cell arrays, each with seven elements. These index the driver line (KC sub-type) which are indicated by “lineNames” and “anatomicalNames”. For the remaining variables, each element of the cell array is a 3-dimensional array. The first element indexes the cell number. The second element indexes the odor (tabulated below). The third element indexes the repetition.

|  |  |
| --- | --- |
| Index | Odor |
| 1 | Clean air |
| 2 | Mineral oil |
| 3 | sulcatone |
| 4 | 2-heptanone |
| 5 | ethyl acetate |
| 6 | benzaldehyde |
| 7 | 2-pentanol |
| 8 | 1-octanol |
| 9 | isopentyl acetate |

The variables:

* “baseline” contains the spikes occurring between 3.5 and 0.5 seconds before the odor presentation.
* “odourOn” and “odourOff” contain the spikes occurring up to 1.8 seconds after the odor onset or offset respectively. As explained in the methods, there is some jitter in the exact timing of the odor onset/offset edges, which results in a minimum odor pulse of 1.8 seconds. These are aligned with the respective on/off edge with a hardware signal and are used for the significance classification.
* “stimComplete” contains the spikes occurring between 0 and 4 seconds after the odor onset. These are the rasters used for the temporal classification.
* “on\_significant” and “off\_significant” contain logical values indicating if the response passes the significance test. All five repetitions of a cell-odour response have the same value.

**MBON\_data.mat**

Matlab file containing the data used in figure 5. The file contains a single variable, a 3 by 33 cell array “MBON\_spikeTrains”. The first row contains the data from the data from the early-trained odor. The third row contains data from the late-trained odor. The first 16 columns contain the responses to the pre-training (control) odor presentation. The final 16 columns contain the responses to the testing odor presentation. The remaining rows and columns are filled with NaN.