**3D reconstruction:**

SCRIPTS:

Here we provide the code to train a Statistical Shape Model (SSM) and to use it for refining the 3D reconstruction.

For training the SSM use the script *train\_shape\_pamameters\_cl.m* (see help therein). Using this function also enables to generate a movie showing changes in body shape along the directions of the eigenposes (**Supplementary Movie 2**).

To refine the raw 3D poses with the SSM use the script *refine\_3D\_cl.m* (see help therein). Temporal smoothing and the regularization parameter α (see eq.3) can be modified inside the script (lines 21 & 23). *refine\_3D\_cl.m* in turn makes use of *reconstruct\_procrustes\_fminunc\_cl.m* (see help therein). This function provides the refined 3D reconstruction by minimizing the cost function in eq.3.

To validate 3D reconstruction by comparing raw and refined 3D use the script *compare\_raw\_refined\_3D\_cl.m* (**Supplementary Figure 2**). This script also compare eigenposes projections with more heuristic measures of neck-tail distance, nose-tail distance and head-body angles on the XY and YZ planes (**Supplementary Figure 3**).

In order to calculate all measures of postures and movements displayed in **Figure.1c** and employed throughout the manuscript use script *calculate\_measures\_postures\_movements.m* (see also help therein). To match these measures with manually annotated actions as in Supplementary Figure.4 use the script *validate\_measures\_manual\_annotation\_cl.m* (see help therein) that also genearates all the panels in said figure.

To calculate mean±sem for all measures across the 3 stimuli use the script *fig\_mean\_response\_cl.m* (see help therein). This script enables also to generate **Figure.2a** and performs statistical comparisons between responses associated with pairs of stimuli that are implemented in *test\_mean\_difference.m.* To generate **Figure.3a** use *example\_locomotion\_elongation.m*.

DATA:

All raw and refined 3D data can be found in *data\_3D\_all.mat* respectively as *Yraw, Yrefined* variables. To generate this file use the following commands:

load('data\_3D\_all\_part1.mat');

load('data\_3D\_all\_part2.mat');

flag\_val = [flag\_val1; flag\_val2];

Yraw = [Yraw1 Yraw2];

Yrefined = [Yrefined1 Yrefined2];

save('data\_3D\_all','flag\_val','Yraw','Yrefined');

Both *Yraw, Yrefined* are cell arrays where each cell contains data for an individual trial as a 3D matrix. The first two dimensions of each matrix represent respectively body landmarks (dimension1: n=5) and the 3D coordinates for a single frame (dimension2: n=3, respectively X,Y,Z). All frames are concatenated along the 3rd dimension of the matrix (n = 320 frames/trial).The stimulus onset is always at frame 150.

Additionally *data\_3D\_all.mat* also contains the variable *flag\_val*. Each row represents a trial and the columns provide information about that trial (column 1: 1 if 3D reconstruction was successful; column 2: mouse cage ID; column 3: mouse ID; column 4: trial number; column 5: stimulus value). Stimulus value in 5th column of *flag\_val* is 0 for flash, 1&2 for looming, 3&4 for sound.

All measures of postures and movements can be found in *measures\_postures\_movements.mat*.