**Hippo**

Contat Benjamin R. Kanter (BRK) ([benjamin.kanter@ntnu.no](mailto:benjamin.kanter@ntnu.no)).

Includes 1 feature from Vadim Frolov (VF) ([vadim.frolov@ntnu.no](mailto:vadim.frolov@ntnu.no)).

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**-- Introduction --**

Hippo is a MATLAB toolbox which adds functionality to the [Behavioural Neurology Toolbox](https://www.ntnu.no/wiki/display/kavli/Behavioural+Neurology+Toolbox) (BNT) (VF). It sits on top of BNT, therefore while BNT can be used without Hippo, Hippo requires installation of BNT. Hippo is updated shortly after BNT to ensure the two remain compatible.

The main purpose of this toolbox is to improve analysis efficiency at the level of the user. If exploring and analyzing data becomes faster and easier to do, it will be done more often and more exciting results will be uncovered.

To achieve this goal, the toolbox does the following:

1) automates routine procedures (e.g. BNT input files)

2) increases user interaction

3) performs batch analysis of large datasets

4) stores data in an easily accessible format

5) provides intuitive filtering to extract useful information quickly

**-- Installation --**

Hippo is publicly available for download here: <https://github.com/brkanter/hippo>.

See *\hippo\license and disclaimer info.text* for details about rights and warranties.

Hippo is a constantly evolving toolbox, partly because of its dependence on BNT, and partly because of the development of exciting new tools. Version control is maintained in a remote repository via GitHub.

(Note: If you want to simply have a copy of the code and are not interested in future updates, go to the webpage listed above, click the green button *Clone or download*, click *Download ZIP*, and extract the files to your preferred directory.)

The easiest way to keep up-to-date is to use [Git](https://git-scm.com/downloads) and [TortoiseGit](https://tortoisegit.org/download/), which is Windows software that allows you to use Git commands without doing so from the command line. To clone the Hippo remote repository to your local machine, open Git Bash and navigate to your preferred directory (e.g. cd Desktop). Type the following and hit enter:

git clone https://github.com/brkanter/hippo.git

You now have a local clone, which is a folder called hippo. Move this folder anywhere you like on your MATLAB path.

**-- Updates --**

Simply right-click on the Hippo folder --> TortoiseGit --> Pull --> OK. You are now up-to-date.

(Note: If you choose not to use Git, you can simply follow the installation steps above and download the files again each time, replacing the old files. This is not recommended.)

**-- Toolbox contents --**

The toolbox functions are organized into subfolders, some of which are MATLAB packages (+) to prevent namespace issues:

+ *calc*: specific analyses (e.g. spike width, object responses, theta phase)

+ *examples*: examples and instructions

+ *extract*: extracting data of interest

+ *meta*: analyzing multiple recording sessions or entire projects

+ *minions*: various small functions to assist others

+ *plt*: plotting functions

- *BNT extras*: modifications or additions to BNT functions

- *MathWorks extras*: from the MathWorks File Exchange, occasionally with modifications

- *MEX files*: sending information between MATLAB and Neuralynx

**-- Parameters --**

Many functions in Hippo and BNT require parameters (e.g. spatial bin width). Hippo uses a global structure called *hippoGlobe* to store default parameters which are made available to its functions. There are almost no parameters which are hard-coded in Hippo; the functions either prompt the user for input, or use the defaults from *hippoGlobe*.

The values in *hippoGlobe* are initially set using a MATLAB startup file (startup.m). See *examples.startupExample* to see how to make one, and make sure this file is above BNT on your path, otherwise it will not be used. You must have *hippoGlobe* to use Hippo (though you do not need to use a startup file to create it).

**-- Getting started –**

Ensure that your parameters are correct by typing *hippoGlobe* at the command line. If you get an error, run your startup file to initialize *hippoGlobe.*

Type *exploreDataBNT* at the command line and select a recording session where you have already cut some clusters. The data will be loaded by BNT, and you should see a plot with the path of the animal and a list of all the clusters that were found. Note that you did not have to explicitly make a BNT input file; it was created automatically for you by Hippo. Now that the data is loaded, you can use any BNT functions you like to explore your data (e.g. *data.getPositions, data.getSpikeTimes*, *analyses.map*). Try combining BNT and Hippo functions like this: *calc.ISI(data.getSpikeTimes([2 1]),1);*

Penguin is a graphical user interface for analyzing data from a single recording session. Type *penguin* at the command line to get started. There should be no instructions needed, as the interface is designed to be intuitive and user-friendly. Simply load data by clicking *Video folder* or *MClust*. The latter (from VF) loads data directly from an open MClust session and will include all clusters exported to the MClust main window, even if they are not yet saved.

Perhaps the highlight of Hippo is its meta analysis capabilities. Preprocess all of your data from an experiment (or more than one) using *emperorPenguin,* which outputs an Excel file of your results. You could stop here and look at the data in Excel, but at this point you don’t have access to things like rate maps. When you’re ready to look at many experiments together, follow the steps provided in *examples.metaAnalysisWorkflow* to get your data back into MATLAB*.* Soon you will have all of your data in a single neat MATLAB array. See *examples.analysisIntro* for a full guide explaining how to quickly extract the information you want from this array.

**-- Help --**

Help is provided at the top of all Hippo files. Simply type *help filename* at the command line or open the .m file.

For bug reports, questions, comments, and suggestions, please contact BRK ([benjamin.kanter@ntnu.no](mailto:benjamin.kanter@ntnu.no)) for Hippo and VF ([vadim.frolov@ntnu.no](mailto:vadim.frolov@ntnu.no)) for BNT.