**Hippo**

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Contains add-ons from Vadim Frolov (VF) ([vadim.frolov@ntnu.no](mailto:vadim.frolov@ntnu.no)).

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**-- 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 is 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>.

Simply click the green button *Clone or download*, then click *Download ZIP*. Extract the files to your preferred directory.

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

**-- Updates --**

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

The easiest way to keep up-to-date is to use TortoiseGit, which is Windows software that allows you to use Git commands without doing so from the command line. It is available from the Kavli Software Center (Programvarebibliotek) or from their website: <https://tortoisegit.org/download/>. If you have this installed before cloning the Hippo repository (see installation above), then the directory into which the files are extracted will automatically become a local Git repository.

The first time you download the files, you need to specify where new changes can be accessed. Right-click on the Hippo folder --> TortoiseGit --> Settings. On the left panel, under the heading Git, click Remote. In the URL field, enter: https://github.com/brkanter. Click OK, and it will ask if you want to retrieve the latest changes now, which you do.

From now on, you can simply right-click on the Hippo folder --> TortoiseGit --> Pull --> OK. You are now up-to-date.

If you choose not to use Git at all, 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 whole experiments, or whole projects

+ *minions*: various small functions to assist others

- *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 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 an experiment (or more than one) using *emperorPenguin,* which outputs an Excel file of your results. When you’re ready to look at many experiments, follow the steps provided in *examples.metaAnalysisWorkflow.* 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.

**-- 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.