# Manual: Atlas-based imaging data analysis tool at histological resolutions AIDAhisto

Niklas Pallast
Department of Neurology
University Hospital Cologne

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## 1 Introduction

AIDAhisto provides accurate and fast results for cell nuclei as well as immunohistochemical stainings of neurons, astrocytes and immune cells in the mouse brain with respect to the associated regions of the Allen Brain Reference Atlas (ARA). The transformation between the atlas as a source and the brain slice as a target image was conducted by a landmark based registration.

## 2 Installation

AIDAhisto is provided as a freely available cell-counting tool written in Python 3.6 as well as Matlab (Matlab Version R2018a, The MathWorks Inc., Natick, USA)

### 2.1 Installation with Matlab

1. A current version of Matlab is required.

2. Download the folders `/Matlab` and `/testImages` by using this link **/Matlab and /testImages should be located in the same directory**

3. set /Matlab as your "Current Folder" in Matlab and type run_example.mat in the "Command Window"

## 2.2   Installation with Python

1. Download the folders /Python and /testImages by using this link
   **/Matlab and /testImages should be located in the same directory**

2. Download & Install Python 3.6 or higher using Anaconda and enter the command to install necessary packages
   pip install numpy=1.14.3 argparse=1.4.0 scipy=1.2.1 matplotlib=3.0.3

3. set /Python as your current folder in the command window of your System and open the GUI by typing python AIDAhisto_gui.py

# 3   Usage of AIDAhisto

The input fields can be as .jpeg, .tiff or .png. Here you can find detailed information about the image input. The command line examples are given with in file /Matlab/run_example.mat for usage with Matlab in the file /Python/run_example.mat for usage with Python. and can be identically applied to other data. In both cases a detailed help is documented in the program code. The test dataset is freely available and can be downloaded from the file https://doi.org/10.12751/g-node.70e11f. If the user does not want to work with the command line, a Generic User Interface (GUI) can be used. The GUI starts with the command python AIDAhisto_gui.py which opens the window shown in Figure 1
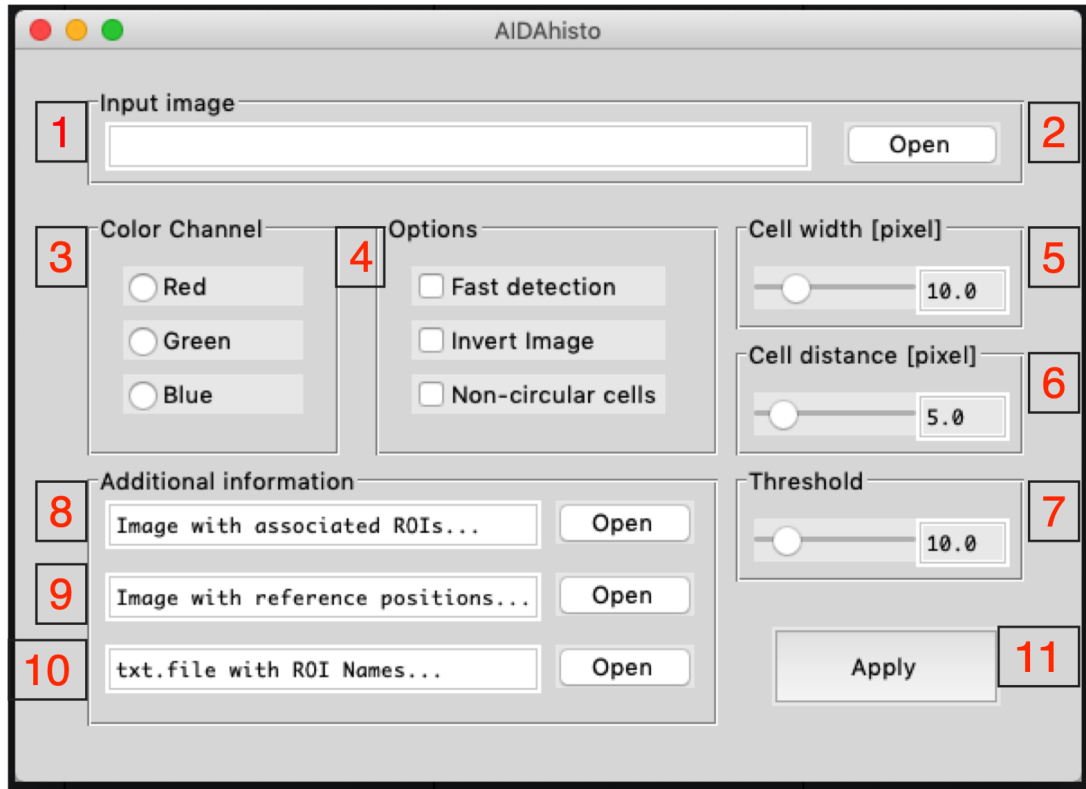
Figure 1: Description of the user interface to process with all provided input parameters.

The user only can choose an image file and adapt the cell width (5) to run AIDAhisto, but we also provide some paramateres to optimize the output and to meet all individual requirements of manifold investiagtions. Therefore, the following is a detailed explanation of the numbering in Figure 1:

1. Path the the file of the input image with the postfix `.jepg, png, tiff`

2. Press button to open file dialog and select a image file

3. Choose the color channel that should be evaluated. If only one channel is present, the first channel will always be examined.

4. 
   - For very large images, the process can be accelerated by choosing *Fast detection*

- If the cells are dark and the background is bright, the image should be inverted by choosing *Invert image.*

- If the cells are not round and have a different shape choose *Non-circular cells.*

5. Choose the cell size in pixels.

6. The minimum cell distance is pre-setted but can also be adapted.

7. The automatically calculated threshold value can be adjusted and weighted here.

8. If regions are superimposed with the image, the region image can be selected here.

9. You can enter the image of a previous investigation here and take it as a reference.

10. If certain names should be noted in the output file instead of the pixel value, the name of the respective pixel value can be entered here as a text file.

# 4  Allen Mouse Brain Atlas Database

In order to simplify the search for specific region numbers (e.g. 582 Caudoputamen) and list the related parental and child regions, we have summarized the ARA data available from (©2017 Allen Institute for Brain Science. Allen Mouse Brain Atlas (ccf3)) in an online database software, which we are using also for managing research data https://doi.org/10.1093/database/bay12. To use the database, create an account here https://ninoxdb.de/de/templates/research and import via the "Import archive" function this file.