

# JuGEx – JuBrain Gene Expression Toolbox

## Intro:

This document describes the installation of JuGEx (version 1.0). It was written by Sebastian Bludau and Thomas W. Mühleisen, INM-1, Research Centre Jülich, Germany. Latest changes to the document at 24<sup>th</sup> Feb 2018.

## Code availability:

The workflow and GUIs of the toolbox are based on a script distribution coded in MATLAB (version R2015b, 64bit) by MathWorks (<https://de.mathworks.com>). All codes are freely available at <http://www.fz-juelich.de/inm/inm-1/jugex>. Questions about the code to Sebastian Bludau ([s.bludau@fz-juelich.de](mailto:s.bludau@fz-juelich.de)).

## Dependencies:

- You need to run the latest version of the SPM toolbox, freely available at <http://www.fil.ion.ucl.ac.uk/spm/software/spm12/>.
- Make sure that your VOIs are registered to the MNI<sub>152</sub> reference space. If not, you will extract wrong and non-corresponding tissue samples through the Allen Brain API.

## Installation:

1. Unzip the downloaded file.
2. Add the new folder and subfolders to the Matlab search path (more information about this issue at [https://mathworks.com/help/matlab/matlab\\_env/add-remove-or-reorder-folders-on-the-search-path.html](https://mathworks.com/help/matlab/matlab_env/add-remove-or-reorder-folders-on-the-search-path.html)).
3. Type the command “Jugex” into the MATLAB console. This will start pre-checks and create project folders.
4. Copy your VOI files to the “maps” folder which was automatically created by the “Jugex” script.

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5. Parse your gene list into a “Jugex” readable format (more information about input and output file formats by the MATLAB command “help parse\_aba\_probes\_file”) and copy it to the automatically created “gene\_list” folder.
6. Type the command “Configuration”. This will start the first GUI to download and extract gene expression data of the user-specified VOIs (note that “Configuration” will be called automatically by the “Jugex” script if you use it for the first time).
7. Type the command “Analysis”. This will start the second GUI to analyze the extracted gene expression data.
8. Type the command “Visualization”. This will start the third GUI to visualize the extracted data and the results.

## JuBrain maps:

The currently available maps of the JuBrain atlas for the adult human brain are described by the JuBrain Cytoarchitectonic Atlas Viewer at <https://www.jubrain.fz-juelich.de>.

## Please cite our work as:

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