# MAsP App User Manual

05/2022

- **Introduction**

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Introduction

MAsP is a R Shiny-based application developed for processing spatial quantitative proteomic data. This app generates customizable protein distribution maps and offers post-processing functions, such as correlation of maps and clustering, identification of region-specific, non-random protein distribution patterns.

Though MAsP has been developed to process the data generated by our novel pipeline of Micro-scaffold Assisted Spatial Proteomics (MASP), it can also be used to process data from other platforms, as long as protein abundance/ratio/Z-score along with coordinate information are provided.
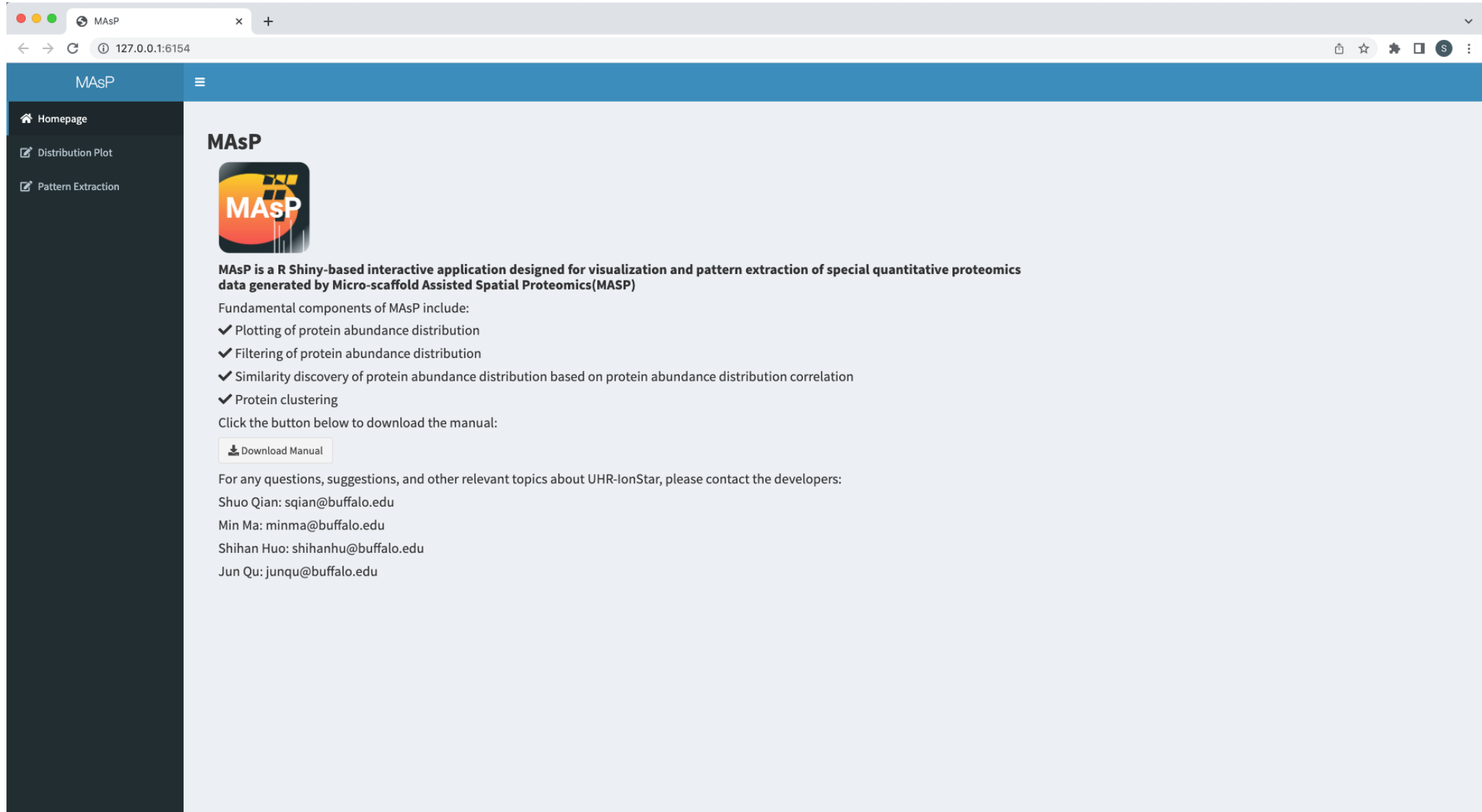
Generation of protein distribution map following accurate protein quantification by UHR-IonStar

Precise mapping   > 5000 protein distribution maps   Post-processing functions

Protein of interest   Correlated distribution   Correlation   Clustering
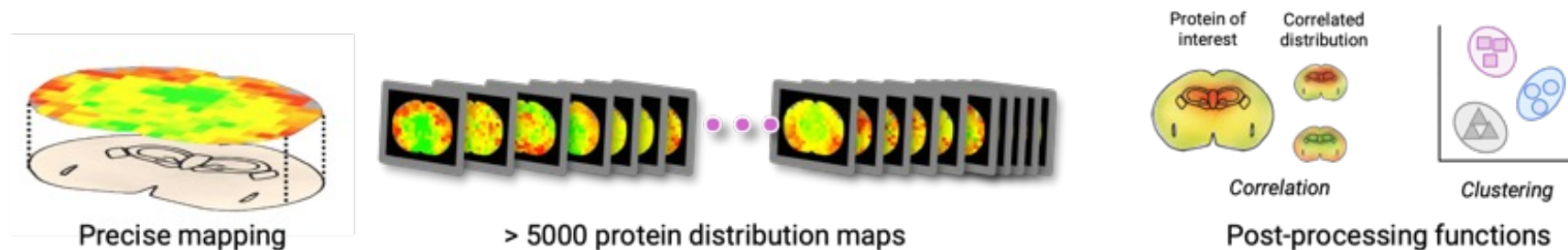
Setup

If the app was installed properly, the web interface would pop up after running the app starting code:

Application

A sample data, which is from our project of measuring mouse cerebral protein distribution using the MASP pipeline, is provided for demonstration. In this project, a total of 5023 proteins were mapped across 208 spatial locations which cover a whole mouse brain slice.

Input datasets

- Spatial protein abundances
  - Row name: protein names
  - Column name: location

- Protein location information

Generation of Distribution Maps

Functions:

- **Location preview:** MAsP automatically generate a location plot read from the location file, helping the user to visualize and confirm different tissue locations.

- **Generation of single protein distribution map:** MAsP creates an abundance/Z-score distribution map for any protein selected by the user. Several parameters, such as data scaling, colors of map, value boundaries, can be personalized by the user.

- **Batch mode for multiple protein distribution maps:** The user can choose batch mode if the user wishes to create multiple protein distribution maps, one for each unique protein. All the distribution maps will be automatically saved in the directory that the user selects.

MAsP

Homepage

Distribution Map

Pattern Discovery/Extraction

Distribution Map

Location Preview

Input the full/partial protein name/accession (not case sensitive)

This preview plot is generated after inputting the location information file.

Apply a tissue shape template

The values exceeding the range would be set to the upper or lower bound.

Protein Distribution Map

Heatmap for Protein P04370:MBP_MOUSE

Data Upload

Upload quantitative file (.csv):

Browse... | Test_data.csv

Upload complete

Upload location information (.csv):

Browse... | Locations.csv

Upload complete

Upload tissue shape template (.png):

Browse... | Brain_cover.png

Upload complete

Input the name of protein you would like to illustrate:

P04370:MBP_MOUSE

☑ Convert data to Z-score

☑ Add tissue shape templete

☐ Make the plot with transparent background while downloading

☑ Plot with legend

Choose the range of map color display:

◉ No limit

◯ Inter-quantile range

◯ Customized

Input the upper bound for protein values (if customized):

2

Input the lower bound for protein values (if customized):

-2

Input the upper color for the distribution map:

Heatmap for Protein P04370:MBP_MOUSE

Protein Distribution Map

6-digit HTML color code or word of a simple color name (e.g., red, green) will work too.

Set the width and height for the output plot.

☑ Plot with legend

Choose the range of map color display:

⦿ No limit

◯ Inter-quantile range

◯ Customized

Input the upper bound for protein values (if customized):

2

Input the lower bound for protein values (if customized):

-2

Input the upper color for the distribution map:

#FF0000

Input the middle color for the distribution map:

#FFF59D

Input the lower color for the distribution map:

#00FF00

✏ Draw Distribution Map

Map saving options:

Global plot width (inches):

4 ——— 8 ——— 20

Global plot height (inches):

4 — 6 ———— 20

⬇ Download current map

Batch mode

Upload a list containing protein names (.csv)

Browse... No file selected

Input the middle color for the distribution map:

#FFF59D

Input the lower color for the distribution map:

#00FF00

🖊 Draw Distribution Map

Map saving options:

Global plot width (inches):

4   8   20

4   6   8   10   12   14   16   18   20

Global plot height (inches):

4   6   20

4   6   8   10   12   14   16   18   20

⬇ Download current map

Batch mode

Upload a list containing protein names (.csv)

Browse...   No file selected

/Users/shuo/Desktop/Russell/Qu lab/Spatial_app/MAsP/inst/shi

⬆ Select the Output Folder

A small widget will pop up after clicking these buttons for guiding the user selecting the output file directory.

Plot settings are inherited from the previous settings, or user can change them before plotting.

🖊 Generate Selected Distribution Maps

Pattern discovery/extraction

Functions:

- **Data filtering:** To identify proteins with non-random, region-specific distribution patterns, MAsP uses the first value of variance explained (VE) in singular value decomposition (SVD) as a filter to remove protein distribution maps with low VE values *(i.e.* random distributions without a recognizable pattern)*, which is necessary for further pattern extraction and clustering. The user can set a customized filter threshold and we recommended 0.25-0.35.

- **Clustering of protein distribution maps based on pattern similarity:** For the protein distribution maps surviving the above step, the maps with similar regional distribution patterns can be grouped by the spectral clustering algorithm, which is a density-based clustering algorithm that are typically used for image processing. A PCA plot and a dataset with clustering labels will be generated.

- **Identification of protein maps correlating with the map of a protein of interest:** Proteins with correlated distribution patterns could imply co-localization of these proteins, which may provide highly valuable information on spatially organized biological processes. Using this approach, we devised a Protein Correlation module to identify proteins that are potentially co-localized with the target protein of interest selected by the user. Two options are provided

Pattern Discovery/Extraction

Plot Area

VE Rank Plot

The median VE of all the proteins. It is okay to choose median as threshold if it is larger than 0.3

PCA Plot with Labels from Spectral Clustering

Find proteins with pattern by the first value of variance explained (VE) in singular value decomposition (SVD)

✏ Perform Singular Value Decomposition on the Protein Quantitative file

Missing values will be forcely imputated because SVD requires missing data free.

⬇ Download imputated dataset   ⬇ Download VE rank plot

Set the threshold of VE value:
○ Median
● Customized

Input the customized VE cutoff value:

0.3

⬇ Download VE filtered protein dataset

Spectral Clustering on filtered proteins

✏ Perform Spectral Clustering on SVD-filtered protein file

⬇ Download protein file with clustering labels

⬇ Download PCA plot grouped by clustering labels

Find proteins with similar distribution comparing to the target protein

Input a name of protein:

PCA Plot with Labels from Spectral Clustering

PCA plot for Spectrum Clustering result

Correlation Rank Plot
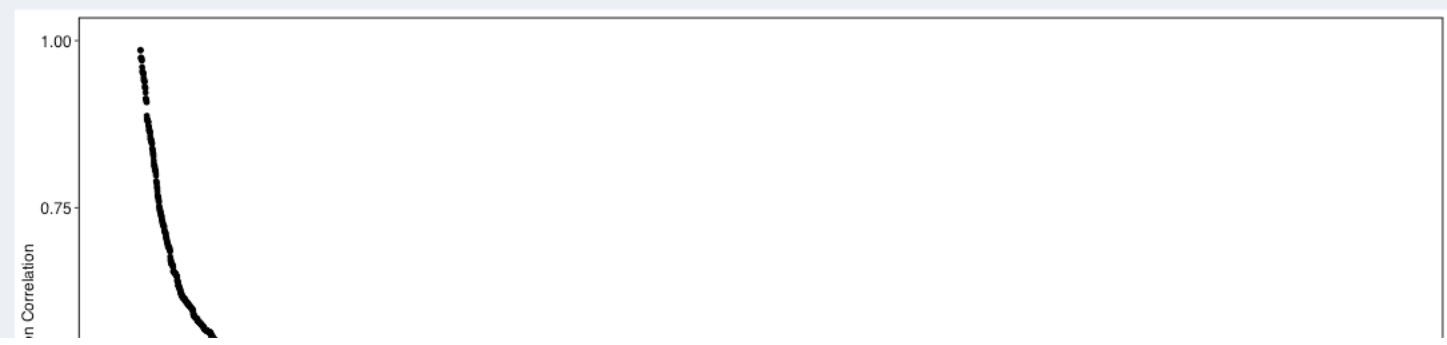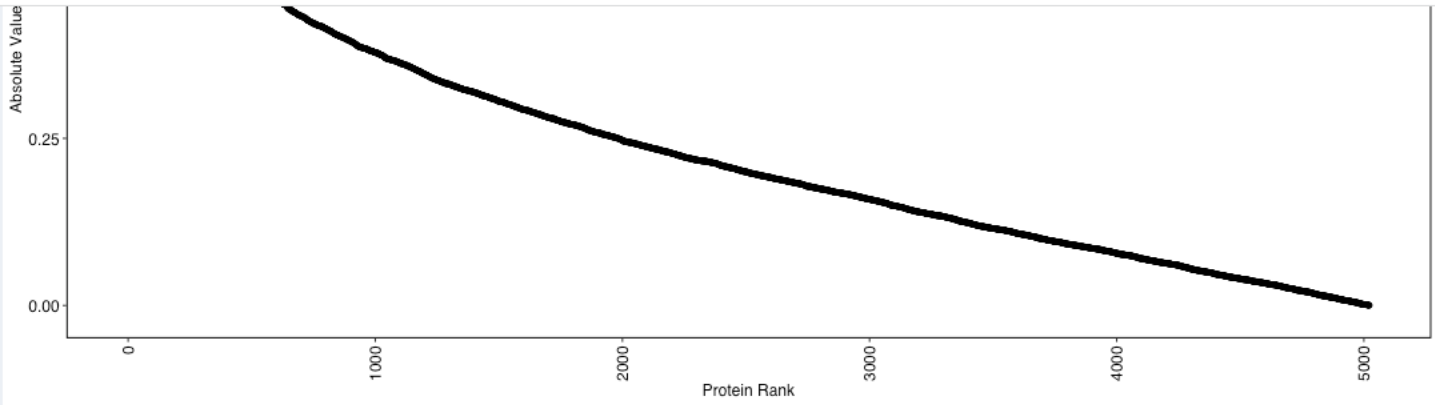
TOP3 Correlated Proteins

Heatmap for Protein P04370:MBP_MOUSE

Heatmap for Protein P16330:CN37_MOUSE

Heatmap for Protein P20917:MAG_MOUSE

Heatmap for Protein Q9DCU2:PLLP_MOUSE
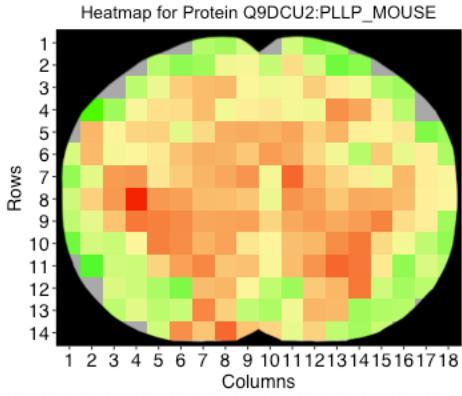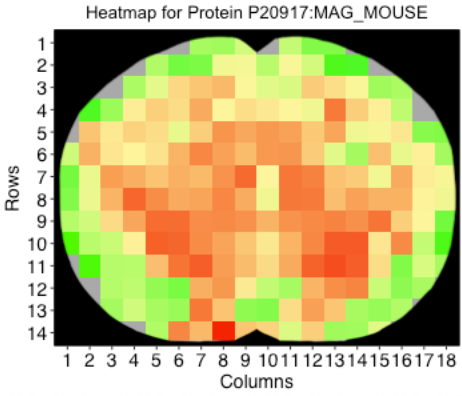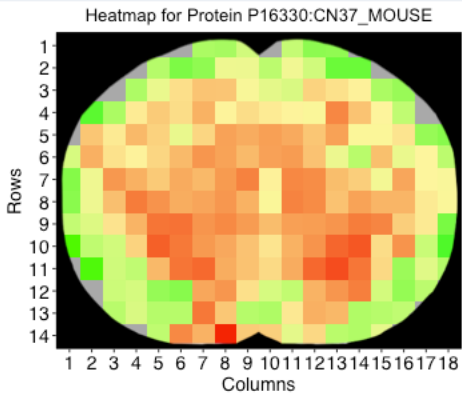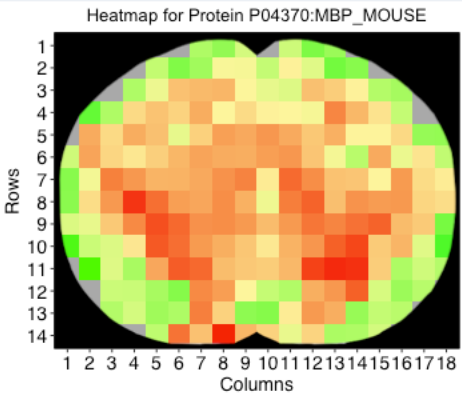
Thank you for using MAsP!

For any questions, suggestions and other relevant topics about MAsP, please contact the developers:

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Relevant articles:

- Shen, Xiaomeng, et al. "IonStar enables high-precision, low-missing-data proteomics quantification in large biological cohorts." *Proceedings of the National Academy of Sciences* 115.21 (2018): E4767-E4776.
- Wang, Xue, et al. "Ultra-High-Resolution IonStar Strategy Enhancing Accuracy and Precision of MS1-Based Proteomics and an Extensive Comparison with State-of-the-Art SWATH-MS in Large-Cohort Quantification." *Analytical chemistry* 93.11 (2021): 4884-4893.
- Fonville, Judith M., et al. "Robust data processing and normalization strategy for MALDI mass spectrometric imaging." *Analytical chemistry* 84.3 (2012): 1310-1319.