MAsP App User Manual

05/2022

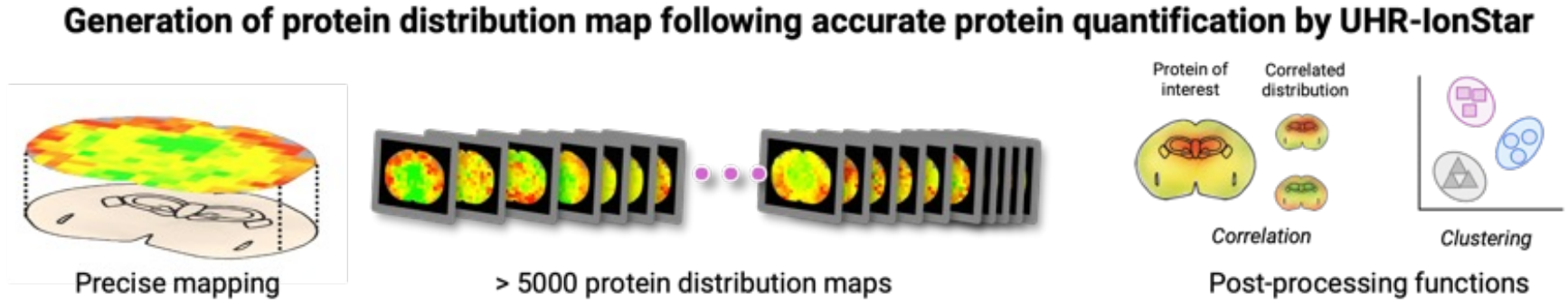
Outline

- Introduction
- App setup
- Application

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.

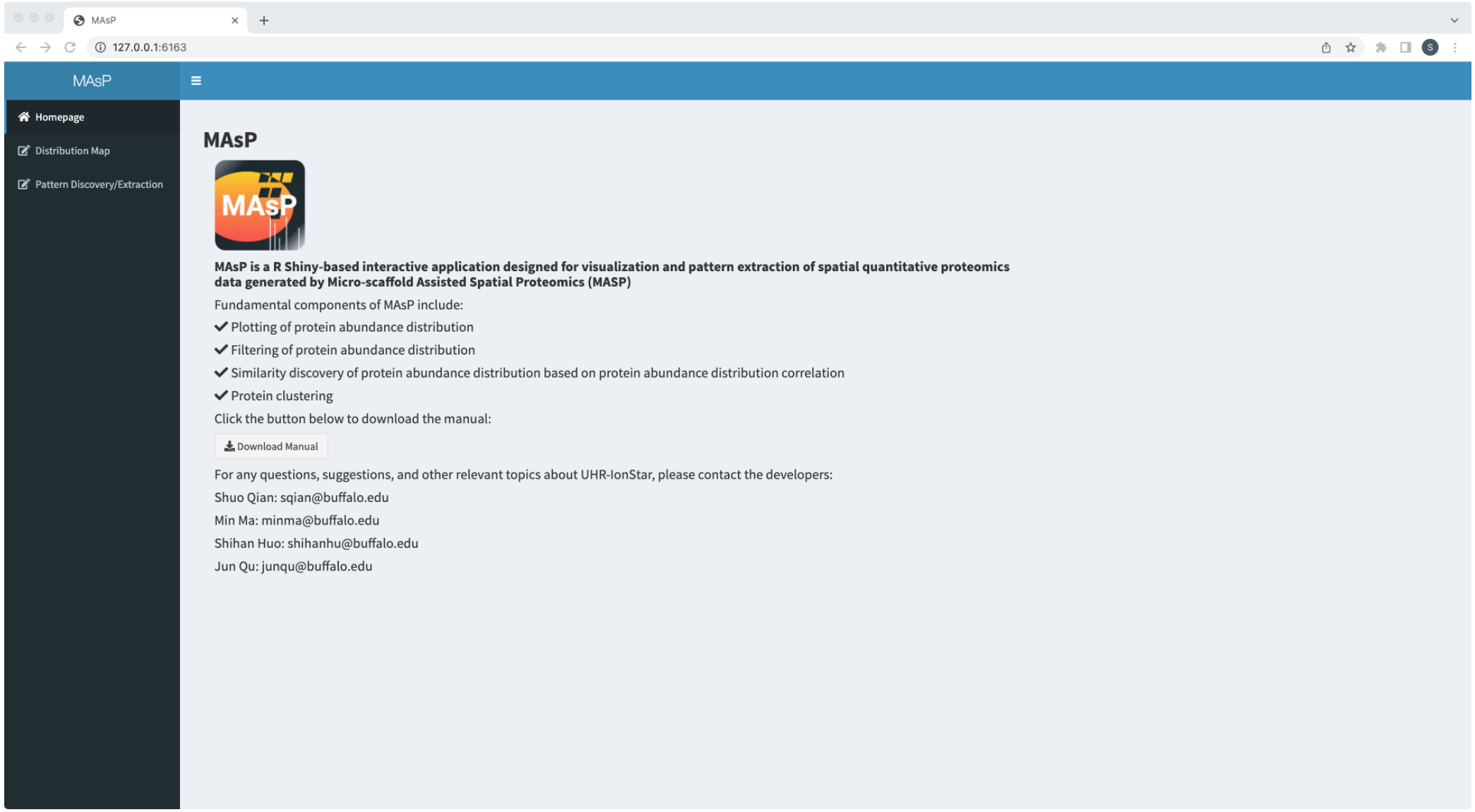
Though MAsP has been developed to process the data generated by our novel pipeline of Micro-scaffold Assisted Spatial Proteomics (MASP), it can also be used to process data from other platforms, as long as protein abundance/ratio/Z-score along with coordinate information are provided.



https://github.com/JunQu-Lab/MAsP

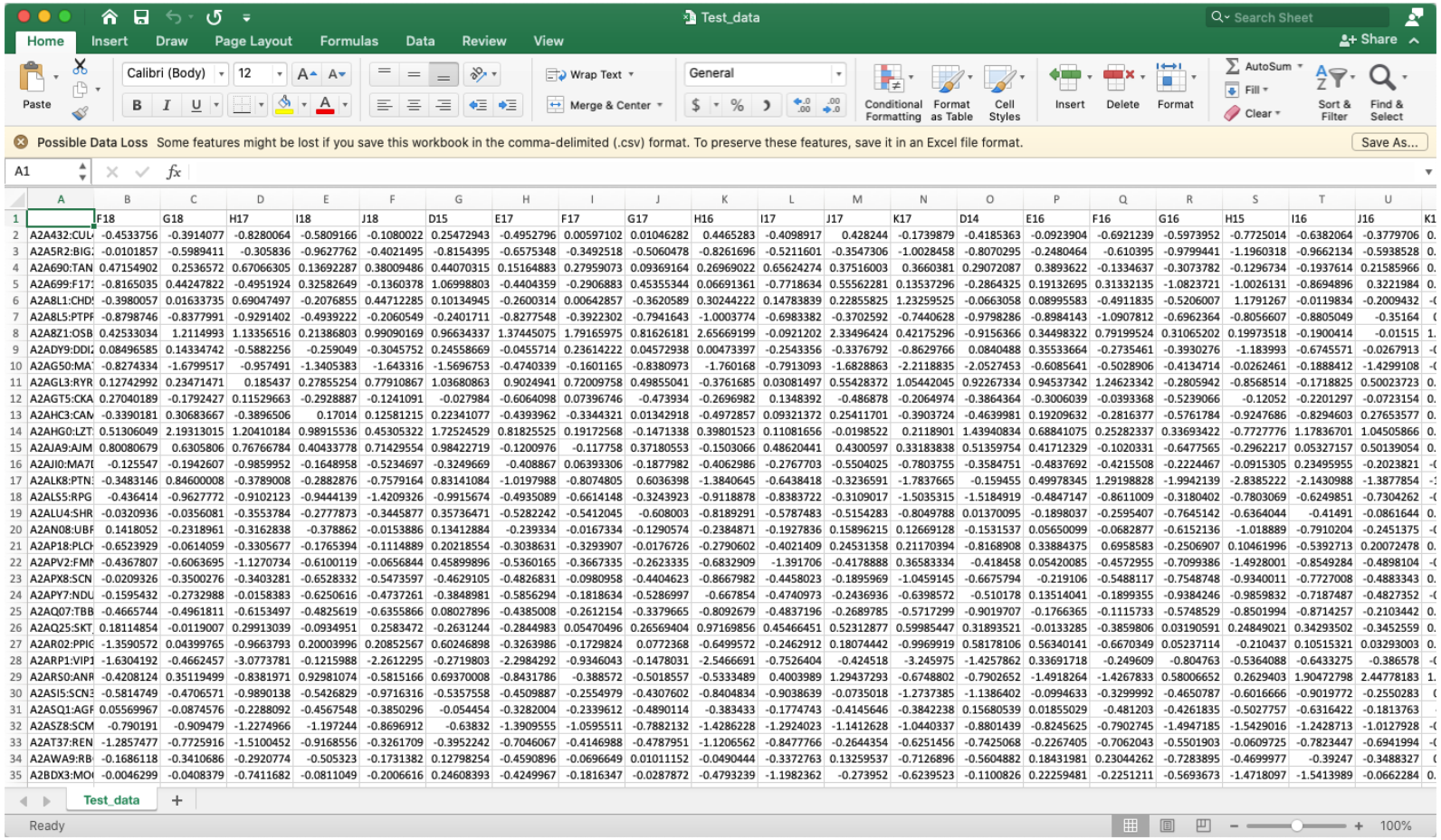
Setup

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

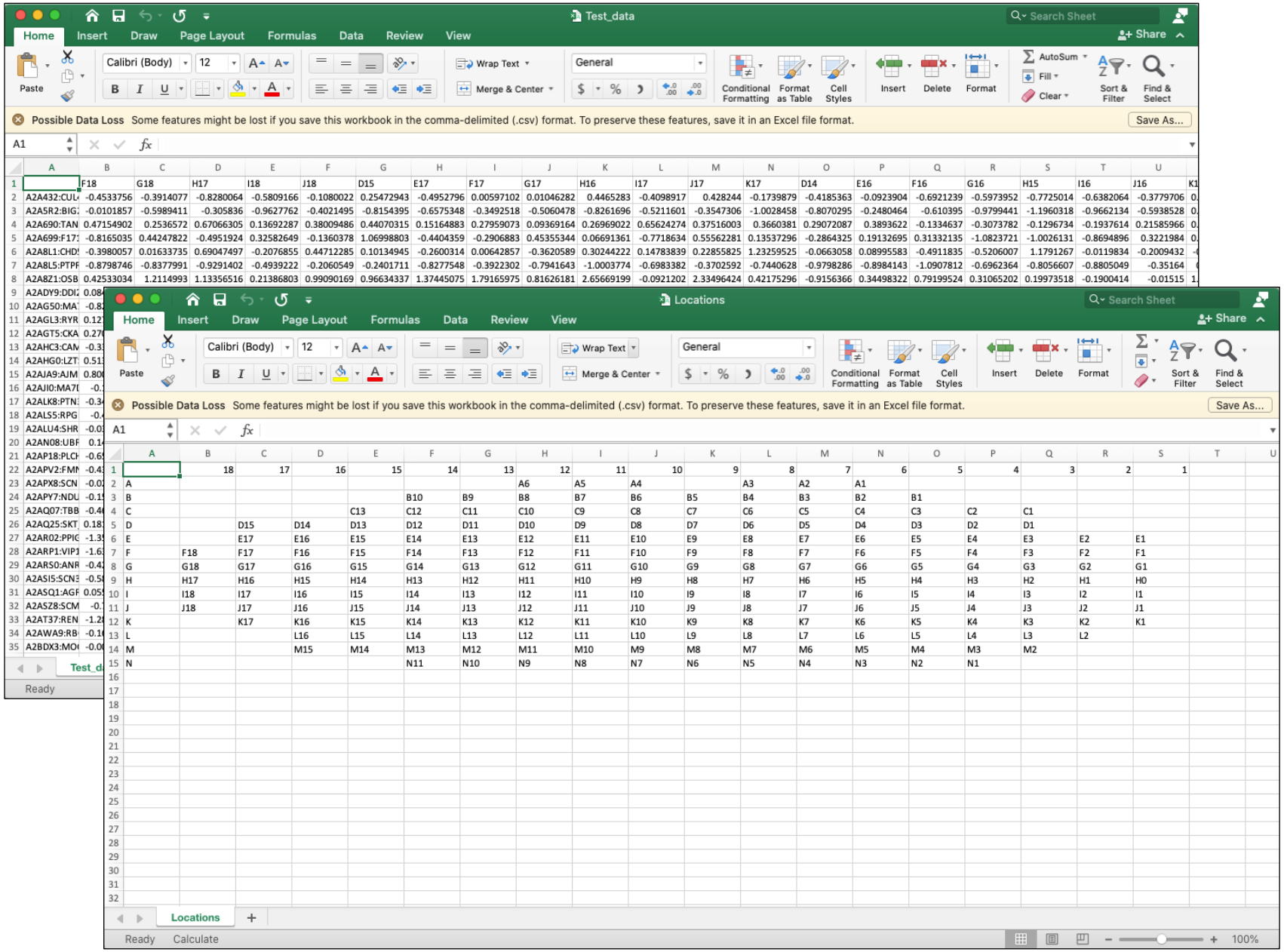


Application

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.



	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U
1		F18	G18	H17	I18	J18	D15	E17	F17	G17	H16	I17	J17	K17	D14	E16	F16	G16	H15	I16	J16
2	A2A432:CUL	-0.4533756	-0.3914077	-0.8280064	-0.5809166	-0.1080022	0.25472943	-0.4952796	0.00597102	0.01046282	0.4465283	-0.4098917	0.428244	-0.1739879	-0.4185363	-0.0923904	-0.6921239	-0.5973952	-0.7725014	-0.6382064	-0.3779706
3	A2A5R2:BIG	-0.0101857	-0.5989411	-0.305836	-0.9627762	-0.4021495	-0.8154395	-0.6575348	-0.3492518	-0.5060478	-0.8261696	-0.5211601	-0.3547306	-1.0028458	-0.8070295	-0.2480464	-0.610395	-0.9799441	-1.1960318	-0.9662134	-0.5938528
4	A2A690:TAN	0.47154902	0.2536572	0.67066305	0.13692287	0.38009486	0.44070315	0.15164883	0.27959073	0.09369164	0.26969022	0.65624274	0.37516003	0.3660381	0.29072087	0.3893622	-0.1334637	-0.3073782	-0.1296734	-0.1937614	0.21585966
5	A2A699:F17	-0.8165035	0.44247822	-0.4951924	0.32582649	-0.1360378	1.06998803	-0.4404359	-0.2906883	0.45355344	0.06691361	-0.7718634	0.55562281	0.13537296	-0.2864325	0.19132695	0.31332135	-1.0823721	-1.0026131	-0.8694896	0.3221984
6	A2A8L1:CHD	-0.3980057	0.01633735	0.69047497	-0.2076855	0.44712285	0.10134945	-0.2600314	0.00642857	-0.3620589	0.30244222	0.14783839	0.22855825	1.23259525	-0.0663058	0.08995583	-0.4911835	-0.5206007	1.1791267	-0.0119834	-0.2009432
7	A2A8L5:PTPF	-0.8798746	-0.8377991	-0.9291402	-0.4939222	-0.2060549	-0.2401711	-0.8277548	-0.3922302	-0.7941643	-1.0003774	-0.6983382	-0.3702592	-0.7440628	-0.9798286	-0.8984143	-1.0907812	-0.6962364	-0.8056607	-0.8805049	-0.35164
8	A2A8Z1:OSB	0.42533034	1.2114993	1.13356516	0.21386803	0.99090169	0.96634337	1.37445075	1.79165975	0.81626181	2.65669199	-0.0921202	2.33496424	0.42175296	-0.9156366	0.34498322	0.79199524	0.31065202	0.19973518	-0.1900414	-0.01515
9	A2ADY9:DDI	0.08496585	0.14334742	-0.5882256	-0.259049	-0.3045752	0.24558669	-0.0455714	0.23614222	0.04572938	0.00473397	-0.2543356	-0.3376792	-0.8629766	0.0840488	0.35533664	-0.2735461	-0.3930276	-1.183993	-0.6745571	-0.0267913
10	A2AG50:MA	-0.8274334	-1.6799517	-0.957491	-1.3405383	-1.643316	-1.5696753	-0.4740339	-0.1601165	-0.8380973	-1.760168	-0.7913093	-1.6828863	-2.2118835	-2.0527453	-0.6085641	-0.5028906	-0.4134714	-0.0262461	-0.1888412	-1.4299108
11	A2AGL3:RYR	0.12742992	0.23471471	0.185437	0.27855254	0.77910867	1.03680863	0.9024941	0.72009758	0.49855041	-0.3761685	0.03081497	0.55428372	1.05442045	0.92267334	0.94537342	1.24623342	-0.2805942	-0.8568514	-0.1718825	0.50023723
12	A2AGT5:CKA	0.27040189	-0.1792427	0.11529663	-0.2928887	-0.1241091	-0.027984	-0.6064098	0.07396746	-0.473934	-0.2696982	0.1348392	-0.486878	-0.2064974	-0.3864364	-0.3006039	-0.0393368	-0.5239066	-0.12052	-0.2201297	-0.0723154
13	A2AHC3:CAM	-0.3390181	0.30683667	-0.3896506	0.17014	0.12581215	0.22341077	-0.4393962	-0.3344321	0.01342918	-0.4972857	0.09321372	0.25411701	-0.3903724	-0.4639981	0.19209632	-0.2816377	-0.5761784	-0.9247686	-0.8294603	0.27653577
14	A2AHG0:LZT	0.51306049	2.19313015	1.20410184	0.98915536	0.45305322	1.72524529	0.81825525	0.19172568	-0.1471338	0.39801523	0.11081656	-0.0198522	0.2118901	1.43940834	0.68841075	0.25282337	0.33693422	-0.7727776	1.17836701	1.04505866
15	A2AJA9:AJM	0.80080679	0.6305806	0.76766784	0.40433778	0.71429554	0.98422719	-0.1200976	-0.117758	0.37180553	-0.1503066	0.48620441	0.4300597	0.33183838	0.51359754	0.41712329	-0.1020331	-0.6477565	-0.2962217	0.05327157	0.50139054
16	A2AJI0:MA7	-0.125547	-0.1942607	-0.9859952	-0.1648958	-0.5234697	-0.3249669	-0.408867	0.06393306	-0.1877982	-0.4062986	-0.2767703	-0.5504025	-0.7803755	-0.3584751	-0.4837692	-0.4215508	-0.2224467	-0.0915305	0.23495955	-0.2023821
17	A2ALK8:PTN	-0.3483146	0.84600008	-0.3789008	-0.2882876	-0.7579164	0.83141084	-1.0197988	-0.8074805	0.6036398	-1.3840645	-0.6438418	-0.3236591	-1.7837665	-0.159455	0.49978345	1.29198828	-1.9942139	-2.8385222	-2.1430988	-1.3877854
18	A2ALS5:RPG	-0.436414	-0.9627772	-0.9102123	-0.9444139	-1.4209326	-0.9915674	-0.4935089	-0.6614148	-0.3243923	-0.9118878	-0.8383722	-0.3109017	-1.5035315	-1.5184919	-0.4847147	-0.8611009	-0.3180402	-0.7803069	-0.6249851	-0.7304262
19	A2ALU4:SHR	-0.0320936	-0.0356081	-0.3553784	-0.2777873	-0.3445877	0.35736471	-0.5282242	-0.5412045	-0.608003	-0.8189291	-0.5787483	-0.5154283	-0.8049788	0.01370095	-0.1898037	-0.2595407	-0.7645142	-0.6364044	-0.41491	-0.0861644
20	A2AN08:UBF	0.1418052	-0.2318961	-0.3162838	-0.378862	-0.0153886	0.13412884	-0.239334	-0.0167334	-0.1290574	-0.2384871	-0.1927836	0.15896215	0.12669128	-0.1531537	0.05650099	-0.0682877	-0.6152136	-1.018889	-0.7910204	-0.2451375
21	A2AP18:PLC	-0.6523929	-0.0614059	-0.3305677	-0.1765394	-0.1114889	0.20218554	-0.3038631	-0.3293907	-0.0176726	-0.2790602	-0.4021409	0.24531358	0.21170394	-0.8168908	0.33884375	0.6958583	-0.2506907	0.10461996	-0.5392713	0.20072478
22	A2APV2:FMN	-0.4367807	-0.6063695	-1.1270734	-0.6100119	-0.0656844	0.45899896	-0.5360165	-0.3667335	-0.2623335	-0.6832909	-1.391706	-0.4178888	0.36583334	-0.418458	0.05420085	-0.4572955	-0.7099386	-1.4928001	-0.8549284	-0.4898104
23	A2APX8:SCN	-0.0209326	-0.3500276	-0.3403281	-0.6528332	-0.5473597	-0.4629105	-0.4826831	-0.0980958	-0.4404623	-0.8667982	-0.4458023	-0.1895969	-1.0459145	-0.6675794	-0.219106	-0.5488117	-0.7548748	-0.9340011	-0.7727008	-0.4883343
24	A2APY7:NDU	-0.1595432	-0.2732988	-0.0158383	-0.6250616	-0.4737261	-0.3848981	-0.5856294	-0.1818634	-0.5286997	-0.667854	-0.4740973	-0.2436936	-0.6398572	-0.510178	0.13514041	-0.1899355	-0.9384246	-0.9859832	-0.7187487	-0.4827352
25	A2AQ07:TBB	-0.4665744	-0.4961811	-0.6153497	-0.4825619	-0.6355866	0.08027896	-0.4385008	-0.2612154	-0.3379665	-0.8092679	-0.4837196	-0.2689785	-0.5717299	-0.9019707	-0.1766365	-0.1115733	-0.5748529	-0.8501994	-0.8714257	-0.2103442
26	A2AQ25:SKT	0.18114854	-0.0119007	0.29913039	-0.0934951	0.2583472	-0.2631244	-0.2844983	0.05470496	0.26569404	0.97169856	0.45466451	0.52312877	0.59985447	0.31893521	-0.0133285	-0.3859806	0.03190591	0.24849021	0.34293502	-0.3452559
27	A2AR02:PPIC	-1.3590572	0.04399765	-0.9663793	0.20003996	0.20852567	0.60246898	-0.3263986	-0.1729824	0.0772368	-0.6499572	-0.2462912	0.18074442	-0.9969919	0.58178106	0.56340141	-0.6670349	0.05237114	-0.210437	0.10515321	0.03293003
28	A2ARP1:VIP1	-1.6304192	-0.4662457	-3.0773781	-0.1215988	-2.2612295	-0.2719803	-2.2984292	-0.9346043	-0.1478031	-2.5466691	-0.7526404	-0.424518	-3.245975	-1.4257862	0.33691718	-0.249609	-0.804763	-0.5364088	-0.6433275	-0.386578
29	A2ARS0:ANR	-0.4208124	0.35119499	-0.8381971	0.92981074	-0.5815166	0.69370008	-0.8431786	-0.388572	-0.5018557	-0.5333489	0.4003989	1.29437293	-0.6748802	-0.7902652	-1.4918264	-1.4267833	0.58006652	0.2629403	1.90472798	2.44778183
30	A2ASI5:SCN	-0.5814749	-0.4706571	-0.9890138	-0.5426829	-0.9716316	-0.5357558	-0.4509887	-0.2554979	-0.4307602	-0.8404834	-0.9038639	-0.0735018	-1.2737385	-1.1386402	-0.0994633	-0.3299992	-0.4650787	-0.6016666	-0.9019772	-0.2550283
31	A2ASQ1:AGF	0.05569967	-0.0874576	-0.2288092	-0.4567548	-0.3850296	-0.054454	-0.3282004	-0.2339612	-0.4890114	-0.383433	-0.1774743	-0.4145646	-0.3842238	0.15680539	0.01855029	-0.481203	-0.4261835	-0.5027757	-0.6316422	-0.1813763
32	A2ASZ8:SCM	-0.790191	-0.909479	-1.2274966	-1.197244	-0.8696912	-0.63832	-1.3909555	-1.0595511	-0.7882132	-1.4286228	-1.2924023	-1.1412628	-1.0440337	-0.8801439	-0.8245625	-0.7902745	-1.4947185	-1.5429016	-1.2428713	-1.0127928
33	A2AT37:REN	-1.2857477	-0.7725916	-1.5100452	-0.9168556	-0.3261709	-0.3952242	-0.7046067	-0.4146988	-0.4787951	-1.1206562	-0.8477766	-0.2644354	-0.6251456	-0.7425068	-0.2267405	-0.7062043	-0.5501903	-0.0609725	-0.7823447	-0.6941994
34	A2AWA9:RB	-0.1686118	-0.3410686	-0.2920774	-0.505323	-0.1731382	0.12798254	-0.4590896	-0.0696649	0.01011152	-0.0490444	-0.3372763	0.13259537	-0.7126896	-0.5604882	0.18431981	0.23044262	-0.7283895	-0.4699977	-0.39247	-0.3488327
35	A2BDX3:MO	-0.0046299	-0.0408379	-0.7411682	-0.0811049	-0.2006616	0.24608393	-0.4249967	-0.1816347	-0.0287872	-0.4793239	-1.1982362	-0.273952	-0.6239523	-0.1100826	0.22259481	-0.2251211	-0.5693673	-1.4718097	-1.5413989	-0.0662284



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.

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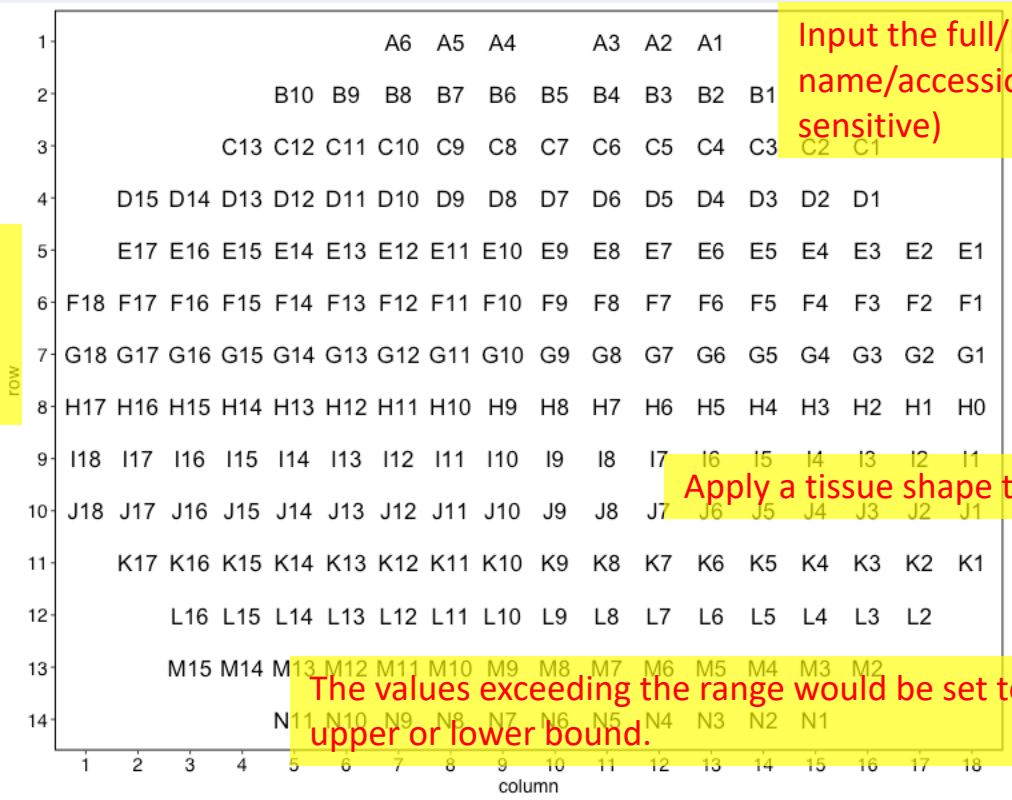
MAsP

- Homepage
- Distribution Map
- Pattern Discovery/Extraction

Distribution Map

Location Preview



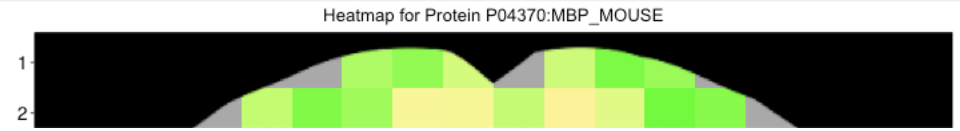
This preview plot is generated after inputting the location information file.

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

Apply a tissue shape template

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

Protein Distribution Map



Data Upload

Upload quantitative file (.csv):

Browse... Test_data.csv

Upload complete

Upload location information (.csv):

Browse... Locations.csv

Upload complete

Upload tissue shape templete (.png):

Browse... Brain_cover.png

Upload complete

Input the name of protein you would like to illustrate:

P04370:MBP_MOUSE

- [x] Convert data to Z-score
- [x] Add tissue shape templete
- [ ] Make the plot with transparent background while downloading
- [x] Plot with legend

Choose the range of map color display:

- (•) No limit
- ( ) Inter-quantile range
- ( ) Customized

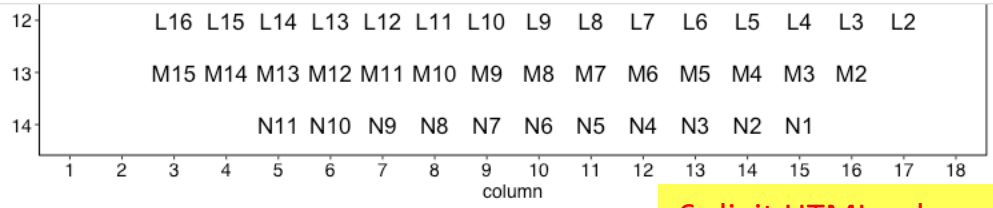
Input the upper bound for protein values (if customized):

2

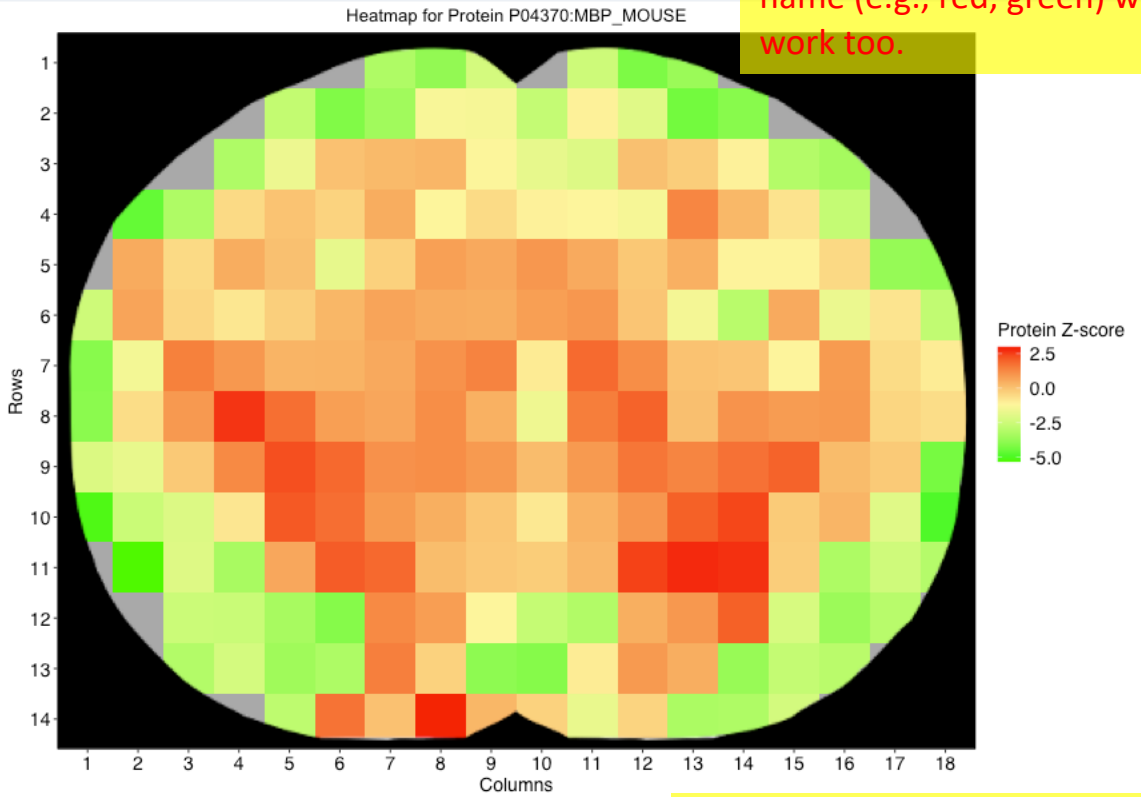
Input the lower bound for protein values (if customized):

-2

Input the upper color for the distribution map:



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): 8

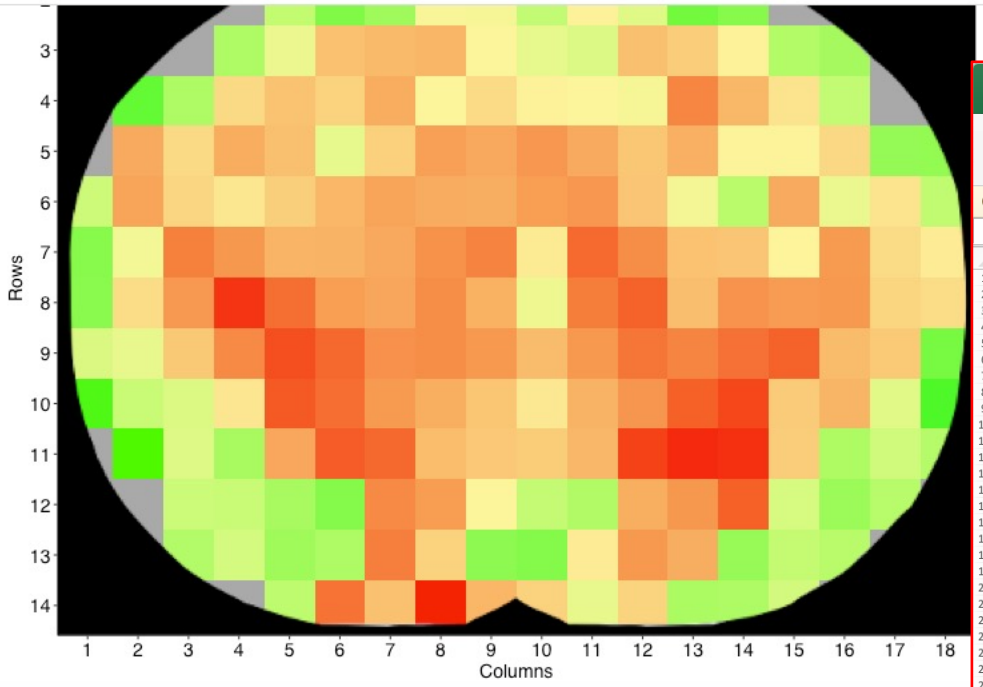
Global plot height (inches): 6

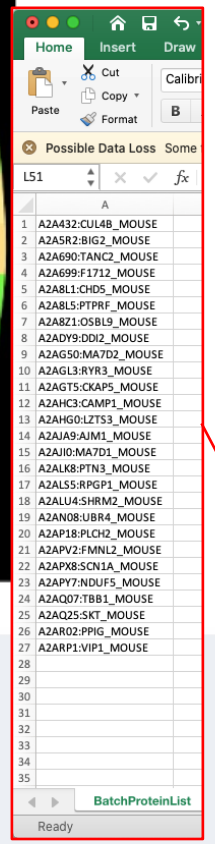
Download current map

Batch mode

Upload a list containing protein names (.csv)

Browse... No file selected





#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):

Global plot height (inches):

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

MAsP

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MAsP

Homepage

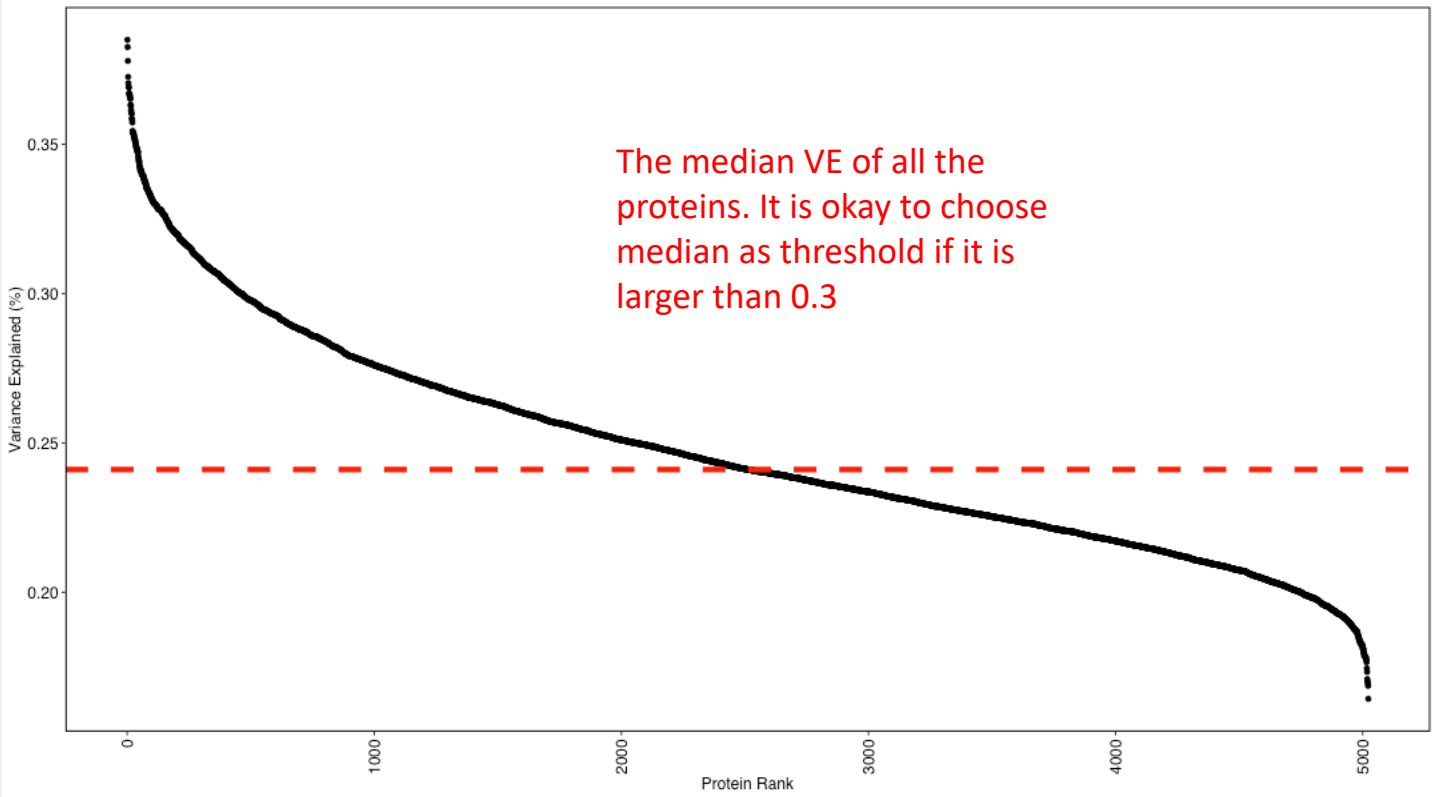
Distribution Map

Pattern Discovery/Extraction

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

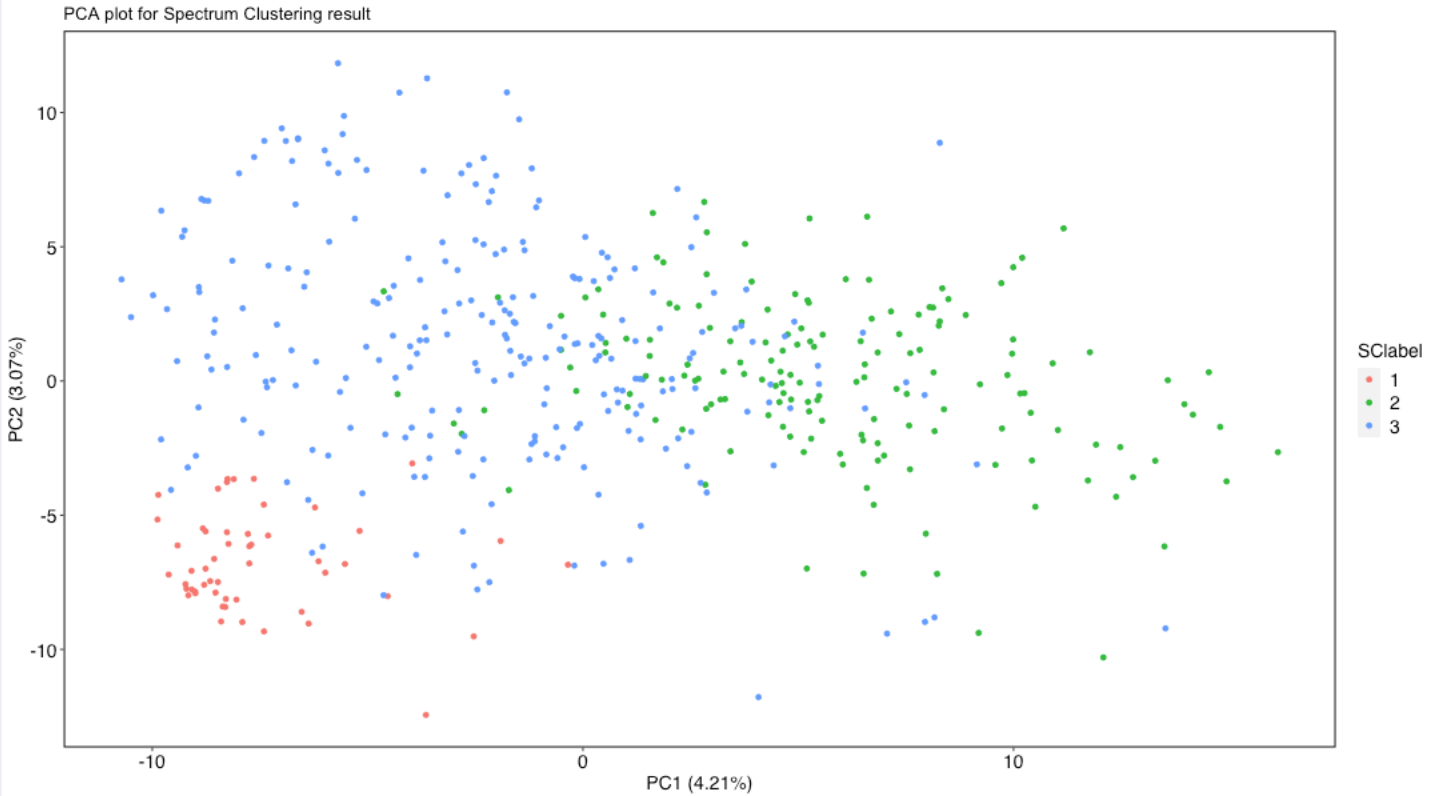
Find proteins with similar distribution comparing to the target protein

Input a name of protein:

MAsP

127.0.0.1:3930

PCA Plot with Labels from Spectral Clustering



Correlation Rank Plot

Input a name of protein:

P04370:MBP_MOUSE

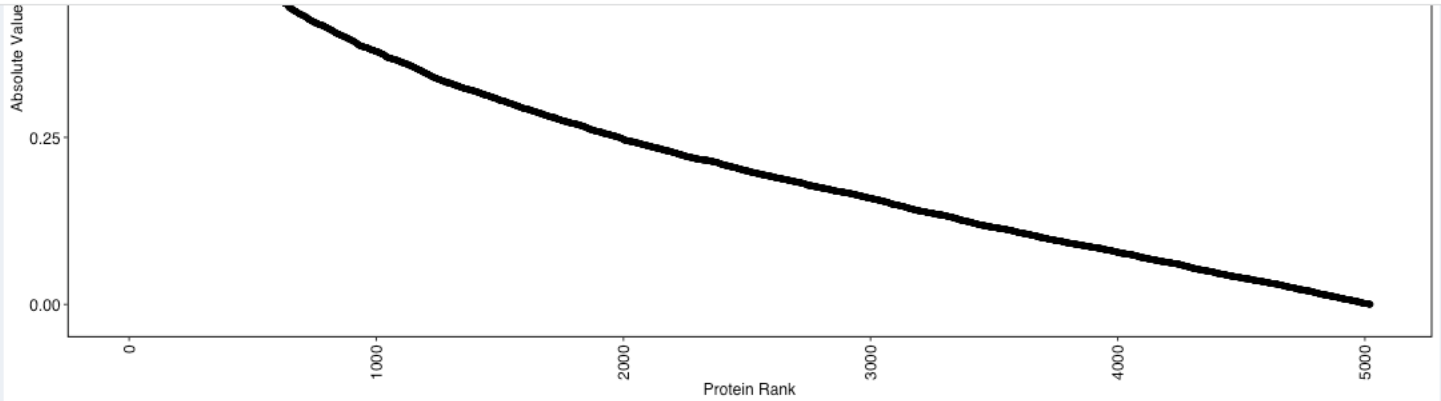
Select the correlation type:

- (•) Pearson Correlation
- ( ) Cosine Similarity

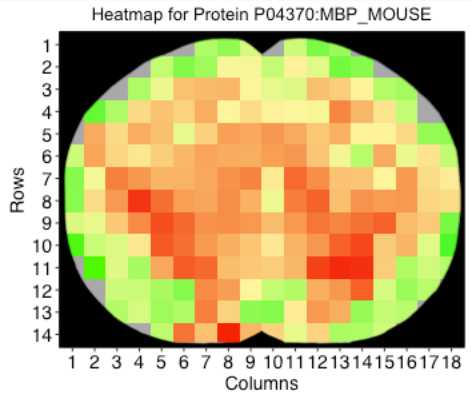
Find correlations

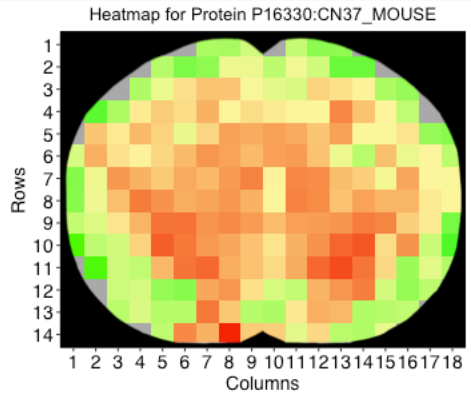
Download correlation rank data

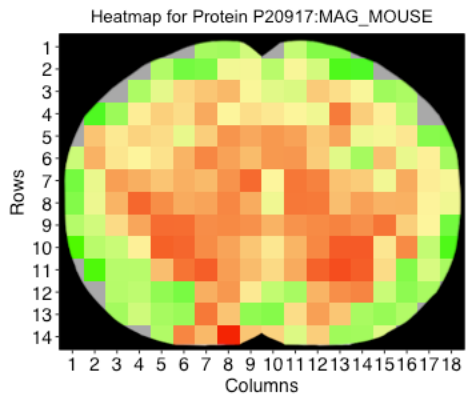
Download correlation rank plot

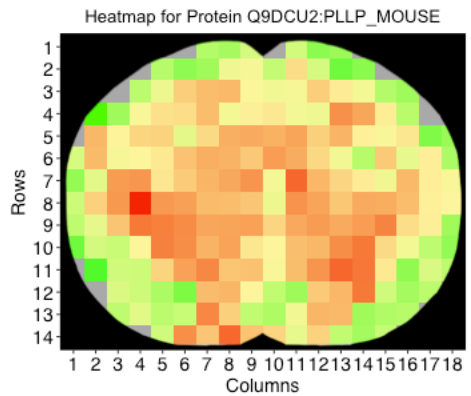


TOP3 Correlated Proteins









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.