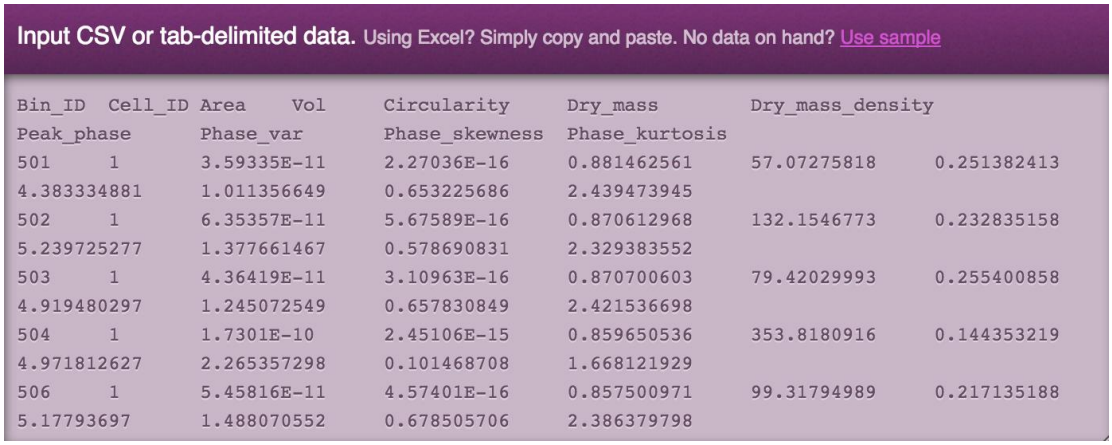
Basically, this graphical user interface allows us to view the relationship between any two of the parameters of particular types of biological cells in the form of scatter plot.

Here are the steps of inputting data (dataset 1 is taken as an example):

1. All the data stored inside the excel file needs to be converted into json format by using this online converter:
   https://shancarter.github.io/mr-data-converter/
   Copy all the content in the excel file and paste it onto this region:




   *The format of the excel file should be like this:

| | A | B | C | D | E | F | G | H |
|---|---|---|---|---|---|---|---|---|
| 1 | Bin_ID | Cell_ID | Area | Vol | Circularity | Dry_mass | Dry_mass_c | Peak_phase |
| 2 | 0 | 1 | 2.42775E-10 | 3.56719E-15 | 0.877264 | 479.6605 | 0.134465 | 4.188837 |
| 3 | 5 | 1 | 2.52975E-10 | 3.33603E-15 | 0.872593 | 313.2902 | 0.093911 | 2.632174 |
| 4 | 6 | 1 | 3.11839E-10 | 4.87084E-15 | 0.873489 | 975.2055 | 0.200213 | 7.746293 |
| 5 | 7 | 1 | 1.86831E-10 | 1.94566E-15 | 0.872289 | 157.8533 | 0.081131 | 1.760488 |
| 6 | 9 | 1 | 2.65122E-10 | 3.61983E-15 | 0.878279 | 360.532 | 0.099599 | 3.59896 |
| 7 | 10 | 1 | 2.74192E-10 | 3.8567E-15 | 0.887979 | 516.3151 | 0.133875 | 4.418086 |
| 8 | 11 | 1 | 2.63214E-10 | 3.19269E-15 | 0.887978 | 256.7875 | 0.08043 | 2.212968 |
| 9 | 12 | 1 | 2.50289E-10 | 3.58426E-15 | 0.888966 | 497.7414 | 0.138869 | 4.767494 |
| 10 | 13 | 1 | 2.62513E-10 | 3.16595E-15 | 0.900019 | 309.6586 | 0.097809 | 2.599648 |
| 11 | 14 | 1 | 2.24906E-10 | 2.71536E-15 | 0.852557 | 289.6876 | 0.106685 | 2.722471 |
| 12 | 15 | 1 | 2.25684E-10 | 2.92207E-15 | 0.882427 | 287.1104 | 0.098256 | 2.973019 |
| 13 | 16 | 1 | 1.29057E-10 | 1.43866E-15 | 0.795801 | 422.4806 | 0.293662 | 7.406054 |
| 14 | 17 | 1 | 3.06817E-10 | 4.91341E-15 | 0.865899 | 856.7765 | 0.174375 | 6.725735 |

   *Basically, the names of the parameters can be arbitrary. However, for “Bin_ID” and “Cell_ID”, they are fixed and cannot be changed to any other names. In addition, the names of the parameters (i.e. names in row 1) cannot be separated by space (e.g. Dry mass). You can simply connect them by adding an “underline”, i.e. Dry_mass.

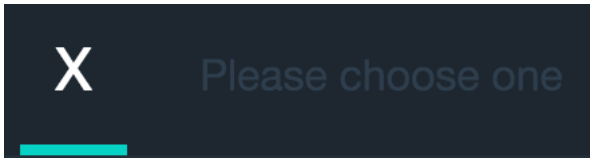
2. Open the folder “dataset”. Copy and paste the output onto “dataset1.json”, which is inside the folder “Dataset 1”.
   *All the content in the dataset1.json should be replaced, except the non-bolded words shown in the following:


```
var dataset1 = [{"Bin_ID":0,"Cell_ID":1,"Area":2.42775E-10,"Vol":3.56719E-
15,"Circularity":0.877264182,"Dry_mass":479.6604877,"Dry_mass_density":0.134464647,"Peak_phase":4.188836501,"Phase_va
r":1.451201474,"Phase_skewness":-0.317814331,"Phase_kurtosis":1.966183424},
{"Bin_ID":5,"Cell_ID":1,"Area":2.52975E-10,"Vol":3.33603E-
15,"Circularity":0.872593091,"Dry_mass":313.2902429,"Dry_mass_density":0.093911004,"Peak_phase":2.632174331,"Phase_va
r":0.387194995,"Phase_skewness":-0.006714225,"Phase_kurtosis":1.798173086},
{"Bin_ID":6,"Cell_ID":1,"Area":3.11839E-10,"Vol":4.87084E-
15,"Circularity":0.873489168,"Dry_mass":975.2054871,"Dry_mass_density":0.200212983,"Peak_phase":7.746292613,"Phase_va
r":4.610475519,"Phase_skewness":-0.059548915,"Phase_kurtosis":1.758581673},
```

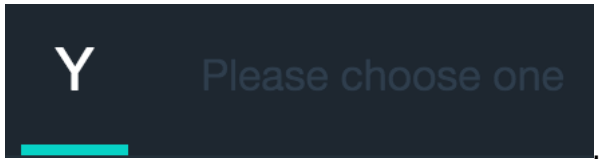

3. Put all the images of cells inside the folder “img”, which is inside the folder “Dataset 1” as well.
   * The images should be in “png” format and they should be like this: 2_1 (the first number is Bin_ID and the second number is Cell_ID).

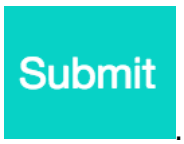
After inputting the data, the steps of using it are shown in the following:

1. Double-click “index.html”.
2. Choose a parameter for x-axis from




   and another parameter for y-axis from

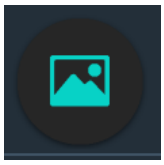



3. Click the “submit button” 

.
4. Choose the dataset to be displayed from 
.

Most importantly, there are some additional functions (other than scatter plot), which are shown in the following:

1. When the cursor is moved to a particular point, the parameters and also the image of that cell will be popped out.
2. Different scales, including linear scale, log10 scale and log2 scale can be chosen individually for x-axis or y-axis from 

.
3. All the points will be changed to their corresponding cell images by clicking this button  and after that, all the images can be changed back to the points by clicking this button  .
   *This button will only appear after any one of the datasets has been chosen to display.
4. Density map (heat map) can be viewed by clicking this button  and by clicking the same button one more time, the density map will be returned to the original scatter plot.
5. This button  is for “reset zoom”.
6. When the “histogram check box” is checked, a group of points can be chosen by dragging out a rectangular gate. Then, the global and also local histograms of all the parameters will be displayed in a pop-up window. If you want to choose another group of points, you can click the cross button located at the top-right corner of the pop-up window and repeat the processes mentioned above.
7. “Shift + p” is the shortcut for outputting the current scatter plot.

Remarks:

1. The maximum number of dataset to be input is 5.
2. The number of parameters of all the datasets should be the same.
3. Only one dataset is allowed to display in order to use the “histogram” function. In addition, the scales of both x-axis and y-axis need to be linear.
4. Using “Chrome” will be better for this interface, but using other browsers should be fine as well.
5. When there are too many input data, it may take some time to load the images or density map. Therefore, it is suggested to use the image-viewing and density-map functions after zooming into a particular region of interest.