# Crayfish User Guide

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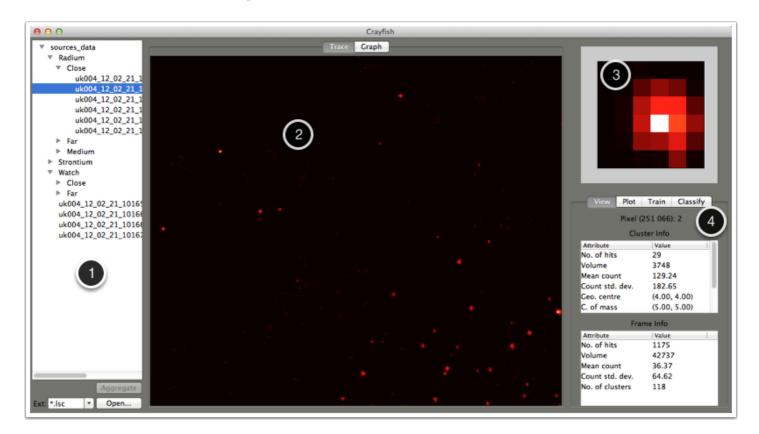
#### 1. Introduction

Crayfish is an application designed to aid in the development of algorithms for the classification of the radioactive particle traces produced by Medipix detectors. It shows a visual display of the particle traces detected, along with tabulated statistical information about the selected frame and cluster. It can also plot the properties of clusters on either a scatter graph or a histogram. The user can manually assign classes to clusters and then use these assignments to train machine learning classification algorithms. The output of these classification algorithms can then be seen from within the software and on the graphs it plots.

#### 2. Installation

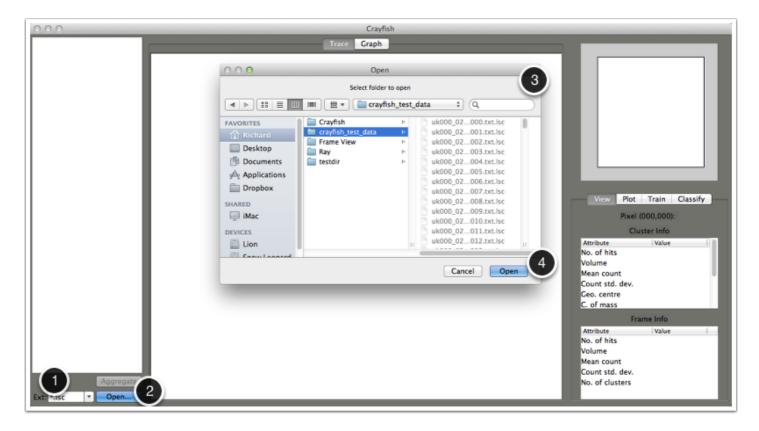
See README.md

## 3. User Interface Layout



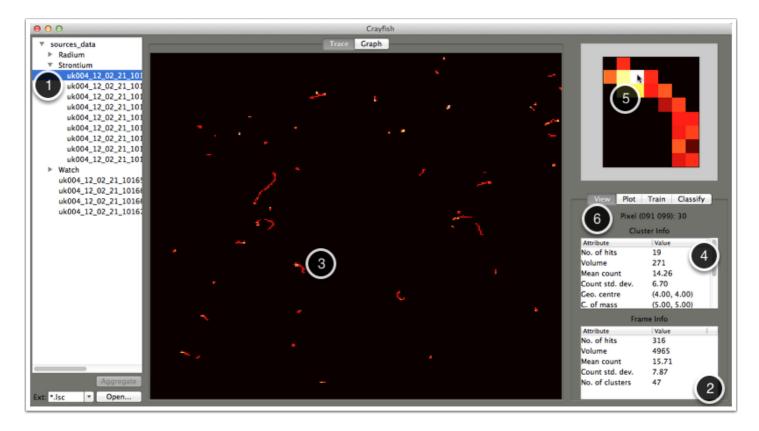
- 1. Frame browser
- 2. Large trace view
- Cluster trace view
- 4. Action tabs

# 4. Opening a Folder



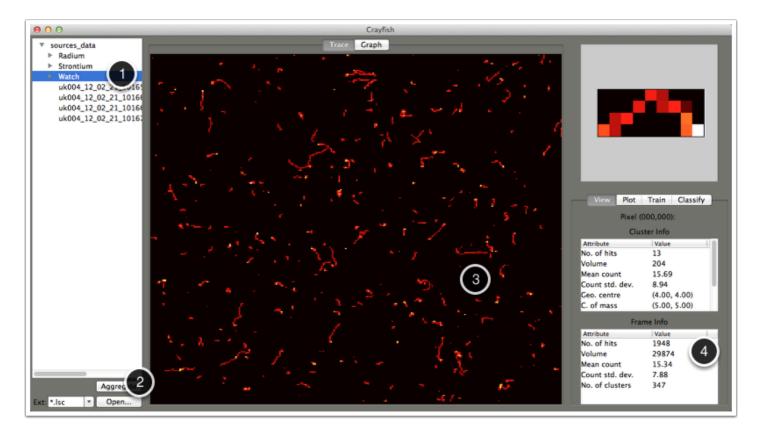
- 1. Select the desired frame extension from the drop down menu, or enter one of your own.
- 2. Click the Open button.
- 3. Select the desired folder in the file dialog.
- 4. Click Open.

# 5. Viewing a Frame



- 1. Select a frame in the frame browser.
- 2. Information about the frame will be displayed in the frame info table.
- 3. Click on a cluster in the large trace view. This will select the cluster.
- 4. Information about the cluster will then be displayed in the cluster info table.
- 5. A zoomed image of the cluster will be displayed on the cluster trace view. Hover over a pixel in this trace view...
- 6. ...and information about the pixel its location and its value will be displayed on the pixel information line.

## 6. Aggregating a Folder



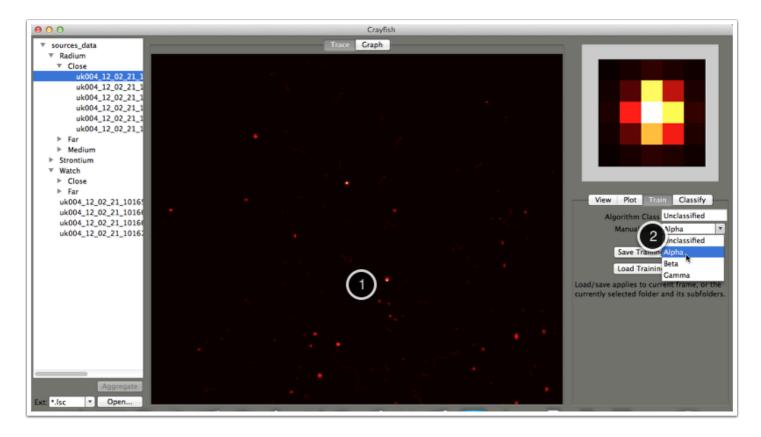
- 1. Select the folder to you wish to aggregate in the frame browser.
- 2. Press the Aggregate button. The software will then aggregate all files in the folder and its subfolders. This process may take some time depending on how many frames there in the folder and how densely populated these frames are.
- 3. The trace zoom will then display the whole folder as if it were one frame, calculating the sum value for each individual pixel.
- 4. The frame info table will display information about the aggregate frame.

Please note that the previously selected cluster will remain selected.

You will not be able to select clusters on the aggregate frame trace view as this doesn't make sense - it is likely that many of the clusters from different frames will overlap. The "No. of Clusters" field in the frame info table is correct however, and displays the total number of clusters found during the aggregation process.

The aggregate frame is cached until either the program is closed or the frame browser is reloaded with the same, or a different, top level folder.

# 7. Manually Assigning a Cluster Class



- 1. Select the cluster using the trace view.
- 2. Use the drop-down menu on the Train tab to assign the cluster's manual class.

# 8. Saving Training Data



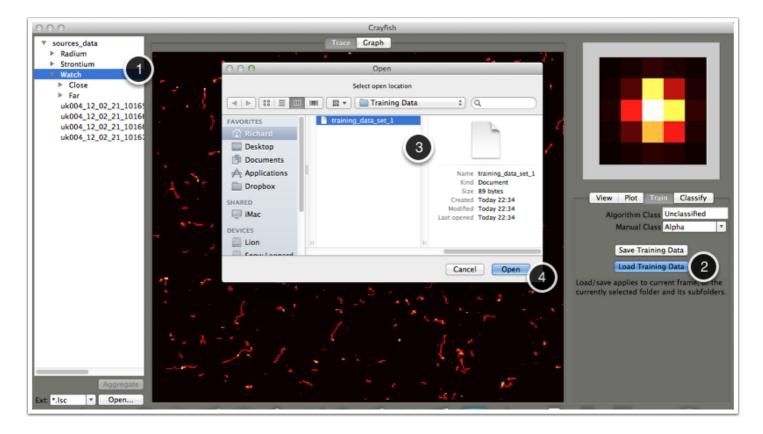
- 1. Select a frame or aggregate a folder .
- 2. Click the "Save Training Data" button.
- 3. Select a location and filename in the file dialog.
- 4. Click Save.

The software will then save a training data file in the desired location.

The training file will contain information about the properties and assigned classes of any cluster in the selected frame/aggregate frame that has a manual class that is not "Unclassified".

This file can then be used as the training data for machine learning algorithms (see later section), or reopened into the Crayfish.

# 9. Loading Training Data



- 1. Select the frame you wish to load the manual class information into, or aggregate a folder.
- 2. Click the "Load Training Data" button.
- 3. Select the file in the file dialog.
- 4. Click Open.

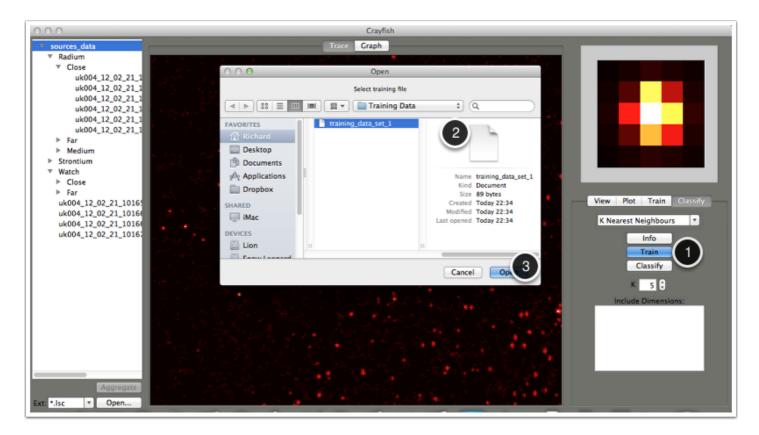
Loading training data back into the software is useful if you wish to adjust training data saved in a previous session, or append further data to it.

# 10. Selecting and Viewing Info About a Classification Algorithm



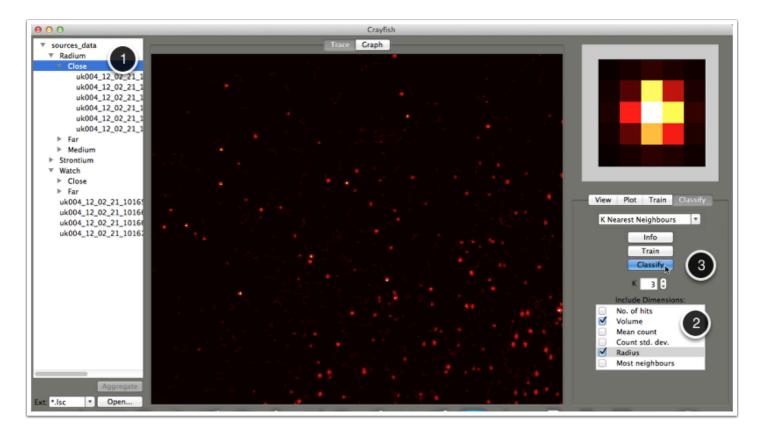
- 1. Select an algorithm using the drop-down menu on the Classify tab.
- 2. Press the Info button.
- 3. A window will be displayed with details about the algorithm and its parameters.

# 11. Training a Classification Algorithm



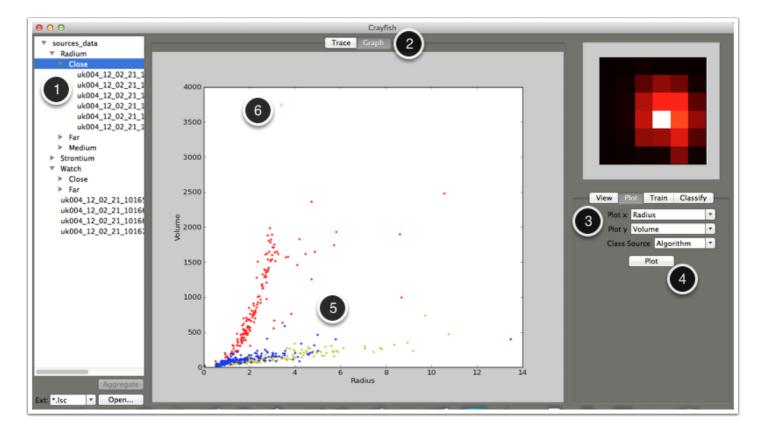
- 1. Click Train.
- 2. Select the training file.
- 3. Click open.

# 12. Running a Classification Algorithm



- 1. Select the frame you wish to classify, or aggregate a folder.
- 2. Set the algorithm parameters as required. View the algorithm information pop-up for more information about the available parameters of the selected algorithm.
- 3. Click Classify. Depending on the algorithm and the given parameters this may take some time.

# 13. Plotting a Scatter Graph



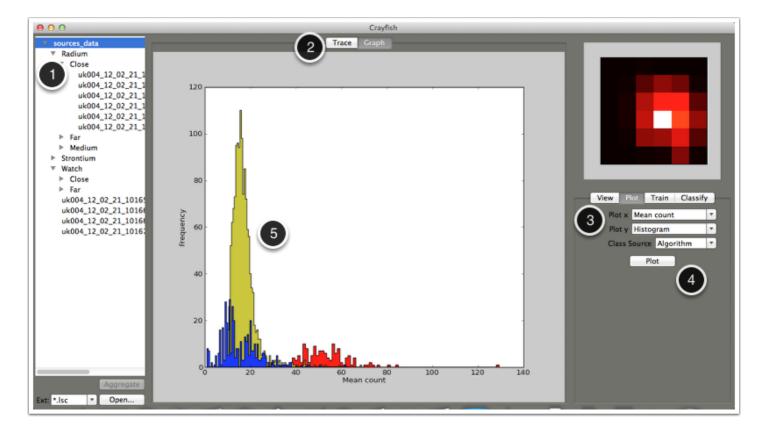
- 1. Select the frame you wish to plot, or aggregate a folder.
- 2. Select the Graph view tab.
- 3. Select the desired attributes for each axis. Then select the source for class colouring either the manually or algorithmically assigned particle trace class.
- 4. Click Plot.
- 5. The graph is plotted with different colours corresponding to the different classes (see below).
- 6. If the currently selected cluster is part of the plotted frame or aggregate frame, it is depicted as a light blue diagonal cross.

The colours for the classes are as follows:

Black: Unclassified

Red: Alpha Yellow: Beta Blue: Gamma

# 14. Plotting a Histogram



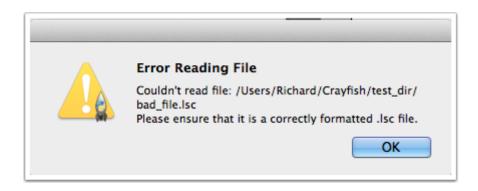
- 1. Select the frame you wish to plot, or aggregate a folder.
- 2. Select the Graph view tab.
- 3. Select the desired attribute for the x-axis. Select histogram for the y-axis. Select the source for class colouring either the manually or algorithmically assigned particle trace class.
- 4. Click Plot.
- 5. A histogram is plotted for each of the cluster classes.

Again, the colours for the classes are as follows:

Black: Unclassified

Red: Alpha Yellow: Beta Blue: Gamma

#### 15. Error: Cannot read file



The specified file could not be opened. Check that is a correctly formatted .lsc file.

.lsc files have the following format:

// An optional number of comment and metadata rows, delimited by two forward slashes.

// The data then follows in the following format, one line per pixel:

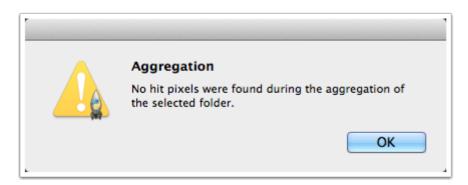
<x co-ord>, <y co-ord> <value>

<x co-ord>, <y co-ord> <value>

. . .

<x co-ord>, <y co-ord> <value>

### 16. Error: No hit pixels found during aggregation



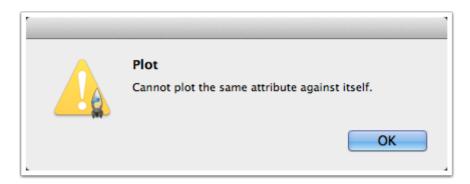
No clusters were found during the aggregation process. This is likely to happen if you try to aggregate an empty folder. The aggregation process will not be completed, and the software will return to the state it was in before the aggregate button was pressed.

#### 17. Error: No frame selected



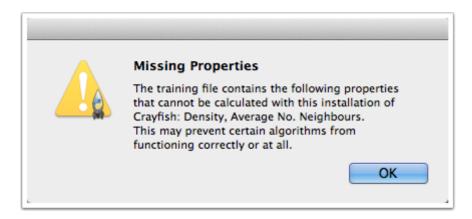
You have selected a folder in the frame browser but have not yet aggregated the folder since selecting it. Either aggregate the selected folder or select a single frame. A folder must be aggregated before it is plotted, classified or training data is loaded or saved from it.

## 18. Error: Cannot plot same attribute against itself



You cannot plot the same attribute against itself on a scatter graph. Change one of the axes to another attribute, or to look at one attribute only, set the y-axis to "Histogram".

# 19. Error: Missing properties



The training file you are trying to load contains attributes that cannot be calculated with the version of Crayfish you are running. This may prevent algorithms from working correctly. It is recommended that you do not continue using the algorithm, but instead save a new training file with the version of the Crayfish you are currently using. You could also contact the author of the training file to ascertain which version of Crayfish they are using and ask if they have added any custom attributes.

## 20. Error: Algorithm not yet trained



You are trying to run a machine learning algorithm without first loading training data. Select a training data file by clicking Train.