READ ME

1 Image Analysis Tool

This application window is part of an **Image Processing Workflow** application. It allows users to configure various parameters related to image processing, particularly focusing on Gaussian filtering and image analysis. Below is a detailed breakdown of the components in the window:

Input Fields

- **Gaussian Window**: A numeric input field where the user specifies the size of the Gaussian window for image filtering. For example, a default value of **121** can be used.
- **Gaussian Sigma**: A numeric input that defines the standard deviation for the Gaussian filter, affecting the smoothness of the filtering effect. The default value is **40**.
- **Dtime**: This input field represents a time-related parameter, such as the time-step used in processing or image acquisition, with a default value of **1E-5**.
- **Grid Size - Image Size**: A drop-down menu allows the user to select a grid size for the images, with options ranging from **8 to 64**, defining the resolution or sampling grid size for the image processing task.

Checkbox Option

- **Enable Advanced Fitting**: A checkbox labeled **Enable Advanced Fitting (takes longer time)** allows the user to enable advanced image fitting techniques, which may provide more precise results but take longer to compute.

File and Directory Selection

- **Select .tif Images**: A button labeled **Select .tif Images** allows users to select image files in the `.tif` format, commonly used for high-quality scientific images.
- **Select Output Directory**: This button allows the user to choose where the processed output files will be saved. It is currently marked as **No output directory selected**.

Output Excel File Name

There is a text field where the user can specify the name of the Excel file in which the output data will be saved. The default value is `output_data.xlsx`.

Log/Status Area

A large text area is present below the file name input field. This space can be used for logging the progress of the image processing workflow, displaying statuses, or indicating errors.

Run Workflow Button

At the bottom of the window, there is a button labeled **Run Workflow**, which initiates the image processing workflow using the selected input parameters and files.

Summary

This application window is designed for scientific image processing tasks. It allows for custom Gaussian filtering, grid size selection, and advanced fitting techniques. Users can select input `.tif` image files and configure output settings, with results saved in an Excel file.

2 Data Analysis Tool

This application is a graphical user interface (GUI) designed for running data analysis based on two model options: a **Simple Model** and a **Model with Background (BG)**. Users can load data, set bounds, exclude data points, customize output preferences, and save their analysis results.

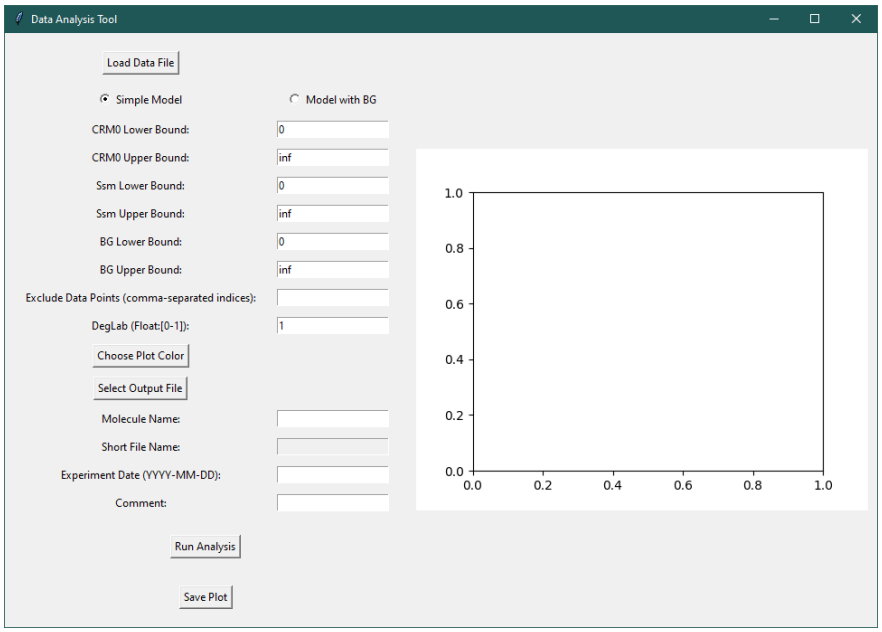

Figure 1: Start up screen of the application

Features

- **Model Selection**:
  - **Simple Model**[1]: A basic analysis model without background contribution.
  - **Model with BG**: Includes an analysis with background contribution.
- **Bound Settings**: Set custom lower and upper bounds for CRMO, Ssm, and BG.
- **Exclude Data Points**: Manually exclude data points by specifying their indices.
- **DegLab Parameter**: Adjust the degree of labeling (Float[0-1]).

[1]Combining Fluorescence Fluctuations and Photobleaching to Quantify Surface Density: `https://pubs.acs.org/doi/10.1021/acs.analchem.1c05513`

- **Select Output file**: Choose an existing output Excel file or create a new one.
- **Metadata Input**: Add information such as Molecule Name, Short File Name (extracted from the Excel file), Experiment Date, and Comments.
- **Run and Save Analysis**: Execute the analysis and save the plot as an image file.

How to Use

1. **Load Data**:
   - Click the *Load Data File* button to select and upload your data file.
   - **Input Data File**: The tool expects an Excel file to be loaded. If the Excel file doesn't contain 'CRMmoy', 'CRmoy' and 'CRMsem' as headers, it will raise an error.
2. **Model Selection**:
   - Choose between the *Simple Model* or the *Model with BG* by selecting the corresponding radio button.
3. **Set Bounds**:
   - Input values for the bounds (CRMO, Ssm, and BG), or leave the default values (0 for lower bound, inf for upper bound) for no restrictions.
4. **Exclude Data Points**:
   - If you wish to exclude certain data points from the analysis, provide their indices in the input box, separated by commas (e.g., 1,3,5). The first row is equal to 0!
5. **DegLab Parameter**:
   - Set the *DegLab* value, which should be a float between 0 and 1. Example: If you are using a mixture of 1:1 Molecule with no label and molecule with label, then the DegLab = 0.5.
6. **Select Output File**:
   - Click the *Select Output File* button to choose a location and filename where the analysis results will be saved. This step needs to be performed only once every time the application is opened.
7. **Enter Metadata**:
   - Input optional information such as Molecule Name, Short File Name, Experiment Date, and any additional comments.
8. **Run Analysis**:
   - Click the *Run Analysis* button to execute the analysis and display the plot.
9. **Save Plot**:
   - Click *Save Plot* to save the generated plot to the file specified in the *Select Output File* step.