Getting Started

Prerequisites

Matlab: You will need at least Matlab version 2015a with the curve fitting and optimisation toolboxes. I recommend installing all the toolboxes anyway.

New Matlab is more graphics-intensive purely so the figures look prettier, so you may want to disable anti-aliasing for improved performance. To do this, type the following command into the terminal:

```
set(groot,'DefaultFigureGraphicsSmoothing','off')
```

Unfortunately, there does not seem to be a way to permanently do this in Matlab's settings, so you must do this each time you open Matlab.

Dexter: For Dexter synchronisation to work, Dexter must be outputting the current run number into a text file at the end of the run (as in the RbCs version).

Network: The image analysis program computer must be able to see the Dexter computer on the network.

Installation: Go to https://github.com/anarakonjac/absorption-image-analyser and click "Clone or download" and "Download ZIP". Unzip it and save the contents to a folder on your computer. Instructions on updating the image analyser can be found later in this document.

Setup

1. Open up a Matlab terminal and navigate to the folder with all of the image analysis files. Type `ImageAnalyser` in the command window and press "enter". This will open the GUI.
2. Click on "File" then "Configure". This opens the configuration file editor.
    a. Choose number of species or two via the pop-up menu. You can change this selection at any time.
        - "Single Species" is for running with a single species only in the first tab.
        - "Two Species (simultaneous)" is for collecting data for two species simultaneously, i.e., a single experimental run simultaneously images both species with two sets of A, B, and C camera images taken.
        - "Two Species (separate)" is for collecting data for two species, but not at the same time, i.e., one experimental run collects images for one species and a separate run collects images for the other.
    b. Set paths to relevant folders.

- “Set Storage Path” is the parent folder for where the A, B, and C images are stored according to date. The program will generate its own folder structure.
    - **Note:** it’s important that folders for future dates are not present. The image analyser relies on this to figure out if it’s a new day or not for some internal data handling.
- “Set Log File Path” is where DAT files will be stored. These files can later be opened in a program of your choice (Origin, Excel, Matlab, Python, etc.). Two types of log files are stored:
    - Saved data log files that store only data that you choose to save, including GUI values such as frequency.
    - Daily log files of every processed image. The data stored is numerical data from the data plotter.
- “Set Dexter Sync File” is the TXT file generated by Dexter that stores the latest Dexter file number for synchronisation purposes. It should be called “currentfile.txt”.
- “Load Variable File” (optional) is the text file generated by Dexter in the multirun configuration that stores the file number and associated variable value. If you load this file, then the variable value will be automatically imported into the image analyser.
- “Set Image Path” is where your camera images are stored immediately after acquisition. Species 1 and 2 can have the same image path, but the paths still need to be specified individually.
- “Load Fourier Filter” (optional) loads a Fourier filter of your own design. The filter should be a matrix of the same size as your image. It should be called `filter_sp1` or `filter_sp2` and saved in a MAT file.
    - You can generate the filter using whatever method you want, but you need to import it into Matlab and then save it as a MAT file using the following command:
      `save('filterfilename_species1','filter_sp1')`
    - Your MAT file name can be whatever you want, but the Fourier filter must be named as specified here.
- “Fringe Removal Path” (optional) sets the path to the probe images you would like to use in order to construct the “perfect” probe image for subtraction. You must select a B file in that folder, but it doesn’t matter which one you choose as long as it’s for the appropriate species.
    - Choose the file numbers you would like to use for fringe removal. Using more images gives a better result, but can be more computationally intensive.
    - **Note:** you MUST chose a B image!

c. Enter relevant quantities.
- “Number of rotations” rotates your camera images. There is some pre-existing redundancy in the code, so if you don’t want any rotation, you should select “3”. You will quickly see if it’s right or not.

        - “Pixel Size” is the pixel size of your camera at a given binning. E.g., if your camera has a pixel size of 2.6 μm and your binning is 2x2, then set the pixel size to 5.2.
        - “View Angle” is the angle of your dipole trap relative to your imaging axis. It is used to calculate the cloud size relative to the dipole trap axes rather than the imaging axis.
        - “I/I_sat (Classic mode)” is simply I/I_sat.
        - “I_sat_eff” is the effective saturation intensity in counts per pixel used in pixel-by-pixel I/I_sat mode or high intensity imaging mode. This is a value that you have to calibrate (see accompanying guide on how things are calculated).
            - If you change your binning, you will have to adjust this value.
    d. Save the configuration file using “Save Config File”. This is optional. All the data entered so far is stored in the configuration file editor is stored already, but saving your file means that you can reload it later without having to re-enter any information. Additionally, the name of your configuration file is saved when you save your data in the main GUI.
        - If you are ever in doubt of what the current configuration settings are, load the configuration file in the command window by typing `load configdata`. To see the variable names stored, type `whos -file configdata` and the variables will be listed.
    e. Close the config file editor GUI. Settings will be stored in `configdata.mat` at this point.
3. The first time you run the main GUI in a given session, you must select the relevant options in the drop-down menus and text boxes. You must also click the tick boxes on and off. This stores the GUI settings. If you are only running one species, you can ignore the second species tab. The different options are as follows:
    a. Analysis Options
        - Species: self-explanatory! Choosing the species will load the relevant properties of that species (mass, transition wavelength, etc.).
            - Species-specific settings are correct for Rb, K, and Cs (I think), but please check `elementproperties.m` to make sure.
        - Mode: there are four options.
            - “Classic” is what we usually use. We specify I/I_sat and assume it’s the same across our whole cloud, even though the probe beam intensity is not uniform.
            - “px-by-px” takes into account the variation in probe intensity, effectively giving you a pixel-by-pixel intensity of your probe beam. To use this setting, you must experimentally determine an effective saturation intensity (I_sat_eff) as explained in the accompanying guide.
            - “High Intensity” lets you image at probe intensities around 10 times I_sat. This is useful in certain situations (see accompanying guide).

        - “Faraday” is for use with Faraday imaging and does a simply subtraction of the A and B images. The resulting image is not the optical depth.
    - Sum or Cut: choose whether to display cross-sections of the column sums or slices (cuts) through the cloud center.
    - Fit type: choose between a Gaussian fit or a bimodal Thomas-Fermi fit.
        - The Thomas-Fermi fit is not always reliable. You may need to adjust some initial guess parameters in `bimodal_findstart.m` for the program to better guess where the thermal cloud ends and the BEC begins.
        - Improvements are planned for future updates!
b. Synchronisation
    - Variable Sync: automatically imports the quantity being varied in multirun as well as the corresponding label.
    - Override Dexter Sync: **don’t use this!** It’s only for testing and when you are trying to use the imaging program without running Dexter for some reason.
        - The program does not cope well with running manual mode and synchronisation on the same day due to the potential for clashing file numbers.
    - Manual Counter: **don’t use this!** It’s only for testing. You can enter a number, and the program will automatically increment it as new images are acquired.
c. Parameters
    - Mostly self-explanatory! If you enter these and save the data for an image, they will be stored along with the rest of the outputs.
d. Plot Options
    - Set ROI: drag the mouse along the area you want to zoom into.
        - Sometimes this bugs out and I don’t know why. If that happens, click zoom out once or twice and then try setting the ROI again.
        - You must zoom out before selecting a new ROI.
    - Zoom Out: zooms out!
    - Use ROI: this keeps whatever ROI you’ve selected for future images.
    - Square ROI: keeps the ROI square. The box you make when choosing your ROI must be somewhat square-ish, or you might get an error.
    - Use Fourier Filter: exactly that.
    - Remove Fringes: select an ROI where your atoms are located, and the program will find the “ideal” probe image based on supplied probe image files.
        - If you always want exactly the same ROI for your atoms, you can input your own coordinates into `removefringes_sp1.m` or `removefringes_sp2.m`

        - This is very slow if you use a full 1000 x 1000 px image, but speed improves considerably if you use a smaller ROI. The ROI can be defined either in Solis or by selecting using the image analyser.
    - Choose a colourmap. Parula is the new Matlab default and should look better when printing in black and white.
    - Select your OD scale.
4. Results: Unless otherwise noted, results are in pixels. See accompanying document on how each quantity is calculated.
5. If it's the first time you've opened the GUI in a Matlab session, go to the Data Plotter tab. Choose the axes from the drop-down menu. Matlab will beep at you and display a lot of angry red text in the command window because there is no data to plot yet, but just ignore it. Also click in the "Range" text box and hit enter, and do the same for "Variable Label". You may also need to click on the appropriate species selection button.
6. Check that the program is looking for camera images with the appropriate file names. The program looks for images with a specific name, such as "data001.asc", "data002.asc", and "data003.asc", etc. for the A and B images, respectively. Check your naming scheme and alter it as required in `newdatamenu.m` and `newdatamenu_sp2.m` accordingly. It's right at the top of the m-file.

Using the Program

1. To load an image, click "New Data". This assumes freshly acquired images exist. The A (atoms), B (probe), and C (dark background) images will be processed and stored in the year-month-day file structure.
    a. In two species (simultaneous) mode, clicking "New Data" will load data for both species. In two species (separate) mode, you'll have to click "New Data" in the appropriate tab.
    b. **Caution:** You must only click "New Data" once the Dexter run is **complete**. To synchronise the image analysis program to Dexter, Dexter writes the current run number to a text file. This happens at the *end* of the run. If you click on "New Data" too soon, the image file number will correspond to the *previous* Dexter run. If there is already an image file with that number present, the image analysis program will complain. If there isn't, then the file number will correspond to the previous run and *the image file number will be incorrectly synchronised!*
2. To load an old image, click "Old Data" and choose the file you want. It doesn't matter if you click on the A, B, or C file.
3. To save data, click on "Save Data". This will save whatever you entered in the "Parameters" box as well as the name of the configuration file you used. This is all stored in a DAT file. This data will be reloaded if you open a saved image via the "Old Data" button.

    a. In two species (simultaneous) mode, clicking “Save Data” saves the data for both species.
4. If you would like to export the *x* and *z* axis fits, go to “Export” then “Export Fit Data” for the appropriate species. This will generate some CSV files that can be imported elsewhere.
5. If you would like to export the absorption images, go to “Export” then “Export Absorption Image” for the appropriate species. This opens the absorption image in a separate figure for saving and printing.
6. The Data Plotter plots data! If you are plotting two species, it will have two *y* axes for each plot. Choose which species are plotted using the radio buttons. You can plot whichever variables you want against each other. There are two modes for the data plotter:
    a. Plot today’s data (default). The fit data for every image acquired throughout the day is saved in a MAT file, regardless if you have saved the data or not. You can choose which files to plot via the “Range” box. This accepts the following:
        - “1-end” (default), “2-end”, “*n*-end” for any integer *n*.
        - Fixed ranges, e.g., “5-10”.
        - A selection of images, e.g., “2-10,15,18,20-25”.
    b. Plot saved data. Click on the “Plot Saved Data” button to enable this. It will prompt you to choose a directory. Only data that has been saved via “Save Data” can be plotted this way. Make sure that the species selection in the species tabs matches what you are plotting. This is how the data plotter knows which file names to look for.
        - To return to plotting today’s data, simply click the “Plot Saved Data” button again.
7. If you would like to export data from the plots as a CSV, go to “File” then “Export Plotter Data”. This will export all the possible plot variables. The CSV file has the following column format:
   `File number; variable; NOD; Nx; Nz; N_pxsum; Tx; Tz; PSD; OD; npk; sigma_x; sigma_z; center_x; center_z`
   If you are in two species mode, data from the second species will be saved in a separate file. The element name is automatically prepended to whatever file name you select.
8. If you would like to export the plots themselves, go to “File” then “Export Plots”. This will replot the data in a new Matlab FIG file. In this figure, you can do the following, and probably more:
    a. Print your plot.
    b. Edit plot characteristics. To access this, go to “Tools” then “Edit Plot”. Then you can change labels, add titles, change markers, etc.
    c. Perform basic fitting. Go to “Tools” then “Basic Fitting”. This will let you fit lines and polynomials. If you want to do anything more sophisticated, you will have to use other means.
    d. Save in a format of your choice.
        - PDF, PNG, etc. if you just want the image.

        - FIG if you would like to open this in Matlab for editing later. You can also extract data from Matlab figures using the following in the command window:

```
figure(61)
subplot(2,3,n)   % where n is the plot you want
h = findobj(gca,'Type','line');
x = get(h,'Xdata');
y = get(h,'Ydata');
```

        - SVG if you want to open the plot in Inkscape and make it beautiful.
9. You can create a figure of all plottable data vs the variable by going to “File” then “Export All Plottable Data”. This opens a landscape A4 sized figure that is ready for printing.
    a. Before you print, go to “Print Preview” and adjust the settings (orientation, centering, size, etc.), because Matlab’s default print settings are rubbish. Once you have set your print settings, save them by clicking “Save As” on the top left on the right of “StyleSheet”. As long as you don’t close the figure, you don’t need to reload the stylesheet.
10. You can also use the image analysis on your own office computer.

Things to watch out for

1. The program can’t deal with Dexter file number “0”. You’ll have to run Dexter once at the beginning of the day to get rid of run 0. Sorry!

Update Procedure

When performing an update, I would recommend against simply downloading and using the entire collection of files from GitHub again as you might lose your settings. Instead, just update the files that have had changes. The following procedure is recommended:

1. Make a copy of your image analysis folder just in case things go wrong.
2. Download the zip file for the image analysis program.
3. Copy across only the files that have changed since your last update.
    a. **Don’t copy any `.mat` files!** Doing so will overwrite your settings.

Troubleshooting

1. You get errors when attempting to make an ROI.
    ➢ Click “Zoom Out” a couple of times and try again. This is an intermittent problem that seems to have been present in the old version too.
2. Matlab complains about one of the `.mat` files not being a binary (e.g., `maindata.mat`, `configdata.mat`).
    ➢ If the file is `maindata.mat`, `configdata.mat`, `mainstate.mat`, or `configstate.mat`, simply delete the file. These files store the states and variables of the GUI, so if you delete any of them, you’ll have to go through

and reset all the GUI elements (pop-up menus, tick boxes, text boxes) as in step 3 in Setup.