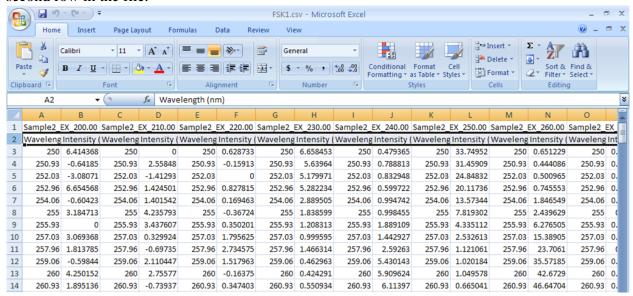
## Fluorescence Resolution using PARAFAC (PARAlell FACtor analysis): A Guide

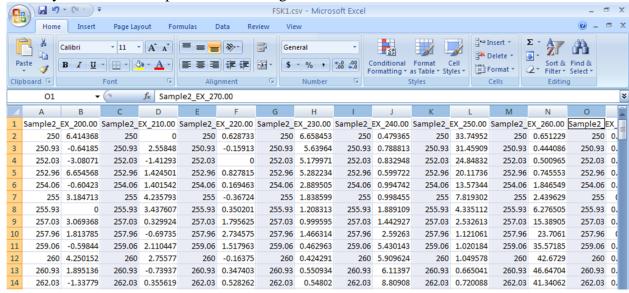
The following is a step by step procedure to resolve 3-D fluorescence data using PARAFAC. The 3D fluorescence spectra obtained from the spectrometer should be saved in the .csv format. The .csv file must be modified to fit the format as mentioned below. Once simplified, preprocessing of the data may begin.

#### **Section 1: .CSV File PREP:**

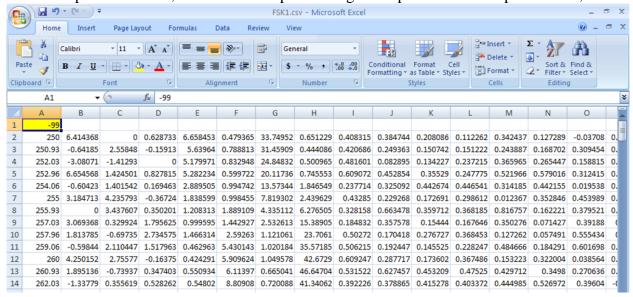
- 1. Open the .csv fluorescence file.
- 2. The second row contains headings for each column (wavelength and intensity). Remove the second row in the file.



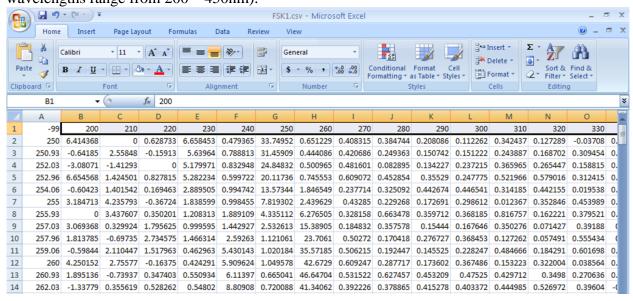
3. Every other column repeats the wavelengths used for the scan. Remove these columns.



4. In the top left hand cell, remove the sample heading and replace it with the placeholder, -99.



5. In row 1, add the wavelengths used for scan along the top of each column (In most cases, the wavelengths range from 200 - 450nm).



## **Section 2: PRE-PROCESSING DATA (Scatter Removal):**

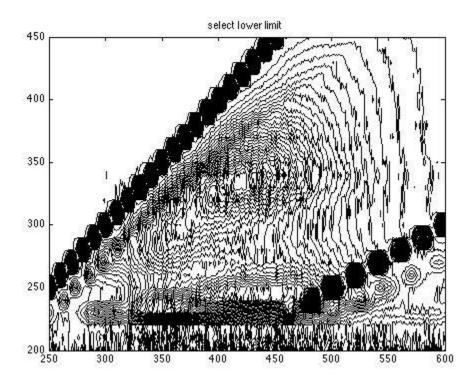
This next section describes how to preprocess the .csv files when absorbance corrections are not needed. If correcting for absorbance, disregard this section and refer to Section 3.

- 1. Open scatterremoval.m
- 2. Change the file name to match the .csv files being preprocessed.

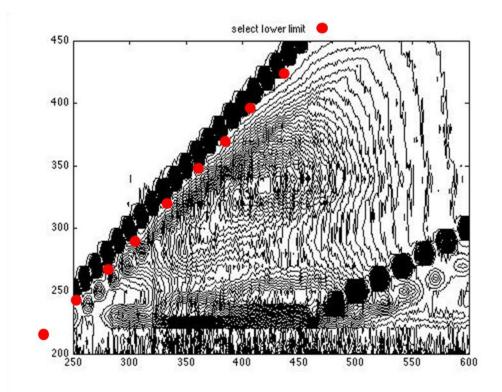
```
names=strvcat(...
'filename1', ...
'filename2', ...
'filename3');

for ii=1:size(names,1)
    name=names(ii,:);
    txt=['preprocess_fluor_data_csv_file ',name]; eval(txt);
end
```

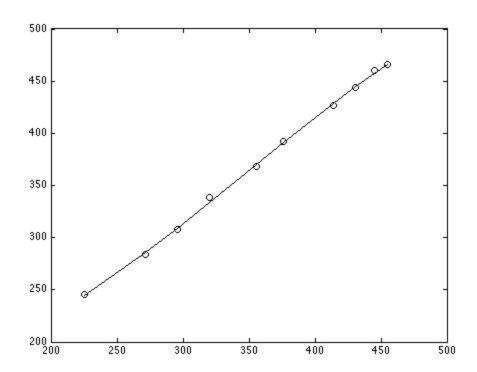
- 3. Press the run m-file (green triangle) play button.
- 4. The following figure (1) will pop into a new window on screen



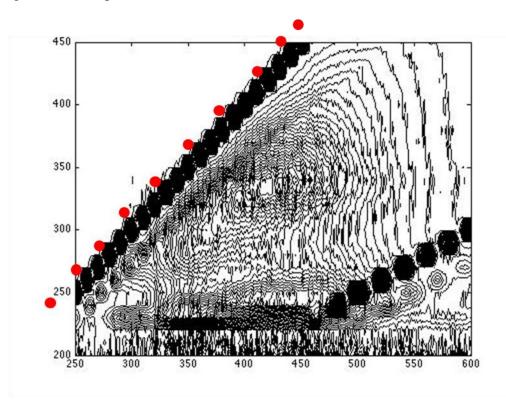
## 5. Select 10 points on the lower limit with mouse



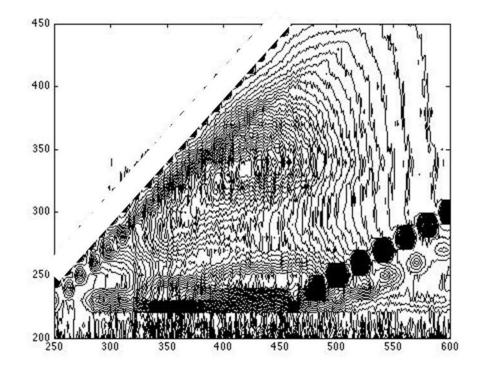
## 6. The following figure (2) will appear



7. Figure (2) will close and Figure (1) will reappear asking you to select the upper limit using the mouse. Again select 10 points.



8. Figure (2) will reappear, then close and figure (3) will appear.



- 9. Repeat steps 5 through 7 for the lower scattering.
- 10. Repeat process for all files. Once all files are complete, the figure of the last line to be fitted to remove the scattering will remain on screen.
- 11. Continue to Section 4.

# Section 3: PRE-PROCESSING DATA (Scatter Removal) WHILE CORRECTING FOR ABSORBANCE

This next section describes how to preprocess the .csv files when correcting for inner filter affects. Absorbance spectra for each sample will need to be obtained (medium speed, 200 – 650nm).

- 1. Open the abs\_correction.m and preprocess\_fluor\_data\_csv\_file\_abs\_corr.m MATLAB files.
- 2. In the abs\_correction.m file, change the file name to match the .csv files being preprocessed.

```
preprocess fluor data csv file abs corr('filename', wavelength, A)
```

3. From the UV-Vis spectrum for the sample, copy and paste the wavelength and absorbance data into the data vector.

```
data=[...
649.9916992 0.0023519103
648.9721069 0.002460845
647.9522705 0.0025235112
646.9321289 0.0024569922
646.0574951 0.0026021234
645.0367432 0.0025036456
644.0157471 0.0025101285
642.9943848 0.0023687498
641.9727783 0.0024299189
640.9508057 0.002375413
639.9285889 0.0025907694
639.052124 0.0028715807
```

- 4. Press the run m-file (green triangle) play button.
- 5. Follow steps 4 9 from Section 3.
- 6. Repeat for each of the samples needing correction.
- 7. Continue to Section 4.

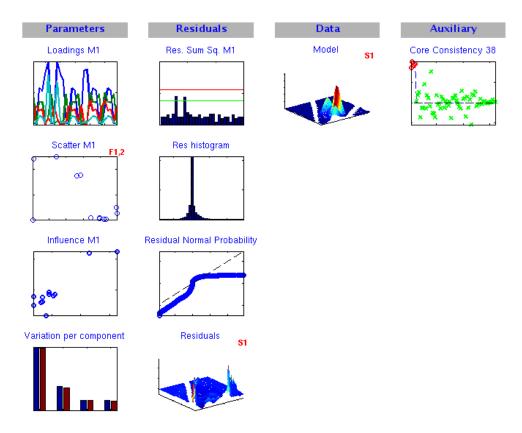
## **Section 4: PROCESSING DATA**

1. Once the Scattering has been removed, open the m-file PARAFAC process mesocosm samples 2009 justaugust.m

2. Change the file name to match the .csv files being preprocessed.

```
names=strvcat(...
'filename1', ...
'filename2', ...
'filename3');
```

- 4. If necessary, the number of components used to describe the data can be changed.
- 5. Press the run m-file (green triangle) play button. At this point a window will pop up which says "Fitting parafac. Please wait". Below the text in the window is a red bar which monitors the progress of the program. Once the bar is completely red, PARAFAC is almost complete.
- 6. Once complete, the window will close and a new window will appear. This window is shown below. The percent of data explained by the fitting will be shown in the title header of the window.



- 7. To obtain a summary of the components for the samples, open the MATLAB file PARAFAC\_summary\_of\_4\_components.m.
- 8. On line 3 of the script, change the load name to match the number of components used to describe the data.

```
clear; clear global
load Hollypracticenumberofcomponents.mat
```

9. If only three components are used to describe the data, comment the final subplot used for component four.

```
%subplot(224); [C,h]=contour(em,EXX,surf4,3,'k'); set(h,'linewidth',2);
%h=xlabel('Emission (nm)'); set(h,'fontsize',12)
%h=ylabel('EXXcitation (nm)'); set(h,'fontsize',12)
%h=title('(d)'); set(h,'fontsize',12)
%set(gca,'linewidth',2)
%set(gca,'linewidth',2)
%set(gca,'fontsize',12)
print components.eps -depsc2
figure(1)
figure(2); clf
subplot(221); plot(conc1,'ko'); xlabel('site'); ylabel('conc');
title('component 1')
subplot(222); plot(conc2,'ko'); xlabel('site'); ylabel('conc');
title('component 2')
subplot(223); plot(conc3,'ko'); xlabel('site'); ylabel('conc');
title('component 3')
%subplot(224); plot(conc4,'ko'); xlabel('site'); ylabel('conc');
%title('component 4')
```

- 10. Press the run m-file (green triangle) play button.
- 11. To have a print out of the concentrations found in each sample for each component, type x = [conc1 conc2 conc3...concn] into the command window.

### **Section 5: SPECTRA FIGURES**

- 1. Open the m-file spectra.m
- 2. Change the file name to match the .csv files being preprocessed.

```
simplereport ('filename', 10, 2);
```

3. To change the number of lines used to describe the data, change the first number after the file name

```
simplereport ('filename', 10, 2);
```

```
OR, in square brackets, list the values at which lines are needed to describe the data. simplereport ('filename', [25, 50, 75, 100, 125, 150, 175, 200, 225, 250], 2);
```

4. The last number in the command line alters the spectra to give you colour or black and white spectra (colour = 2, black and white = 1).

```
simplereport ('filename',10,2);
```

5. Press the run m-file (green triangle) play button.