

Assignment Report – Analysing Fluorescence Data

Done by Group 2A: Gagan Deep, Santosh, Manikandan

- This assignment is based on **real time data analysis**, a simple version is being considered.
- The given data corresponds to size scattering and forward scattering due to cell when light is illuminated on it.
- There are sudden peaks observed in the data which corresponds to presence of cell in the fluid flow.
- To find the location of the cell, we are required to match the peaks from forward scattering data and side scattering data. If both have a peak at the same place, we can confirm the arrival of a cell.
- Firstly, noise is eradicated from the data by using **moving average filter** i.e. average is calculated locally and subtracted from the window of data. The window keeps moving, hence analysing the large set of data giving the required information.
- In this analysis we may find cases where the peak is found only in one of the graphs. In that scenario, we consider it to be an error and do not count it as a cell.
- To find the peaks in the filtered data, we first find the maximum in a small window, and find if it crosses the required threshold to be considered as a peak. If it crosses the limit, the location and value of the peak will be recorded in a file.
- Now after finding peaks, we are also required to find the **Full Width at Half Maximum** of the peak (for the Side Scattered data). This is done by interpolating the filtered data, and then finding the locations corresponding to the half-maximum.
- The interpolation method used is linear interpolation.
- Also, for reference, the values of mean arrival times of cells, mean and median of FWHM, mean width of FWHM have been calculated.
- The text files generated are “filtereddata.txt”, “peakdata.txt”, “FWHM.txt”, “MeanFWHM.txt”.
- The plots of the filtered data for the first 10000 points are given, both for forward and side scattering



