Fluorescence Fingerprinting Protocol (Tara)

Pw: eclipse

- ➔ Scan
- ➔ Setup
    - Cary – Em. Excitation 200 3D mode: Check (450 & 10)
      Start: 250 Medium
      Stop: 600
    - Options – PMT = high
    - Accessories – Multicell #2
    - Autostore – On:Prompt on Start (ASCII csv)
    - OK
- Start with blank: MilliQ and press Start
    - Only want to see Raleigh Peaks
- When scan is complete click on graph then box at top to see 3D plot

UV-Vis

Pw: cary50

* corrects for inner filtering effects for PARAFAC (inner filtering corrections required if A > 0.3 at 254 nm)

- ➔ Scan → Connect
- ➔ Setup
    - Start: 600 Stop:200 Scan Control: Medium
    - Baseline: zero/baseline correction
    - Reports: Select for ASCII (csv)
    - Autostore: On: promt on start
    - Baseline (to start scan)
- ➔ On prompt add onecard to block beam, once done remove card and press START

Cleaning Cuvette:

1. Rinse with MilliQ and pat dry
2. Rinse with Standard/Sample a couple times then fill

Standard:

10 mg C/L Southampton DOC
2.4 µM Tyrosine
1 µM Tryptophan

Cuvette Preparation and Storage:

- Store in MilliQ plus cuvette soap
- Before use put in beaker with MilliQ then add soap
- Heat for at least 10 min in oven @ 40°C

Data Analysis:

- Save data from instrument computers to USB
- Remove text portion (rows) and wavelength (columns)
- 1st box arbitrary value of -99; 2nd box start @ 200 and increase by 10 across row (should end at 450)
- Resave (as short a name as possible)
- Move to same folder as matlab scripts to run analysis
- 10 points to remove Raleigh scattering