



**OceanOptics**

**BioFluid**

Focused Kit

**Spectroscopy Kits**

# BioFluid

When dealing with biological samples, unless you're studying dried bones there is likely some fluid involved one way or another. The average adult is about 60% water by weight, so liquid spectroscopy clearly has value in assessing all the various fluids found in human physiology.

Most biofluid components have some UV activity, which is why each tier of the BioFluid Kit uses the deuterium light source and a UV-g geared spectrometer. This allows relatively quick-and-easy concentration regression to turn your system into a protein meter, as well as a meter and/or identifier for colorimetric or fluorescent markers.

## BioFluids Compatible with Dip Probe:

- Blood Serum
  - *whole blood requires shorter pathlength tip or reflective approach*
  - *both options possible with existing hardware*
- Cerebrospinal Fluid
- Lymph
- Urine
- Saliva
- Cell Culture Media / Buffer





# Components



# System



# Software



# Experiment



# BioFluid

Focused Kit







# Components



## System



## Software

These spectrometer and light source combos turn optical signals into meaningful numbers.

Spectrometers are powered and interfaced via USB, and light sources require standard power.

### Essential | 185-650 nm



ST-UV



DH-2000-S-DUV-TTL

### Enhanced | 220-910 nm



SR-2UVV300



DH-2000-S-DUV-TTL

### Superior | 220-880 nm



HR-2UVV250



DH-2000-S-DUV-TTL



# Components



## System



## Software



## Experiment

# Bulk Dip Probe



## T300-RT-UV-VIS

Dip this probe into your sample solution for transmission readings. Ensure no bubbles are trapped in the optical path by whisking the probe through the fluid.

Go on. Dive right in.

Track protein concentration or component ratios in real-time, in vessels as small as a beaker or as large as an industrial tank. The standard  $\frac{1}{4}$ " diameter allows quick integration into bioreactor head ports.

The standard  $\frac{1}{4}$ "  
diameter of the dip  
probe allows for...

HJBS EPRHTGJREAP

EPRA FEFH AG GHJLRAG

LACFGHBBEAP

MERREPTB

Hint: H = E



# Components

## System

## Software

**Pro Tip:** Use a ring stand or lab clamp to hold the probe in place. To minimize probe movement, you can place the fluid vessel on a removable support to swap fluids while keeping the probe mounted.



Connect one probe fiber leg to the light source SMA port, and the other fiber leg to the spectrometer SMA port.



The provided tip provides a 10mm total pathlength, but is only a 5mm gap. This is because the light travels the 5mm distance twice (*there&back*)





# Components



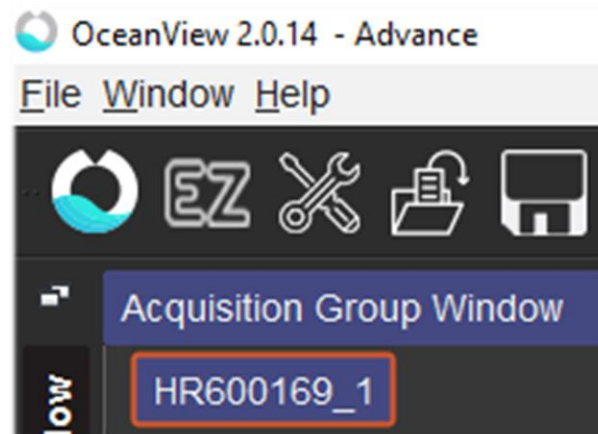
# System



# Software



# Experiment



Click the OV icon



Select **Absorbance**, and then **Absorbance Only**





# Components

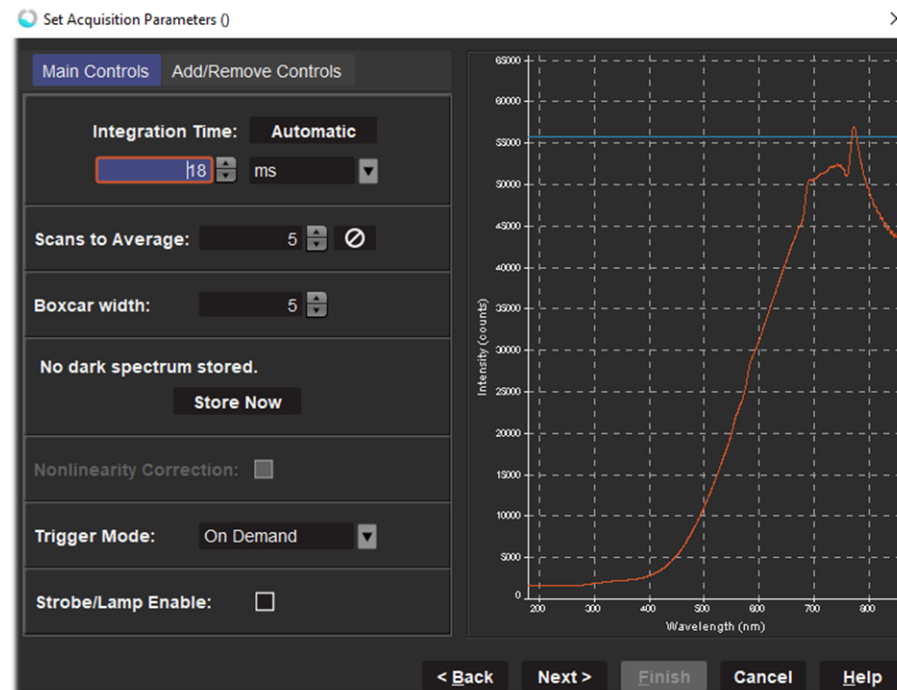


# System



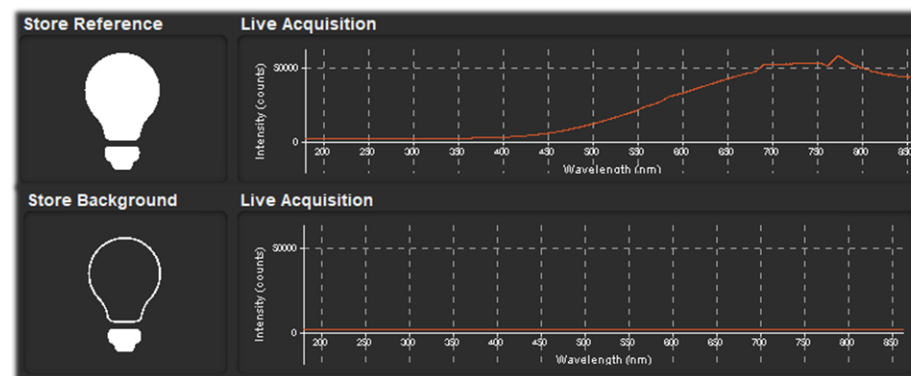
# Software

**Pro Tip:** Scans-to-Average averages individual pixels over time, while Boxcar averages neighboring pixels to smooth the spectrum. The former increases scan time, but the latter does not. However, high Boxcar can begin to mute sharp peaks that may be important to your work.



*Total Scan Time =  
Integration Time x  
Scans to Average*

Hit 'Automatic' button to auto-set Integration Time



Take light reference with light source on and reference fluid present

Take dark/background reference with light source off



# Components



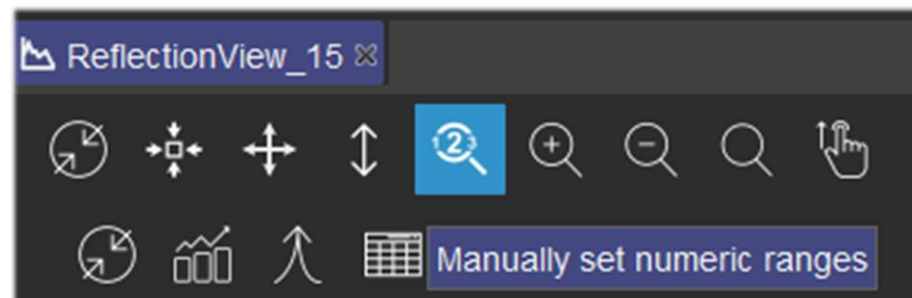
# System



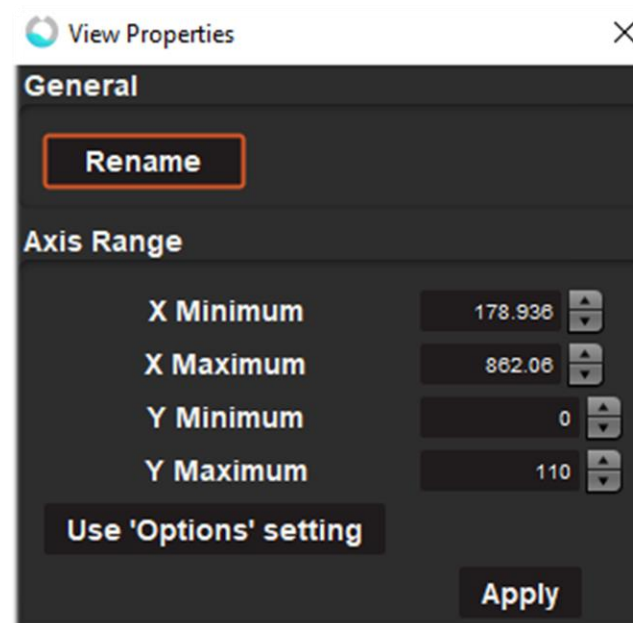
# Software



# Experiment



Use arrow and magnifying buttons to move and zoom around the graph. The magnifying glass with numbers in it allows you to manually set the x- and y-axis range.



# Components

## System

## Software

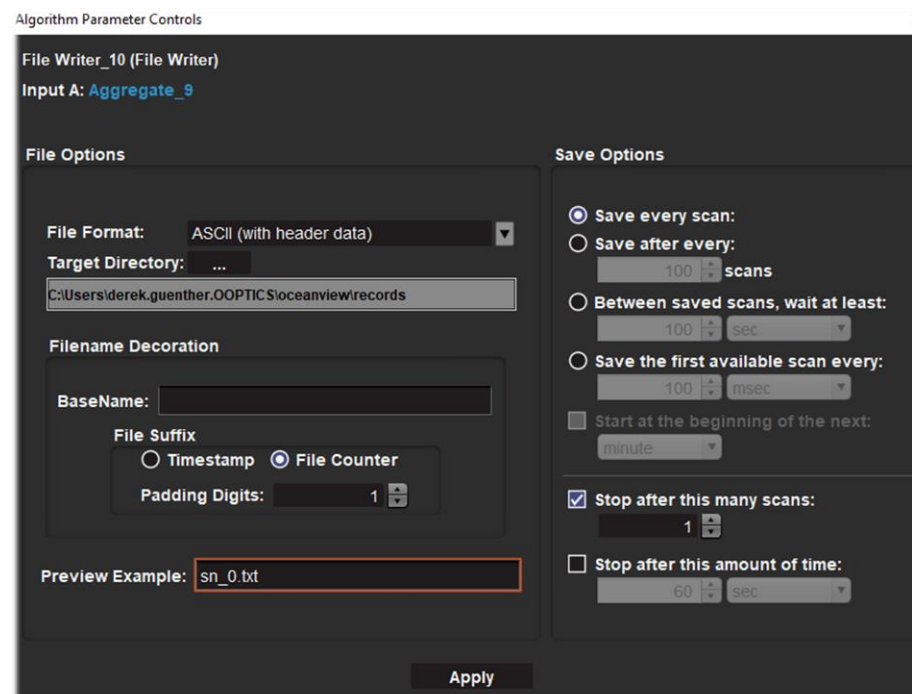
**Pro Tip:** Standard *ASCII* file type will save each spectrum to an individual file in column format. Changing File Format to *Time Series* or *Append Series* will place all spectra in a single compiled file in row format.



Select the gear icon to configure data save parameters.

Configure your file format, location, and naming convention on the left.

Configure the frequency and intervals of data logging on the right.

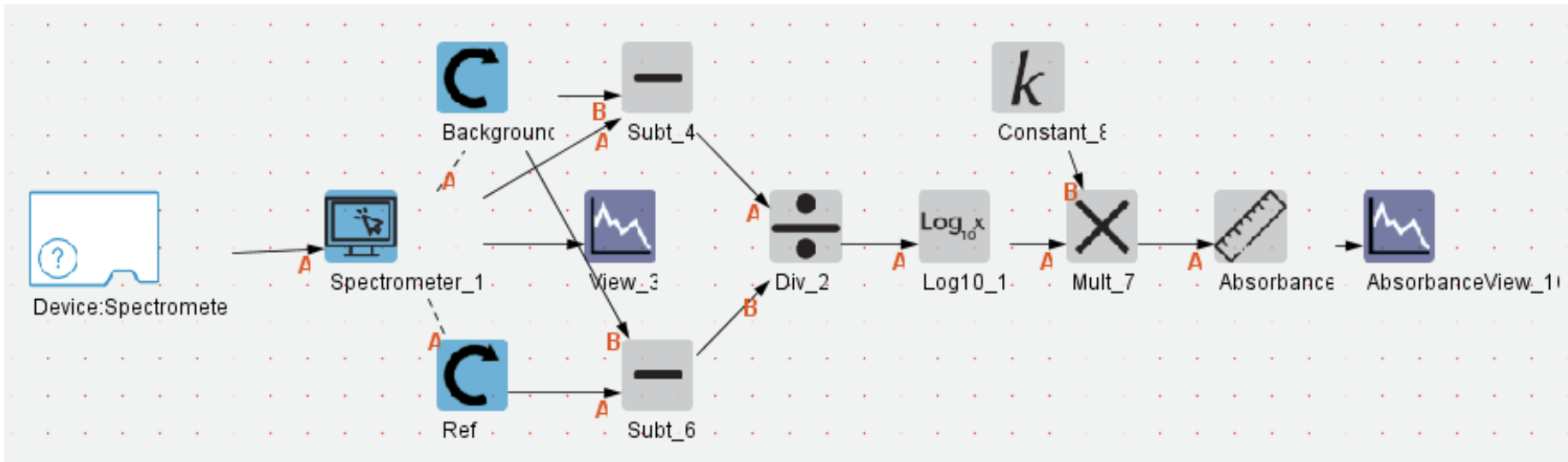


Don't forget to press 'Apply' before exiting!

# Schematic

OceanView's Schematic interface is a powerful feature that allows highly-customizable spectral math and numerical methods to be implemented. Wizards are useful tools to build the core foundation of a schematic, which can then be modified by the user however may be needed.

The below schematic is generated by the Absorbance Wizard.  $Absorbance = \log \left( \frac{I_0 - I_{Dark}}{I - I_{Dark}} \right)$



Can you track how the above equation is represented in the schematic nodes to the left?



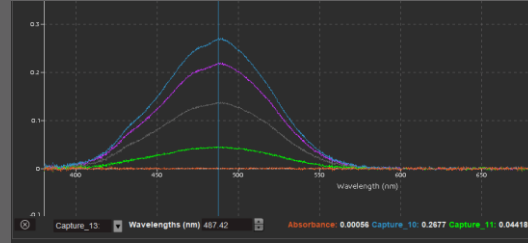
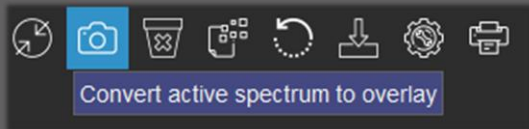


# 1 Assemble System and Complete Absorbance Wizard

from prior steps

use water as reference fluid

# 3 Click Camera icon to freeze overlay



for each 100mL sample

# 2 Make Protein Dilutions

With the provided protein powder,  
dissolve 1-gram in 100mL of water (10g/L)

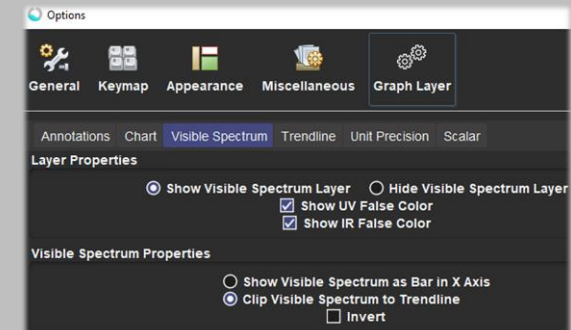
Take 25mL and q.s. to 100mL (2.5g/L); repeat for 0.625g/L

# 4 Click on the peak location.

Note the values for each trend  
below the plot.

# 5 In Excel or similar program, use the values to plot concentration vs. absorbance to generate a calibration regression.

Pro-Tip: To see the full ROYGBV spectrum in the graph, right-click in the graph and go to Graph Layer Options. Go to Visible Spectrum and select Show Visible Spectrum Layer and Clip to Trendline.



# Experiment





EASY INTEGRATION INTO PIPE OR  
REACTOR COMPRESSION FITTINGS

Cryo-Quip Solution:



[oceanoptics.com](https://www.oceanoptics.com)