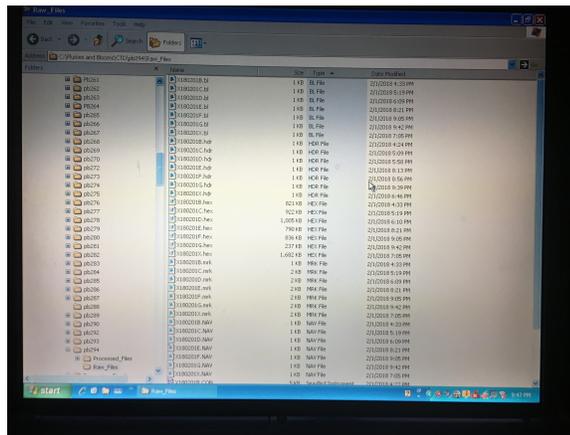


# Earth Research Institute CTD Data Processing Protocol

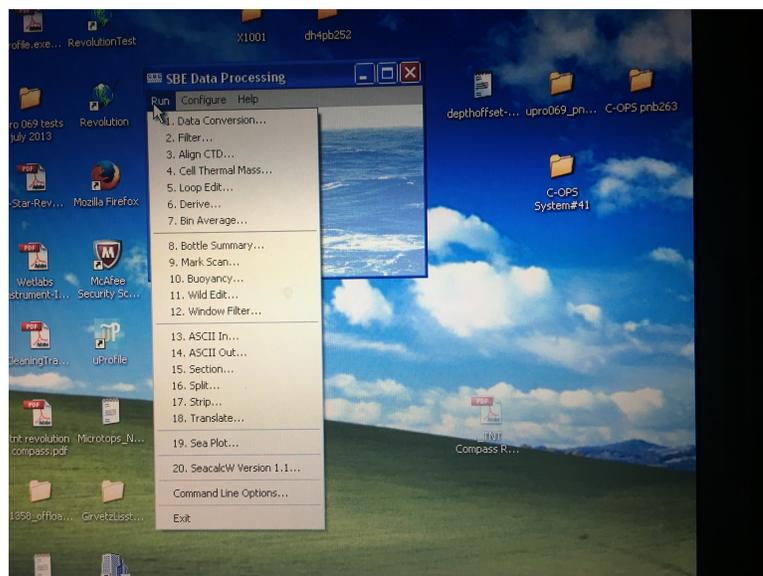
Stuart Halewood – ([halewood@eri.ucsb.edu](mailto:halewood@eri.ucsb.edu))

## Data import and management:

1. Make sure you are using a Windows operating system and that you have the required software loaded, in this case we use Seabird Datproc.exe
2. Ensure that you have all of your CTD profiles in one folder. Check that you have files for each cast or station and that they are in .hex format.



3. Disregard any deck tests and copy all your actual profiles into a folder with the cruise name and Raw\_files. This will be where we will be importing our .hex files from.
4. Within the Seabird Data Processing software there are various separate processing modules that will each apply a variety of calculations and variables. The product is then output in a form of your choosing to be further interpreted by the next module. The modules all have the extension .psa  
In the below image you will see the list of all available modules (.psa) listed under the **RUN** tab.

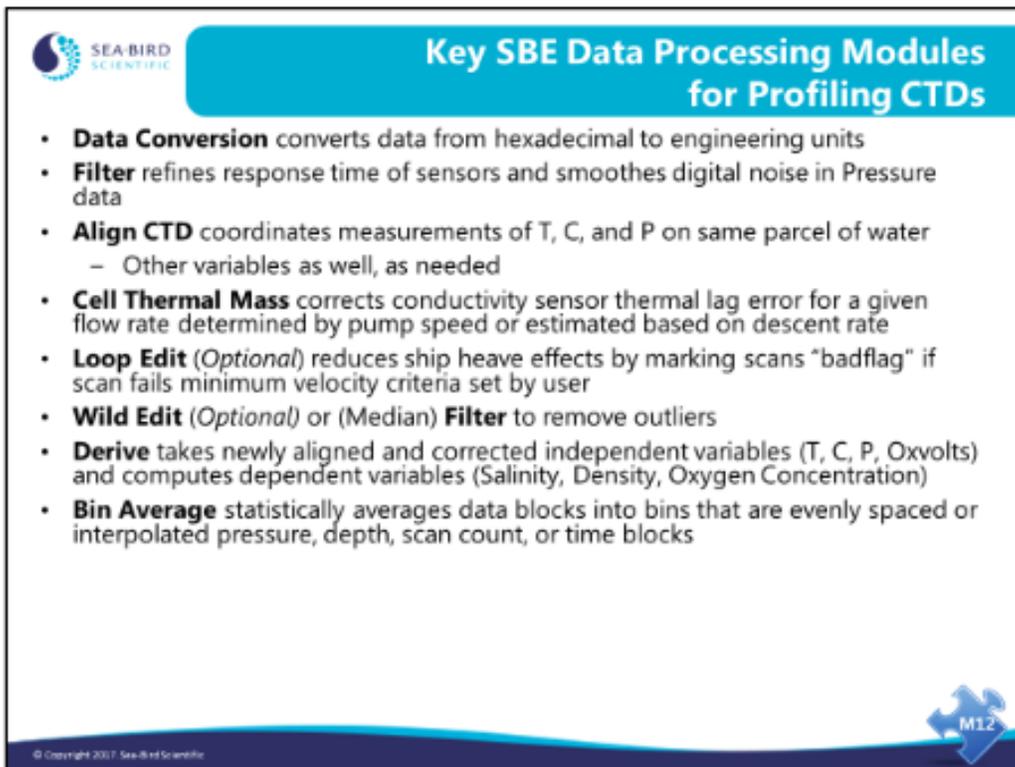


The Seabird Training manual lists a .PSA As:

A .psa (program setup) file is used by Seasave V7 and by each module in SBE Data Processing to remember the way the program was set up. You can save the .psa file to a desired filename and location, and then use it when you run the software the next time, to ensure the same setup

A .psa file is created by Seasave V7 to store program settings, such as instrument configuration(.conor .xmlcon)file name and path, serial ports, water sampler, TCP/IP ports, serial data output, etc. as well as size, placement, and setup for each display window.

A .psa file is created by each module in SBE Data Processing to store program settings, such as input filename and path, output filename, and module specific parameters (for example, for Data Conversion: variables to convert, ascii or binary output, etc.).



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## Key SBE Data Processing Modules for Profiling CTDs

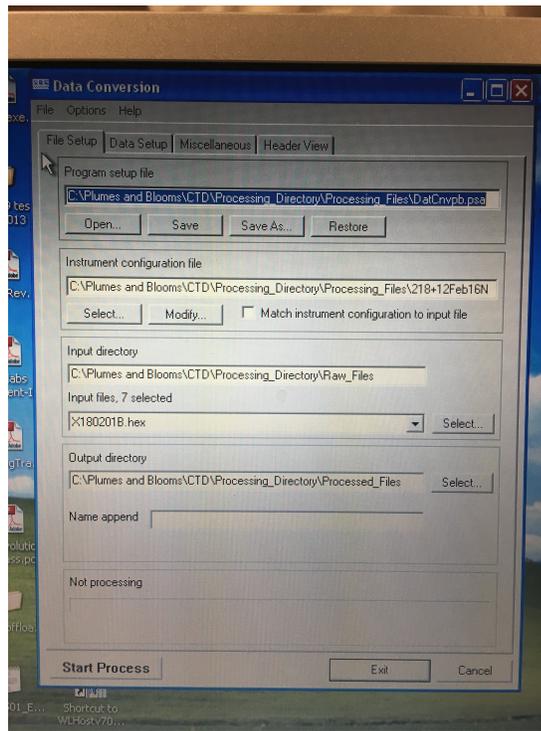
- **Data Conversion** converts data from hexadecimal to engineering units
- **Filter** refines response time of sensors and smoothes digital noise in Pressure data
- **Align CTD** coordinates measurements of T, C, and P on same parcel of water
  - Other variables as well, as needed
- **Cell Thermal Mass** corrects conductivity sensor thermal lag error for a given flow rate determined by pump speed or estimated based on descent rate
- **Loop Edit** (*Optional*) reduces ship heave effects by marking scans "badflag" if scan fails minimum velocity criteria set by user
- **Wild Edit** (*Optional*) or (Median) **Filter** to remove outliers
- **Derive** takes newly aligned and corrected independent variables (T, C, P, Oxvolts) and computes dependent variables (Salinity, Density, Oxygen Concentration)
- **Bin Average** statistically averages data blocks into bins that are evenly spaced or interpolated pressure, depth, scan count, or time blocks

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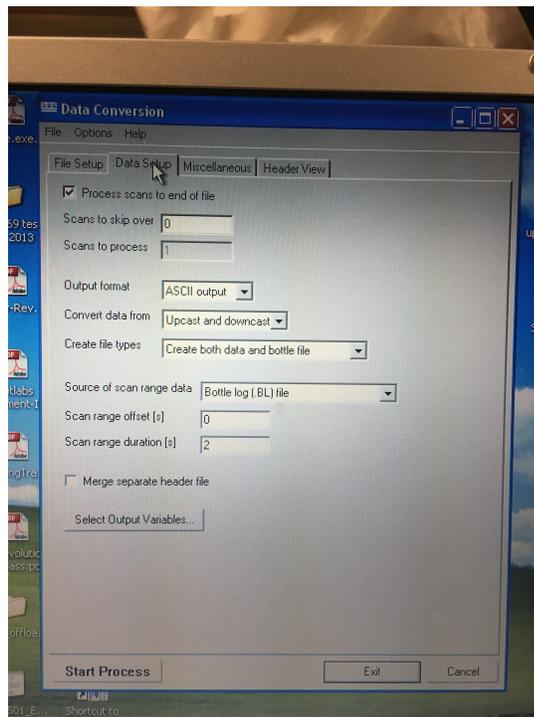
M12

5. Starting with the first module of the list we select Data conversion (**DatCnv.psa**). This module convert the raw data into scientific units. Our particular module is called **DatCnvPB.psa** this has been named and saved after we have opened the module and set it up in our required way for PB (Plumes and Blooms). All of our .PSA files are stored in one Processing\_Files directory under the main Plumes and Blooms directory.

**NOTE- Please make an archived copy of all your Raw data as you cannot reverse the process once you have converted the data in a .PSA module**

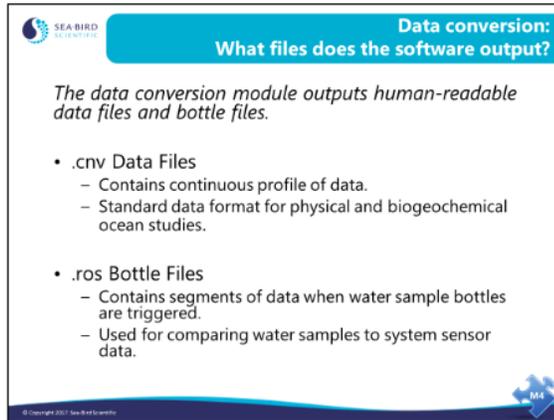


6. Under the File Setup tab check that the Instrument file matches the one for your specific CTD .con (or xml.con) file. That is the file that contains all the calibration coefficients and configuration of all sensors on your CTD rosette package.
7. Make sure that the input folder is the one with your correct raw data .hex files and that the output folder is the specified one that you want your final data to be stored in.
8. Clicking on the Data Setup tab allows us to enter the number of scans to skip, the data output format (ASCII) whether to process the downcast and upcast etc. The Plumes and Blooms setup can be seen below.



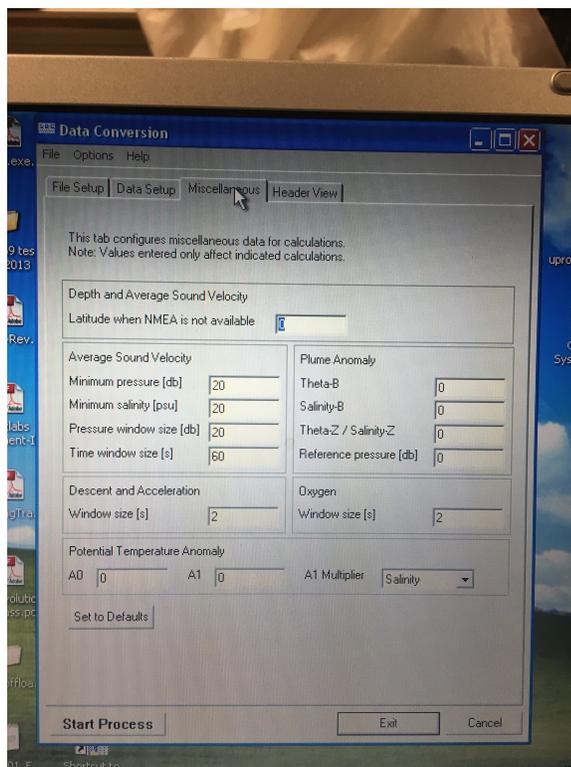
9. Within the Data Setup tab you can then select the 'Specific Output Variables' button. From the Seabird manual:

The output variables dialog allows you to select a table of items that will be calculated and the order in which they will be calculated. Note that the list on the right reflects the information in the selected configuration(.con or .xmlcon)file only data measured by the sensors indicated in the configuration file, and data that can be calculated from those measurements, are available for output. Data that can be calculated from the measurements are included in Data Conversion to allow you to get a quick look at the derived variables.

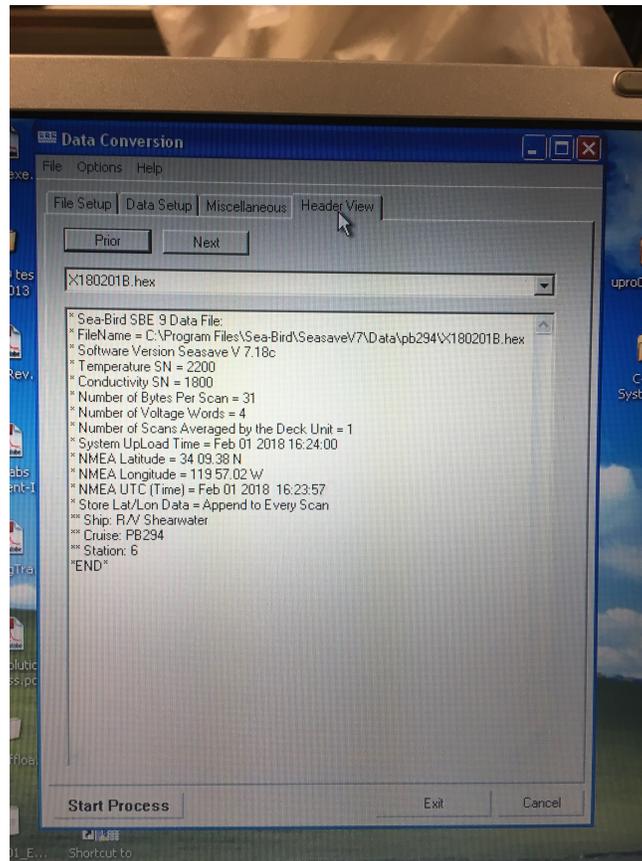


The data conversion process also writes a file with data collected while water bottles were being closed. You choose the time window of data you want written to the file. For example, you might select to have all scans collected starting 5 seconds before the bottle closes and ending 5 seconds after the bottle closure written to the file. The .ros file contains the selected output variables as well as the scan number and associated bottle number for the output scans. Like the .cnv file, the .ros file also contains an error flag column.

10. The next Tab is the Miscellaneous tab that defines additional parameters required for output of specific variables, such as depth, average sound velocity, and oxygen. Entries on this tab are used only if you are calculating and outputting the associated variables to the .cnv file. Below is our PNB setup.



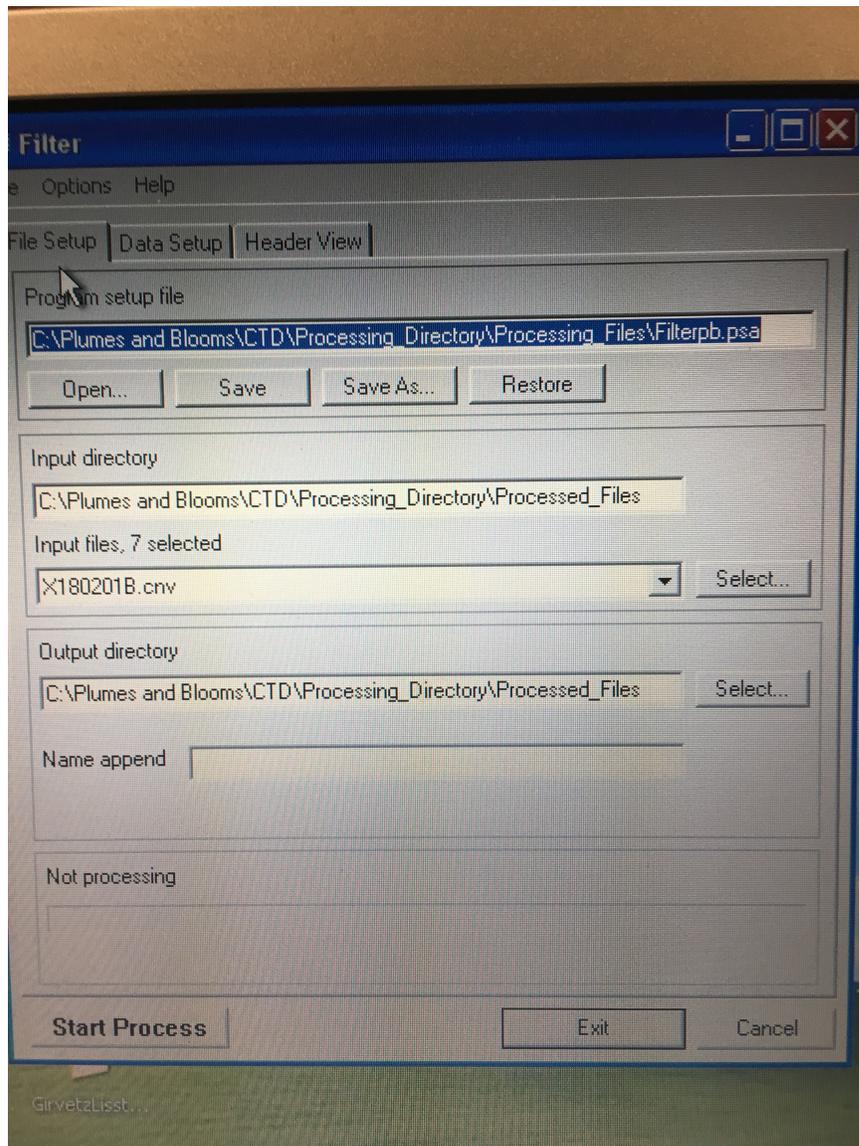
11. The last Tab is the 'Header View' which provides a record of the Configuration you are using and which modules you have used sequentially. The Header is updated each time you manipulate the data with a .PSA. The header view can reassure you that you are working with the instrumentation you think you are.
12. It is wise to keep checking the header when you see it on the relevant .PSA modules so you do not miss a processing step. Below is the beginning header from the PNB data processing.



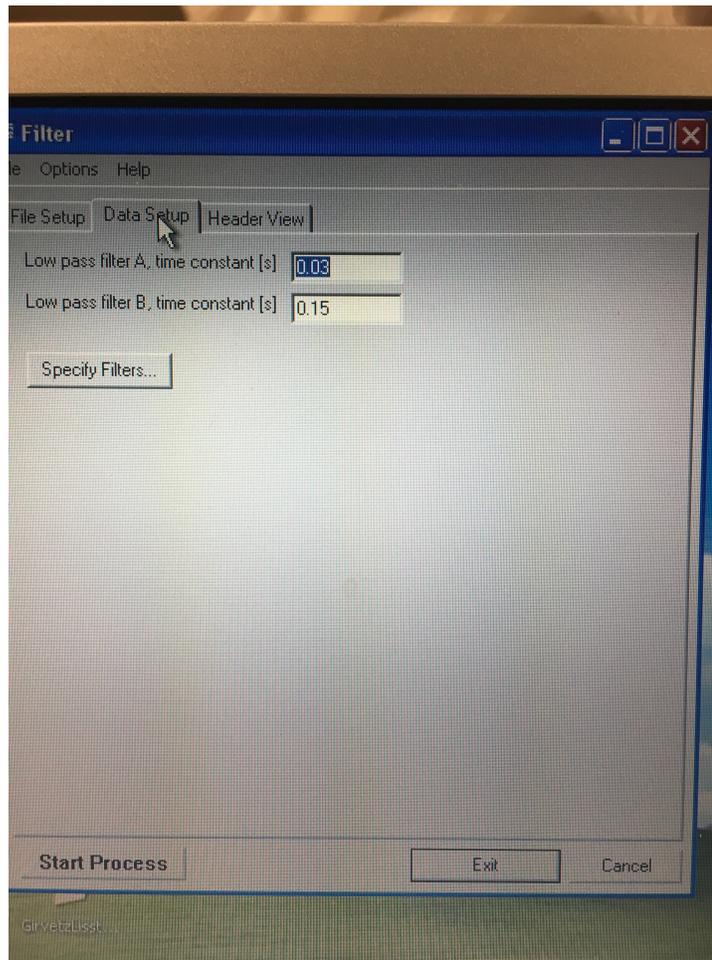
### 13. Filtering Data:

It is very desirable to match the time constants of the temperature and conductivity sensors. This improves salinity data in conditions of sharp gradients. The conductivity sensor has a time constant that depends on pumping rate; it can range from 10 millisecond at a fast pumping rate to very large if no water is moving through the cell.

Below is an image of the Plumes and Blooms FilterPB.PSA setup



The input files are selected as normal and then the 'Data Setup' tab is selected:



The time constants are entered to bring the temperature and conductivity values in line with each other.

Filtering is done for two reasons:

- To match the time constants of the temperature and conductivity sensors.
- To smooth the pressure signal to minimize digitization noise in preparation for removing loops in the data with Loop Edit. When smoothing pressure, use a filter that is approximately four times the sample rate:

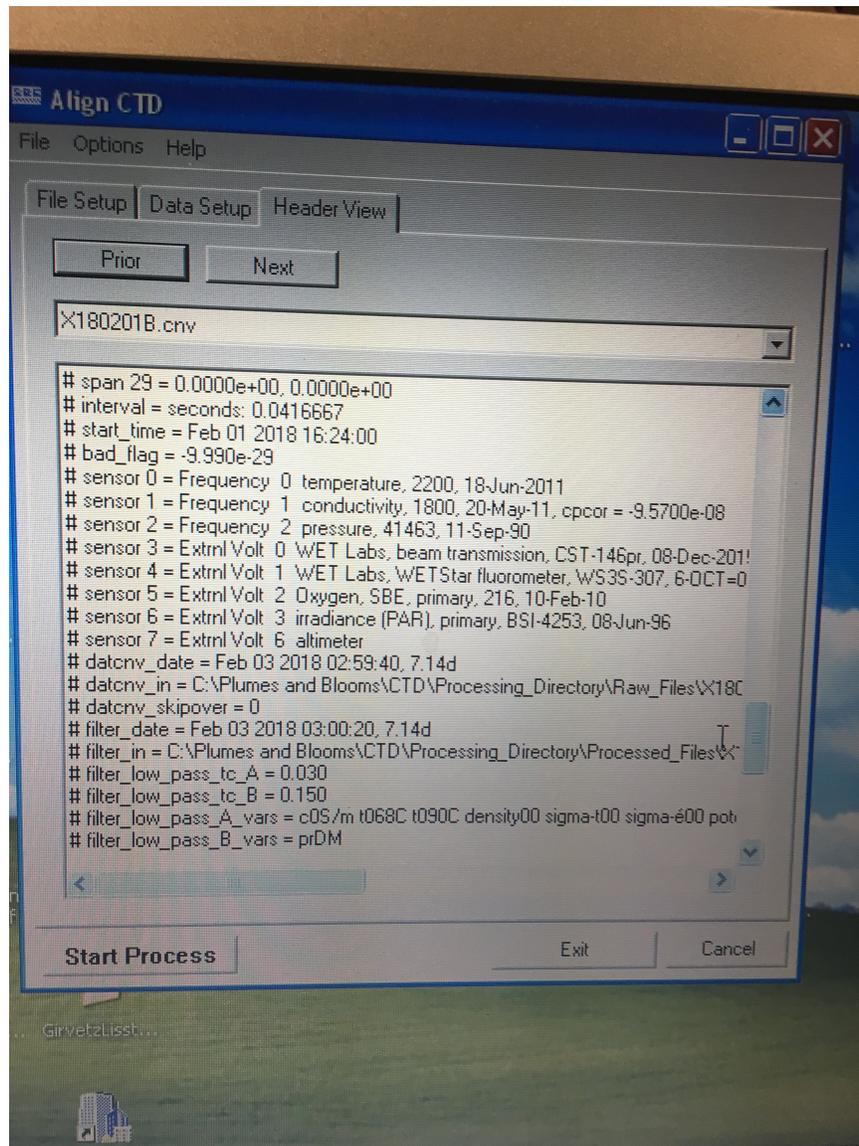
-SBE 9 Plus samples at 24 Hz (0.04167 sec),  $4 \times 0.04167 = 0.15$  sec

-SBE 25Plus samples at 16 Hz (0.0625 sec),  $4 \times 0.0625 = 0.25$  sec

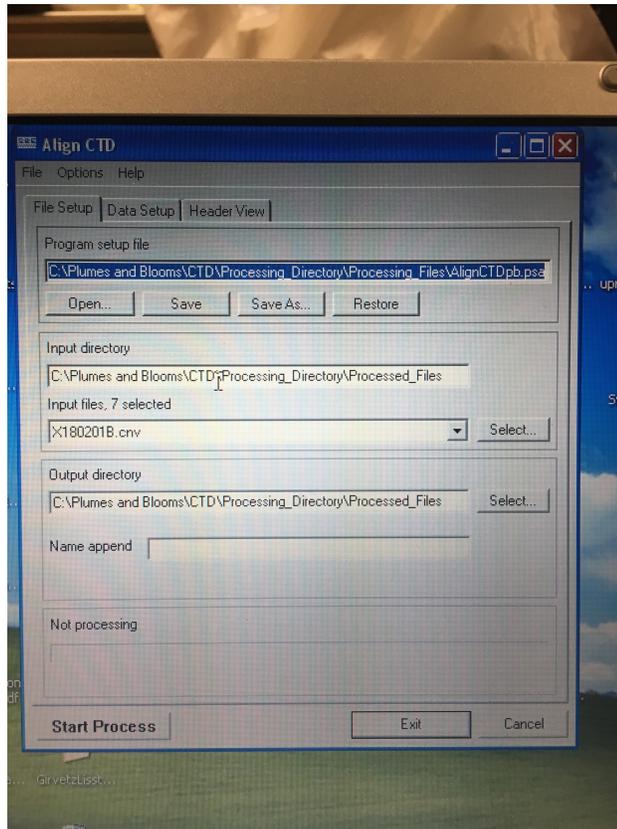
-SBE 25 samples at 8 Hz (0.125 sec),  $4 \times 0.125 = 0.5$  sec

-SBE 19Plus or 19plus V2 samples at 4 Hz (0.25 sec),  $4 \times 0.25 = 1$  sec

14. At this time its good to check the 'Header' tab and confirm what the last 'Filter' PSA has applied:



15. The next module we use is the 'Align' PSA. Again in our case this is the AlignCTDPB.psa:

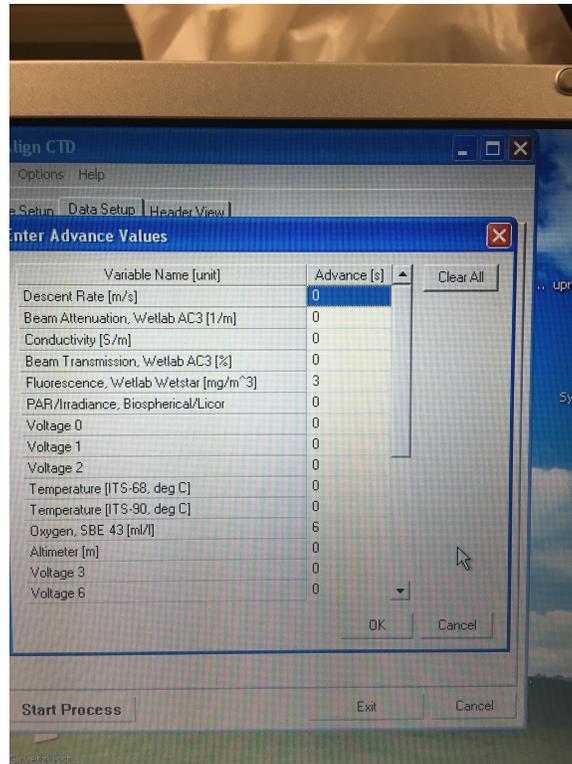


Because the 911plussystem is well characterized, an alignment of the data stream is done automatically in the 11plus before data is transmitted to your computer. With the TC duct in place, an alignment of 1.75 data scans (or 0.073 seconds) is done on incoming data. A linear interpolation between scans is done to implement the alignment of a non-integer number of scans.

Misalignment that differs from the nominal values can arise from plumbing changes, which can influence pumping speed. A slower pumping speed increases a water parcel's residence time in the TC plumbing, and will require a larger shift in data scans. A faster pumping speed will decrease the residence time in the TC plumbing and require a smaller alignment value.

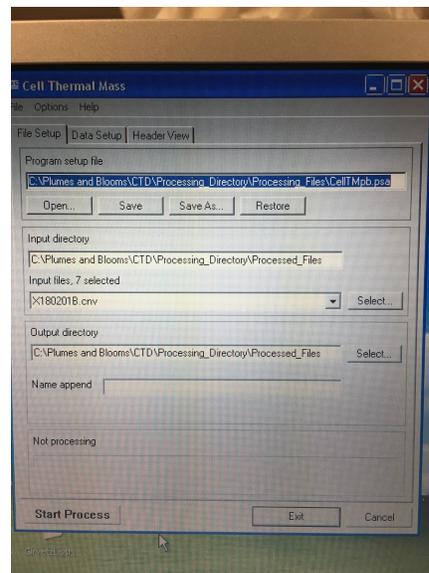
Note that the advance values are given in seconds and are relative to the pressure channel.

Entering the 'Data Setup' tab allows you to input advanced delays in seconds for all other parameters:



After applying your values check that you are up to date in the 'Header' tab and move on to the 'Cell Thermal Mass' module.

16. For our Plumes and blooms project we have the below 'CellTMpb.psa'



### Conductivity Cell Thermal Mass

The conductivity measurement has temperature dependence. The conductivity cell itself is constructed of glass and plastic, and as such has a thermal mass. When the cell goes from warm water into cold, the water that passes through the cell is slightly warmed as it transits the cell, resulting in a conductivity measurement that is high of correct. Conversely, when the cell comes

up from cold water into warmer water, the water that passes through the cell is cooled slightly, resulting in a conductivity measurement that is low of correct. This heat transfer can be modeled and corrected.

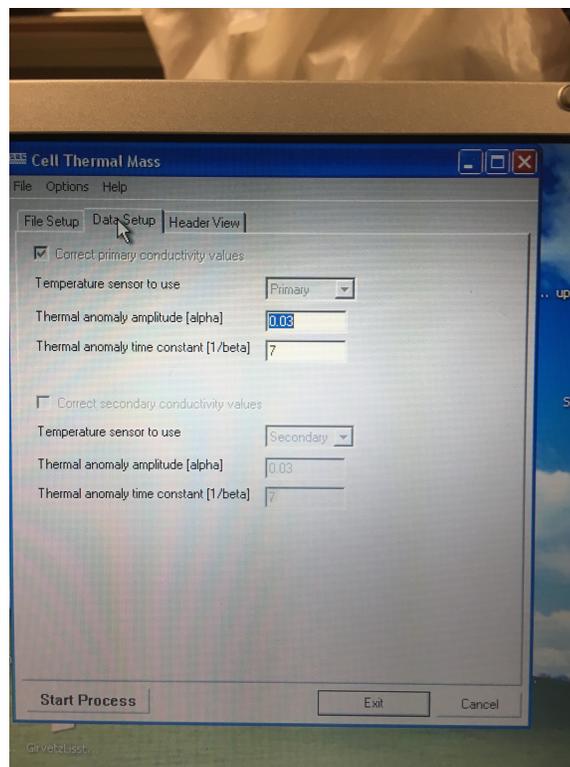


**Effect of Conductivity  
Cell Thermal Mass**

- Glass conductivity cell stores heat
- A warm cell warms water moving through it
  - Will read warm of correct (High)
- A cold cell cools water moving through it
  - Will read cold of correct (Low)
- Water in cell is a different temperature than the thermometer measured a moment earlier
- When salinity is computed, it will be in error

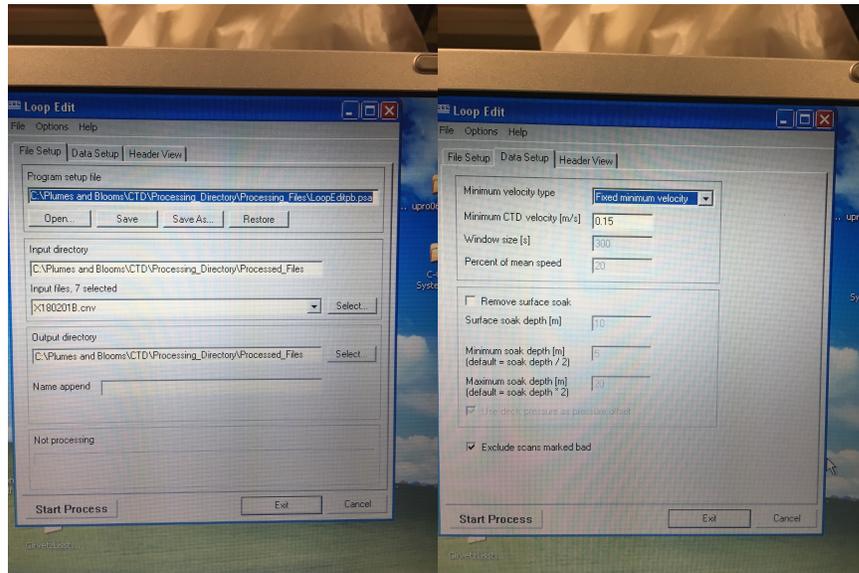
  
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below are the corrections entered for our plumes and Blooms module



17. The next 'Loop Edit' module marks data collected when the CTD package loops through the water or decelerates sharply. Minimum Velocity can be specified as well as the surface soaking being removed here.

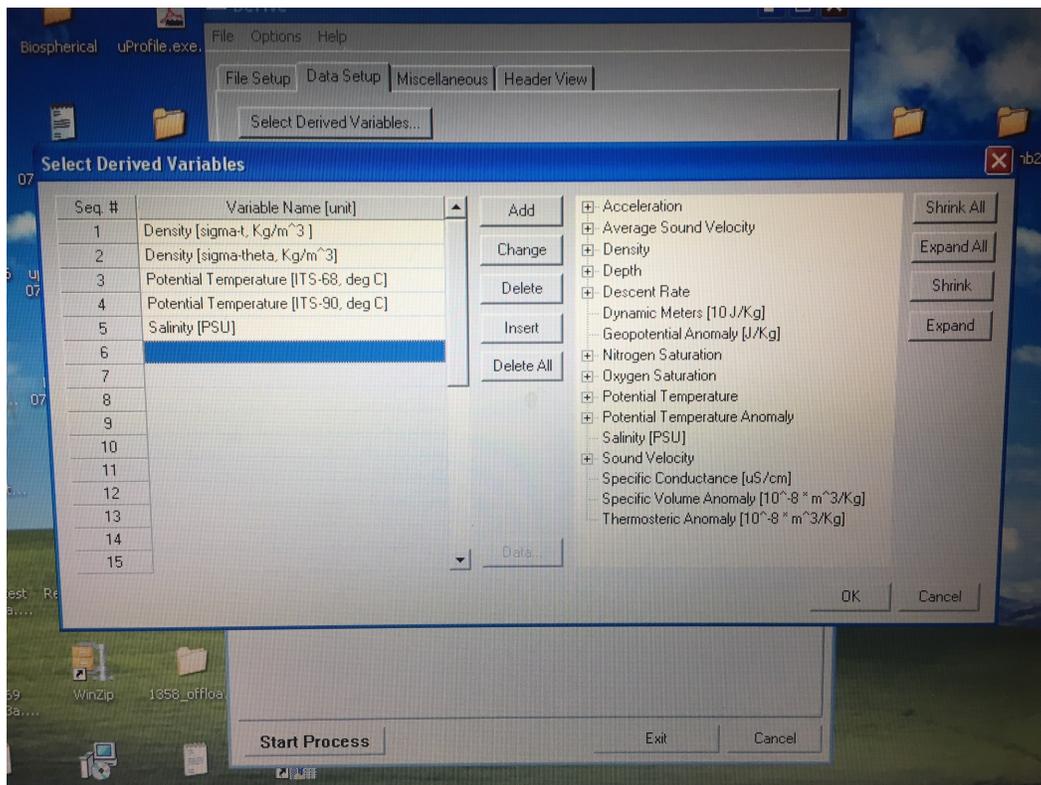
Plumes and Blooms images are shown below for 'LoopEditPB.psa'



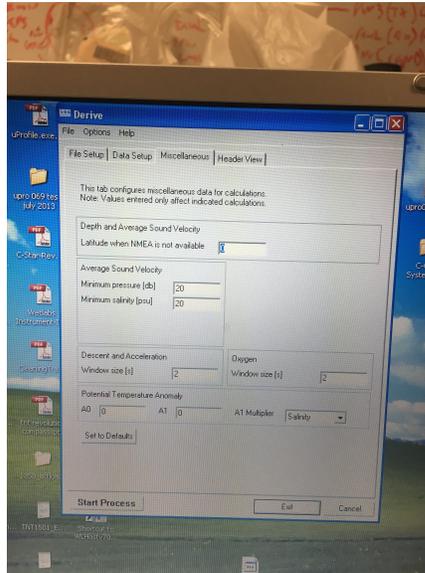
Again now is a good time to check the 'Header' tab to see if you have missed any steps

18. Moving on to the 'Derive.psa' Allows us to take the newly aligned and corrected independent variables i.e. T,C,P, OxVolts and computes the dependent variables (Salinity, Density, Oxygen concentration etc.)

Our screenshots for the Plumes and Blooms Derivepb.psa are below:  
Click on the 'Data Setup' then Selecting the derived variables:



Then select the Miscellaneous tab:



19. Moving on now to the 'Bin Average' module:

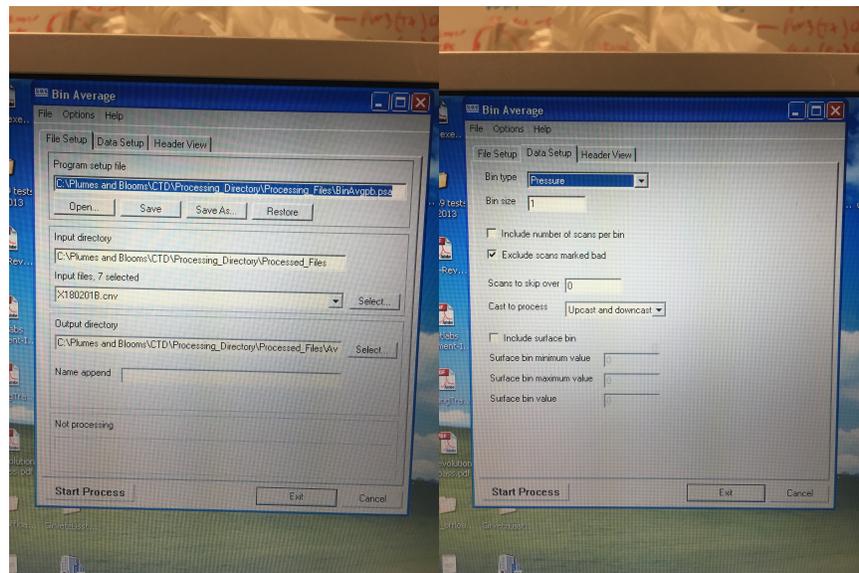
 **Bin Averaging**

- Reduces size of a data set by statistically estimating data values at even intervals (e.g., every meter or 10 meters)
- Can work in depth (meters), pressure (decibars), time, or by scan
- Can bin average upcast, downcast, or both
  - If bin averaging upcast and downcast, keeps upcast bins and downcast bins separate
- Surface bin is treated separately

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Bin averaging is a means of reducing your data set to a more tractable, and perhaps a more meaningful, size. The Bin Average module makes a statistical estimate of data values at a user-prescribed interval based on the surrounding data. You can bin data on the even meter or 10 meters. You can bin data with a bin size that represents the resolution of your instrument. For time series measurements, you can bin on time interval.

For our Plumes and Blooms project (BinAvgpb.psa) purposes our settings are as below

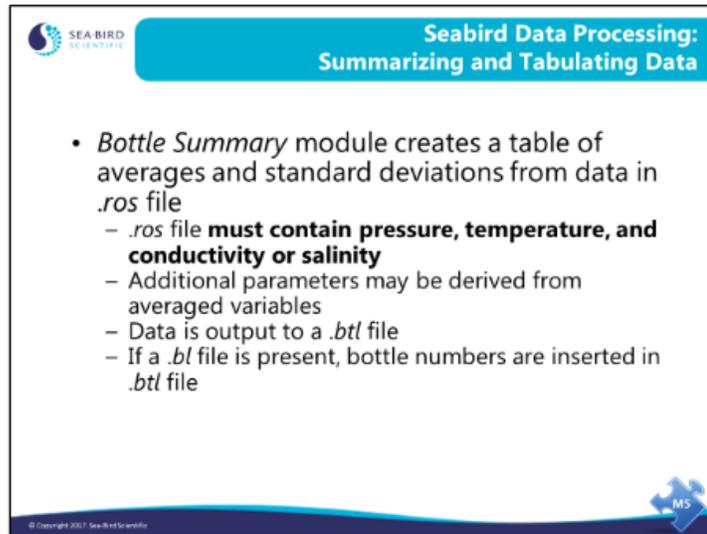


Ensure that in the output directory you have an Average folder for these average values.

### Data Setup

The Data Setup tab allows your choice of pressure, depth, time, or scan bins. You can include the number of scans per bin in the output file, which is useful for evaluating data from instruments with a low sample rate. Bins with 1 sample in them are not very accurate statistically. You can skip data that you acquired while checking out your instrument before the cast started. Similar to previous processing, you can process the upcast, downcast, or both. Earlier in this module, we discussed techniques for removing suspect data. These data are marked in the data set as bad scans. When setting up Bin Averaging, you may exclude scans marked bad by previous processing steps. As mentioned earlier, the surface bin is handled separately. Note that in our example the surface bin is not included, because we are binning on a 1-meter interval. If you bin on a small interval, it is very difficult to calculate a surface bin. For example, with 1-meter bins, a surface bin would run from 0 to 0.5 meters with value 0.25 meters; depending on the profiling and sampling speeds, there would be few samples within that depth. The surface bin is useful for a coarser bin size. For example, with 10-meter bins, the first bin starts at 5 meters and runs to 15 meters. You can succeed in calculating a surface bin that runs from 0 to 5 meters with value 2.5 meters.

20. We now move onto the Bottle Summary module which was created back when we first did the Dat Cnv.psa. The BottleSum.psa is as follows:



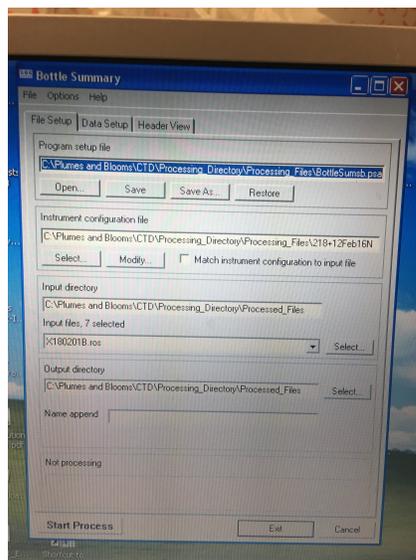
The slide features the Seabird Scientific logo in the top left corner. The title bar at the top reads "Seabird Data Processing: Summarizing and Tabulating Data". The main content is a bulleted list describing the Bottle Summary module. In the bottom right corner, there is a small blue icon with the number "15" and a copyright notice "© Copyright 2017 Seabird Scientific" in the bottom left corner.

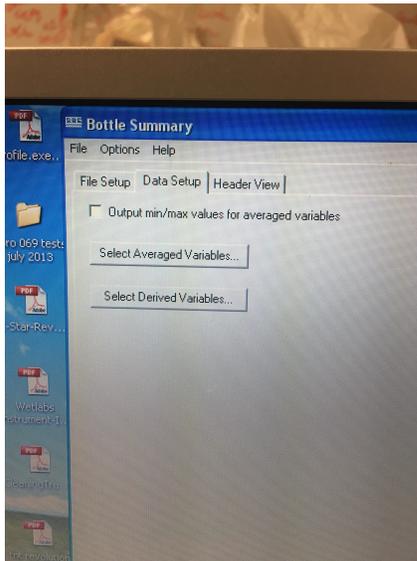
- *Bottle Summary* module creates a table of averages and standard deviations from data in .ros file
  - .ros file **must contain pressure, temperature, and conductivity or salinity**
  - Additional parameters may be derived from averaged variables
  - Data is output to a .btl file
  - If a .btl file is present, bottle numbers are inserted in .btl file

### Bottle Summary: Summarizing Water Sample Data

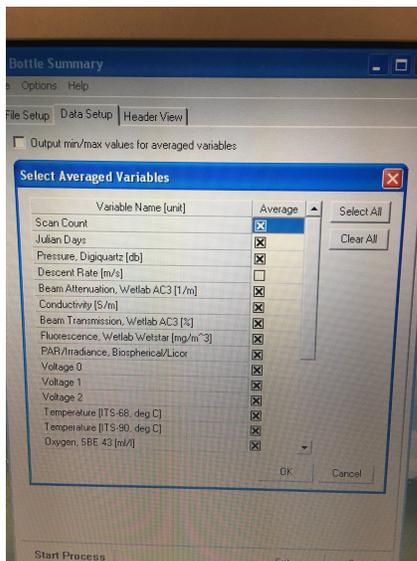
The .ros file created by Data Conversion contains a set of data scans for each water sample taken. The Bottle Summary module takes the process one step further by averaging the scans for each water sample into a single line of data that contains averages and standard deviations for each of the parameters in the .ros file. In addition, you may add derived parameters to this list. The derived parameters are calculated from the averages of the data contained in the .ros file.

The Plumes and Blooms (BottleSumb.psa) series of setup images are given here:





Note that extra derived variables selected under the 'Data Setup' tab and output in the .Ros file.



21. For our final set of modules we move to the ASCII Out module. We run this module twice.

Once for values including the header data (ASCII\_Outsub.psa) and once for the data without the header values (ASCII\_Outsuball.psa)

Note that both modules we are inputting the data from the Average folder.



This should be the final step in the CTD data processing and now the data can be passed onto Matlab or other processes.

Seabird states:

ASCII Out Transforms a Sea-Bird formatted file and produces a single column file or data in text format. These can now therefore be used in Excel and other non-Sea-Bird programs.