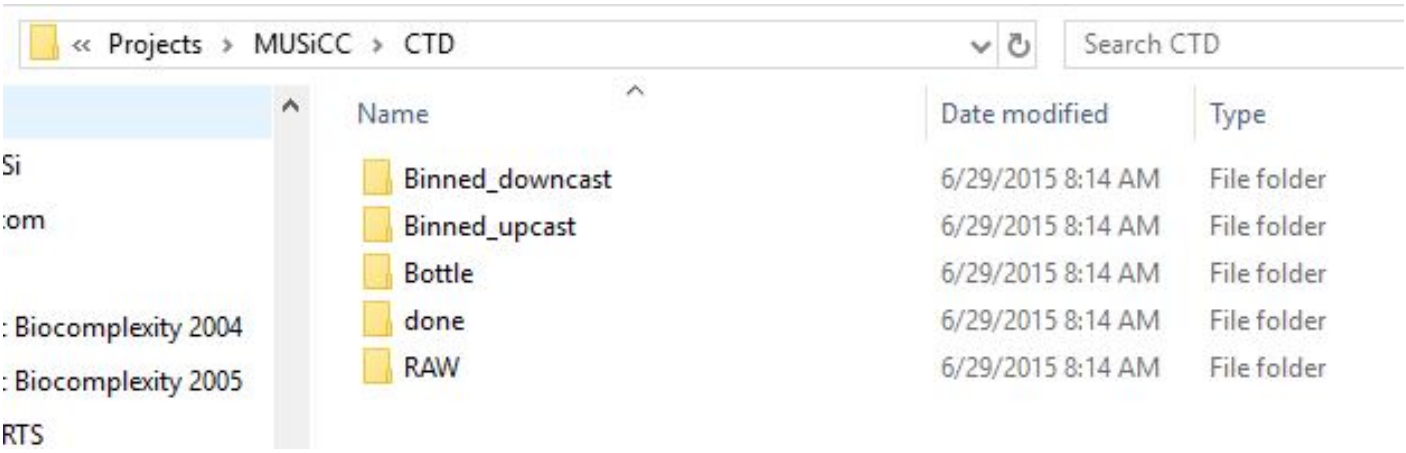
SBEDataProc

Scripts to be run

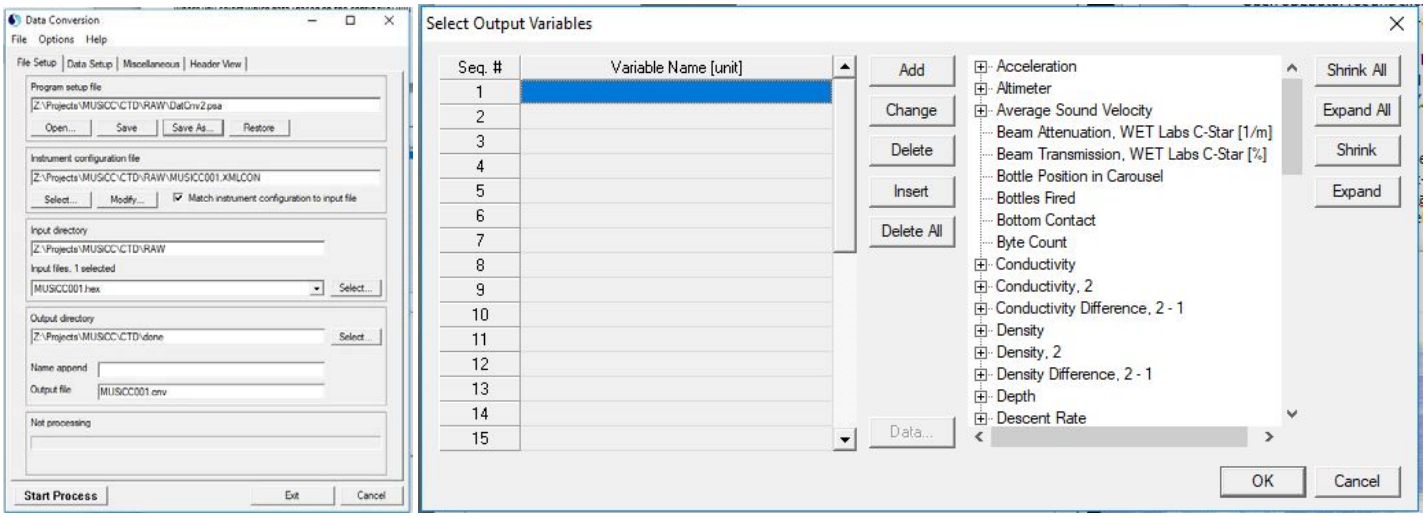
Data Conversion – converts raw hex file to ascii with header
Bottle Summary – creates bottle files
Loop Edit – removes data loops due to ship motion
Wild Edit- removes wild outliers
Bin Average – averages data into depth or pressure bins
Split – separates upcast and downcast into 2 files

Each script has a *.PSA file – this file refers back to the configuration file in order to set up the parameters, input file, output file, filenames and file locations. The first time you run each script, SeaBird creates a default setup file for that script and puts it in your local directory (based on your windows login). Once you set up the script with your parameters, names and locations, you need to SAVE THAT PSA TO YOUR WORKING DIRECTORY. Your working directory will be the place you put all your raw files --- *.hex, *.hdr, *.bl, *.con (or *.xmlcon). All other processed files will go into a different directory. Below is how I typically set up the directory structure using the project name as the top directory.



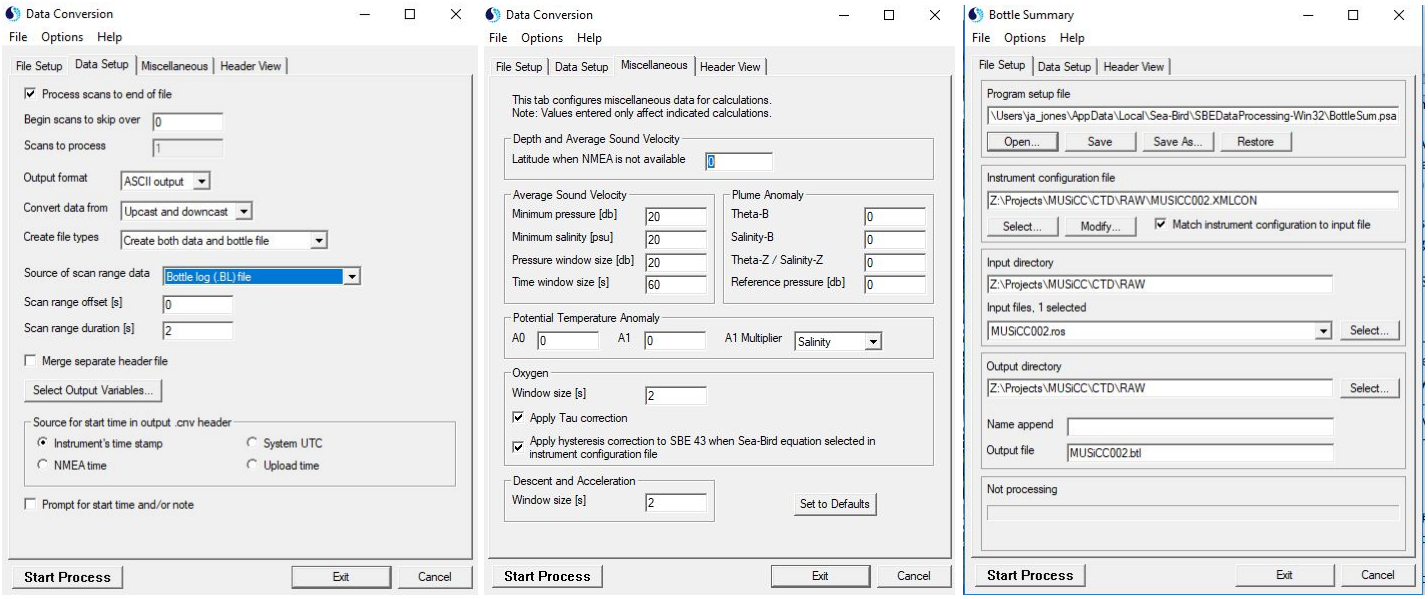
DATCNV.PSA

Open SBEDataProc and click on Run. Select Data Conversion from the dropdown list. The system will generate a new PSA file for you (click okay) and open a new window.
FILE SETUP TAB
Under INSTRUMENT CONFIGURATION FILE, select the configuration from your raw working directory – checkmark the MATCH INSTRUMENT CONFIGURATION TO INPUT FILE box. Under INPUT DIRECTORY, select your raw working directory, under OUTPUT DIRECTORY, select your done directory. Under OUTPUT FILE be sure you have your filename with CNV extension. For DATCNV, do not append anything – the *.cnv file that is generated here you know is from DATCNV.
DATA SETUP TAB
Here is where you setup the parameters to process – this is based on your config file so if the configuration is incorrect, you will not see the correct options. This is also where you put the SCANS TO SKIP OVER value.
OUTPUT FORMAT – select ascii
CONVERT DATA FROM – select upcast and downcast (unless you only want the downcast data, whatever works for you is fine!)
CREATE FILE TYPES – select BOTH DATA AND BOTTLE files or you won't get the data associated with your bottle trip
SOURCE OF SCAN RANGE DATA – when you setup the config/rosette you have to make sure you tell the system to log the bottle trips and you'll get a *.BL file associated with each *.hex file. This file is used to generate the *.BTL file which is the ascii form of the bottle data.
SELECT OUTPUT VARIABLES – this will look familiar (based on what you said when we looked at it in the ET area), this is where you select which data (based on the config file) will be processed and output to the ascii file. Once you click on Select Output Variables a window will open



From here you will choose your parameters from the right and put them in the order you want on the left. The order I generally use is as follows:
depSM: Depth [salt water, m]
prDM: Pressure, Digiquartz [db]
t090C: Temperature [ITS-90, deg C]
t190C: Temperature, 2 [ITS-90, deg C]
c0S/m: Conductivity [S/m]
c1S/m: Conductivity, 2 [S/m]
sal00: Salinity, Practical [PSU]
sal11: Salinity, Practical, 2 [PSU]
sigma-é00: Density [sigma-theta, kg/m^3]
sigma-é11: Density, 2 [sigma-theta, kg/m^3]
flECO-AFL: Fluorescence, WET Labs ECO-AFL/FL [mg/m^3]
CStarTr0: Beam Transmission, WET Labs C-Star [%]
CStarAt0: Beam Attenuation, WET Labs C-Star [1/m]
sbeox0Mm/Kg: Oxygen, SBE 43 [umol/kg]
par: PAR/Irradiance, Biospherical/Licor

Some of those won't be needed but pick whatever works for you! Once you have this part set up, the rest of the scripts are easy ☺



Since you won't have access to the NMEA string, you can use the instrument time stamp (as above). I've never used the PROMPT FOR START TIME AND/OR NOTE here, this just makes one more step when you do the processing. If you think you need to add something during processing you can use this option.

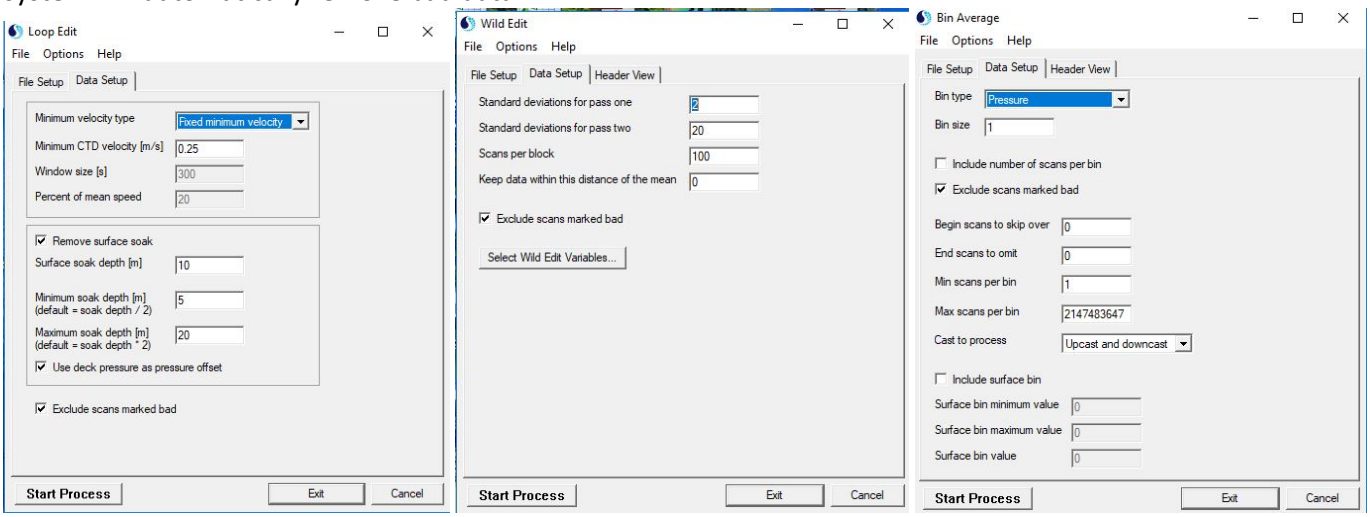
MISCELLANEOUS TAB
Be sure to add the latitude here as you don't have a NMEA string. The rest are calculated fields and you can do what you need to do with them – I've never needed them for our data.

HEADER VIEW – this just shows you the header and lists the parameters you've selected. It's easy to look here quickly to see if you're missing anything.

Save the DATCNV.PSA file to your working directory.

BOTTLESUM.PSA
BOTTLE SUMMARY – select #9 from the dropdown menu. Set up this file the same as the datcnv file. You do not need a name append here either, this script will generate a *.btl file and save it to the directory you choose (bottle).
DATA SETUP TAB – you can select the min/max if you want, I never use it. Select the variables you want output – I usually just click SELECT ALL. You can select derived variables here the same way you selected variables in DATCNV. I generally don't derive any variables here unless someone specifically asks for something.
HEADER VIEW TAB – again, easy way to see what you've picked without running the script.

LOOPEDIT.PSA
LOOP EDIT – select #5 from the dropdown menu. Set up the input/output parameters using your DONE directory. This is where you'll add the first NAME APPEND. I use L – this will save the file as filenameL.cnv so you know it's been run through loopedit.
DATA SETUP TAB – this is where you can remove your SOAK. Be sure to check EXCLUDE SCANS MARKED BAD so the system will automatically remove bad data.



WILDEDIT.PSA
WILD EDIT – select #12 from the dropdown menu. Set up the input/output parameters using your DONE directory. REMEMBER – the input file here is filenameL.cnv and you need a new letter to append – I use W so the output file will now be filenameLW.cnv.
DATA SETUP TAB – here you can set your stats for determining a wild value. The system values are fine, also check EXCLUDE SCANS MARKED BAD. I usually select all variables for wild edit.

BINAVG.PSA
BIN AVERAGE – select #8 from the dropdown menu. Set up the input/output parameters using your DONE directory. Here the input file will be filenameLW.cnv and you can append B for output filenameLWB.cnv.

DATA SETUP TAB – select pressure or depth bins and the size of the bin. Also select EXCLUDE SCANS MARKED BAD. The default values of min scan=1 and max scans=some enormous number are fine. Since you're not starting data collection at the surface, you won't need to include the surface bin.

SPLIT.PSA

SPLIT – select #17 from the dropdown menu. Set up the input/output parameters using your DONE directory. Here your input file will be filenameLWB.cnv and you do not need to append anything as split separates the files into ufilenameLWB.cnv and dfilenameLWB.cnv – you can move those into up and down directories easily later.

Now that all the PSA scripts are set up with your directory structure, go back and run them in the above order and check your output files to be sure you have what you want. Check the header structure to make sure the data is all there. Watch for funky errors where loopedit or wildedit suddenly starts removing bins – if this happens, uncheck EXCLUDE SCANS MARKED BAD, rerun the scripts and look for individual bad values – these are indicative of a bad termination. You can remove the values individually if needed but the system removes the entire scan if 1 variable is bad. I've had that happen, the termination would periodically short during comms and some values would be bad. You need to check this before the BIN AVERAGE script otherwise those funky values get averaged into your depth/pressure bin!

I'm sorry I didn't get a chance to go over this with you, I hope this all makes sense! Please check it on your test run and we can tweak it via email.

Good luck!!!
Janice