Processing hydroacoustic data with ESP3 and ShinyApp

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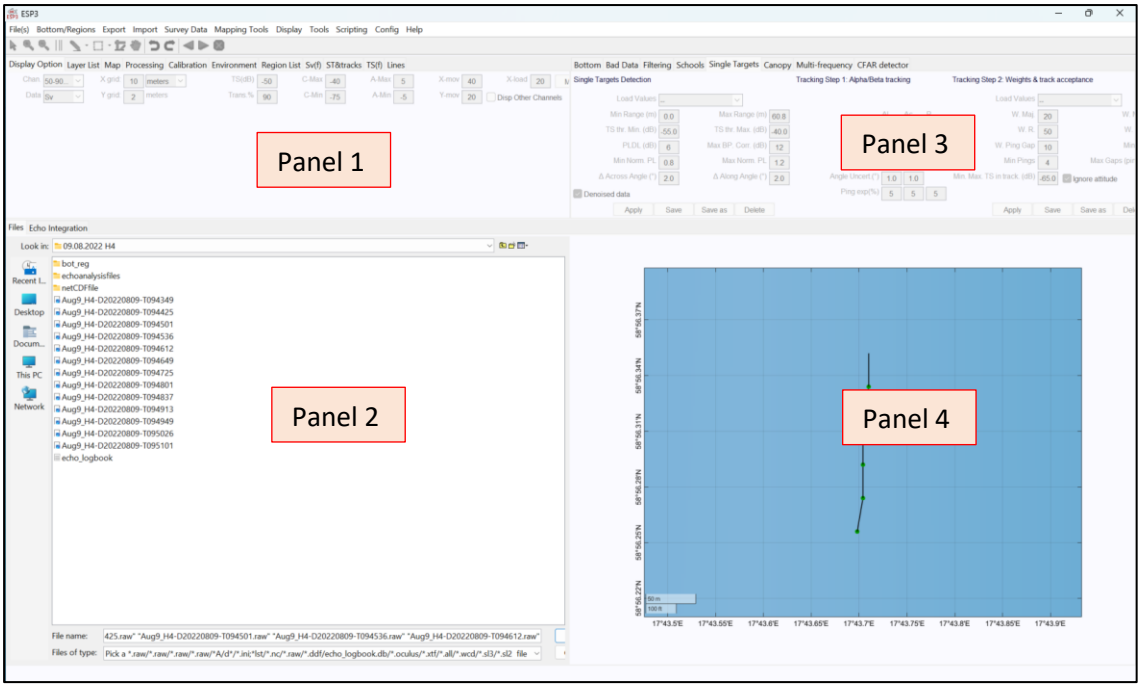
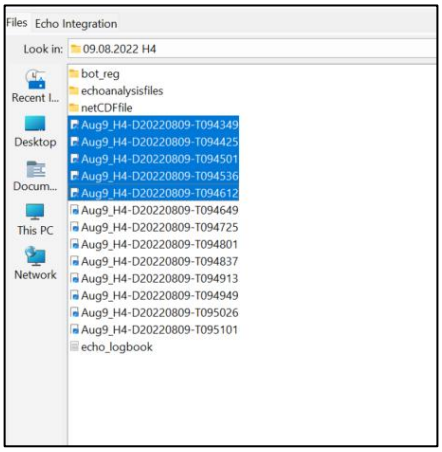
A) ESP3 workflow (Echo Sounder Package; *https://bitbucket.org/yladroit/esp3/src/master/*)

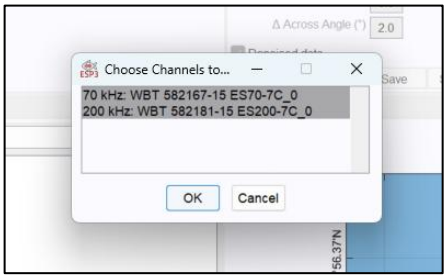
- Launch ESP3 (could take some minutes). This is what you should see (4 panels):



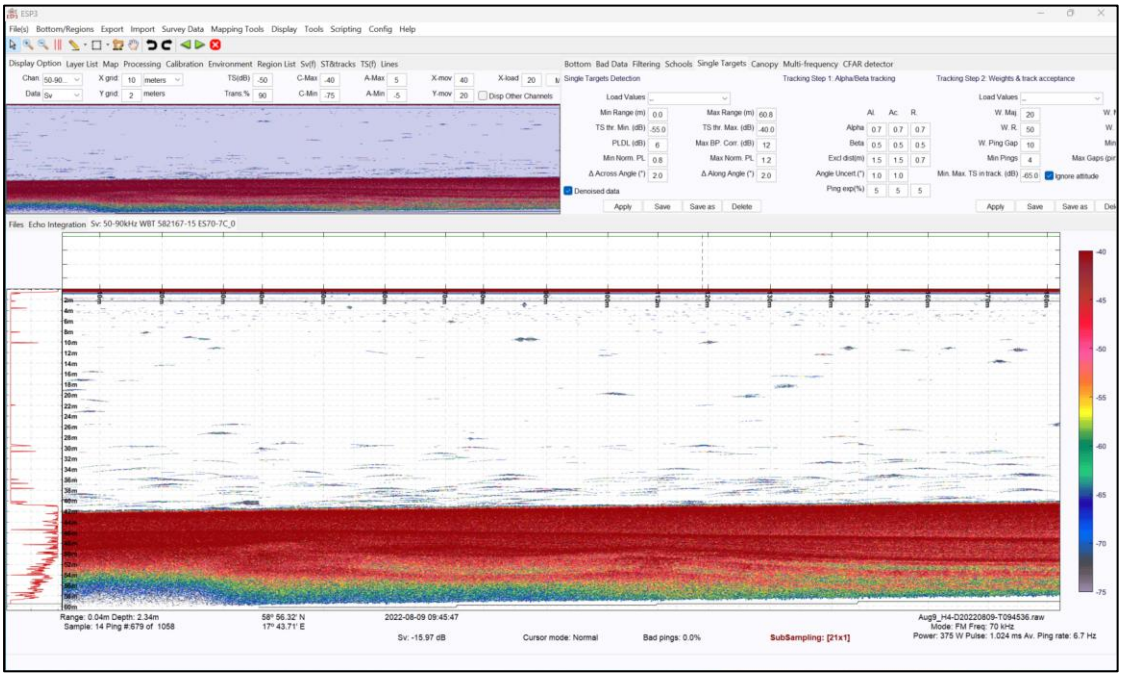
- In the "Files" window of the Panel 2 go to the echogram file folder, select files of interest from the transect (ctrl + left mouse click for multiple file selection) and drag them in the "Display Option" of the above Panel 1;
(the first 5 files in this case)



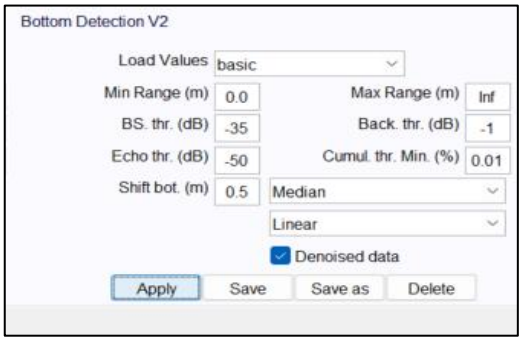
- Choose channel (70 or 200 kHz frequencies in our case): you could select only 70 kHz since is the best channel for "fish echoes" detection (200 Hz for zooplankton or jellyfish). Loading of the files could take a while if multiple files are loaded;



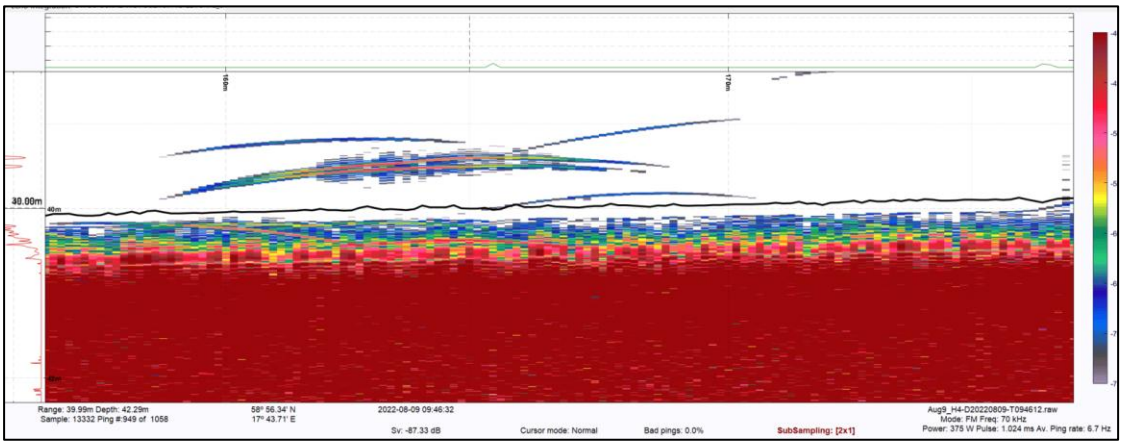
- Now you should see something like this: In this example the echogram is quite “good” but in other cases it may be necessary to manually apply some cleaning in the “bad” regions of the echogram (but that is not the purpose of this user manual).



1) Bottom detection and exclusion:



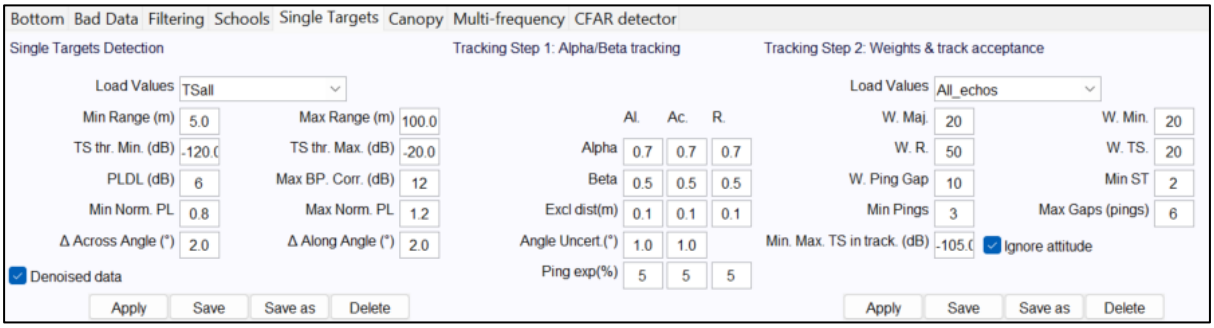
- In Panel 3 go to the “bottom” window. In the *Bottom Detection V2* part, select the “basic” option in *Load Values*. Change the *Shift bot. (m)* to at least 0.5 and then *Apply*. This parameter adds extra meters (50 cm in this case) to the “real” bottom detected by the algorithm. It is a sort of safety buffer to be sure we exclude the bottom;
- Now you should be able to see a black line around 40 meters in bottom Panel (Panel 2 and 4 are now merged). That is the bottom line detected (shifted up by 50 cm). Everything below this line will not be considered in the following analyses/steps.



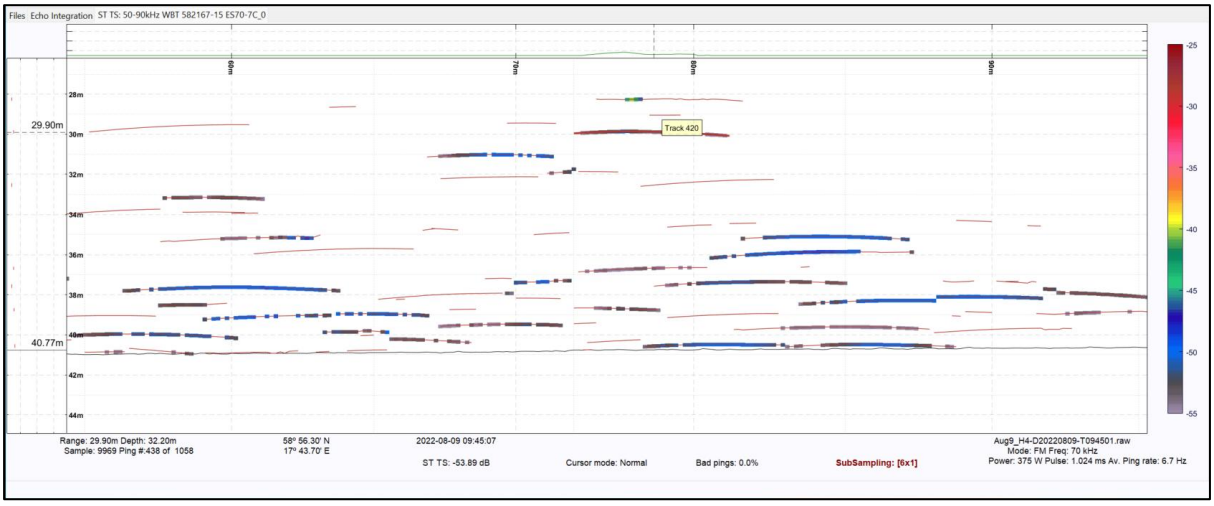
2) Single Target and Echoes detection:

- In Panel 3 go to the “Single Targets” window. In the *Single Targets Detection* and *Tracking Step 1&2* parts, change the parameters accordingly to the one showed below and then *Apply* both. Important: TS min -120 to max -20 for *Single Targets Detection* and TS min.max -105 in *Tracking Step 2;*

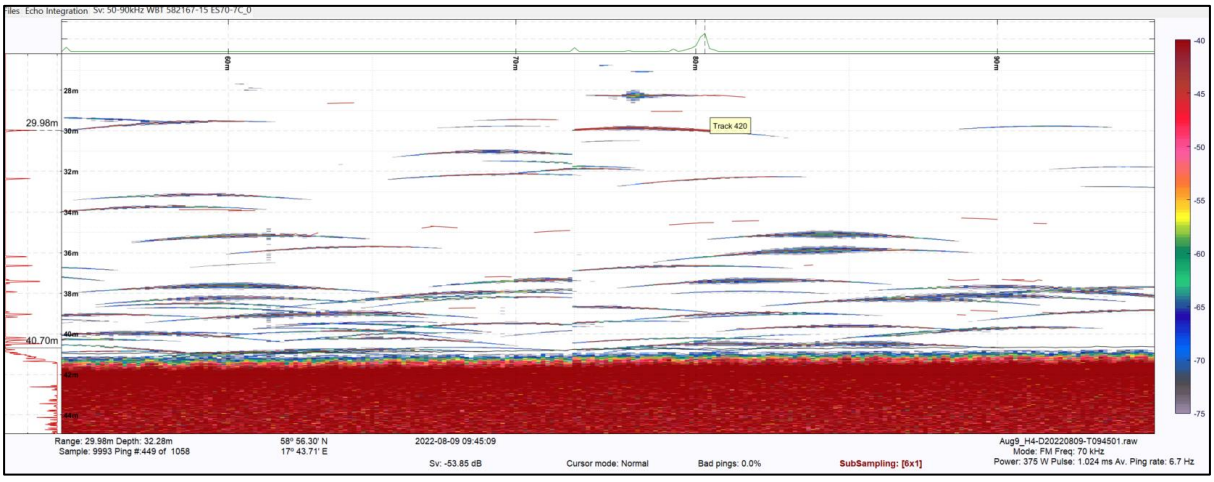
(“TSall” and “All_echos” are saved options I created; you can do the same pressing the *Save as* button)



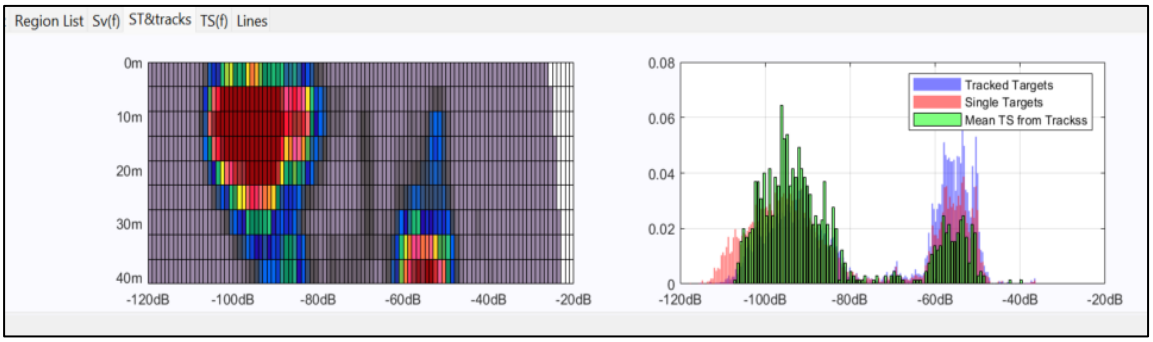
- Now you should be able to see colorful dots and several brownish lines (first figure; in Panel 1 “Display Option” -> *Data=ST TS*). The dots are the single targets detected and the lines the tracked echoes (more single targets “merged” in one total echo). Track 420 highlighted;



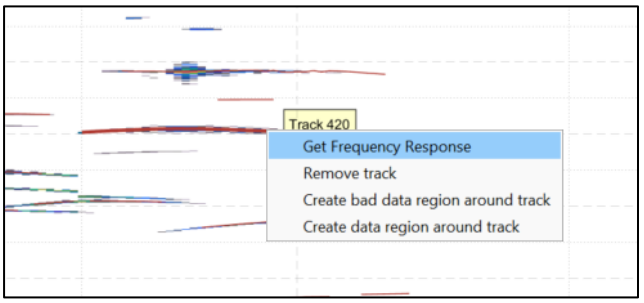
Below, Panel 1 “Display Option” -> *Data=Sv.* Track 420 highlighted;



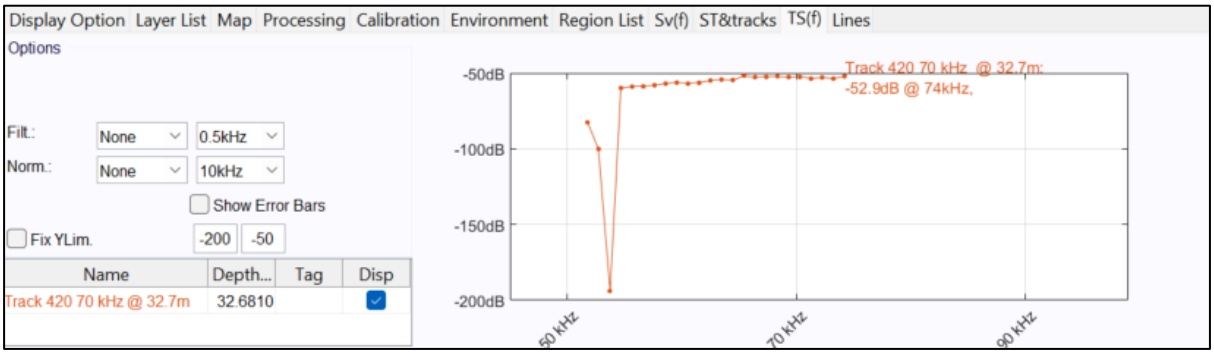
- In Panel 1 “ST&tracks” you can explore the TS plots and histograms.
  Mean TS from Tracks (green part of the histogram) reveals two modes. The first component (mode around -100 dB) could be formed by weak-reflection targets such as bubbles, plankton, jellyfish etc. while the second component (mode around -55 dB) are probably fish. Also, the position of the two components in the water column is different; -100 dB is located in the pelagic layer while the -55 dB is closer to the bottom (first plot);



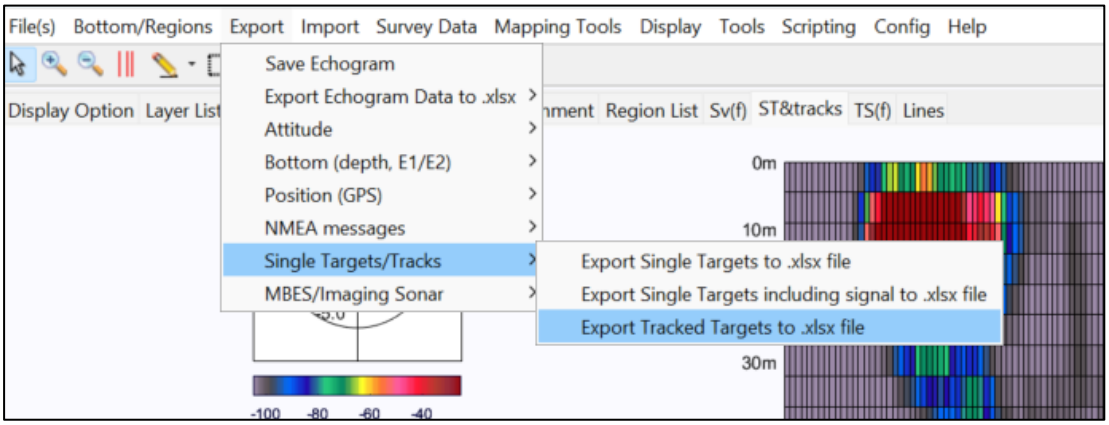
- Frequency response of tracks (e.g., Track 420) can be explored as follow:
  Right mouse click on the track of interest -> *Get Frequency Response;*



- Then go to “TS(f)” in Panel 1. In this case around -50 dB at 70 kHz. Most probably a fish; (don’t look at the first drop since is a calibration problem at that specific frequency)

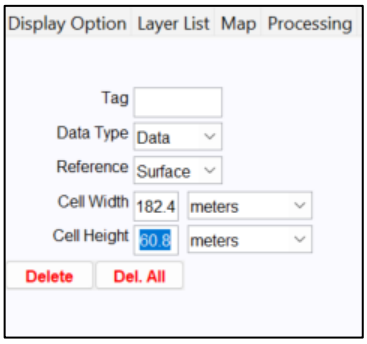


- Export the tracks as excel file: “Export” (top command bar) -> *Single Targets/Tracks* -> *Export Tracked Targets to .xlsx file.*
  Important: This file is the db containing the TS-echoes histogram you will need for the ShinyApp processing part.

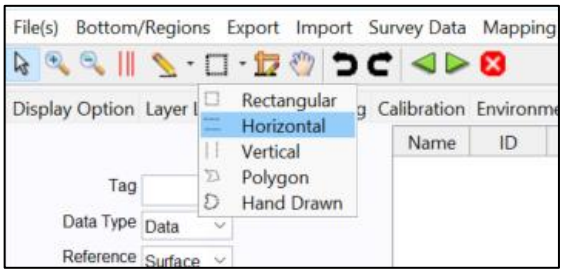


3) Echo integration of the transect:

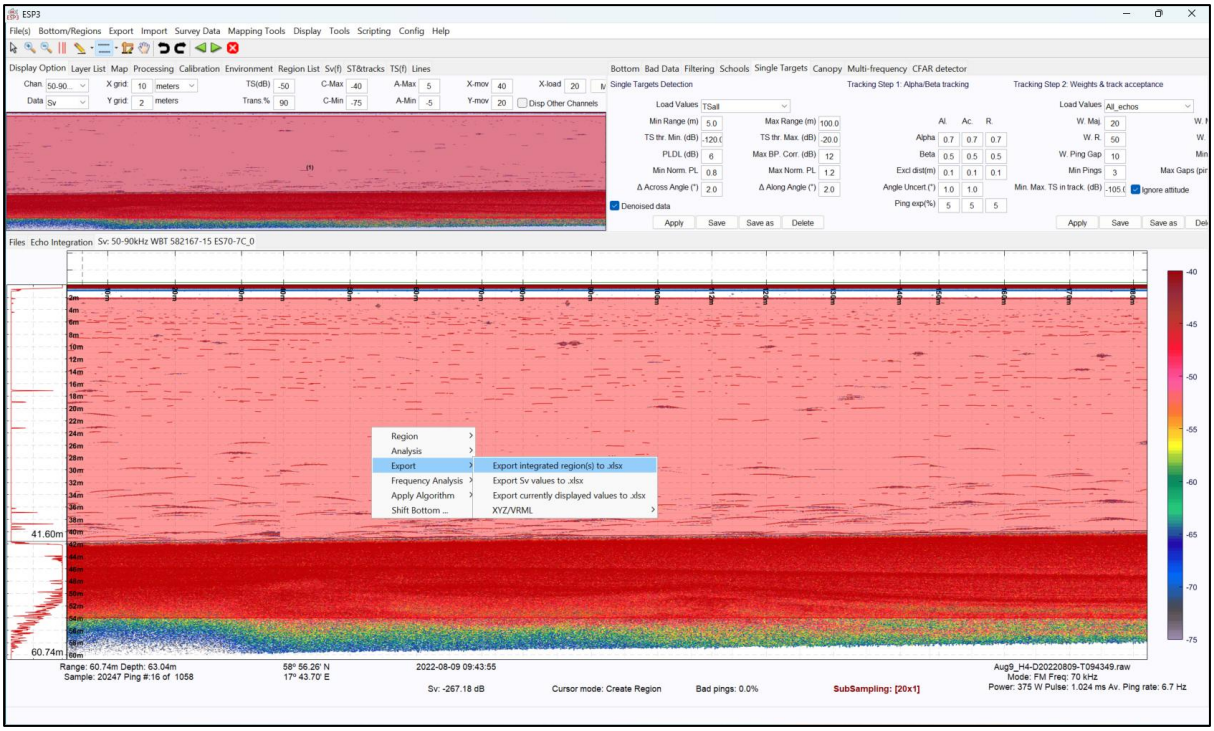
- In Panel 1 go to the “Region list” window. In *Cell Width* and *Cell Height* put a very large number (e.g; “9999”) so to force ESP3 to automatically put the max values recorded in the echogram. Also, check that *Data Type* is on *Data* and both *Cell Width* and *Cell Height* are in *meters;*



- Then click the icon of the Area creation in the shortcut command bar and select *Horizontal;*

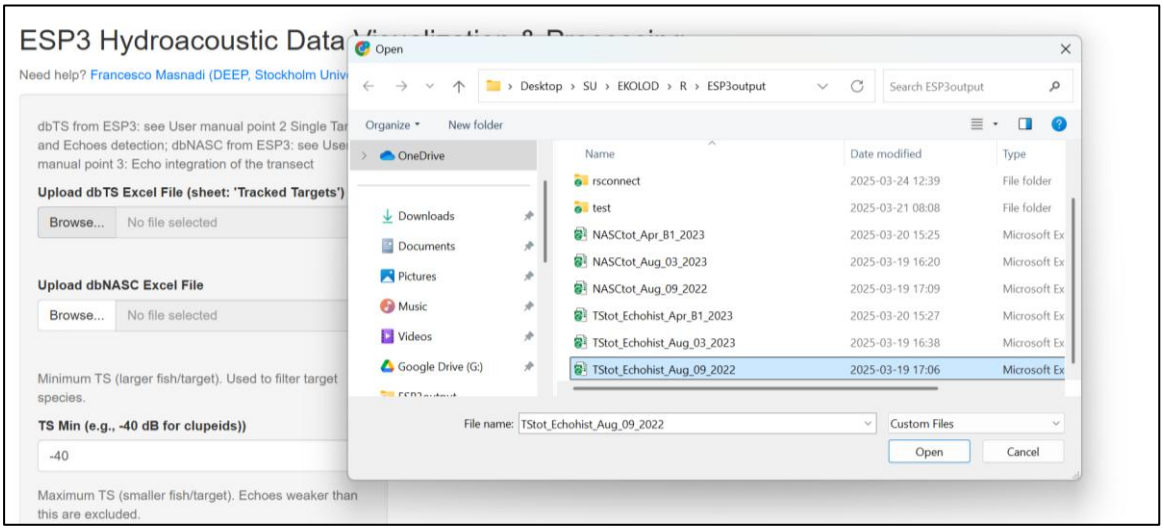


- Create/draw a horizontal region from the surface (usually starting a few meters below the surface to avoid possible disturbances from waves/ship hull etc., e.g.; 2 meters deep) to below the bottom line (it doesn't matter how low, as the data will only be analyzed down to the bottom line);
- Mouse right click on the region (red color means the region is active, green color the region is inactive) -> *Export* -> *Export integrated region(s) to .xlsx file.*
  Important: This file is the db containing the total NASC value you will need for the ShinyApp processing part.

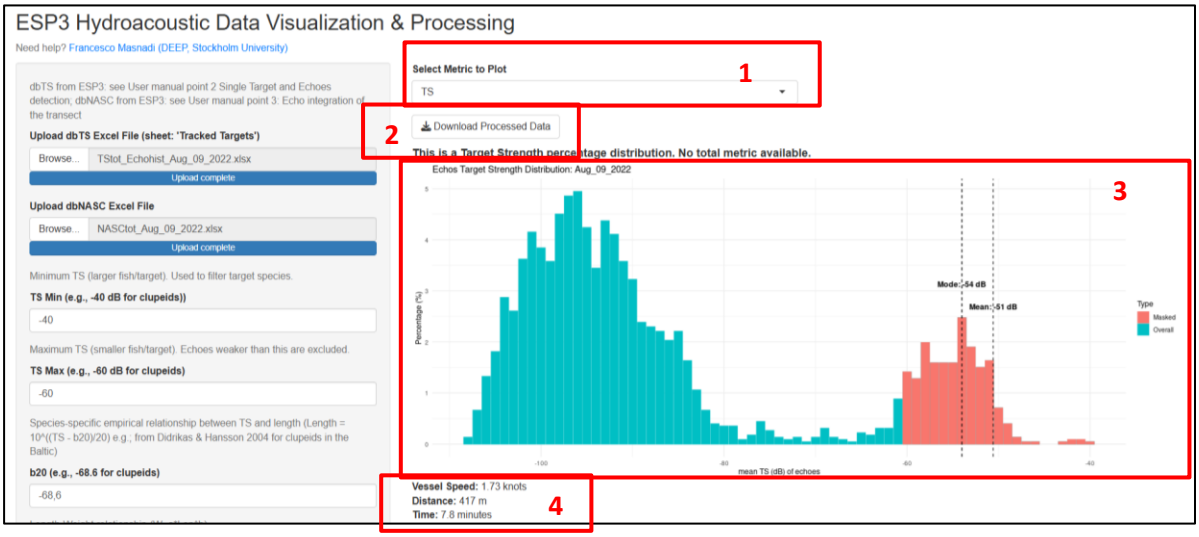


B) ShinyApp workflow (*https://shiny.posit.co*)

- Go to the app webpage: https://framasnadi.shinyapps.io/Ekolod_projectAPP/
- Upload both dbs via “Upload dbTS” and “Upload dbNASC Excel file” (from *Browse* navigate to your folder and select the correct db);



- Once both files are uploaded you should see something like this:



1 – Select the metric to plot from these: *TS, NASC, Abundance, Biomass*

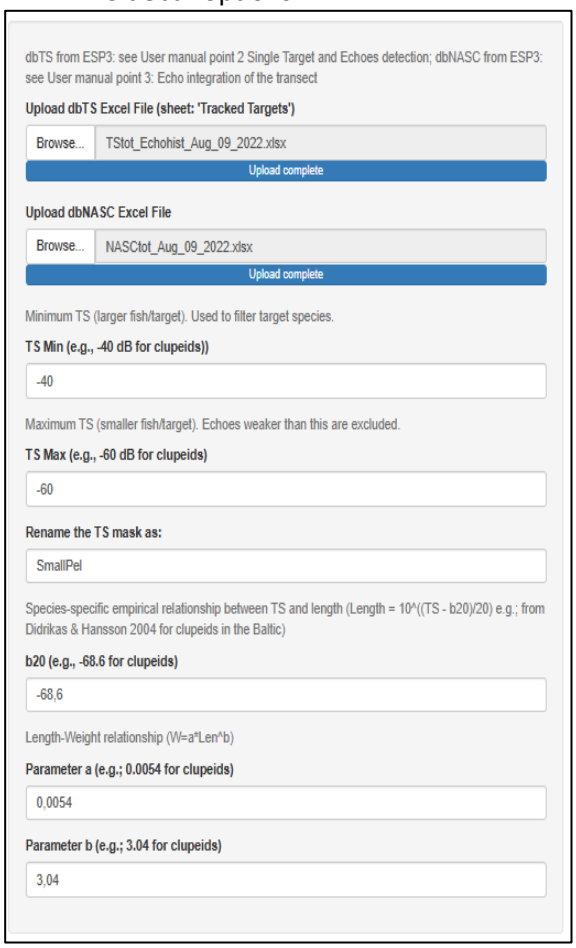
I. *TS*: Target Strength percentage distribution (no total metric available);
II. *NASC*: Overall and “Masked” Nautical Area Scattering Coefficient (m^2/m^2nmi^{-2});
III. *Abundance*: Overall and “Masked” number of targets per hectare;
IV. *Biomass*: Overall and “Masked” kg per hectare.

2 – Download the final dataset with processed data as .csv (both by TS and Total values).

3 – Histogram showing the selected metric by Target Strength bin and Type (Overall vs “Masked”). Mode and mean are also presented.

4 – Summary info of the transect analysed.

- Sidebar options:



→ dbTS upload menu (see above)

→ dbNASC upload menu (see above)

→ Minimum TS value for filtering data as desired

→ Maximum TS value for filtering data as desired

→ Rename the mask/filter. This will be the name saved in the final db

→ Species-specific b20 value from literature (directly affecting Masked Biomass histogram)

→ Parameters a & b of Length-Weight relationship (directly affecting Masked Biomass histogram)