**Instructions for creating and testing Pamguard’s Matched Click Template Classifier**

*Note: you will need PAMPal v. 0.14 or higher*

1. Process data with a click detector as usually done with PamguardBeta
2. Create a click template (only needs to be done once per species, but if a species makes a variety of click types, you can use multiple templates)
   1. Use a database that contains examples of the species you’d like to make a template of
   2. Look for the best click, create a separate event per species with just that one click in it
      1. Best click= high SNR aka Wigner has a dark blue background (preferred), Click Spectra plot shows a large difference in the amplitudes between background noise and the signal
      2. The eventType should be “TC” (for template click)
   3. Save an XML file for the Pamguard settings (especially important if you decimated your data within Pamguard)
   4. Run CreateClickTemplDirectFromPamGuard v3.r
      1. Figure out your click duration (ms) based on species (line 30). Some guidelines are provided below, but this should include the duration of time that your click is above the typical noise level.
         1. Sperm whale: 0.8 ms
         2. Beaked whale: 1.8 ms (if including long, broadband beakers like BWC), 0.5 ms (if shorter duration, “traditional” beakers)
         3. Kogia: 0.16 ms
      2. May have to also adjust the template duration based on what species you’re interested in (line 32). Some guidelines are provided below, but this should be roughly twice your click duration (to provide some zero-padding on each end of your click template).
         1. Sperm whale: 1.5 ms
         2. Beaked whale: 3.0 ms (if including long, broadband beakers like BWC), 1.0 ms (if shorter duration, “traditional” beakers)
         3. Kogia: 0.3 ms
      3. May need to adjust your bandpass filter depending on your signals (lines 34 & 35)
         1. Sperm whales: 1-20 kHz
         2. Beaked whales: 16-90 kHz
         3. Kogia: 100-160 kHz (or to Nyquist freq if sample rate < 320 s/sec)
      4. Adjust lines 39-50 to point to the correct paths as explained in the R file
      5. Check to see if there are NAs in the csv and if so change them to nothing in an ASCII text editor (like Notepad++).
      6. Should be good to go after that
   5. Within PamguardViewer (v 2.00.16e or higher)
      1. Add Modules> Classifiers> Matched template click classifier
      2. Settings> Matched click template
         1. Use the + button to add multiple templates (note: running 6 templates at one time has not been a problem).
         2. Keep the generic dolphin click for the Reject template, or (if you want to base your classification only on the “match” correlation) select “None” for the reject template.
         3. Change the Match template to what you created in step 2.d
            1. Use the downward arrow to upload the csv you created in step 2.d
            2. Start with a Match threshold of 0.8 (for v2.01.05) or 0.15 (for v2.00.16e) under the Matched Template Parameters. This will be an iterative process. You want to find a value that yields a high fraction of template matches for strong SNR clicks of the given type but has a low number of false positive matches. Note, a beaked whale click may match with multiple similar beaked whale templates.
         4. Save the configuration file with your newly created classifiers
3. Create a backup of the binaries and database- using the Matched Click Template Classifier changes the shape of the clicks in the Bearing Time plot (and also good to have if you have to backtrack)
4. Load the database into PamguardViewer
   1. Settings> Matched click template> Reclassify clicks> Reprocess data (all of it)
      1. Check the box for erase everything in the database
      2. This will take a while. Close out of Pamguard when done
5. Create a backup of the database and binaries at this step as steps 6 and 7 will be trial and error and once you’ve run those steps and aren’t happy with the results you will need to delete the binaries and database you were working with and resort to this backup to run steps 6 and 7 again. Alternatively, if you didn’t save a backup, you can re-run the basic click classifier in PamGuard Viewer (deleting old binary and database values) which will also delete the click template classifications and allow you to start over.
6. Run ReadPamGuardBinaries v10.R
   1. Change path on line 26 to where your binaries and databases are stored
      1. Database needs to be located within the BinaryStorage folder
7. Run MakePamGuardEventsFromTemplateClassifier v4.R
   1. Set the path on line 10 to be the same as the path from step 6.a in this instructional document
   2. You will need to adjust lines 16 and 17 to work for your dataset and every one is different. If you see a lot of detections in the R Console then you will have to abort and start back at step 5 of this document