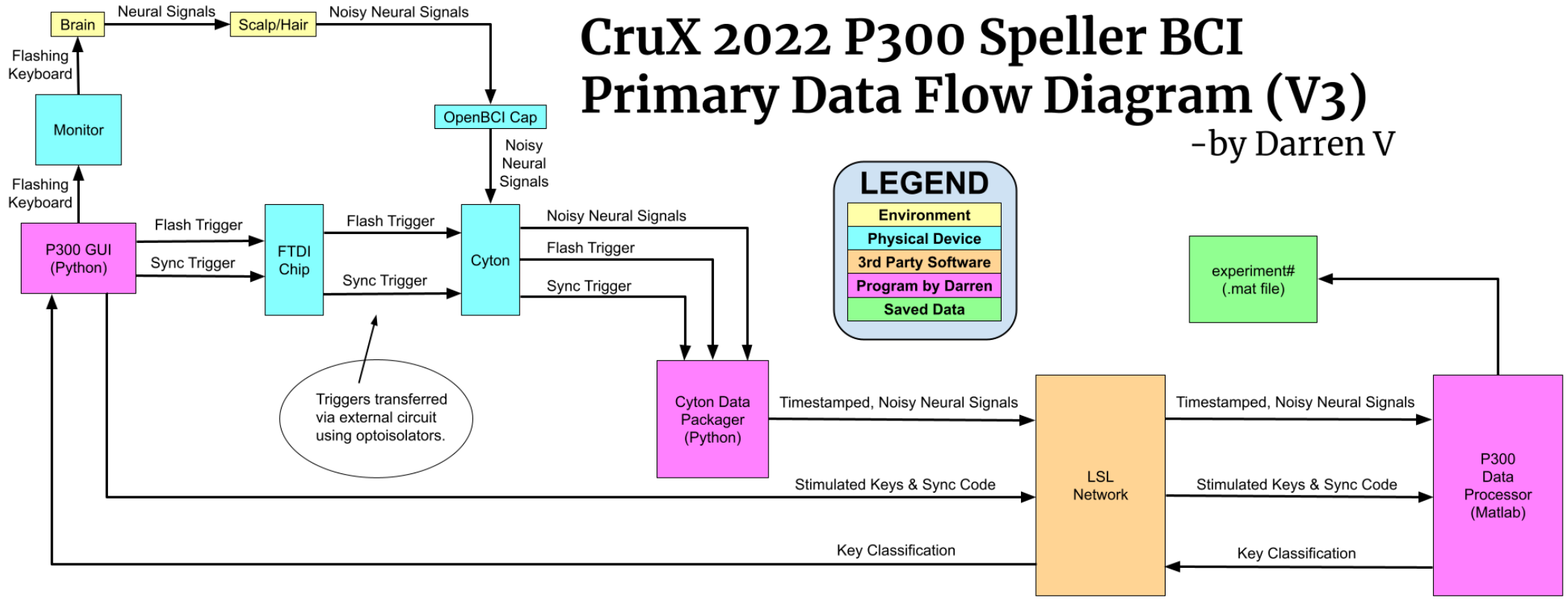
CruX 2022 P300 Speller BCI Primary Data Flow Diagram (V3)

-by Darren V



Both Modes

"Flash Trigger" is a signal that alternates (high/low) *every* single time the P300 GUI flashes.

"Stimulated Keys" is a boolean vector that corresponds to each character code and indicates if the given key was flashed or dull for the given trial.

Training Mode

"Sync Trigger" is a signal that alternates (high/low) every time the P300 GUI flashes the target character.

"Sync Code" is the character code for the target character of the given trial.

Validation Mode

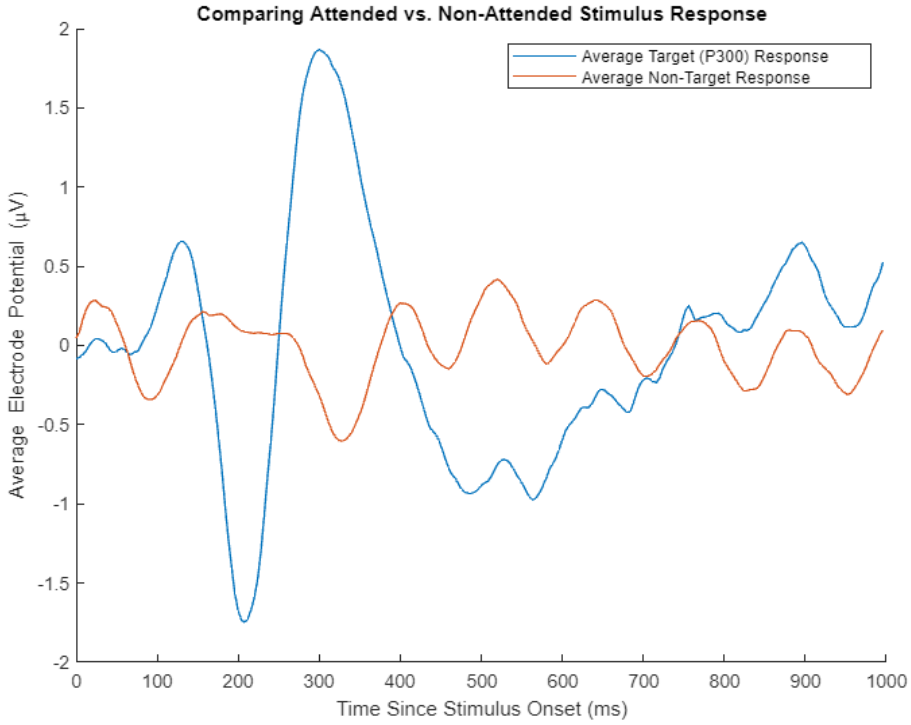
"Sync Trigger" is a signal that alternates (high/low) periodically to help validate data synchronization.

"Sync Code" is a binary value that indicates whether or not the given trial is a sync trial (i.e. Sync trigger *should* have alternated on this trial).

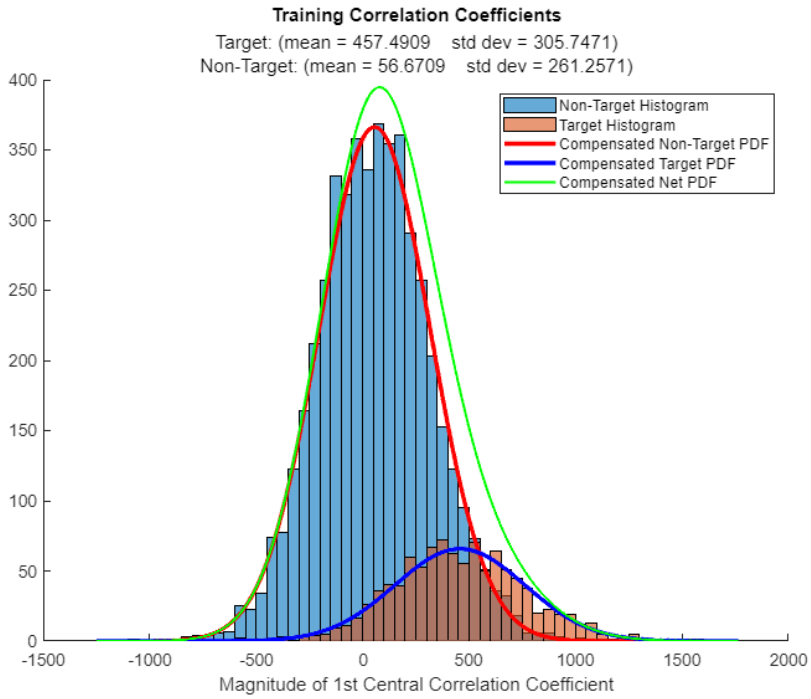
Using Iterative Cross-Correlation as a Minimal-Training, Interference Resistant Demodulation/Classification Method: Analysis and Validation

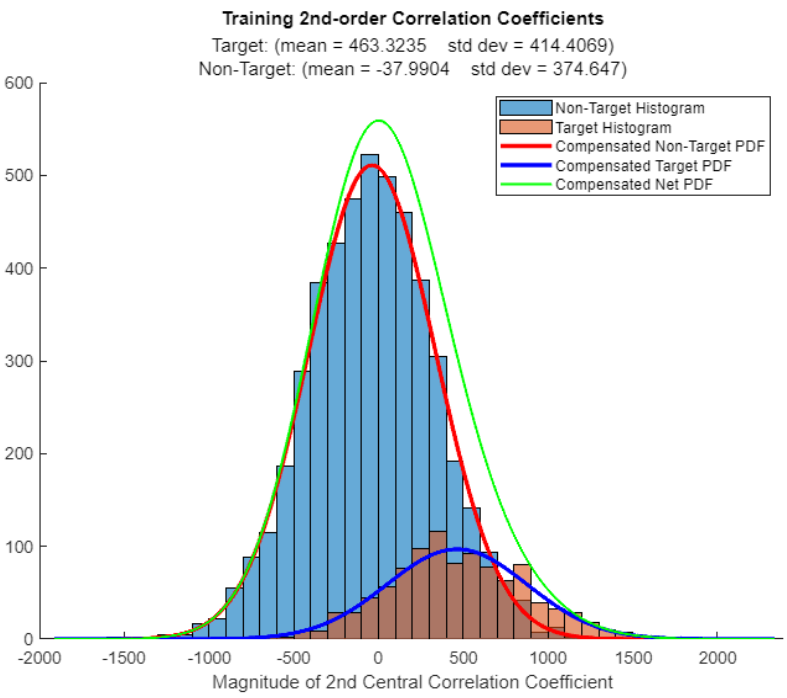
Access to the Github for this project is available upon request.

The data listed below and on the following pages introduce and justify the core of the logic behind my BCI's classification method. Not included (for the sake of length), however, are several methods for classification that were implemented, tested, and shown to be ineffective or not as effective as the chosen method. Also not included are details on how GPT-NEO was used as a causal language model to produce word suggestions, how character n-grams were used to produce dynamic character thresholds, how probabilities were dynamically weighted to reduce type-I errors, how the signal characteristics were updated *while* making live classifications, or technical details such as trigger and synchronization handling. Lastly, not included is the reasoning behind or explanation why iterative cross correlation reduces inter-trial interference, inter-stimulus interference, and training time.

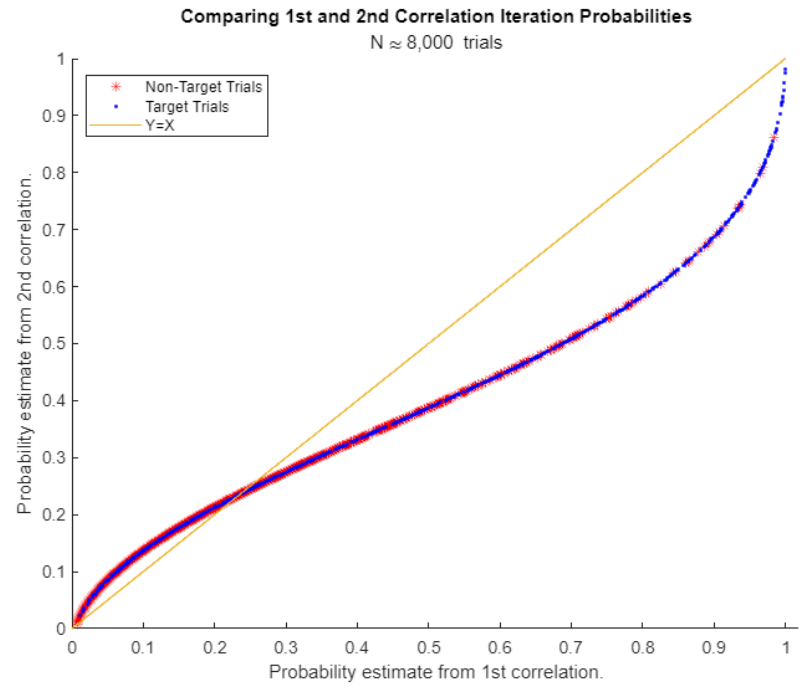


The above graph illustrates the difference between the average non-target response and target (P300) response over N≈15,000 total trials, (about 30 minutes worth of data). Given a high enough number of sample trials, ostensibly, the orange curve would be a flat line at 0_{uV}, and the blue curve would exhibit an ideal N200 deflection and P300 inflection, followed by a refractory period before returning to a flat line. Because of interference from peripheral stimuli, we instead see a low-amplitude steady-state visually evoked potential at the flash frequency, $\approx 8.33_{Hz}$ in this instance. This specific frequency can then be removed with a notch filter to improve signal discrimination. Noting that these two average responses are clearly distinct, the challenge, then, is demodulating individual trial signals and determining the likelihood that the trial was a target response or non-target response.

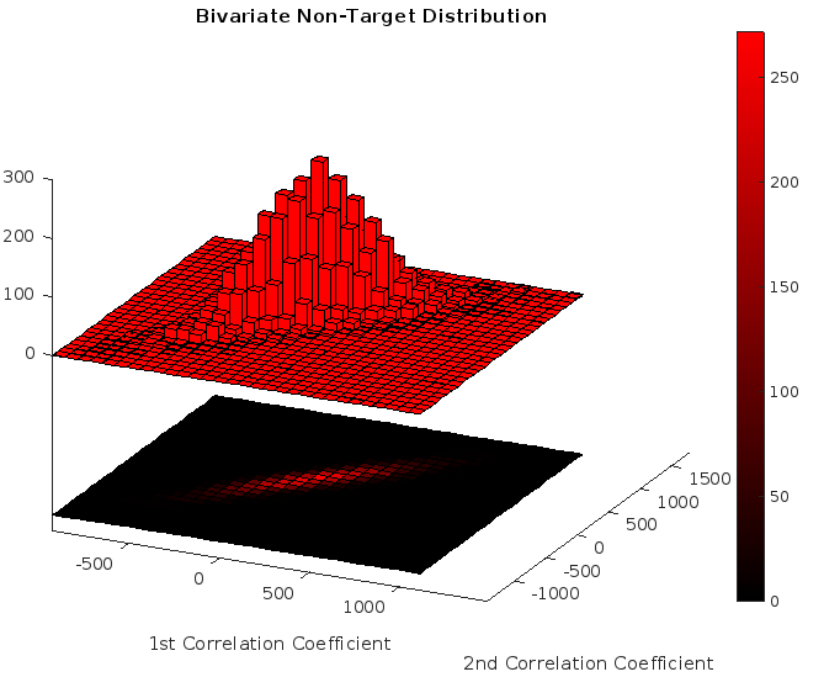


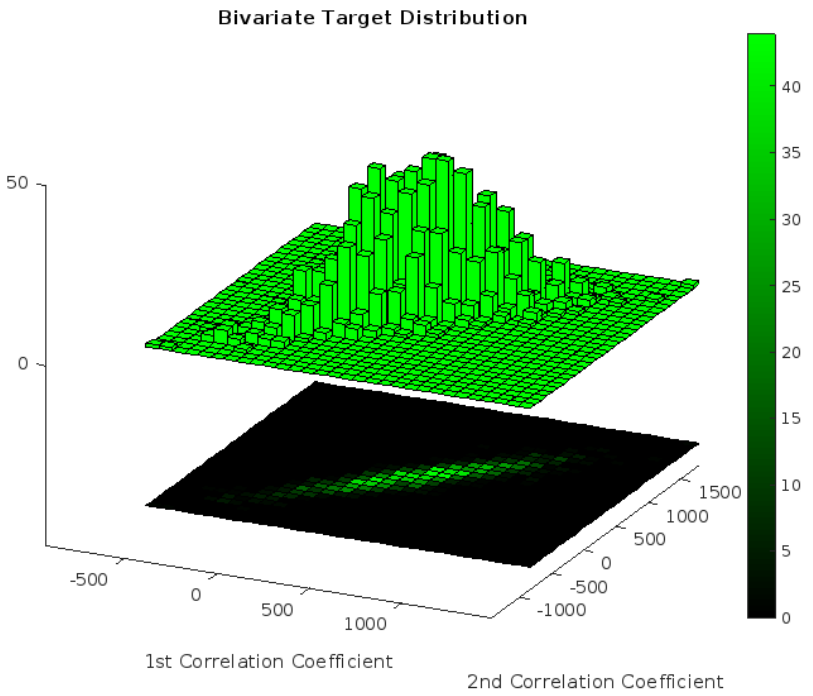


The two above graphs, (shown for N≈8,000 total trials), show that the calculated central cross-correlation coefficients can be treated as random variables sampled from target and non-target distributions, both of which are highly normal. The left graph shows the target and non-target histograms for the central correlation coefficient of the cross correlation between each trial and the average target response. The right graph shows the target and non-target histograms for the central correlation coefficient of the cross correlation between the previously mentioned cross correlation for each trial and the average first cross correlation for target trials. Notably, the distributions become narrower and more normal as further iterations are performed (as a result of the central limit theorem). Each distribution set has a net resolution space (percent area under the net PDF which is not intersected by both distributions) of ≈75%. Thus, it is clear that either can be used as a valid demodulator. It is unclear from these graphs alone, however, whether or not the discriminatory information is independent between these two distribution sets (i.e. if any information is actually *gained* by performing more than one iteration of cross correlation).

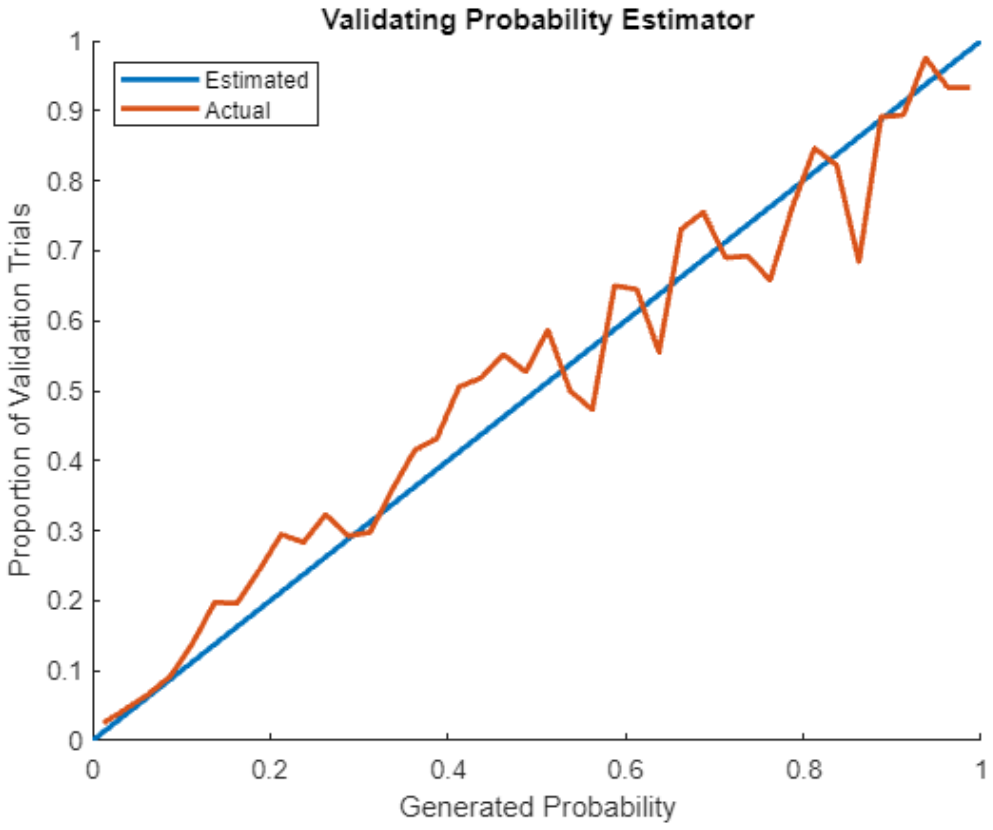


The graph to the left shows that the probability estimates from the first and second cross correlations are non-linear, particularly in the region of $p_1 \approx [50\%, 90\%]$, indicating that, so long as each of p_1 and p_2 are calculated from valid normally sampled distributions, information is gained. This analysis can be performed iteratively, and, so long as the new iteration's prediction, p_n, is calculated from a valid normally sampled distribution and the curve deviates from the n-1 dimensional line with a slope of 1 in all dimensions more than the previous curve, p_n can be said to add new information to the trial estimate. The most notable *drawback*, particularly during live analysis, of performing more correlation iterations is the increased processing time. Also, diminishing returns seem to appear after only 4 or 5 iterations, (i.e. the net information gain appears to be logarithmic w.r.t. the number of iterations performed).





The above graphs show the bivariate histograms (drawn on the same plane to illustrate the separation of means) which can be used to generate bivariate normal statistics to estimate a probability that a given trial is a target trial given some 1st and 2nd correlation coefficients. We say that using n iterations of cross correlation to generate an estimate is using n^{th} degree correlation. Thus, this is using 2^{nd} degree correlation. Also verifying that new information is gained, the average magnitude of the 'distance' between two points from the two different distributions is greater in this 2-dimensional frame than in the 1 dimensional frame on the previous page. Much like parsing the light apart from two stars near to one another when viewed through a telescope, this increase in separation yields a greater ability to discriminate which sample came from which distribution.



The graph to the left validates that the *analytically generated* key probabilities, shown in blue, closely match the actual percentage of positive trials at that generated probability, shown in orange. This confirms the appropriateness of performing these statistical analyses on the correlation results to generate key probabilities. By then treating each of the stimuli as independent trials and compounding samples over time, the target key probability will eventually converge to 100% and all other keys to 0%. The optimization problem then becomes choosing key decision thresholds. (displayed probabilities generated using 3^{rd} degree correlation and corresponding trivariate normal distributions)