**User Review Traces**

Orignally by Bob Rawle, Kasson Lab, University of Virginia, 2016

Updates by:

Bob Rawle, Williams College 2024

Notes: Updates to make things flow easier. Prompts for user. Easy start script. Specific parameters for analyzing Sendai virus. Ability to correct wait time, not just the designation. Etc.

To begin:

To start the program, run the function Start\_User\_Analysis.

\*\*Can also use the An\_Easy\_Start\_… script as well

Before starting the program, the options should be specified in Setup\_Options\_User\_Review.

Basic description:

This program takes the .mat output file from the Trace Analysis script and then allows the user to easily review how well the automated analysis did. There usually is the need to correct a variety of traces which have been incorrectly categorized (maybe there was a focus event which the program thought was fusion, maybe the parameters weren’t fine tuned).

The output of this program is a new .mat file which contains a data structure of all the analyzed traces (corrected and reviewed). This can be used to create CDFs, etc.

See the Reference Guide for Prompt Codes on how to correct the trace analysis. And please don’t hesitate to reach out Prof. Bob Rawle if you have questions!