Tremor Quantification Device Instructions (for HIFU)

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General notes:

- Be patient with the software. After pressing a button, give it a few (\sim 2-5s) to think.
- Anytime you type text (ex. naming patient ID and trials), the software will
 delete any spaces. So if you want to name something "upside down spiral" it
 will turn out as "upsidedownspiral". Instead of spaces, use "_" or "-" (ex.
 "upside_down_spiral").
- (Don't worry about this only included in case needs to be done) From time to time, it is good to update the software (I will contact Dr. Cleary whenever I make changes to software). The instructions for this are:
 - Open "Git bash" app logo is the windows-like 4 parted diamond with red, green, yellow, and white squares.
 - o Type "cd /c/hifu/Spiral-Drawing" then enter
 - o Type "git pull" then enter
 - o If there is anything to update you will see a paragraph of text, if not, it will say "Already up to date"
 - You can close out after that
- If you would like to see where the data you have collected is located (possibly to transfer it to drive, or to locate the report PDF to put in patient chart), there should be a shortcut on the Desktop screen of a folder named "HIFU-cases" (it is located at C:\hifu\HIFU-cases\). In that folder, there is a folder with the patient ID. Open it, and this is where the PDF report as well as the data are located.

Launching application: Shortcut to the application should be on the home Desktop screen of the devices. To launch, double click on the "SpiralDrawUI.py" icon on the desktop

1. <u>Starting Case</u>

Starting a case is done by either

- a. Inputting a new patient id (for research the coding was p### = ex. p210 for the 210th patient in the study) to allow for identification. Then click "Start Case".
- b. (To load previous patient) Select a patient id from the list area it should highlight blue. Click "Load Case"

If done correctly, The typing field as well as the start and load case buttons should be grayed out. The "Finish Case" button should now be enabled (clickable). This can be clicked at any time to change the patient being treated (no progress will be lost).

2. Starting a new Recording

Summary:

- 1. Hand pen to the patient
- 2. Navigate to "Trial Setup" tab
- 3. When they have the pen in hand they will draw in, select the proper "Trial Name" and device and press "Record"
- 4. Switch to the "Draw spiral" tab
- 5. Have patients draw all spirals and the line
- 6. Press "Done" <u>underneath each spiral</u> you want to save (**Still on the "Draw Spiral Tab"**) Patient should still be holding pen in their hand
- 7. Switch to "Trial setup" tab and press "Done"
- 8. Right after the screen no longer says "Recording..." you can take the pen from the patient's hand and wait for the reading to download from the accelerometer (over Bluetooth).

Recording happens in 2 ways: the reading from the accelerometer, and the spiral itself. The "Trial setup" tab starts the recording of the accelerometer and saves any spirals drawn with the same trial name.

To start a new recording, the "trial name" field must be completed. Selecting the corresponding radio buttons names the trial (Ex. preop = spiral in prep room, intraop1 = baseline before sonications, intraop# = subsequent recordings)

- The intraop field has a number next to it; it will advance automatically as trials are completed.
- If you desire a different name, use the "other field"
- Current trials cannot be named the same as previous trials (recording will not start if they are named the same). Previous trials are listed in the box on the right side of the screen
- Test radio button can be used for testing, and is a good idea to do at the start of the day, or whenever you want to make sure the device works properly. All steps will be the same, just it will not display any information collected (accelerometer or spirals) on the UI.

The proper device must also be selected in the "Select device" field by selecting the proper radio button. If you would like to only use drawn spirals (rare), select "No accel" radio button.

After selecting a valid trial name as well as a valid device, you can click "Record". If done properly, the display status text on the 'Trial setup screen will say Recording...".

NOTE: The recommended practical way to start trials is to hand the pen to the patient (in the hand you are recording the spiral), and ask them to just hold it up. Then, when the pen is in their hand, press "Record", and then have them draw the spirals. Same when stopping recording after the spirals have been drawn, have the patient hold up the pen in their hand, stop the recording, then take the pen from them. Recording only happens from the time the screen displays "Recording..." and the time you press "Done." When the device says "Downloading data, and resetting, it is no longer recording from the accelerometer. The reason for doing it this way is so that the accelerometer contains as much as the patient's tremor as possible without recording the motion of transfer of the pen into the person who is recording the spirals' hand.

After the accelerometer is recording, spirals can be acquired either on paper or on the tablet. If they are done on paper, simply administer them on paper. If you wish to record the spirals on the tablet, after you see the "Recording..." confirmation on the Trial setup" tab, switch to the "Draw Spiral" tab.

- The patient can now use the pen to draw the spirals (will show up in blue).
- While the trial is running (before you press "done" on the "trial setup" tab), you must save any spirals you want to save by pressing "done" underneath the drawing. This will save it with the same name as the trial.
 - o Ex. f you only want to save 1 of the spirals and not the others, simply only press "Done" on that spiral, and it will be saved, you can then clear the others.
- "Clear drawings" button will clear all of the drawings on the tab.

3. Finishing a Recording

After the recording is done, and you have saved all of the spirals drawn by pressing "Done" underneath each individual spiral (if spirals were drawn on tablet), you can finish the trial and accelerometer recording by pressing the "Done" button in the "Trial setup" tab

- Recommend to press "done" when the pen is still in patient's hand to not record the movement of the transfer of the pen in the analysis.
- The device will say "Downloading data...", then "Resetting BT", then "Done. Ready for next trial". If it says "Download failed.", just make sure the pen is nearby, wait a few seconds and click "Done" again to retry the download

4. Analyzing data

Summary:

- 1. Navigate to the "View progress" -> "Graph settings" tab.
- 2. Select case from the "Accelerometer" list (should highlight blue) and press "Set as baseline"
- 3. Click "Analyze Accelerometer" (This will also automatically plot the analysis)

- 4. To view, the plots, navigate to "View Progress" -> "Graphs" tab.
- 5. Click "Generate PDF" Button to make and save a PDF report to the folder where the patients data is stored (in C:\hifu\HIFU-cases\<pt_id>)

To analyze the data, switch to the "View Progress" tab. Within this tab, go to the "Graph Settings" tab. From here, you can plot any spirals (should they exist), and the raw accelerometer traces.

To plot the progress, and the accelerometer PSDs, though, the data must be analyzed. To do this, a valid trial from the list must be displayed under the "Current Baseline" text. The baseline is normally "intraop1", but any trail can be selected at your discretion.

• <u>Set baseline</u>: Choose a trail from the "Accelerometer" list (it should hightlight blue). Press "Set as baseline" button. At this point, that trial name should appear in bold under the "Current baseline" text.

At this point, click "Analyze accelerometer" This will analyze the accelerometer data with the baseline set as the selected baseline, and plot it on the "Graphs" tab. You can also click the "Generate PDF report" button at this point to save a PDF report of the case to save to the patients chart (can be done either after every recording, or at the end – each time you press the generate report button it will overwrite the previous PDF report).

6. Advanced techniques

How the program stores data:

- The base folder is C:\hifu\HIFU-cases
- Data is stored in folders named with the patient ID
 - o The PDF report is also located here
- The analysis folder within the folder with the patient ID shows up if there has been a previous analysis started. The best way to view the information in this

folder is to start the program and go to the "Graph" tab or view the PDF report.

- Deleting all data from one patient:
 - O Close out of the software if it is open in python
 - Navigate to "HIFU-cases" folder (either Desktop shortcut or C:\hifu\HIFU-cases)
 - O Delete the folder with the patient ID as well as the .txt files with the patient ID (3 items); (ex. if pid is p206, delete p206 folder, p206.txt and p206_spials.txt files)
 - Next time you start the software, the patient will not show up on the list of previous cases.
- Deleting one trail from a patient (not recommended, only included if needed to be done).
 - o Close out of the software if it is open in python
 - Navigate to "HIFU-cases" folder (either Desktop shortcut or C:\hifu\HIFU-cases)
 - o (Remove accelerometer recordings) Double click on the .txt file named after patient ID (ex. "p206.txt") to open it. Delete the line containing the trial you want to remove (Note: do not leave any empty lines or extraneous spaces in this file when modifying it).
 - O Double click on the _spiral.txt file named after patient ID (ex. "p206_spiral.txt") to open it. Delete the line(s) containing the trial you want to remove (Note: do not leave any empty lines or extraneous spaces in this file when modifying it).
 - Open the folder with the patients id you want to modify. Delete any .csv files with the trail you want (up to 4 for each trial you want to delete 1 for accelerometer, 3 for drawn spirals/line).
 - o Next time you start the software, the patient will not show up on the list of previous accelerometer spirals in the "Trials setup" tab.
 - o Analyze the data again to avoid any potential crashes while plotting