CDP 2.0 Development GUI\*

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**Note**\*: This is not the GUI for the final product, but a GUI for aiding the in the development of the BRADx project with the sole purpose of maintaining a high-level user interface for interacting with their CDP 2.0 unit.

Table of Contents

[Overview 5](#_Toc123225558)

[Current GUI Capabilities 5](#_Toc123225559)

[Update: 12/29/2022 5](#_Toc123225560)

[Image 5](#_Toc123225561)

[Filter 6](#_Toc123225562)

[LED 6](#_Toc123225563)

[Options 7](#_Toc123225564)

[Brightfield 7](#_Toc123225565)

[Auto-Focus 7](#_Toc123225566)

[Save View 8](#_Toc123225567)

[Load View 8](#_Toc123225568)

[Scan Chip 8](#_Toc123225569)

[Home Imager 8](#_Toc123225570)

[LED Intensity 8](#_Toc123225571)

[Relative Moves 8](#_Toc123225572)

[Note 8](#_Toc123225573)

[Thermocycle 8](#_Toc123225574)

[Thermocycler Option Menu 9](#_Toc123225575)

[Cycles Entry 10](#_Toc123225576)

[Thermocycle Temperature Plot 10](#_Toc123225577)

[Temperature Settings Entries 10](#_Toc123225578)

[Time Settings Entries 11](#_Toc123225579)

[Thermocycler Progress Bar 11](#_Toc123225580)

[Thermocycler Image 11](#_Toc123225581)

[Thermocycle Checkboxes 12](#_Toc123225582)

[Start Button 12](#_Toc123225583)

[Load Button 13](#_Toc123225584)

[Save Button 13](#_Toc123225585)

[Home Button 13](#_Toc123225586)

[Build Protocol 13](#_Toc123225587)

[Tips 14](#_Toc123225588)

[Tray Option Menu 14](#_Toc123225589)

[Column Option Menu 15](#_Toc123225590)

[Action Option Menu 15](#_Toc123225591)

[Add Button 16](#_Toc123225592)

[Motion 16](#_Toc123225593)

[Consumable Option Menu 16](#_Toc123225594)

[Tray Option Menu 17](#_Toc123225595)

[Column Option Menu 17](#_Toc123225596)

[Tip Option Menu 17](#_Toc123225597)

[Add Button 18](#_Toc123225598)

[Pipettor 18](#_Toc123225599)

[Volume Entry 18](#_Toc123225600)

[Tip Option Menu 18](#_Toc123225601)

[Action Option Menu 18](#_Toc123225602)

[Pressure Option Menu 18](#_Toc123225603)

[Add Button 19](#_Toc123225604)

[Time 19](#_Toc123225605)

[Delay Entry 19](#_Toc123225606)

[Units Option Menu 19](#_Toc123225607)

[Add Button 19](#_Toc123225608)

[Other 19](#_Toc123225609)

[Options Option Menu 20](#_Toc123225610)

[Add Button 20](#_Toc123225611)

[Protocol Progress Bar 20](#_Toc123225612)

[Action Table 21](#_Toc123225613)

[Start Button 21](#_Toc123225614)

[Load Button 21](#_Toc123225615)

[Save Button 22](#_Toc123225616)

[Delete Button 22](#_Toc123225617)

[Optimize 22](#_Toc123225618)

[Deck Plate Image 22](#_Toc123225619)

[Consumable Option Menu 23](#_Toc123225620)

[Tray Option Menu 23](#_Toc123225621)

[Column Option Menu 23](#_Toc123225622)

[Use Z Checkbox 23](#_Toc123225623)

[Slow Z Checkbox 24](#_Toc123225624)

[Home Button 24](#_Toc123225625)

[Move Button 24](#_Toc123225626)

[Update Button 24](#_Toc123225627)

[Print Button 24](#_Toc123225628)

[Home Z Button 24](#_Toc123225629)

[Home Y Button 24](#_Toc123225630)

[Home X Button 24](#_Toc123225631)

[Tip Size Option Menu 24](#_Toc123225632)

[Note 25](#_Toc123225633)

[Service 25](#_Toc123225634)

[Status 26](#_Toc123225635)

[Configure 27](#_Toc123225636)

[Unit Settings Option Menu 28](#_Toc123225637)

[Relative Move Settings Entries 28](#_Toc123225638)

[Thermocycler Clamp Settings Entries 28](#_Toc123225639)

[Heater/Shaker RPM Settings Entry 29](#_Toc123225640)

[Tip Tray Box Settings Option Menus 29](#_Toc123225641)

# Overview

# Current GUI Capabilities

## Update: 12/29/2022

Currently this GUI is capable of setting up thermocycling protocols with two limitations which will be discussed in the Thermocycle section, generate protocol scripts, optimize and fine tune coordinates on the deck plate, provide debugging tips for certain service tasks, current unit status based on the unit’s primary manager, and configuring the unit. The imaging portion is completed by David Bauer but is not implemented within this GUI currently.

# Image

Figure 1 contains an image of the Image tab, it is currently not fully functional and must be ported over from David Bauer implementation. The purpose of this tab is to enable live imaging of a chip loaded on any of the reader trays. Functionality will include selecting the desired filter, LED, turning on brightfield, auto-focusing, view saving and loading, chip scanning functionality, imager motion, LED intensity control, and fine tuning of the imager position.

A screenshot of a computer

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Figure : Image tab with default settings

## Filter

Filter is an option menu with the following options shown in Figure 2.Each filter option corresponds to a filter wheel location for the imager.

Graphical user interface, application

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Figure : Image tab, Filter option menu options

## LED

LED is an option menu with the following options shown in Figure 3. The default selection is set to *Off* with the interpretation that no LED is currently on. As will be discussed in the LED Intensity section, this option menu is linked to the LED intensity, currently, if you select to turn on any of the LED options, this will set the LED intensity to 100%, this will be changed in the future, but is currently enforced by a the lower level code which will be updated and then that change will be mirrored here in the GUI.

A screenshot of a phone

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Figure : Image tab, LED option menu options and default selection

## Options

### Brightfield

The Brightfield button first changes the filter wheel location to HEX in a blocking fashion depending on the unit (unit A and B cannot have motion while the LEDs are on) then turns on the FAM LED. These changes are indicated with an update to the Filter and LED option menu selections as well as the LED Intensity slider as shown in Figure 4 on the left. When the Brightfield button is clicked again the location of the filter wheel remains at HEX, the LED is turned off, and the LED intensity is set respectively as shown in on Figure 4 the right.

A screenshot of a phone

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Figure : Image tab, Brightfield on (left) and off (right)

### Auto-Focus

This feature is currently nonfunctional; however, it is intended to be used to focus the imager along the Z-axis for the user to find the focal plane, making live imaging before full automation easier.

### Save View

This feature is currently nonfunctional; however, it is intended to be used to save the current view of the imager as seen on the GUI. These saved images would then be automatically sent to the cloud for processing if the user so desires.

### Load View

This feature is currently nonfunctional; however, it is intended to be used load previously saved imager views. In the future image analysis could be included in the GUI, therefore loading in an imager view from a previous run could be useful in analyzing the image from the GUI.

### Scan Chip

This feature is currently nonfunctional; however, it is intended to be used to scan an entire chip avoiding user intervention.

### Home Imager

This feature is currently nonfunctional; however, it is intended to be used home the imager.

### LED Intensity

The LED intensity is controlled by a slide bar in 10% increments, currently only 0% and 100% are functional, i.e. the LED is either fully off or fully on. This will be a configurable parameter for the user at a per LED level in the future.

### Relative Moves

This feature is currently nonfunctional; however, it is intended to be used to set the relative move distance in microsteps in order to control the exact position of the imager for live imaging. Motion along each axis will be controlled by the user’s arrow keys on the keyboard, motion along the x-axis will be controlled by the left and right arrow keys, backwards and forwards will be controlled by the up and down arrow keys, and up and down motion along the z-axis will be controlled by Shift+up and Shift+down arrow keys.

## Note

Motion of the imager itself beyond relative moves will be controlled by the A, B, C, and D keys. The A key will move the imager to a defined position under Thermocycler A, and similar functionality is set for the other thermocyclers.

# Thermocycle

Figure 5 shows the Thermocycle tab with the default settings. This tab allows the user to set specific thermocycle protocols for each of the 4 thermocyclers (A-D). Within this figure is an image of the thermocycler from directly above, Thermocycler A is the first thermocycler in that image (closest to the top right corner of the GUI window), below that is B, C, and D respectively. Tray AB is connected to Thermocycler A and B, while Tray CD is connected to Thermocycler C and D. An overview of this tab is as follows, the user can set the number of cycles, temperatures, times at each temperature, select which thermocycler is running, and control the motion of the trays and thermocycler clamps.

Graphical user interface

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Figure : Thermocycle tab with default settings

## Thermocycler Option Menu

The Thermocycler is an option menu with the options shown in Figure 6.

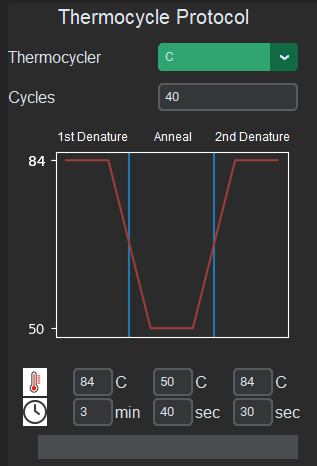
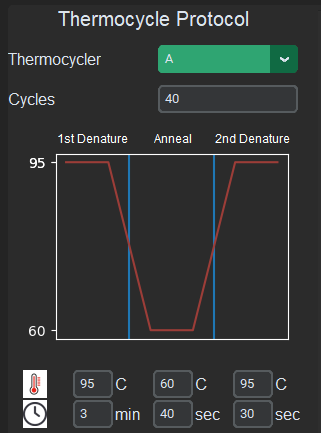
Graphical user interface, application

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Figure : Thermocycle tab, thermocycler option menu options with the default selection (A)

The default option is Thermocycler A, by changing the option in the option menu, this changes control of which thermocycler you are going to set the thermocycling protocol for, i.e. all other portions of the Thermocycle tab will be with respect to the Theromcycler option you have chosen. For example, if you select to work with Thermocycler D, the Thermocycle Temperature Plot will change accordingly, the temperature entries will be according to Thermocycler D. This is illustrated in Figure 7 where the image on the left is the protocol to be run on Thermocycler A and the image on the right is the protocol to be run on Thermocycler C.

Figure : Thermocycle tab, example of setting a different protocol on two different thermocyclers



## Cycles Entry

The Cycles entry currently is controlled by the Thermocycler A and sets all other thermocyclers according to the value set for Thermocycler A. This will be fixed in the future. This means that each thermocycler will run with the same number of cycles. The default number of cycles is 40.

## Thermocycle Temperature Plot

The Thermocycle Temperature Plot is unique to each thermocycler as set by the Thermocycler option menu as discussed in the Thermocycler subsection. The curve is broken into 3 parts, the temperature for the 1st denature step, the anneal temperature, and the 2nd denature temperature. These values are controlled by the Temperature Setting entries as will be discussed in in the Temperature Settings subsection. The uniqueness is shown in Figure 7.

### Temperature Settings Entries

The Temperature Settings entries allow the user to specify the temperature of the 1st denature temperature, the anneal temperature during cycling, and the 2nd denature temperature during cycling, all in Celsius. Changing these entry values for a selected thermocycler will update the Thermocycle Temperature Plot accordingly. The blue vertical bars on the plot separate the three distinct temperature settings, the y-axis in the temperature scale, and the x-axis has no physical meaning.

### Time Settings Entries

The Time Setting entries allow the user to specify how long the 1st denature step is (default is 3 min the current working standard used by the Ann Arbor team on unit A), the anneal time, and the 2nd denature time, both which are in seconds.

## Thermocycler Progress Bar

The Thermocycler Progress Bar is an indication of how much is left in the current Thermocycle protocol run and will be full when the thermocycling protocol is complete.

## Thermocycler Image

The Thermocycler Image as discussed in the overview of the Thermocycle section allows for user interaction. By default the trays are both in their homed position (open) and the heaters are raised in their homed position as seen in Figure 5. The user is able to click on this image to open/close trays and lower/raise heaters. If the image on the GUI does not match the reality of the unit home the trays and readers as discussed in the Home subsection. To be specific, clicking on Tray AB will either open or close the tray, this is only allowed if the image on the GUI indicates that Thermocycler A and B are both in their homed positions. An example of this is shown in Figure 8, on the left side of this figure Tray AB was clicked allowing it to close, this was possible because Thermocycler A and B were both in their homed positions (the image will not change if an action is not allowed assuming that we started the GUI and instrument with trays and heaters homed). On the right and side of the figure it can be seen that the user lowered Thermocycler A while Tray AB was closed, if the user clicks on Tray AB again to open it the image will not change since this action is not allowed and the instrument will act accordingly, to open Tray AB again from this configuration the user must click on Thermocycler A to open it first. A quick note, Figure 8 also shows the difference in images between open and closed trays, as well as raised and lowered Thermocyclers.

A picture containing game

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Figure : Thermocycle tab, thermocycler image with Tray AB closed and all heaters raised (left). Tray AB closed with Thermocycler A lowered which is an example of a case which prevents Tray AB from reopening (right).

## Thermocycle Checkboxes

The Thermocycle Checkboxes allow the user to specify which thermocyclers to use during the protocol (currently it is advised to run no more than 3 at a time), the default thermocycler are shown in Figure 5. Successful thermocycle tests have been performed with 3 thermocyclers at a time but not 4, use at own risk, this is not recommended. These checkboxes only affect what the instrument does when the start button is clicked in the Thermocycle tab as discussed in the Start subsection.

## Start Button

The Start button allows the user to start their defined protocol as set by the user specified options, the instrument will start even if all trays are open and thermocyclers raised so please be aware of this capability. During a protocol run, the start button is disabled and won’t re-enable till the protocol is fully done.

## Load Button

The Load button is nonfunctional currently; however, it is intended to allow the user to load previously saved thermocycling protocols.

## Save Button

The Save button is nonfunctional currently; however, it is intended to allow the user to save the current protocols for all the thermocyclers.

## Home Button

The Home button allows the user to home the thermocyclers, this includes all four thermocyclers first then their respective trays. It also updates the thermocycler image on the GUI to the fully homed positions.

# Build Protocol

The Build Protocol tab allows the user to generate scripts for the CDP 2.0 unit to run, this tab is almost fully functional, the to be finished functionalities are a few of the protocol option such as moving lids and chips, better action table manipulation for editing mistakes or making changes. The user is able to add actions to the Action Table by using the option menus provided, these include tip eject and pickup, motion to specific consumable locations, pipettor functionality (aspirate, dispense, and mix), set delays within the protocol, and include higher level functions such as generate droplets, extraction, pre-amp, or even subsections of a full 8 sample extraction. The user can also save and load protocols which will load them into the Action Table.

A screenshot of a computer

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Figure : Build Protocol tab with the default options selected

## Tips

The Tips portion of the tab allows the user to select from 3 different option menus (Tray, Column, and Action) which together can then be added to the Action Table. By default no Tray or Column is specified, but the default Action is *Eject*. The type of tip in each column of tip tray A, B, C, and D are set in the Configure tab as discussed in the Configure section. The Tips portion of the Build protocol tab is shown in Figure 10.

Graphical user interface

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Figure : Build Protocol tab, tips portion with defaults

### Tray Option Menu

The Tray option menu allows the user to specify which tray they would like to either pickup or eject tips. The options are shown in Figure 10.

Graphical user interface, application

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Figure : Build Protocol tab, tray option menu options for the tips portion of this tab, the default is setting to nothing

### Column Option Menu

The Column option menu allows the user to specify which column of the specified tray to use for tip eject or pickup. The options available to the user as well as the default option are shown in Figure 11.

A screenshot of a computer

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Figure : Build Protocol tab, column options for the tips portion of the tab, and the default set to nothing

### Action Option Menu

The Action option menu allows the user to specify which action they would like to perform. The options available to them are shown in Figure 12.

Graphical user interface, application

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Figure : Build Protocol tab, action options for the tips portion of the tab with the default set to Eject

### Add Button

The Add button for the tips portion of the Build Protocol tab allows the user add their selected options and action to the Action Table, only after clicking this action button will this action be added to the protocol the user is building.

## Motion

The Motion portion of the Build Protocol tab allows the user to specify where they want the pipettor head to move by selecting the consumable and adding it to the Action Table. This portion of the tab is shown in Figure 14.

Graphical user interface

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Figure : Build Protocol tab, motion portion with default settings

### Consumable Option Menu

The Consumable option menu allows the user to select which consumable they are trying to move to. The current available options are shown in Figure 13. It must be noted that the DG8 1000 option is only available for Unit A currently, the DG8 chip holder was custom printed here in Ann Arbor.

Graphical user interface, application

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Figure : Build Protocol tab, consumable options for the motion portion of the tab with the default set to nothing

### Tray Option Menu

The Tray option menu is the same as for the one discussed in the Tray Option Menu subsection, the only difference is that the Tip Transfer Tray is not an option here.

### Column Option Menu

The Column option menu allows the user to select which column of the consumable to use, the options will not be shown here since they are the same as shown in Figure 11.

### Tip Option Menu

The Tip option menu allows the user to select what tip size is currently on the pipettor during the motion. The available options to the user are shown in Figure 14. If the tip is set to *None* and the consumable is not set to *DG8 1000* the pipettor head will not move in the z. Caution must be taken when building the protocol, if you set the tip size to 50 µL but the pipettor has 1000 µL tips on, the pipettor head will move down and bend the tips significantly. In the future further safety features will be included at the GUI level to avoid this issue.

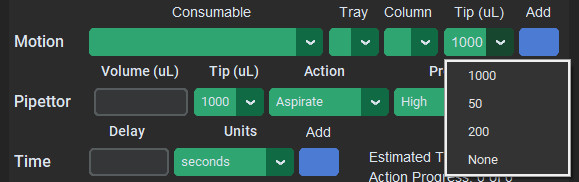


Figure : Build Protocol tab, tip options for the motion portion of the Build Protocol tab with the default set to 1000

### Add Button

The Add button for the Motion portion of the Build Protocol section allows the user to add the motion action to the Action Table.

## Pipettor

The Pipettor portion of the Build Protocol tab allows the user to specify what the pipettor does its current position. The user can specify how much the pipettor aspirates or dispenses as well as the pressure at which this occurs. The Pipettor portion of the Build Protocol tab is shown in Figure 17.

Graphical user interface, text, application

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Figure : Build Protocol tab, pipettor portion with default settings

### Volume Entry

The Volume entry allows the user to specify how much the pipettor should aspirate, dispense, or include in a mix (single aspirate then dispense). The value entered should be given in µL.

### Tip Option Menu

The Tip option menu allows the user to specify the current tip size, the options are the same as shown in Figure 10, however, *None* is excluded since these actions cannot be performed with out a tip.

### Action Option Menu

The Action option menu allows the user to specify the action to take with the pipettor, the options are shown in Figure 18.

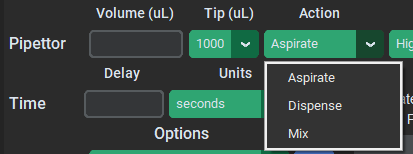


Figure : Build Protocol tab, action options for the pipettor portion of the tab with the default settings shown

### Pressure Option Menu

A screenshot of a computer

Description automatically generated with medium confidenceThe Pressure option menu allows the user to specify the pressure to use during aspiration or dispense (also included in the mix but the pressure is used for both, i.e., if you want one pressure for the aspirate and a different pressure for the dispense use two separate actions rather than a single mix action). The options available to the user are shown in Figure 19.

Figure : Build Protocol tab, pressure option portion of the tab with default settings shown

### Add Button

The Add button for the pipettor portion of the Build Protocol tab allows the user to add the action to the Action Table, the action will not be added if no volume is specified or if an non integer volume is specified.

## Time

The Time portion of the Build Protocol tab allows the user to include delays into the protocol they are building. This portion is shown in Figure 20.

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Figure : Build Protocol tab, time portion of the tab with default settings shown

### Delay Entry

The Delay entry allows the user to specify how long they want the delay to be with respect to the units they select as specified in the Units Option Menu subsection.

### Units Option Menu

The Units option menu allows the user to select the unit to use for the delay amount they want. The options available to the user are shown in Figure 21.

A screenshot of a computer

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Figure : Build Protocol tab, units options for the time portion of the tab with the default settings shown

### Add Button

The Add button for the time portion of the Build Protocol tab allows the user to add the delay action to the Action Table. It must be noted, currently only integer values can be used, decimal values will be included in the future.

## Other

The Other portion of the Build Protocol tab allow the user to add other actions to the Action Table, these are in general more complicated than simple moves, aspirates, or dispenses. This portion of the tab is shown in Figure 23.

Graphical user interface, application, website

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Figure : Build Protocol tab, other portion of the tab with the default setting shown

### Options Option Menu

The options available to the user are shown in Figure 22. Options that are currently not available at the GUI level are labeled as such with a Not Functional tag.

Text

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Figure : Build Protocol tab, other options for the other portion of the tab with the default option set to home pipettor

### Add Button

The Add button for the other portion of the tab allows the user to add the selected option to the Action Table.

## Protocol Progress Bar

The Protocol Progress Bar allows the user to see how far into the protocol they are while it is running. Along with the progress bar filling up the current action number being worked on out of the total number of action is displayed above the progress bar. The estimated time currently is not shown but will be in the future. An example of the progress bar filling up and the action count changing is shown in Figure 24.

Graphical user interface, text

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Figure : Build Protocol tab, progress bar showing progress during a protocol run

## Action Table

The Action Table of the Build Protocol tab allows the user to see what has been added to the protocol being build along with what part of the protocol is being executed during a run. The Action Table is shown in Figure 25. As can be seen from this figure, actions are listed in chronological order, and they will be executed in the order they are shown in the table. Each action in the table is blocking, i.e., during one action, the following action will not be started until the current action is complete. If the user wants to add a new action between two actions already in the table the user should click the first action of the two actions then click the respective add button, this will add the new action below the previously selected action. Further table manipulation will be discussed in the Delete Button subsection. During an actual run the current action in the table will be selected to show which part of the protocol is being run.

Graphical user interface, text, application

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Figure : Build Protocol tab, action table portion of the tab with an example protocol shown

## Start Button

The start button of the Build Protocol tab allows the user to start all the actions starting from the first action in the Action Table. The start button will be disabled during the run and will be re-enabled after the protocol run is complete.

## Load Button

The load button for the Build Protocol tab allows the user to load in protocol files which are currently simple text files with the actions as shown in the Action Table but in the text file, in other words, one action per line. The action text must be exact in these protocol files, so if the user wants to type the protocol file which is not suggested, the wording must be the exact same as would be set for selecting from the GUI.

## Save Button

The save button for the Build Protocol tab allows the user to save the current protocol that is in the Action Table to a protocol text file. These can then be loaded in later.

## Delete Button

The delete button for the Build Protocol tab allows the user to delete one or more selected actions from the Action Table. This is beneficial if you need to restart a run of a protocol and want to start from somewhere that is not the true start of the protocol or if a mistake was made during the protocol building process.

# Optimize

The Optimize tab allows the user to fine tune coordinates for their unit. The Optimize tab is shown in Figure 26.

Graphical user interface

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Figure : Optimize tab with the default settings shown

## Deck Plate Image

The Deck Plate image allows the user to click on any consumable along with any column of that consumable, doing so will fill in the consumable option menu, tray option menu, and column option menu for what was clicked on. If the user wants to move to the selected position the user will have to click the Move button. This tab is meant to be used for fine tuning coordinates or finding new coordinates. Often a coordinate is unknown for new units, a known coordinate can be then used as an initial guess and fine-tuned relative moves can be used to move the pipettor head to the desired location. The chiller is currently not shown in the image since it is not being used but will be added in the future. Currently tray locations and DG8 chip holder locations are not included in the image but can easily be added in the future if needed. The deck plate image can be seen in Figure 26.

## Consumable Option Menu

The consumable option menu allows the user to select where to move on the deck plate, it also allows the user to see what consumable was clicked on in the deck plate image. The available options currently are shown in Figure 27.

Diagram

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Figure : Optimize tab, consumable options available with the default setting shown

## Tray Option Menu

The tray option menu allows the user to select the tray for the selected consumable, also it shows what tray was clicked on in the deck plate image. The options available are the same as those shown in Figure 11 without the tip transfer tray option.

## Column Option Menu

The column option menu allows the user to select the column for the selected consumable, it also shows the user which column was selected when clicking on the deck plate image. The options available are the same as shown in Figure 12.

## Use Z Checkbox

The Use Z checkbox allows the user to select if they want to use Z motion during a move when the move button is clicked. By default it is selected, if the user just wants to move to the x,y position they should unselect the use z checkbox.

## Slow Z Checkbox

The Slow Z checkbox allows the user to specify if they want the Z motion during a move when the move button is clicked to be slow. By default it is filled in, however, if the user wants to use the full speed z velocity they should unselect the slow z checkbox.

## Home Button

The home button allows the user to home the upper gantry pipettor head to the home position, this is a good practice after the unit has been turned on (homing is slow).

## Move Button

The move button allows the user to move the pipettor head to the selected position. Relative moves do not require the user to press the move button, these kinds of moves will be discussed in the Note subsection.

## Update Button

This button is not fully functional, currently it is very similar to the print button, in the future it will update the file containing the coordinates for the unit being tested, this will have to be login controlled to prevent accidental coordinate changing.

## Print Button

The print button allows the user to get the current position of the pipettor head in the terminal that launched the GUI. Since the response is not instantaneous, the printed position is not “accurate”, if you want an “accurate” reading wait till the pipettor is stationary.

## Home Z Button

The home z button allows the user to home the pipettor along the Z axis, this is a slow motion.

## Home Y Button

The home y button allows the user to home the Y axis of the pipettor, this is a slow motion.

## Home X Button

The home x button allows the user to home the pipettor along the X axis, this is a slow motion.

## Tip Size Option Menu

The tip size option menu allows the user to specify what tip size the pipettor has on, this importance of this option dictates how far the pipettor head will move down. All coordinates are currently based on the 1000 µL tips and motion with tips other than these tips move relative to this defined coordinate based on the 1000 µL tip coordinate. The available options are shown in Figure 28.

Graphical user interface, application

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Figure : Optimize tab, tip size options with the default setting shown

## Note

Relative moves for fine-tuning a coordinate can be done using the arrow keys on the keyboard (all motions are with respect to facing the front of the unit). Left and right are performed using the left and right arrow keys. Backwards and forwards are performed using the up and down arrow keys, Lastly, up and down are performed using Shift+up and Shift+down, respectively. The distance moved in these relative moves are set in the Configure tab as discussed in the Relative Move Settings subsection. The defaults for the X, Y, and Z axes are 500, 5000, and 5000 µsteps, respectively. Currently the best way to fine-tune a coordinate is to find the new coordinate, then click the print button to see the coordinate (format is [x,y,z,drip plate]) on the terminal that launched the GUI. This value can then be used to manually update the coordinate in the coordinate.py file for your unit (this is coordinate\_C.py for unit C).

# Service

The Service tab allows the user to select a topic of known issues that have know solutions, these solutions are currently hard coded into the code that creates the GUI but will in the future be pulled from a known unit issue log document. The Service tab with the aspirate topic selected is shown in Figure 29. The idea of this tab is to allow the user to find quick fixes to known issues, this tab is not complete, a service functions portion is to be included with unique options for testing the topic selected. For instance, if the aspirate topic is selected, a service function will be to turn on and off valve 2 to test it is functioning or a function for a quick aspirate test to test air flow in the pneumatic tubes.

Graphical user interface, text

Description automatically generated

Figure : Service tab, aspirate topic selected for an example

# Status

The Status tab allows the user to see the current status of their unit, the status is pulled from the unit status log document on SharePoint and is only up to date as soon as the manager of the unit updates the document. Currently the table is filled on start up but will be changed to update periodically with the last updated date and time. An update button should also be included to make sure the newest log is being used to keep users up to date on their units status. The Status tab is shown for unit A in Figure 30.

Graphical user interface, text, application

Description automatically generated

Figure : Status tab, unit A status shown as an example

# Configure

The Configure tab allows users to configure certain parameters for their unit, any user has access to this tab, in the future certain parameters will be disabled for certain users (such as hard position limits). The Configure tab is shown in Figure 31.

A screenshot of a computer

Description automatically generated with medium confidence

Figure : Configure tab for unit A as an example

## Unit Settings Option Menu

The unit settings option menu is disabled currently and will remain disabled. It can only be changed within the GUI code. The portion of code to change this is shown in Figure 32. This should not be changed unless the user knows what they are doing (i.e. using the same laptop for different units, have the proper software version, and the correct coordinate files). The figure below is only included for completeness.

A screenshot of a computer

Description automatically generated with medium confidence

Figure : Portion of code showing the unit variable for setting the unit settings option

## Relative Move Settings Entries

The relative move setting entries are used to allow the user to set how much they want the relative moves while on the Optimize tab to be, they are un µsteps. The dx, dy, and dz entries correspond to motion along their respective axes.

## Thermocycler Clamp Settings Entries

The thermocycler clamp setting entries allow the user to set what the thermocycler should lower to when the thermocycler image is clicked on in the Thermocycle tab. Changing these settings does not immediately change the position of the thermocycler clamp positions, in other words, if the user lowered the thermocycler with the thermocycler clamp setting at 400000 µsteps then change it to 500000 µsteps the lowered thermocycler will stay at the 400000 µsteps, to move it to 500000 µsteps the user will have to raise double click the thermocycler in the thermocycler image of the Thermocycle tab. The entries are in µsteps.

## Heater/Shaker RPM Settings Entry

The Heater/Shaker RPM setting entry allows the user to set the RPM of the Heater/Shaker during shaking of a protocol run. Similar to the thermocycler clamp settings, this entry does not change the RPM in real time, it is used to fill out the Action Table of the Build Protocol tab, in other words, when you select the *Shake on* option from the other portion of the Build Protocol tab, that action will include the RPM setting that is filled during the addition of that action. This is currently not functional because communication with the Heater/Shaker and scripts are being updated and will be fixed in the future.

## Tip Tray Box Settings Option Menus

The Tip Tray Box Setting option menus are used to specify what tip sizes are in each column of a tip box. By default the first four columns of a tip box are 1000 µL and the rest of the columns are 50 µL.