What's New in Bluestem OS v1.4

For the LI-6800 Portable Photosynthesis System

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Contents

Section 1. Background programs

Section 2. Warmup/system tests

Section 3. File management

Section 4. Fluorescence

Section 5. Matching revisited

Section 6. Soil chamber

Section 7. Other changes

What's new in Bluestem v1.4

Bluestem software version 1.4 for the LI-6800 Portable Photosynthesis System brings a variety of new features and improvements. Here we describe the new features, including file management, USB utilities, trash management, range matching, fluorescence tools, background programs, flow balancing, and soil chamber interface updates.

Section 1. Background programs

Background Programs (BPs) are a new approach to Auto Programs. While they do not replace the Auto Programs, they do provide an alternative with several advantages. You can, for example, easily modify factory-supplied programs, or generate your own from scratch. Also, multiple BPs can be run simultaneously.

A quick overview of BPs is below. The complete guide to writing and using BPs is found at licor.com/documents/be4i41pnc010o1y5084na8ma2i6lzpw5

Accessing

The **Program Builder** button on the Auto Programs page (*Figure 1-1* below) opens the BP's **Open/New** screen, from where one can run or edit existing BPs or create a new BP from scratch.

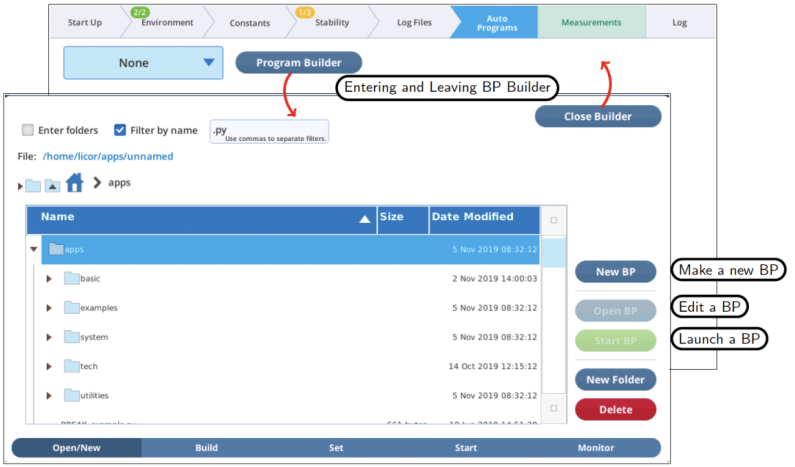


Figure 1-1. BPs buttons and the BP Builder screen.

BPs can be found in the /home/licor/apps folder, and are distributed across several subfolders. In the **basic** folder are several simple BP's that duplicate the functionality of some of the basic Auto Programs. The other BP folders include **examples** (example programs used in the BP user guide), **system** (helper programs used by the system), **utilities** (useful tasks, if you need them), and **tech** (specialty tasks that a technician might use or ask you to run).

Several of the new features in version 1.4 are implemented with the help of BPs, such as *Acquiring range match data* on page 50, *Balanced flow* on page 61, and *Response check test program* on page 66.

Running

BPs can be run by selecting a BP file and tapping Start BP. After that, what happens is entirely up to the BP itself. The files in the basics folder will display a dialog (*Figure 1-2* below) letting the user configure and run, or cancel the program.

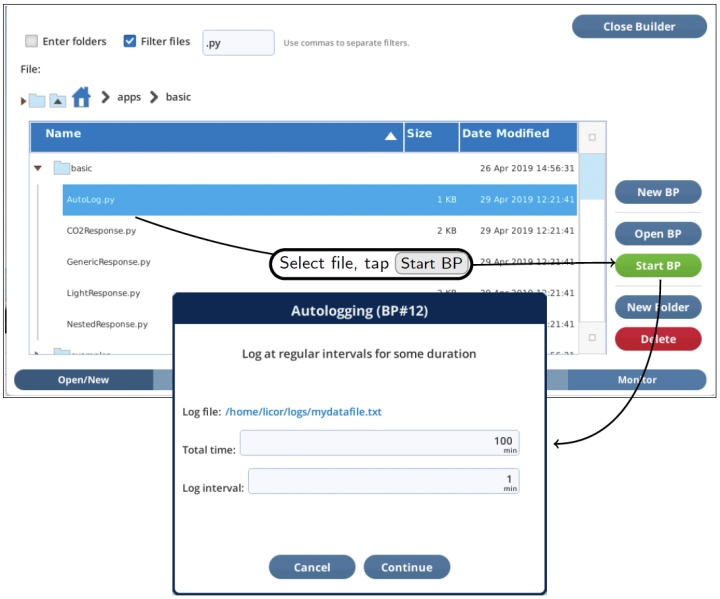


Figure 1-2. BPs in the basics folder have opening dialogs for setting parameters.

Once a BP is running, it can be monitored (and paused, canceled, etc.) from the BP Monitor screen (*Figure 1-3* on the next page).

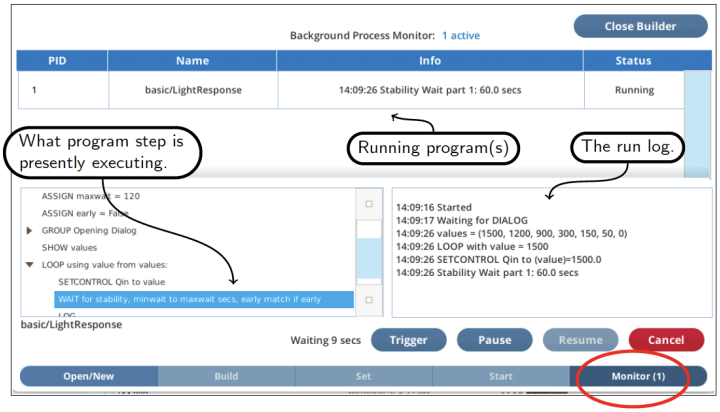


Figure 1-3. Once a BP has been started, you can monitor it in the Monitor *screen.*

Building

The Builder environment lets you make new BPs from scratch, or modify existing BPs. The steps in *Figure 1-4* on the facing page make a trivial BP that waits for 10 seconds then quits, but illustrates the Build, Set, Monitor screens of the Builder environment.

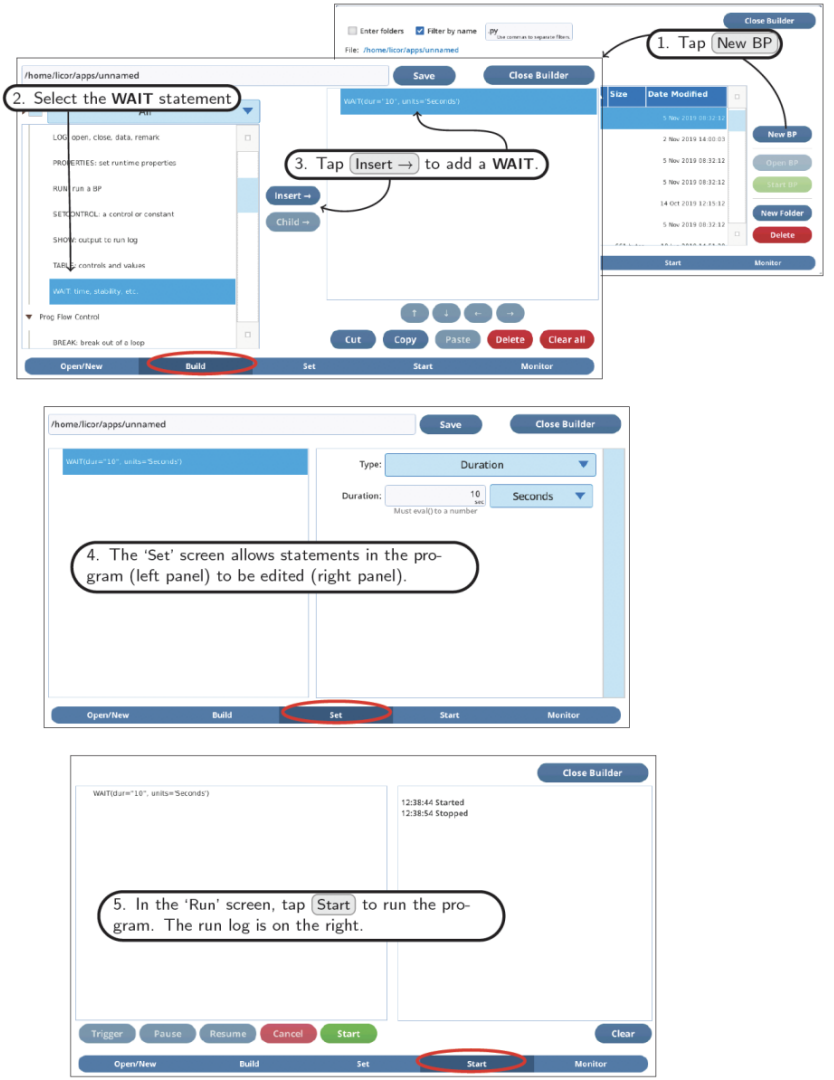


Figure 1-4. **Build** *screen: Add and arrange BP steps.* **Set** *screen: Edit BP steps.* **Start** *screen: Run the program.*

Section 2. Warmup/system tests

Version 1.4 has modified the Warmup/System Tests (*Figure 1-5* below) to differentiate **errors** (serious issues) and **warnings** (things you may or may not need to address). When errors or warnings occur, there will always be one or more suggestions shown to help you address the problem, or determine if it can be ignored.

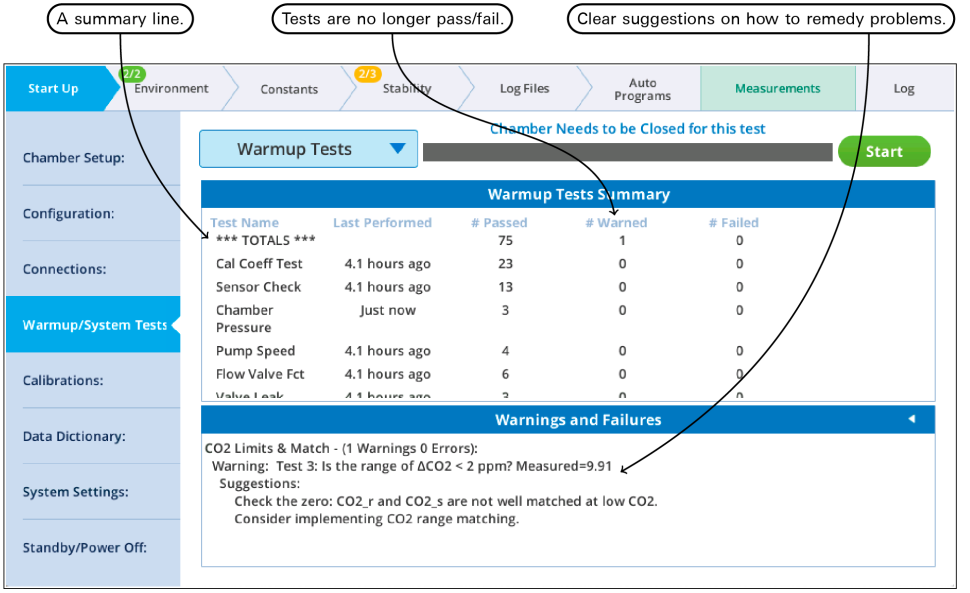


Figure 1-5. The Warmup Tests summary page.

The silent test

All of the system tests that rely on flow rate contain a silent test that checks the state of the flow system. ("Silent" means that output is logged only if there is a problem.) If there is problem with flow, the system test is abandoned, and reasons given.

If the issue is a console leak, the following results:

```
Chamber_Pressure started at 2019-09-25 13:15:34
Overpressure test, Pump=high
```

```
*** Fail *** Test 1: Abandoning Test. System Flow Fault.
    Suggestion:
    Console Flow Leak. Desiccant or Humidifier tube cap loose?
Chamber_Pressure stopped at 2019-09-25 13:15:46
```

If the issue is unexpectedly low flow, the following results:

```
Chamber_Pressure started at 2019-09-25 13:18:35
Overpressure test, Pump=high
*** Fail *** Test 1: Abandoning Test. Expected flow > 100. Measured -0.0.
    Suggestions:
    Is the flow tube from the console firmly connected to the head?
    Is the pump functioning?
Chamber_Pressure stopped at 2019-09-25 13:18:46
```

New and changed tests

The **SodaLime CO2** test has been replaced by **CO2 Limits & Match**. It still checks the soda lime and CO_2 cartridge, but also checks how well the IRGAs are matched at low, ambient, and high CO_2.

The **Drier Humidifer** test has been replaced by **H2O Limits and Match**. It checks the desiccant and humidifier as before, but also how well the H_2O IRGAs are matched at low, ambient, and high humidity.

The reason for the match checking is made clear later in this document. See *Matching revisited* on page 41.

A new test (**Pressure Valve**) checks the chamber pressure overpressure valve for potential interference with the sample cell flow sensor.

Descriptions and details of all tests can be found at:
licor.com/env/support/LI-6800/topics/system-tests.html

Section 3. File management

Version 1.4 introduces a number of file management tools:

A **Trash Folder** is now used to contain all deleted files and folders. Moving unwanted items to the trash can be done from any file viewer that has a Delete button, or by a new utility that allows you to target files using name and date filters. The trash can be browsed, and selected content easily recovered, automatically returned to its place of origin. To recover space, items in the trash can be erased, either all at once or selectively.

A new **Backup / Recovery** utility makes it easy to copy data, settings, and programs to a USB drive. To do a backup, simply insert a drive, select an optional time filter (all files before or after a certain date, or between two dates), and the desired categories: user data, configuration data, and diagnostics. Backups are archived by console serial number and date/time, making it easy to find and browse backed up data. Restoring from a backup is simple and flexible. You can select an entire backup, or narrow it down as far as you like, all the way to a particular folder or file. You also have control over what happens when restoring a file if the original still exists: overwrite it, skip it, or rename it.

For general purpose file copying between a **USB** drive and the LI-6800, there is a utility screen that lets you browse both file systems system side by side, and pick files and folders to copy, putting them exactly where you want them.

Trash

In version 1.4, when a file or directory is deleted, it is moved to a Trash Folder (/home/licor/trash). When items are added to the trash, folders are created as needed so that the deleted item's location in the trash matches its original location. For example, the file

```
/home/licor/logs/mydata/lightcurves/mydata.xlsx
```

would be moved to

```
/home/licor/trash/logs/mydata/lightcurves/mydata.xlsx
```

with all of the intermediate folders (`trash/logs/mydata/lightcurve`) created as needed. Mirroring the directory structure in the trash has two advantages: 1) when browsing the trash, you know where to look to find a file you deleted, and 2) all you have to do to recover an item is to select it; the system knows where to move it based on its location in the trash.

When a file is moved to the trash it will undergo a slight name change if there is a name conflict with something already there. For example, deleting `abc.txt` when there is already a previously deleted `abc.txt` in the trash at the same location will result in the moved item being renamed `abc.txt_0` (or `_1`, `_2`, etc.) to make the name unique.

Moving files to the trash

Any file viewer with a Delete button can move selected files to the trash (*Figure 1-6* below).

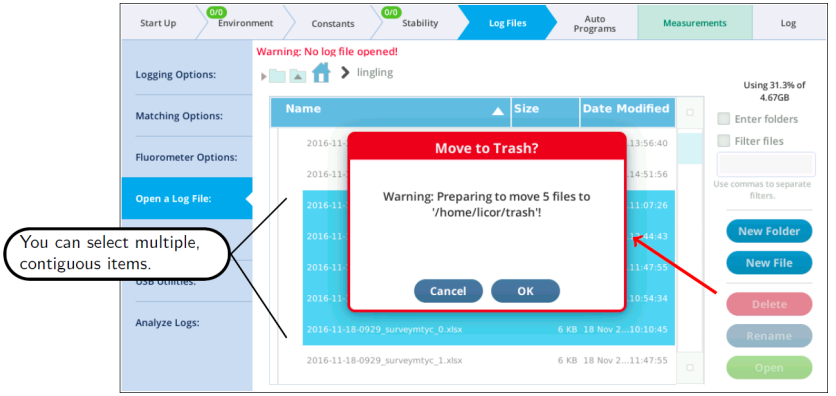


Figure 1-6. **Delete** *buttons in file viewers move items to the trash.*

Suppose you want to remove all fluorometer event .xlsx files that are older than some date. These are distributed in daily folders in the `/home/licor/-logs/flrevents` folder, so stepping through removing them by the Delete button method would be very tedious.

Fortunately, there is a new utility for just this sort of purpose: it is found in the Manage Files screen, accessed by **Log Files > Manage Files > Trash** (see *Figure 1-7* on the next page).

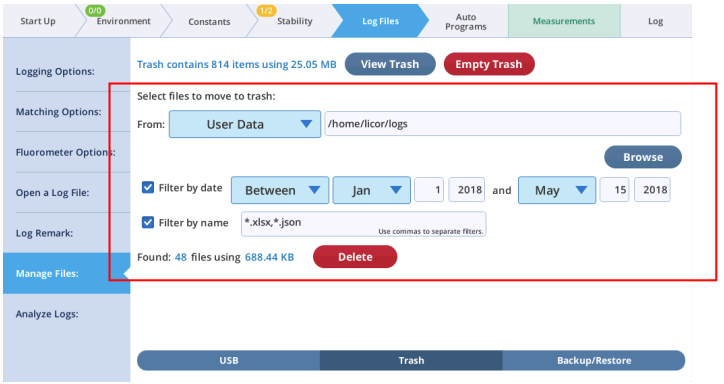
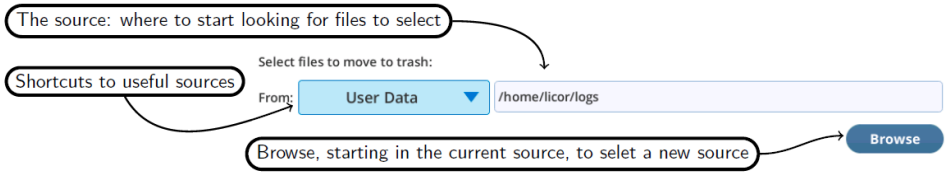


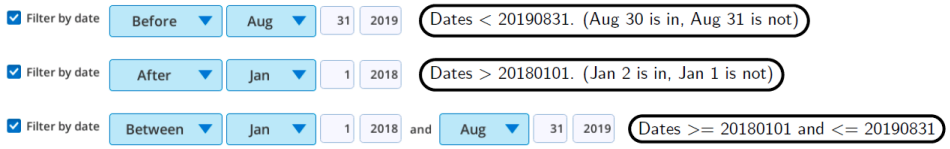
Figure 1-7. A utility for selecting files by name and date filter to move to the trash.

You can target a folder (including all sub-folders), and specify name and date filters. As you edit the target and filters, the system automatically re-scans and indicates the number of files that meet the criteria. The Delete button brings up a dialog that summarizes what will happen, giving you a chance to cancel or proceed.

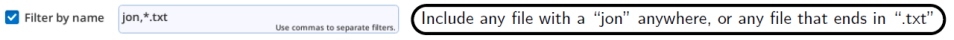
The **source folder** can be selected by editing, picking from a list, or browsing.



The **time filter** can be set to select before, after or between. The before and after are not inclusive (i.e., the date itself is excluded), and the latter is inclusive (the dates are included).



The **name filter** can use Linux wildcards (* and ?). If no wildcards are used, files that contain the filter string anywhere in their name are included. Name filters are not case sensitive. Multiple filters (they are "or-ed") are separated by comma.



The following table illustrates how the name filter behaves.

Filter(s)	File names					
	abc	xyz.txt	Ab.TXT	stXtx	aBXyxT	abc.xlsx
*	✓	✓	✓	✓	✓	✓
.		✓	✓			✓
*.txt		✓	✓			
txt		✓	✓	✓		
ab	✓		✓		✓	✓
xy, *.txt		✓	✓		✓	
????xt			✓		✓	
???.*		✓				✓

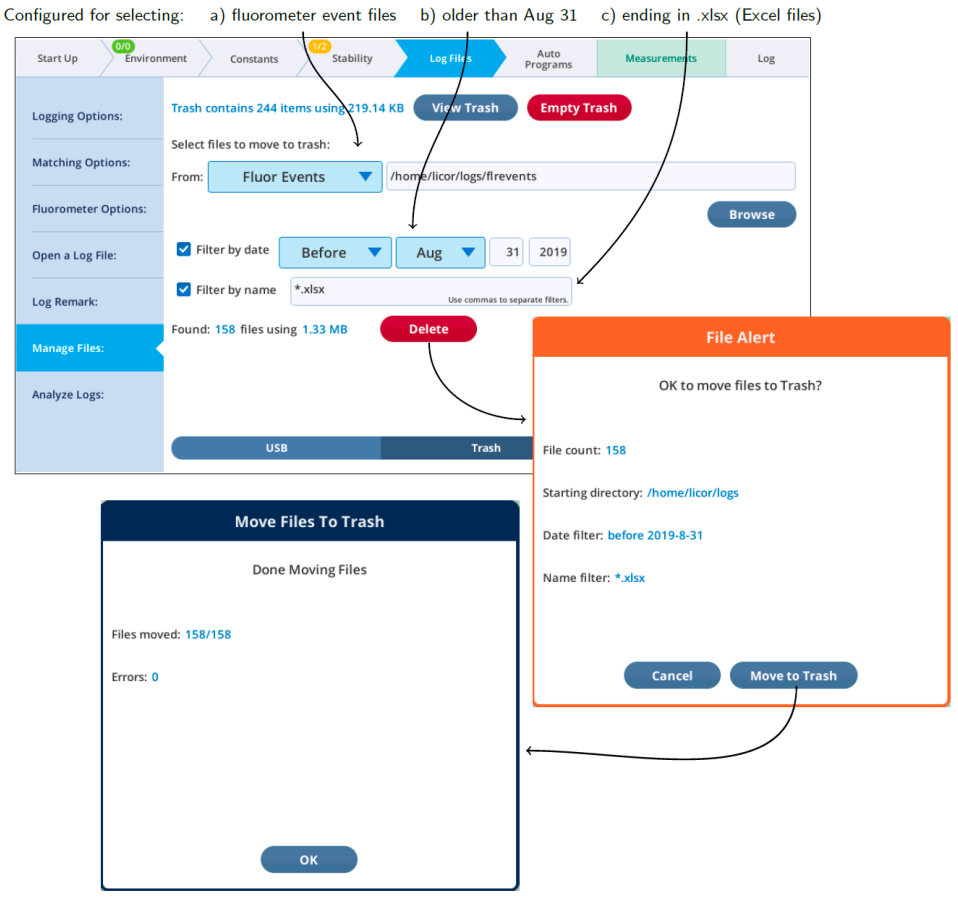


Figure 1-8. A utility for selecting files by name and date filter to move to the trash.

Recovering trash items

To recover items that have been sent to the trash, tap the **View Trash** button. This opens a viewer from where you can select items to recover. Multiple selection (contiguous items) is supported. Note that you can choose what to do in the case of a name duplication.

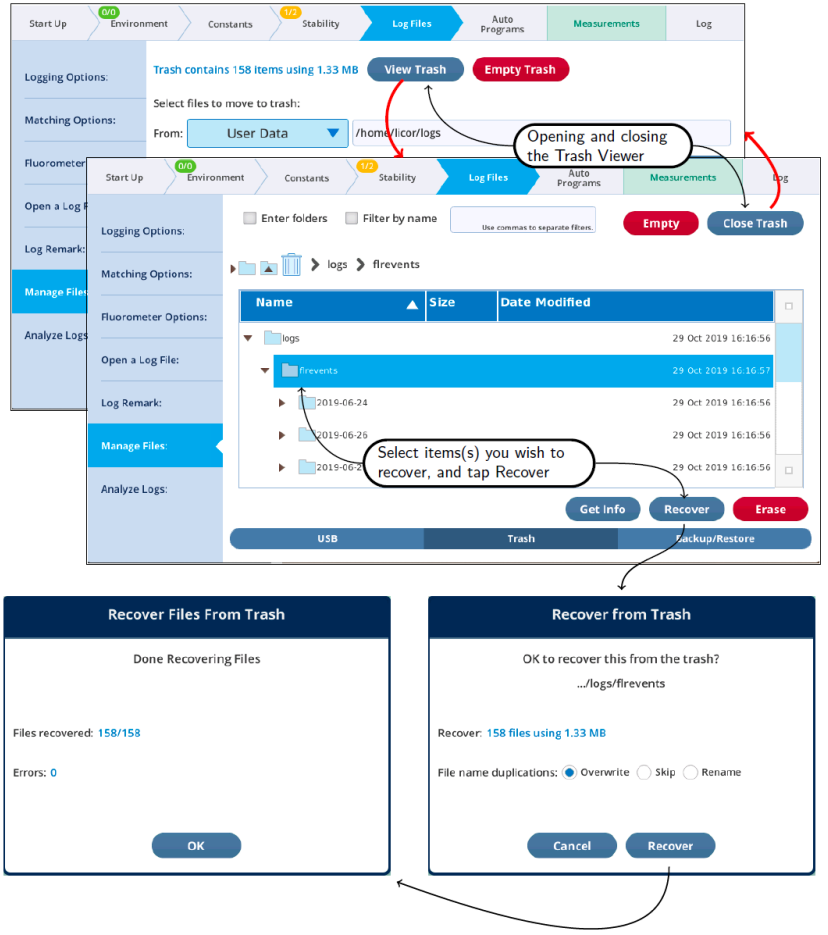


Figure 1-9. The **Trash Viewer** *lets you view and recover items.*

Depending on how you select items to be recovered from the trash, you may see empty folders afterwards (*Figure 1-10* on the next page).

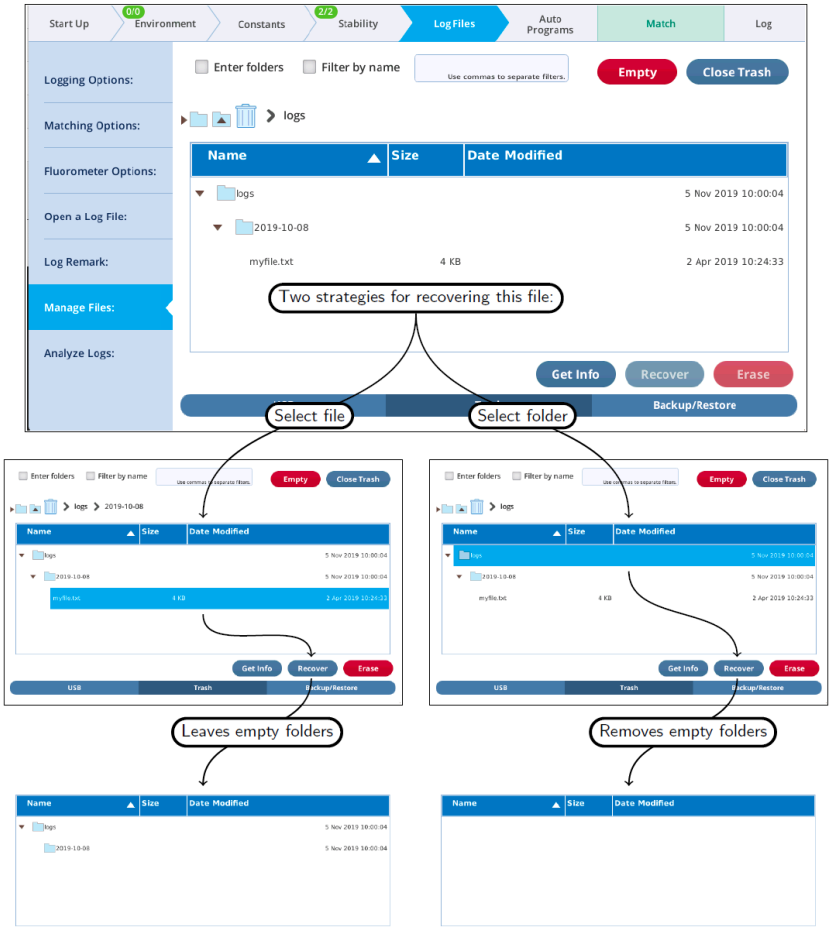


Figure 1-10. Folders emptied when trash is recovered are removed, but only if they are the targeted selection, or a child thereof.

You can remove empty folders by Recover or Erase, although they do not count as files in the ensuing dialogs ("Recover 0 files using 0 bytes"). What actually happens when "recovering" an empty folder is that the system first moves the contents (there are none, it is empty), then erases the folder if it is empty (it is).

Emptying the trash

Moving items to the trash does not free up space on the file system. To do that, items need to be erased from the trash. **Once an item is erased it can never be recovered.** To erase everything, use the Empty Trash button (*Figure 1-11* below, top). Partial erasures can also be done (*Figure 1-11* below, bottom).

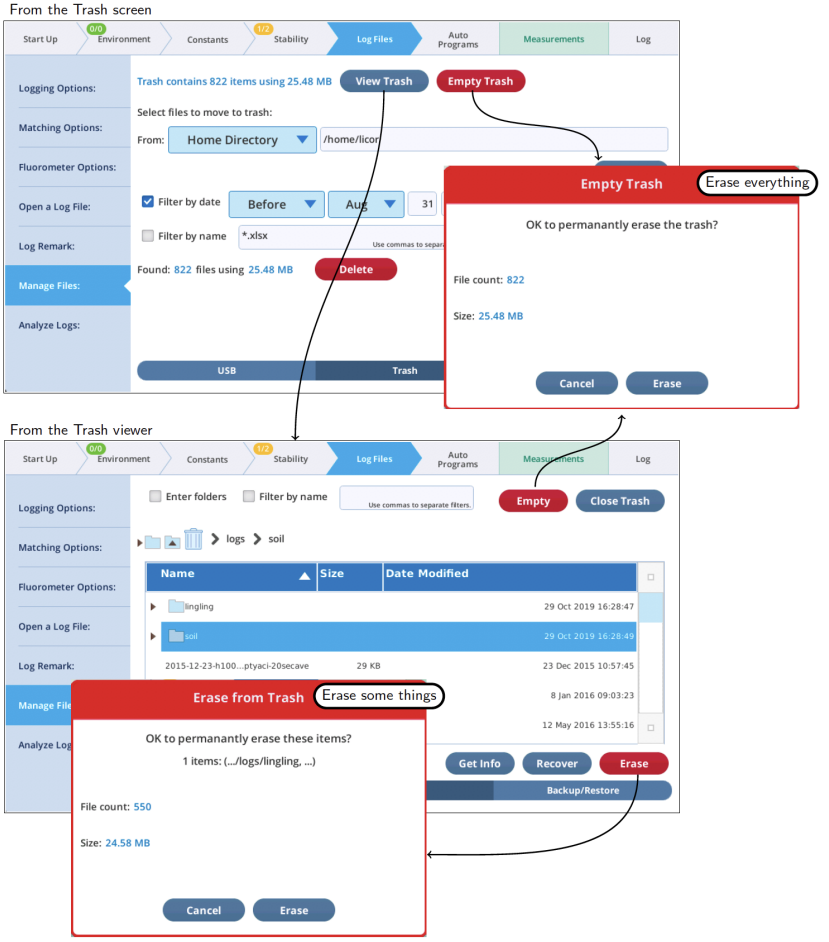


Figure 1-11. Erasing all or some of the trash. **Warning**: *This can't be undone.*

Another method of selectively erasing trash is to point the **Move to Trash** utility to the trash folder, and set the filters to select the files you want to permanently get rid of.

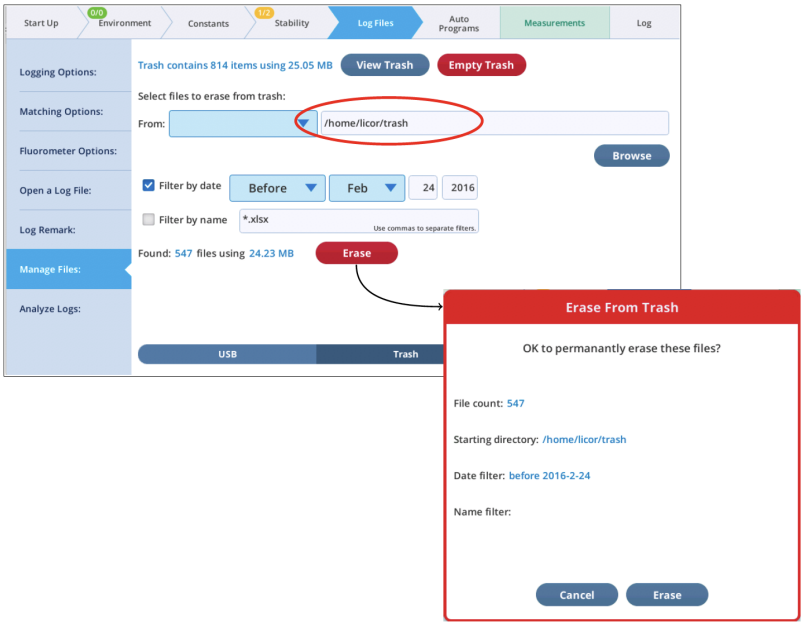


Figure 1-12. Using the **move to trash** *utility to selectively erase items from the trash.*

What's using the space?

You can get information on where file space is being used by the Get Info button available in many of the file broswers. For example, in the **Move to Trash** utility, set the target to the home folder (`/home/licor`), tap Browse, and then tap Get Info.

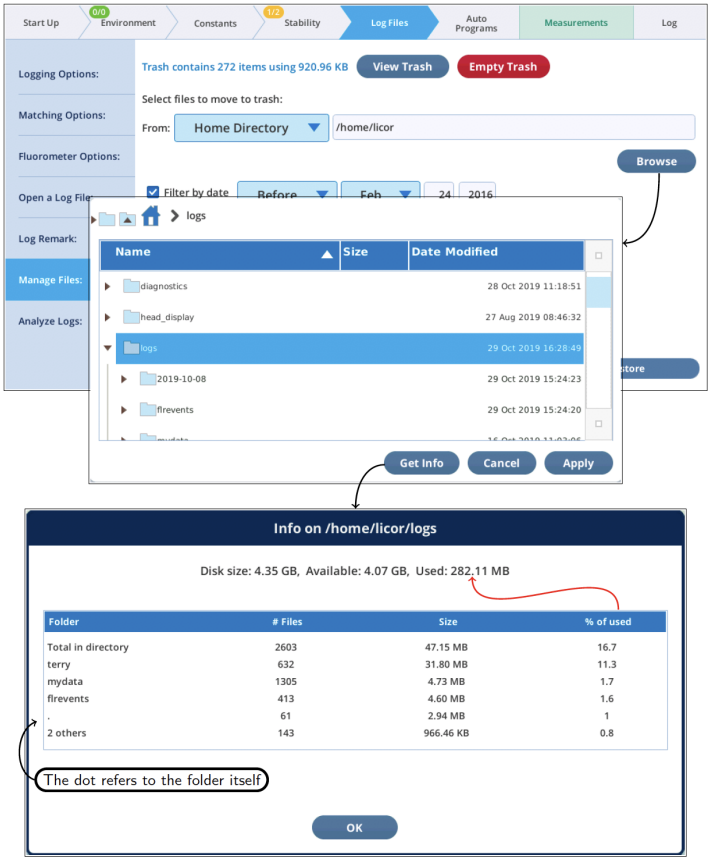


Figure 1-13. The **Get Info** *display for a folder ranks its subfolders folders by size.*

Backup and restore

The **Backup/Restore** page provides utilities for backing up to USB, and restoring files a USB backup to the console. Since backups created on USB are easy to nav-

igate (folder structure is maintained), backing up is also a quick and easy way to get data files from the console to your computer.

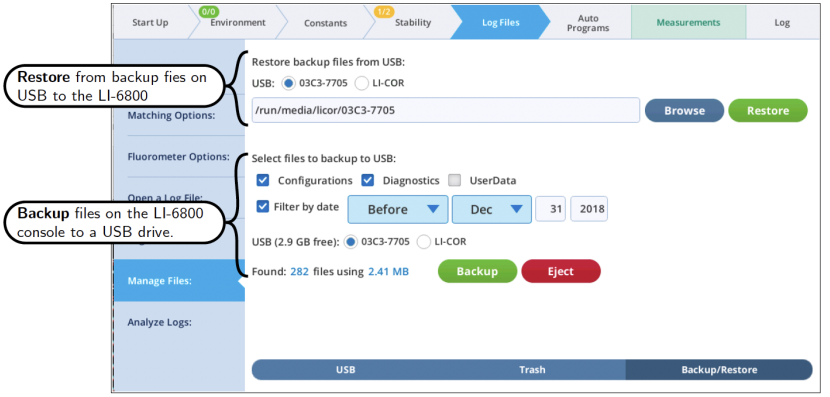


Figure 1-14. The Backup/Restore file management screens.

All backup and restore file operations are "copy", never "move". That is, backing up a file does not remove it from the console, and restoring a file from a backup does not remove it from the USB drive.

For purposes of backup, all LI-6800 console files that might need backing up are divided into three categories: Configurations, Diagnostics, and UserData.

Backups never include factory files, so - in the future - restoring from a backup with a different software version should be safe.

Backups

An example backup is illustrated in *Figure 1-15* on the facing page. In this case, all categories are included, but only those files that have changed prior to the specified date.

To do a complete backup, simply a) uncheck the time filter, and b) check all three file categories.

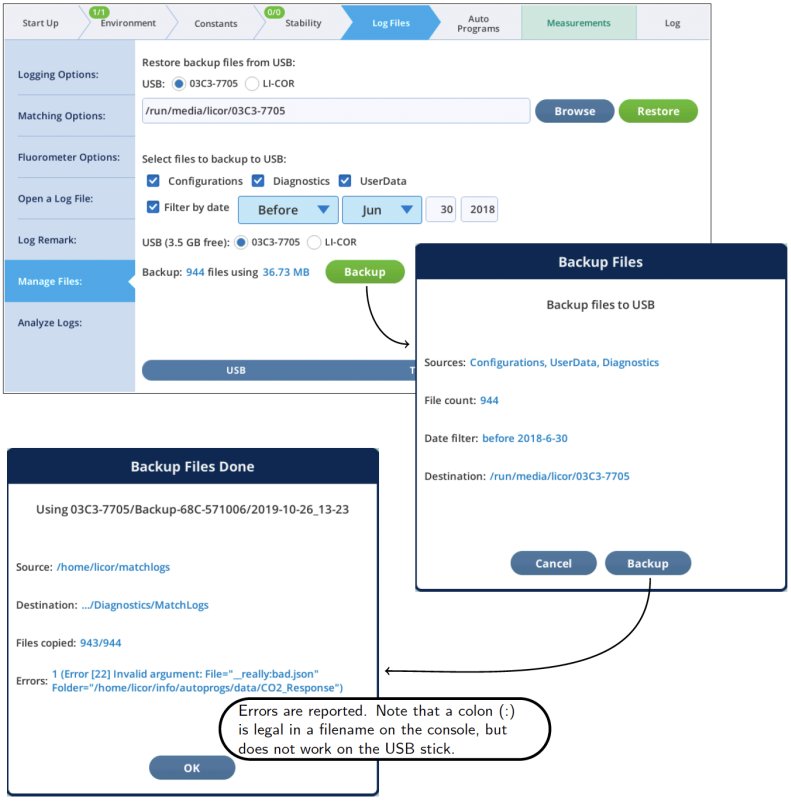
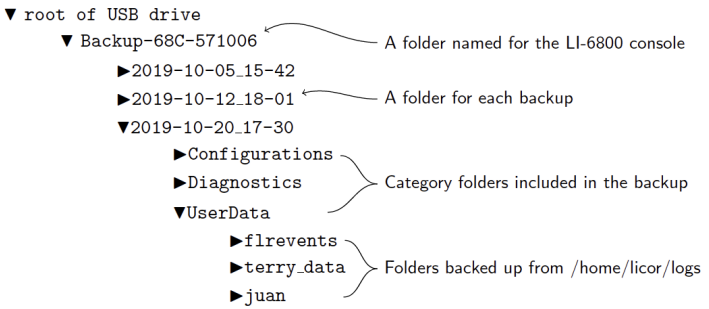


Figure 1-15. Backup and restore.

Every backup goes into a folder on the root of the selected USB drive. The folder is named for the console serial number. For example, backing up console 68C-571006 would cause a folder `Backup-68C-571006` to be created on the USB drive, into which all backup would be written. Each backup event is stored in a subfolder named for the date and time the backup was started. Inside that folder will be a folder for each selected category.

Thus, after a few backups, the folder structure on the USB drive might look like the example below:



Restoring files from backup

To restore from an entire backup, tap **Restore** (*Figure 1-16* below). If no Backup folders are found, then you will be notified.

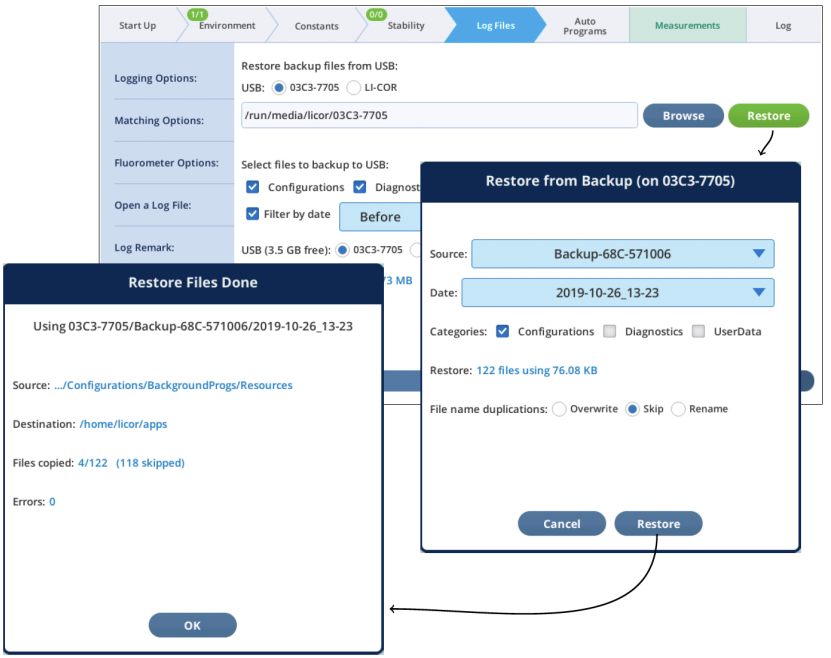


Figure 1-16. Restoring from a USB drive.

To more narrowly focus the restore from backup, follow these steps (*Figure 1-17* on the facing page):

1. Use **Browse** to open a viewer
2. Navigate to the desire folder or file and select it
3. Tap **Apply**
4. Tap **Restore**

Note that if you navigate in step 2 to somewhere that is not within the parentage of a backup folder, your selection will be ignored.

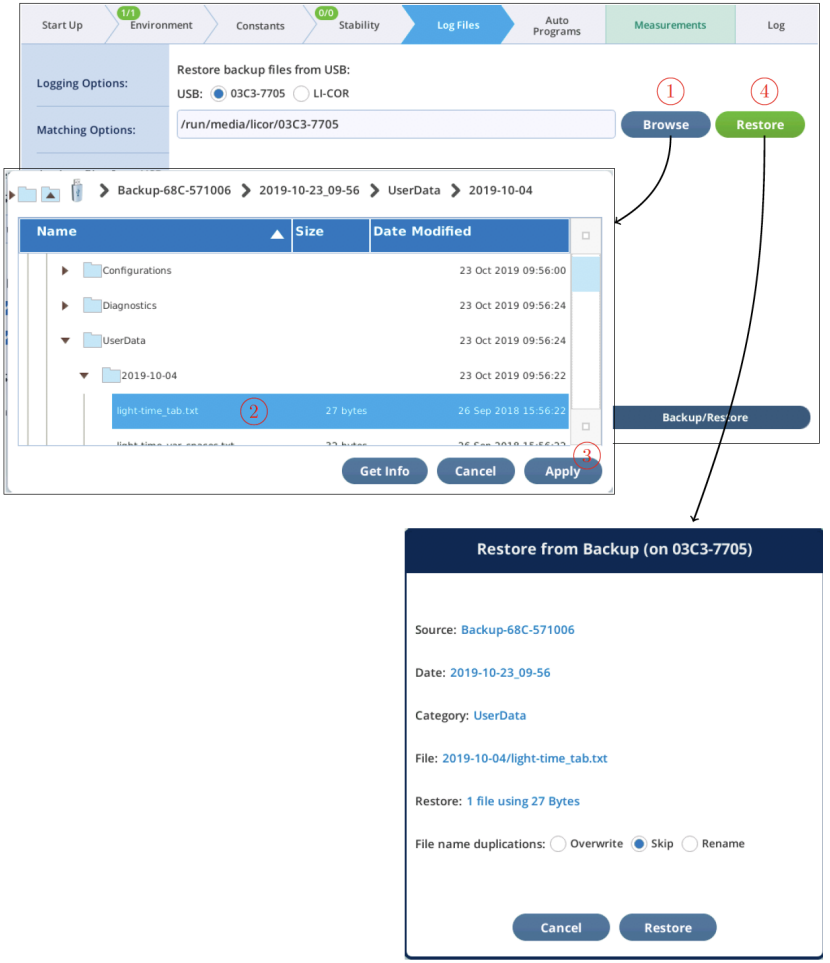


Figure 1-17. Selecting a specific folder or file to restore.

USB utilities

In version 1.4, there is a **USB Utilities** screen, available in two places: **Log Files > Manage Files** and **Start Up > Configuration** (*Figure 1-18* below).

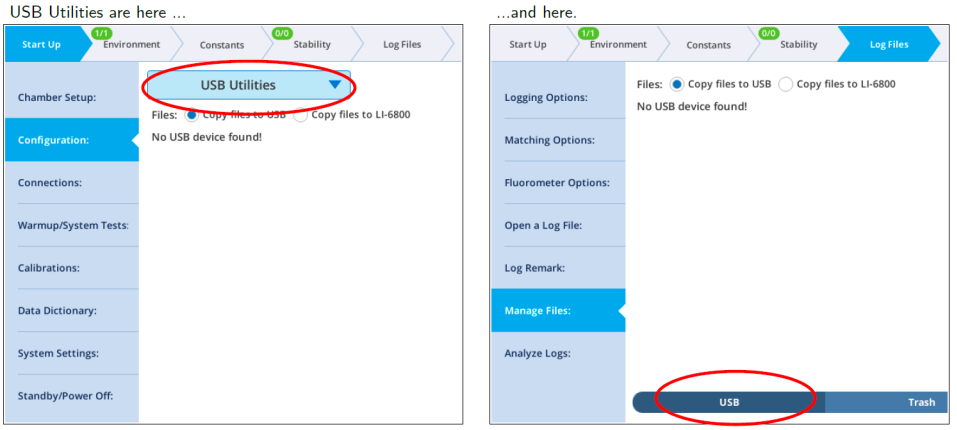


Figure 1-18. The USB Utilities screen locations, with no USB attached.

Inserting a USB drive will, after several seconds, automatically bring up the USB file system in either the source or destination views, depending on how the To/From radio buttons are set (*Figure 1-19* on the facing page). Inserting a second USB drive will produce a radio button selection for which USB drive you wish to use (*Figure 1-20* on page 26).

To copy one or more files or fodlers, select them (tap and drag for multiple, contiguous selection) in the source view, select a folder in the destination view using the Browse button or typing in the edit box, then tap the Copy button. A dialog confirming the copy or reporting a failure is displayed after the copy (*Figure 1-21* on page 26).

To remove a USB drive safely, tap Eject to verify it is safe to remove (*Figure 1-22* on page 27). Note you can continue to use the USB drive after tapping Eject if you choose - it remains functional until you physically remove the drive from the console.

If a USB drive has a space character in the volume name (allowed, but never a good idea), the name in the edit box for the destination volume will show a `nx20` instead of a space. For example, a drive named `DISK IMG` will be shown as

```
/run/media/licor/DISKnx20IMG
```

instead of the expected

```
/run/media/licor/DISK IMG
```

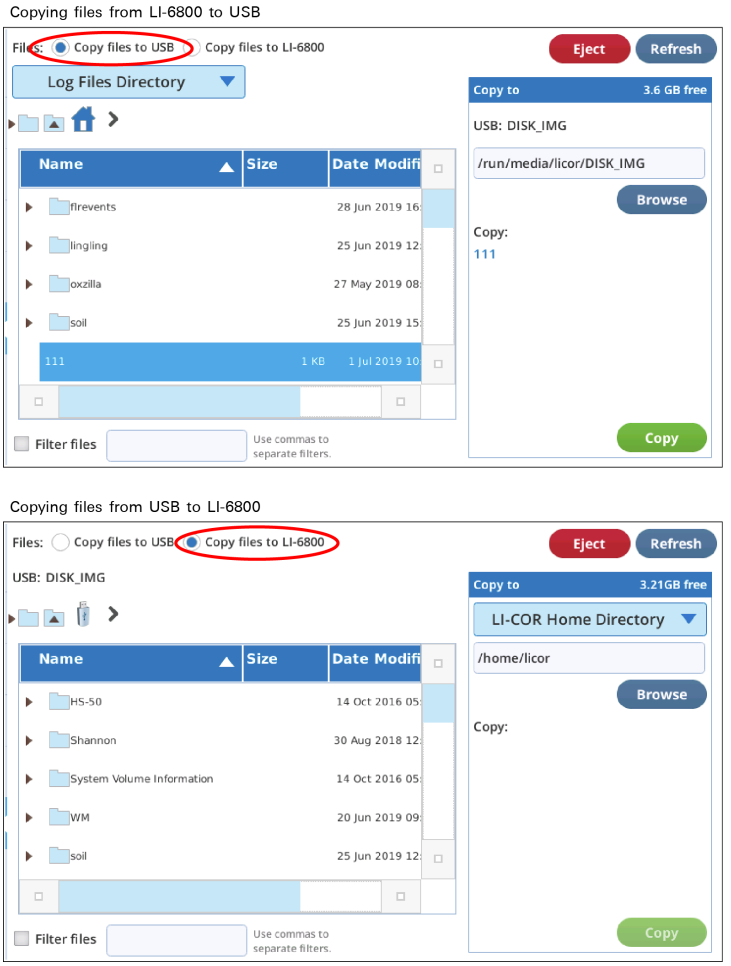


Figure 1-19. USB Utilities displays the source on the left and the destination on the right.

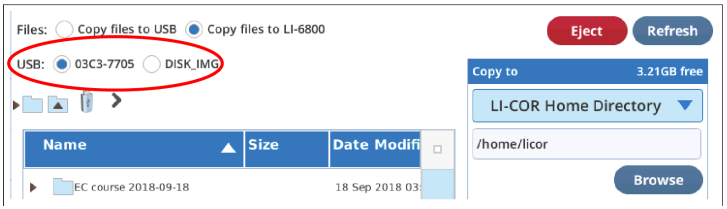


Figure 1-20. If a second USB drive is inserted, radio buttons are provided to select which to use.

Figure 1-21. Copying an item: 1. Select it in the source view, 2. Select a destination, 3. Tap Copy*. Existing files will not be overwritten on the destination, but will bring up the error dialog.*

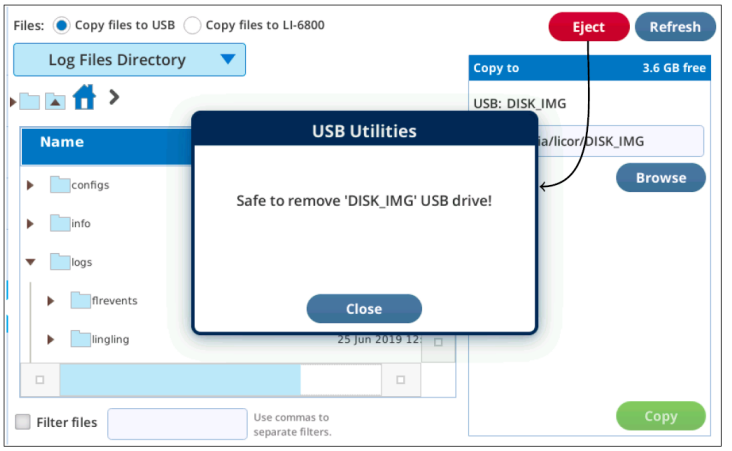


Figure 1-22. Tap **Eject** *to verify it is safe to remove a USB drive.*

Version 1.4 file system folders

Figure 1-23 below illustrates the folder structure implemented in version 1.4 on the LI-6800 console.

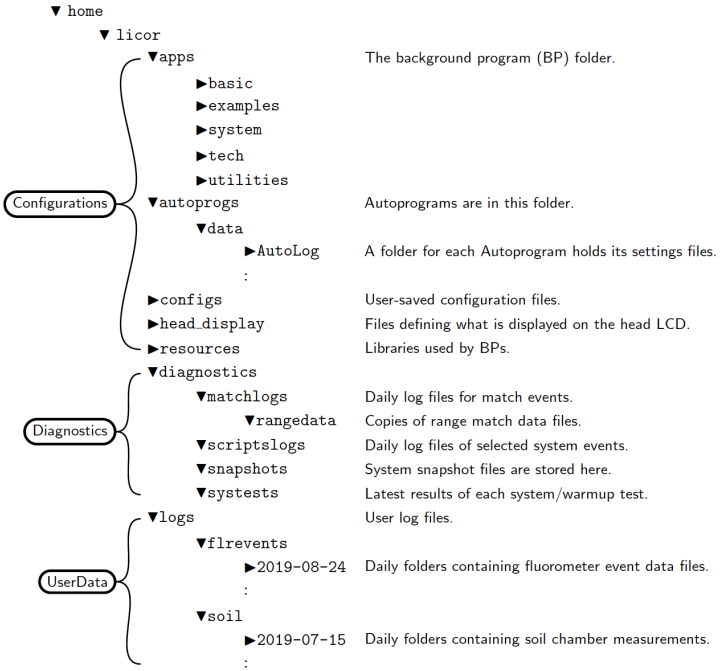


Figure 1-23. The folder structure used in software version 1.4.

For backup and restore utilities group these folders into the three categories shown. The following folders will need "cleaning" periodically by using, for example, the **Move to Trash** utility, since their contents increase with normal instrument operation. Arranged in decreasing order of typical size, the list is:

- `/home/licor/logs` - User log files and associated Excel files
- `/home/licor/logs/flrevents` - Every time a flash or dark pulse event occurs, two files (.xlsx and .json) are added here in daily folders.
- `/home/licor/logs/soil` - Every soil chamber measurement (.json file) goes into daily folders.

- `/home/licor/diagnostics/snapshots` - Each snapshot taken (tap Snapshot on the **System Settings** page) adds a file in this folder.
- `/home/licor/diagnostics/matchlogs` - Matching events are recorded in daily files.
- `/home/licor/diagnostics/matchlogs/rangematch` - Acquiring range match data, and accepting the results, adds a file here.
- `/home/licor/diagnostics/scriptslogs` - Daily files (on days the LI-6800 runs) are added here.
- `/home/licor/apps` - User-created BPs are typically stored in this folder or below.
- `/home/licor/congfigs` - Saved configurations (in the Configurations screen) go in this folder.

Factory files

The folders `/home/licor/autoprogs`, `/home/licor/resources`, and the sub-folders of `/home/licor/apps` all contain special files known as factory files. (They are actually symbolic links to protected files elsewhere in the file system.) They look like normal files as viewed, and can be opened and used, but not overwritten.

Factory files cannot be moved to the trash by the Delete button, or by the **Move to Trash** utility. If this is attempted, factory files will be skipped over, and a dialog similar to *Figure 1-24* below shown.

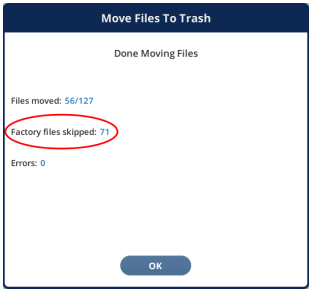


Figure 1-24. Factory files cannot be moved to the trash.

If you do (intentionally or otherwise) manage to get rid of the factroy file, it will automatically be replaced the next time the instrument powers up.

Section 4. Fluorescence

Version 1.4 has several fluorescence related changes and improvements.

Setup Screens: In addition to showing the intended Q pattern based on current settings, the graphs accompanying the setup screens now display the latest flash (or dark) results (F and Q data), allowing you to tune an event's parameters (target, duration, etc.) without changing screens.

Result Screen: The latest dark adapted flash, light adapted flash, and dark pulse continue to be shown on the Results screen. Viewing event details for these and any previous events is now done on the new Files screen.

Files Screen: This new tool allows up to 8 fluorescence events to be viewed simultaneously. These can be captured automatically as they occur, or past event files can be loaded for viewing.

Fluorometer Constants: Previously logged dark adapted events can be loaded from the file system, automatically setting the values of Fo, Fm, Adark, and PS2/1. This greatly aids work flow when making a dark adapted measurements on a number of leaves prior to the associated light adapted measurements.

Setup screens

Each setup screen has a graph that shows the current settings, and also the results of the last event of that type that was made. The time of the fluorescence peak (or minimum, for a dark pulse) is called out on the graph, to aid in setting proper duration times. For flash events, the displayed *F* data are only those points during the flash. This has the affect of zooming in on the upper part of the response. (For more controlled zooming and other options for fluorescence plots, see the **Files Screen.**)

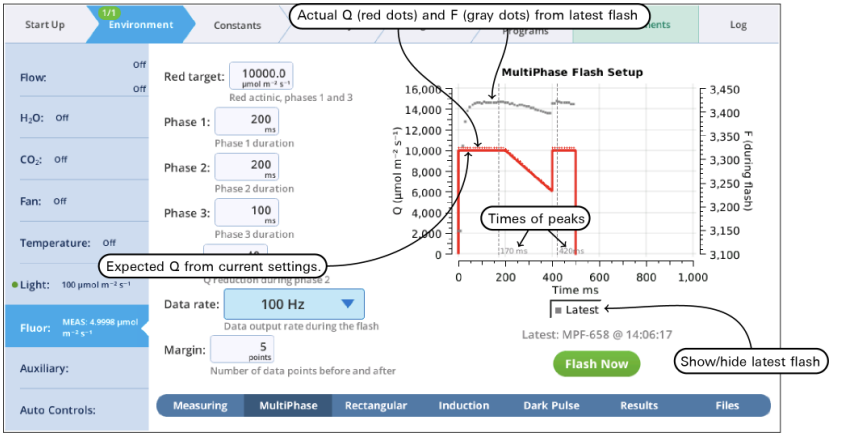


Figure 1-25. An example setup screen for MultiPhase flashes.

Result screen

The Results screen shows the current state of the fluorescence computations (Group name = Flr), and the dark adapted, light adapted, and dark pulse events on which they are based.

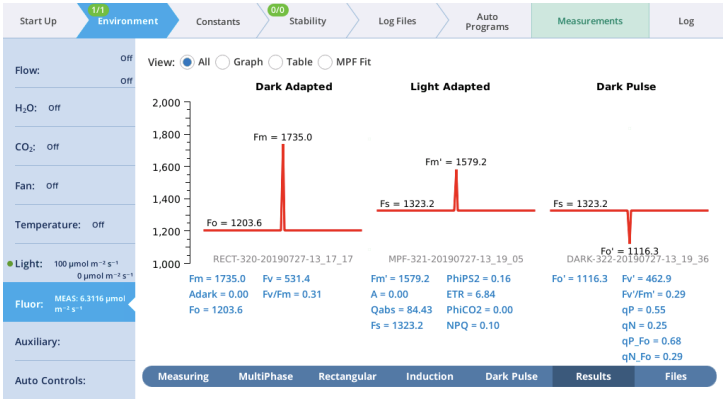


Figure 1-26. The state of the Flr computational group.

When fluorescence events are triggered manually from their setup pages, the dark adapted, light adapted and dark pulse sections are treated independently. When events are triggered as part of logging to a file, the following rules are followed.

- A log that triggers an FoFm will clear the light adapted and dark pulse sections.
- A log that triggers an FsFm' will update the light adapted, but clear the dark pulse section.
- A log that triggers an FsFm'Fo' will update the light adapted and dark pulse sections.

Light adapted vs dark adapted is determined by the following: A flash is dark adapted if the fluorometer actinic is off, or else the measured Q is less than 1 mol m^{-2} s^{-1} at the time the flash occurred.

Files screen

The Files screen allows you to view and compare up to 8 fluorescence events, either by loading them from file, or by capturing when they occur.

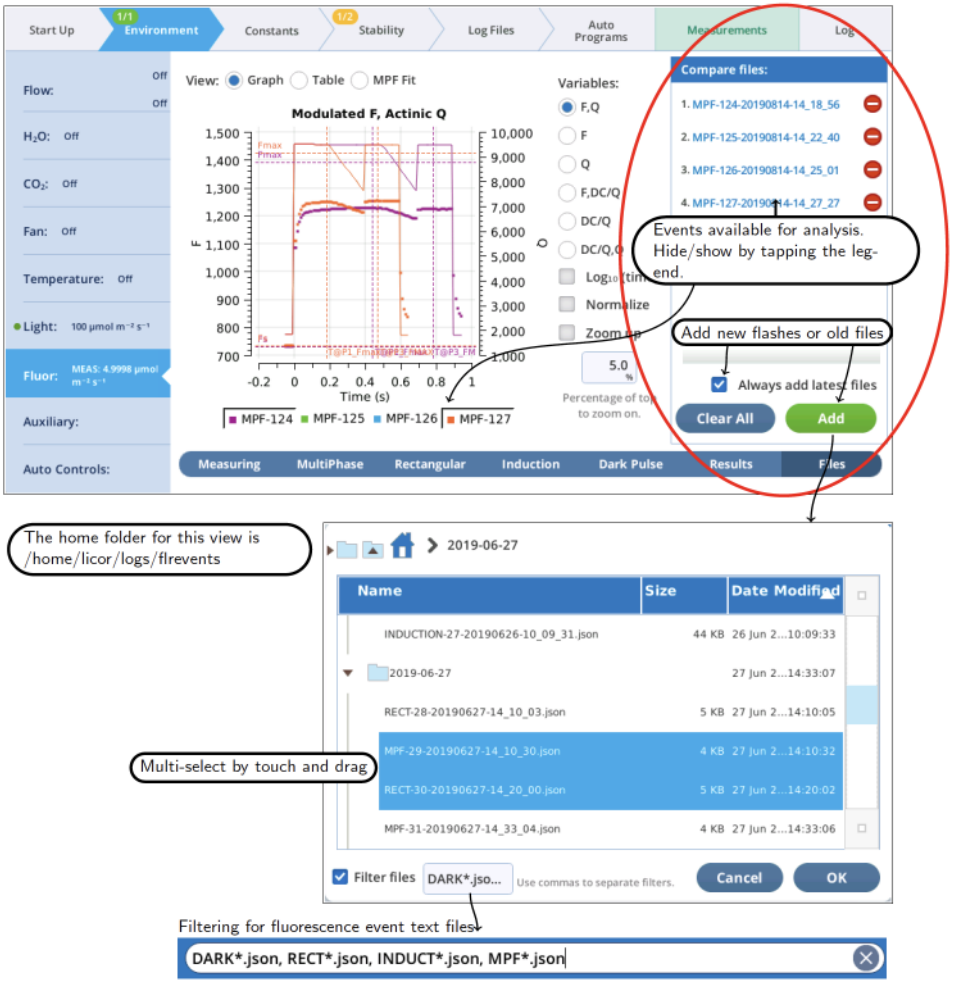


Figure 1-27. The Files Screen can hold up to 8 events.

Graph

Variables that can be plotted are Q (actinic light), F (modulated fluorescence) and DC=Q (non-modulated fluorescence normalized by non-modulated Q).

- **Log_{10}(time)** - Apply a log scale to the time axis, which is useful for looking at an induction flash.
- **Normalize** - Plot each y axis variable as scaled by the maximum value in the data set. In the case of F for a flash event, it is scaled by Fmax.
- **Zoom up** - Change the scaling of each Y axis so that only the top x% of the data is shown.

Figure 1-28 below illustrates these options.

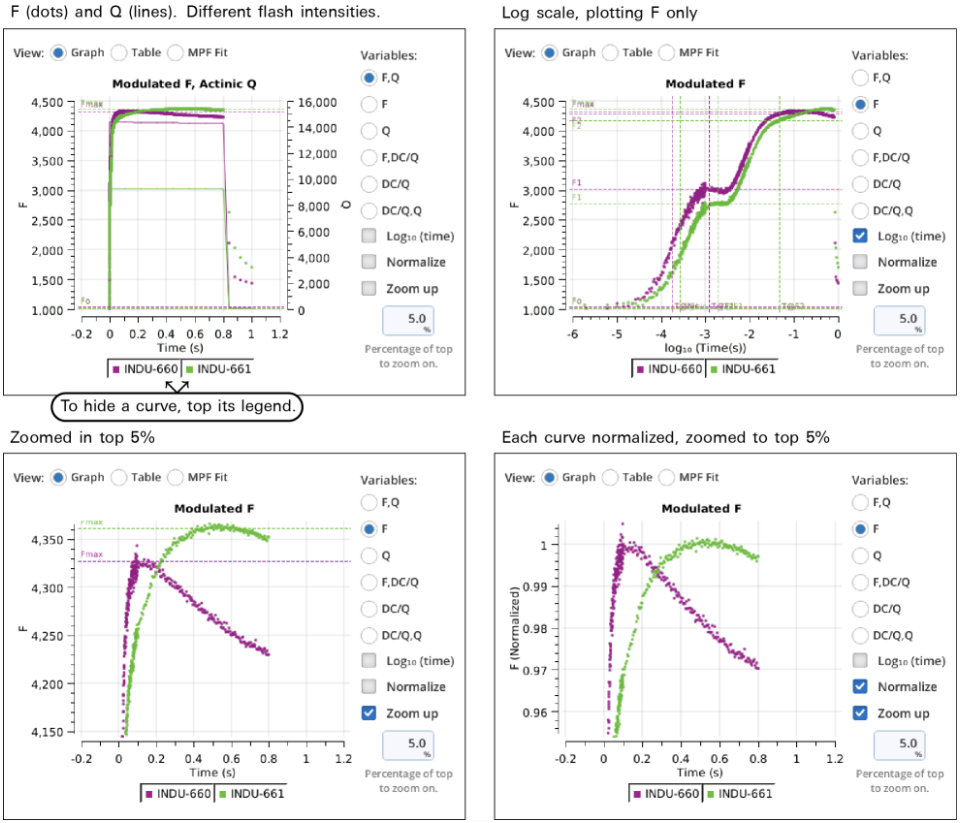


Figure 1-28. Some plot modifiers illustrated using two induction curves.

Table

The Table screen shows all events in tabular form. All single-value items from the fluorometer event file are shown in alphabetical order. If more than one type of event file (MPF, Rectangular, Induction, Dark Pulse) is present, some entries will be blank.

Figure 1-29. The Table view shows all of the single-valued entries in the fluorescence event file.

See Fluorometer Event File Documentation for a description of what the row labels mean. The last row (VERSION) will show 1 for new files, or 1* for pre-version 1 files. Such files are temporarily converted to version 1 when loaded so will appear in the table with all the new entries filled in.

MPF fit

MultiPhase Flash events in the Compare files list will appear on the MPF Fit screen, whose graph shows the Phase 2 regressions. In addition, the Fmax value of the flash is shown (Fmax is whichever is larger: the extrapolated Phase 2 value (P2 INT), or the Phase 1 max (P1 MAXF)). Two validity indicators are also shown, based on the phase 2 regression: the predicted Phase 1 max (P1 PREDF) and the predicted phase 3 max (P3 PREDF). The closer they are to the line the better the phase 2 regression is in predicting phase 1 and phase 3 fluorescence.

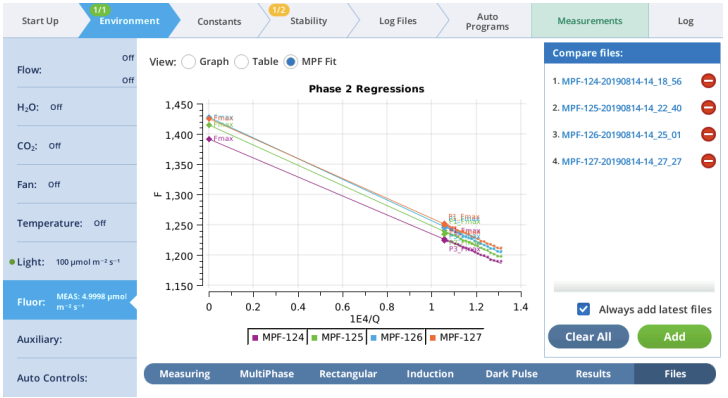


Figure 1-30. The phase 2 regressions of MPF events.

Fluorometer constants

Fluorescence Constants (Fo, Fm, Adark, and PS2/1) can be loaded from a DarkAdapted file. A DarkAdapted file is created when a flash is triggered by an FoFm log event. DarkAdapted files are stored in the flrevents folder, and begin with "DarkAdapted".

Each DarkAdapted file contains Fo, Fm, Adark, and PS2/1, and the name of the flash event. Loading a DarkAdapted file from the **Constants > Fluorometer** page (*Figure 1-31* below) does two things:

1. Sets the constants' values
2. Sets the Dark Adapted data on the Results screen.

Figure 1-31. Set constants and dark adapted results by loading from a previously logged FoFm event.

Fluorometer event file documentation

Table 1-1 below lists the single-value labels in the four types of fluorometer event files (MPF, RECT, INDUCTION, and DARK), and *Table 1-2* on page 40 the multi-value entries. Items marked (new) are only present in Version 1 files.

Table 1-1. Single-value entries in fluorescence event files, Version 1 and prior.

Label	MPF	RECT	IND.	DARK	Notes
DATE	✓	✓	✓	✓	Date of event (see also TIME)
DCmax			✓		Max value of DC/Q fluorescence
DCo			✓		Extrapolated pre-flash for DC/Q
DEVICE	✓	✓	✓	✓	Fluorometer serial number
DURATION		✓	✓	✓	Event duration (ms flash, s dark)
D FARRED PERCENT				✓	Farred power as % of max
D RED PERCENT	✓	✓	✓		Red power as % of max
EVENT ID	✓	✓	✓	✓	Event identifier number
F1			✓		F at 1st inflection
F2			✓		F at 2nd inflection
FMAX	✓	✓	✓		Maximal F
FMIN				✓	Minimal F
Fo (present if dark adapted)	✓	✓	✓		Pre-flash F
Fs (present if light adapted)	✓	✓	✓	✓	Steady state fluorescence
InitSlope			✓		Initial slope of DC/Q
MARGIN	✓	✓	✓	✓	Margin (# of points)
MODRATE	✓	✓	✓	✓	Modulation rate (Hz)
OUTRATE	✓	✓		✓	Data points per second
P1 DELTAF (new)	✓				P1 PREDF - P1 MAXF
P1 MAXF	✓				Phase 1 max F
P1 PREDF (new)	✓				Phase 1 predicted F
P2 INT	✓				Phase 2 regression intercept
P2 INT SE	✓				Phase 2 std. error of intercept
P2 R2	✓				Phase 2 regression R squared
P2 SLP	✓				Phase 2 regression slope
P2 SLP SE	✓				Phase 2 std. error of slope
P3 DELTAF	✓				P3 PREDF - P3 MAXF
P3 MAXF	✓				Phase 3 max F
P3 PREDF	✓				Phase 3 predicted F
P3 Q	✓				Max Q during phase 3

Table 1-1. Single-value entries in fluorescence event files, Version 1 and prior. (...continued)

Label	MPF	RECT	IND.	DARK	Notes
PHASE1 DURATION	✓				Phase 1 duration (ms)
PHASE2 DURATION	✓				Phase 2 duration (ms)
PHASE3 DURATION	✓				Phase 3 duration (ms)
Q@P1 MAXF (new)	✓				Q at phase 1 max F
Q@P3 MAXF (new)	✓				Q at phase 3 max F
QMAX	✓	✓	✓		Maximum Q during flash
QMIN				✓	Minimum Q during dark pulse
Q FARRED SETPOINT				✓	Farred target µmol m^{-2} s^{-1}
Q RED SETPOINT	✓	✓	✓		Red target µmol m^{-2} s^{-1}
RAMP	✓				Percent ramp for phase 2
T@DCmax (new)			✓		Time (s) of DC/Q max value
T@F1			✓		Time (s) of F1
T@F2			✓		Time (s) of F2
T@FMAX (new)		✓	✓		Time (s) of FMAX
T@FMIN (new)				✓	Time (s) of FMIN
T@NIR			✓		Time (s) of half initial rise (F 1 – Fs)/2
T@P1 MAXF (new)	✓				Time (s) of phase 1 max F
T@P3 MAXF (new)	✓				Time (s) of phase 3 max F
TIME	✓	✓	✓	✓	Time (local) of the event
TIMESTAMP	✓	✓	✓	✓	GMT time t value of event (s since 1970)
TYPE	✓	✓	✓	✓	MPF, RECT, INDUCTION, or DARK
T OFFSET	✓	✓	✓	✓	Time shift (s) of event start (In version 1, this is already incorporated into the SECS data.)
VERSION (new)	✓	✓	✓	✓	File version
Q FARRED SETPOINT				✓	Farred target µmol m^{-2} s^{-1}
Q RED SETPOINT	✓	✓	✓		Red target µmol m^{-2} s^{-1}
RAMP	✓				Percent ramp for phase 2
T@DCmax (new)			✓		Time (s) of DC/Q max value
T@F1			✓		Time (s) of F1
T@F2			✓		Time (s) of F2
T@FMAX (new)		✓	✓		Time (s) of FMAX

Table 1-1. Single-value entries in fluorescence event files, Version 1 and prior. (...continued)

Label	MPF	RECT	IND.	DARK	Notes
T@FMIN (new)				✓	Time (s) of FMIN
T@NIR			✓		Time (s) of half initial rise (F 1 – Fs)/2
T@P1 MAXF (new)	✓				Time (s) of phase 1 max F
T@P3 MAXF (new)	✓				Time (s) of phase 3 max F
TIME	✓	✓	✓	✓	Time (local) of the event
TIMESTAMP	✓	✓	✓	✓	GMT time t value of event (s since 1970)
TYPE	✓	✓	✓	✓	MPF, RECT, INDUCTION, or DARK
T OFFSET	✓	✓	✓	✓	Time shift (s) of event start (In version 1, this is already incorporated into the SECS data.)
VERSION (new)	✓	✓	✓	✓	File version

Table 1-2 below lists the time-series data, which is common to all event files. A difference in version 1 files is that the time (SECS) is adjusted by the T_OFFSET value, so that SECS=0 corresponds to the time the flash began (or when the actinic turned off for a dark pulse). In files with no VERSION, the rst value of SECS is 0.

Table 1-2. Table of multi-value entries in fluorescence event files.

Label	Notes
SECS	Time (s). In version 1 files, the 0 value is the time of the flash on or actinic off.
FLUOR	Modulated fluorescence.
DC	Non-modulated fluorescence.
PFD	Photon Flux Density (includes contribution of REDMODAVG).
REDMODAVG	Average flux contribution from the red modulated LEDs.
CODE	Event phase data identifier: 2 = pre-flash margin 3 = rect or induction flash 4 = MPF phase 1 5 = MPF phase 2 6 = MPF phase 3 7 = post-flash margin 11 = pre-dark margin 12 = farred on (actinic still on) 13 = actinic off (farred still on) 14 = farred off 15 = post-dark margin (actinic back on)

Section 5. Matching revisited

A potential matching error

Central to the LI-6800's gas exchange computations is the difference (Δ) between sample and reference gas analyzer readings C_s and C_r. (We are using C for concentration, meaning CO_2 or H_2O). For Δ to be accurate, we need to ensure that $C_r = C_s$ when the IRGAs are receiving identical air streams. We call this condition matching, and it is used to measure correction factor M.

$$M = (C_r - C_s)|_m \quad \text{1-1}$$

where the $|_m$ indicates the readings were made in match mode. M is used to correct subsequent measurements.

$$\Delta = C_s + M - C_r \quad \text{1-2}$$

The value of M is unchanged until another match is performed. How stable is M? There is some relation between sample and reference that likely depends on concentration, time, temperature, and human activity such as zeroing and/or spanning one or both IRGAs. Let's designate this match relationship as function $m(C)$, to emphasize its potential dependency on concentration. We don't really know what $m(C)$ looks like, but every time we match, we capture its value at a particular concentration, time, temperature, etc. Since matching is done at the reference concentration, we can write

$$M = m(C_r|_m) \quad \text{1-3}$$

Question #1: Does frequent matching assure accuracy?

It may not. It turns out that the shape of $m(C)$ is very important. *Figure 1-32* on the next page illustrates the potential problem.

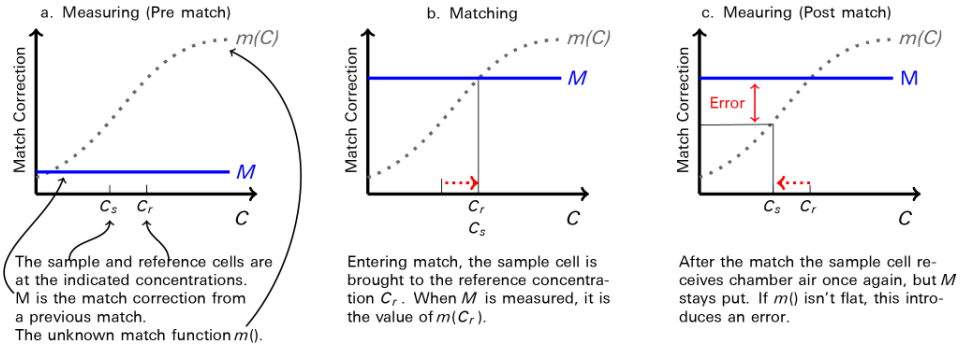


Figure 1-32. Illustration of a hypothetical error function m(C) *and its role in a potential post-match error.*

The post-match error can be expressed as a fraction by

$$E = \frac{m(C_r) - m(C_s)}{C_r - C_s} \qquad 1\text{-}4$$

which is the slope of $m(C)$ over the interval $(C_S; C_r)$. This error (as a fraction or a percentage) is independent of how large or small Δ is. This means that if $m(C)$ has a 1% slope, the post match error in flux will also be 1%.

So, the shape of $m(C)$ is crucial: the more sloped it is, the more you need to re-match if concentration changes, but with each match, there will still be a post-match error. A flat $m(C)$ is good, a sloped $m(C)$ is bad.

Question #2: If $m(C)$ is an unknown function, how can I know the slope?

The match screen in version 1.4 has match graphs for both CO_2 and H_2O. This graph displays the current and previous match values (i.e., values of M). If you do a few matches over a range of concentrations, you will quickly get a sense of the overall slope of $m(C)$ (*Figure 1-33* on the facing page).

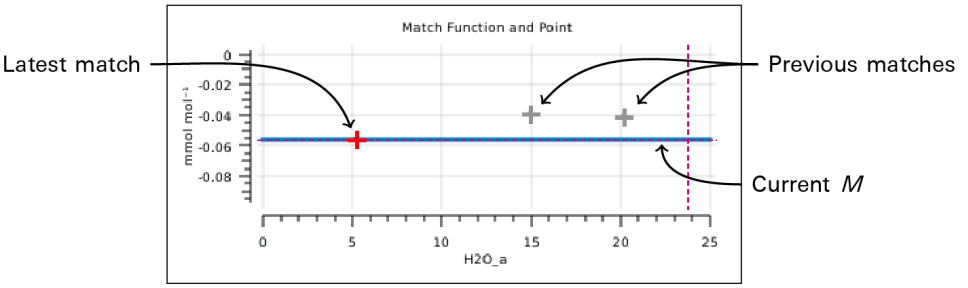


Figure 1-33. The H_2O graph from the match page, shows the history of recent point matches.

In addition, version 1.4 provides a mechanism to acquire "range match" data (*Figure 1-34* below). This is a set of values of *M* taken over the full concentration range in about 5 minutes and shows a very detailed estimate of what *m*(*C*) looks like, over that window of time.

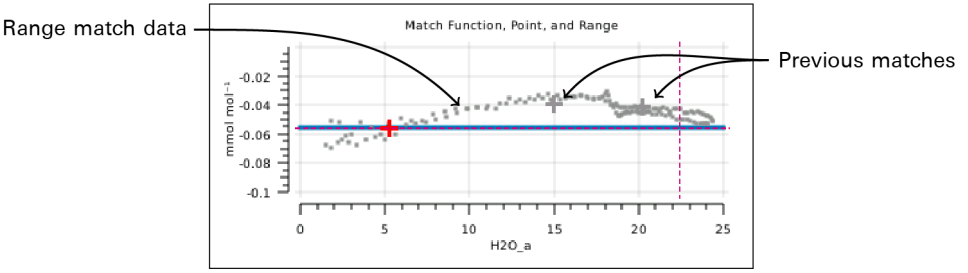


Figure 1-34. The H_2O graph showing recent point matches (+), and range match data (■).

Question #3: Can a sloped *m*(*C*) be corrected (i.e., flattened)?

Yes. A sloped *m*(*C*) means there is a calibration mismatch that you can correct. Values of *M* should go to 0 as concentration goes to 0. If they don't, one or both IRGAs need to be properly zeroed. At high concentrations, large *M* values can be caused by an improperly zeroed IRGA, or when one IRGA (or both) is improperly spanned. *Figure 1-35* on the next page illustrates some examples.

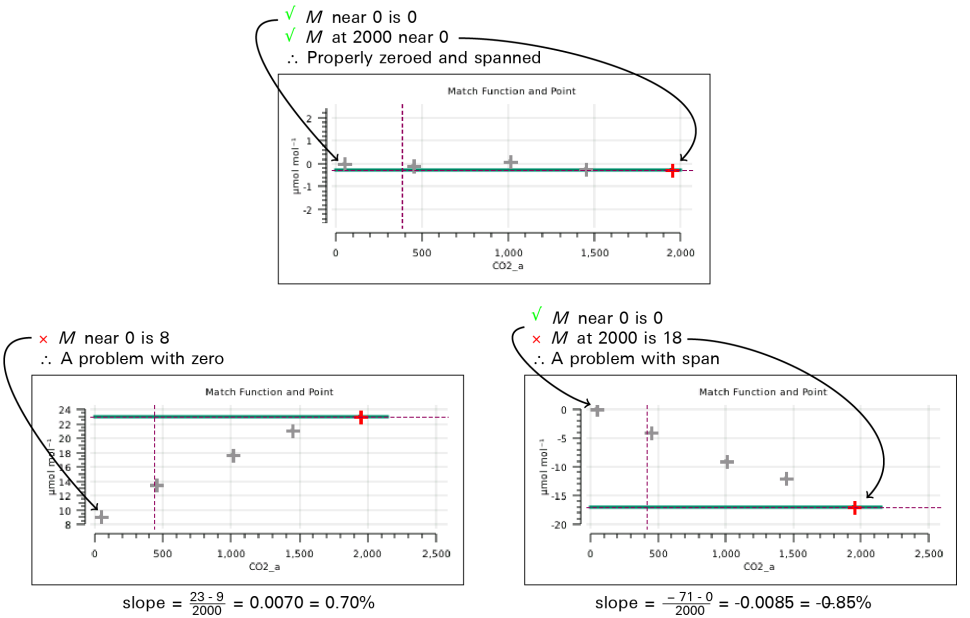


Figure 1-35. Three distributions of CO_2 match points, one with a bad zero, one with a bad span.

Question #4: The post-match error problem stems from the fact that *M* is a constant. Does it have to be?

Version 1.4 allows the match correction *M* to be a 3rd order polynomial based on C_s. It can be fit to range match data, yielding an *M* that continually updates as C_s changes (*Figure 1-36* below). This not only removes post-match errors, but reduces the need to match when concentration changes. In other words, instead of a constant *M*, you can have $M(C) \approx m(C)$.

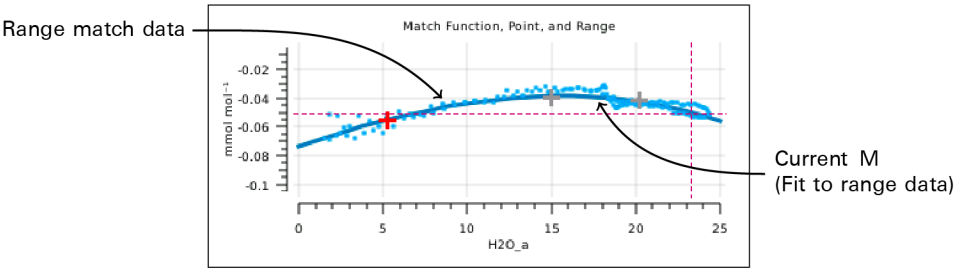


Figure 1-36. The H_2O graph from the match page, with M *fit to the range match data.*

The new match screen

The **Match** screen in version 1.4 has been changed (*Figure 1-37* below). Matching can be triggered by the Auto or Manual buttons on the left. The status table in the center shows exactly how the current value of Δ is being computed. The graphs to the right show matches done since power on (gray plus marks) and the current match value as a function of concentration (solid green or blue curve). Some new features are available through the **View CO_2** and **View H_2O** buttons at the bottom.

Figure 1-37. Getting in and out of the new **Match** *screen.*

The summary table

The summary table (*Figure 1-38* on the next page) makes explicit what the match function is doing. We label it *match*() since the match offset is now potentially a function of uncorrected sample cell concentration.[1]

[1]In general, the match function is a 3rd order polynomial. If the only non-zero coefficient is the offset, then the function is merely a horizontal line: the same value at any concentration.

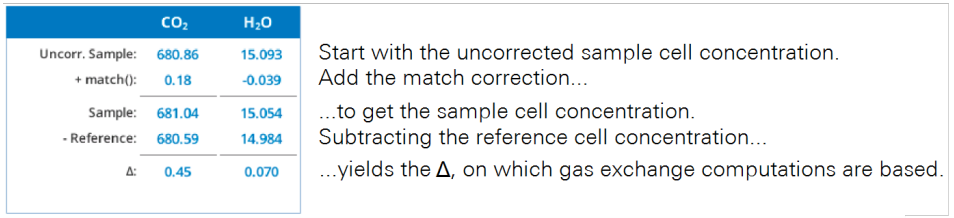


Figure 1-38. Match status table.

During a match, the table changes a bit (*Figure 1-39* below). Since both cells are seeing the same gas, the expected Δ is zero; it is labeled ϵ, since a non-zero value represents an error in the current value of *match()*. There is also a stability indicator, $d\epsilon = dt$, the rate of change of that error with time.

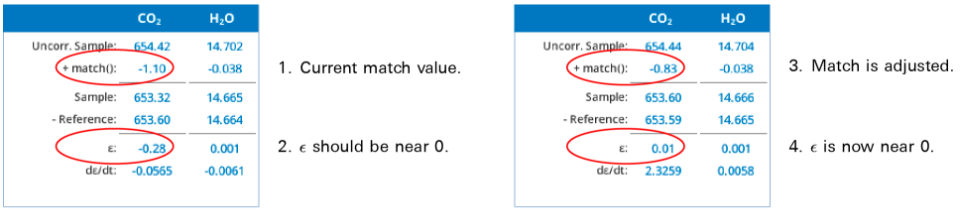


Figure 1-39. Before the match (left), the CO_2 match value is too high by 0.28. After the match adjustment (right), the new match() *gives an* ϵ *much closer to 0.*

The graphs

The graphs on the **Match** page show three things: the current match function (solid colored line), recent point matches (most recent in red), and (if present) range match data. In the example in *Figure 1-40* on the facing page, the H_2O graph (bottom) has range data, with the match function t to them; the CO_2 graph (top) does not.

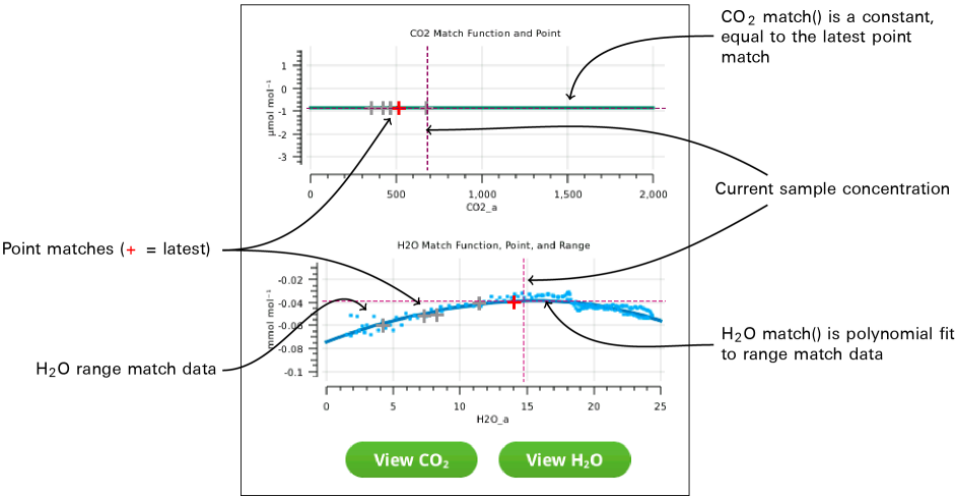


Figure 1-40. Match page graphs.

Managing the details

The View CO2 and View H2O buttons on the match screen open a screen that allows you to manage matching for that gas. If no range data is present (*Figure 1-41* on the next page), there aren't many options other than acquiring range data (Acquire), or removing old match points (Manage).

Figure 1-41. The **CO_2 Match Data** *screen shows an expanded version of the CO_2 graph.*

When range match data is available (*Figure 1-42* on the facing page), you can choose to fit the match function to it, and whether to adjust the fit to the latest point match.

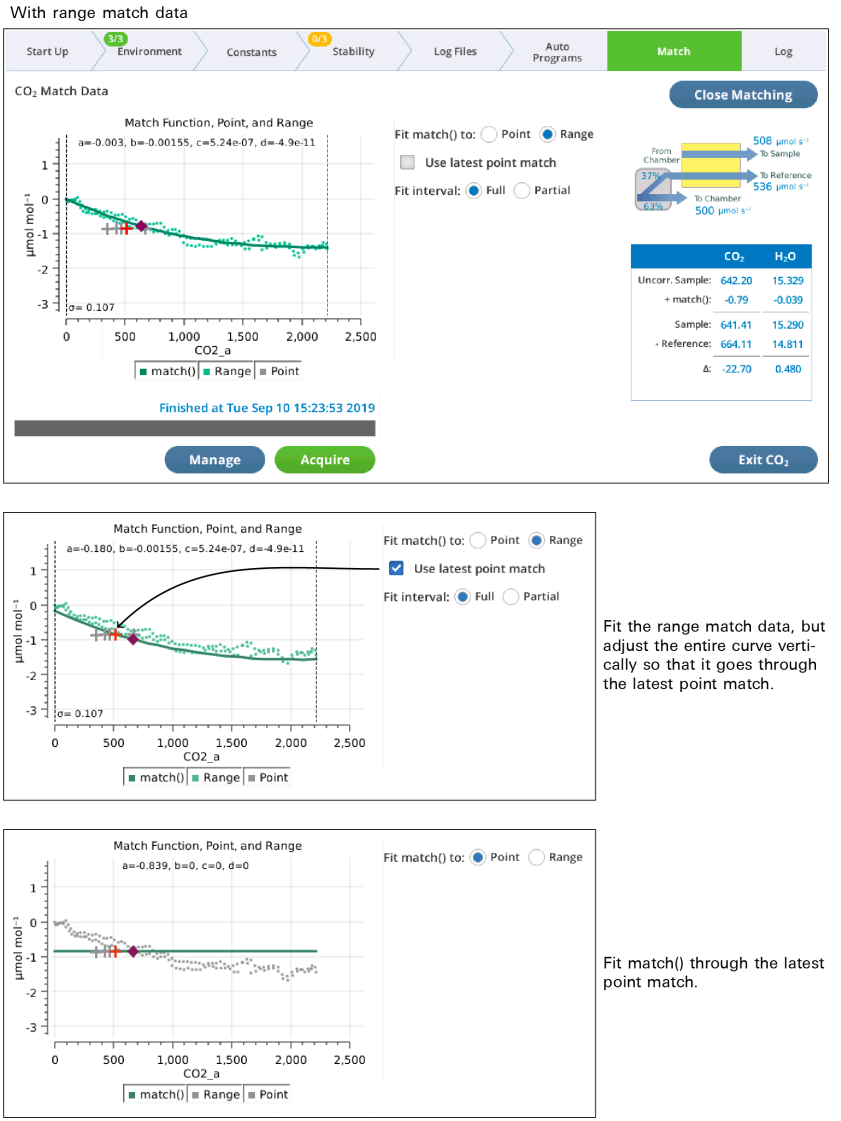


Figure 1-42. If range match data is available, you can select between using it or not.

The match function can be fit to the full range match data set, or to a subset by setting Fit interval to Partial, which selects a narrow band of range match data that

contains the current sample concentration. This band shifts automatically as sample cell concentration changes (*Figure 1-43* below).

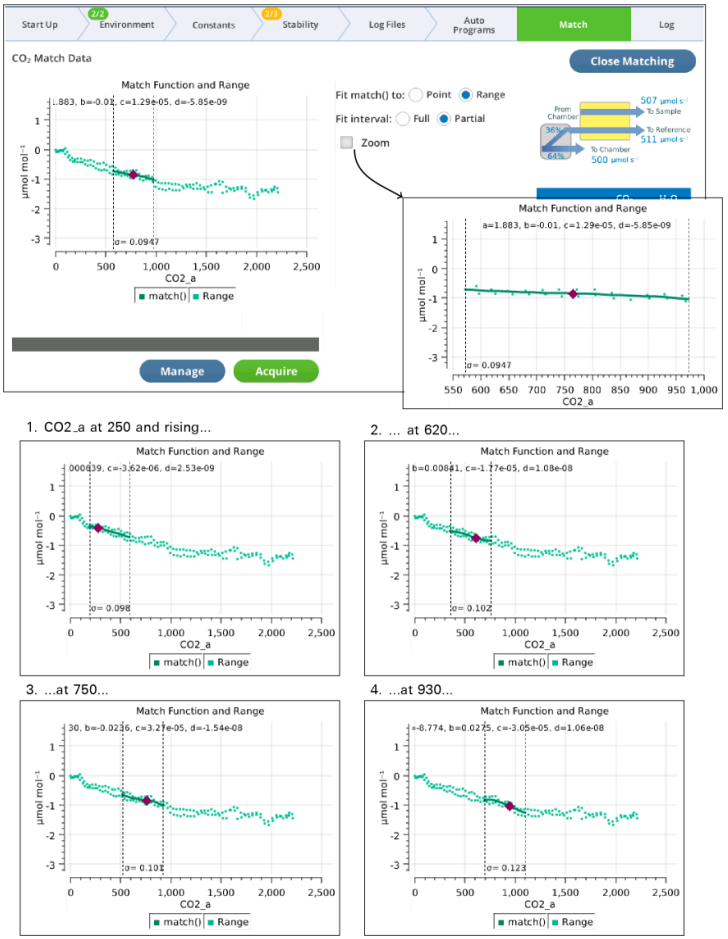


Figure 1-43. When **Fit Interval** *is* **Partial**, *a subset of the range match data is fit. This narrower fit interval shifts automatically as needed to keep the sample cell concentration within its domain.*

Acquiring range match data

The **Acquire** button will launch a program to collect range match data (*Figure 1-44* on the facing page). This process takes a few minutes, and should be done without

any leaf in the chamber, since the chamber receives no air flow during the process.

The **Acquire** program tries to cover as wide a concentration range as possible. For CO_2 this means having fresh soda lime and an adequate CO_2 cartridge. For H_2O, it means having fresh desiccant and a saturated humidifier tube.

Once running, the **Acquire** program does the following: a) Routes all the flow to the IRGA, splitting it between sample and reference. b) Ramps concentration from low to high and back to low. c) Records the concentrations differences between uncorrected sample and reference during the ramp up and back.

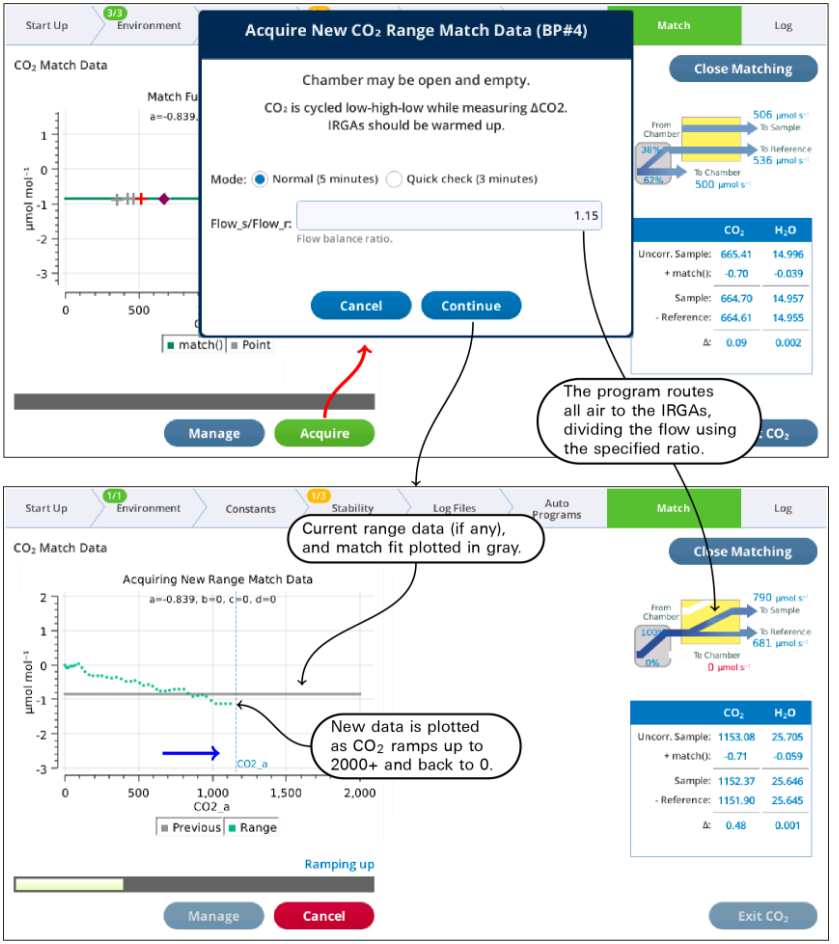


Figure 1-44. Acquiring range match data.

When the program is done, the closing dialog (*Figure 1-45* below) gives you the option of keeping or discarding the new range match data set.

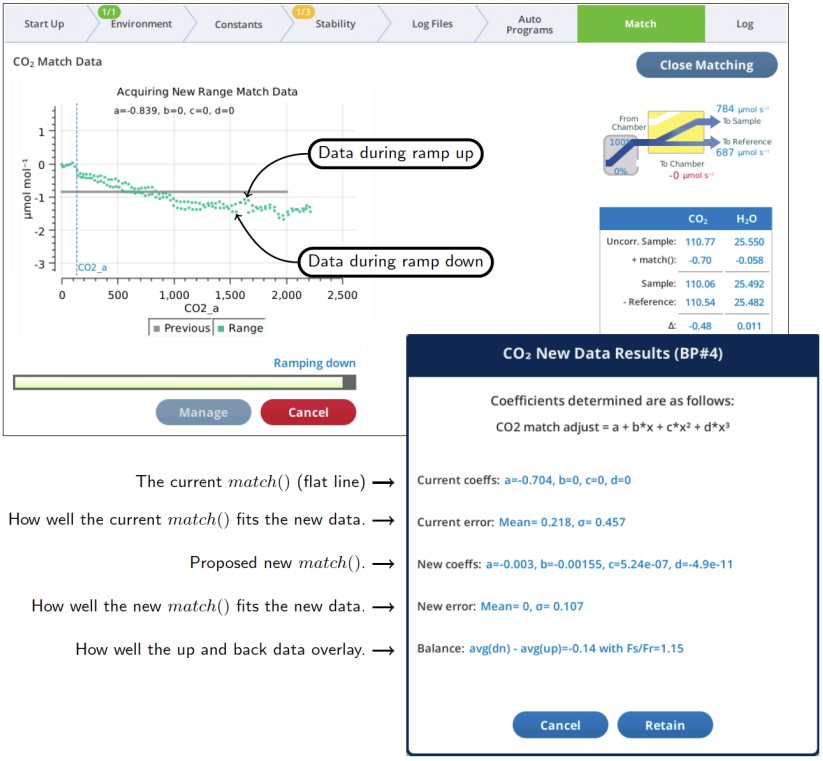


Figure 1-45. The **Acquire** *program closing dialog.*

The ramp up values should overlap reasonably well with the ramp down values. If they don't, you can adjust the Flow_s/Flow_r parameter to compensate. Doing the ramp at a faster rate will exaggerate the difference, so you can run Acquire a couple of times at the faster rate to try and get the best Flow_s/Flow_r value. Then, when you slow it down for a normal run, the overlap will be even better.

- If the "coming back" values are higher than the "going up" values, then Flow_s/Flow_r should be *lowered*.
- If the "coming back" values are lower than the "going up" values, then Flow_s/Flow_r should be *raised*.

Values in the 1.10 to 1.20 range seem typical for CO_2. For H_2O, expect flow ratios to be 1.3 to 1.4.

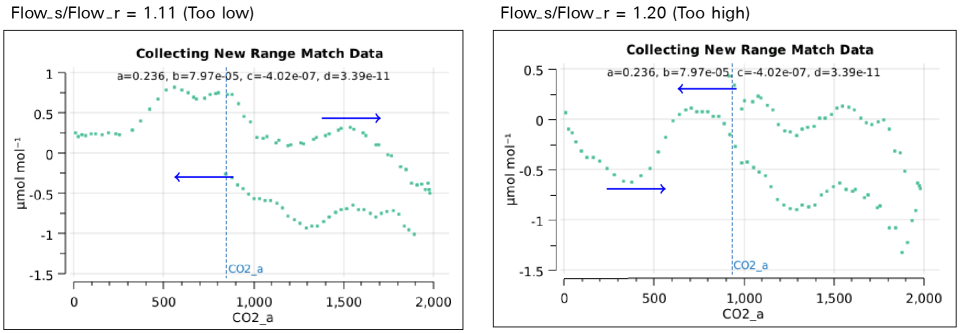


Figure 1-46. The effect of flow ratio on data overlap.

Range match stability

Zero and span

Zeroing and spanning an IRGA will potentially invalidate range match data. In fact, entering those routines will reset the match function to a 0th order polynomial with 0 offset. The range match data is not discarded, but you may need to run **Acquire** after the zero or span adjustments.

Effect of warmup

There is typically a shift in range match data as an instrument warms up. *Figure 1-47* on the next page compares an original range match data set taken when fully warmed up on a prior day (gray data, same in all plots) with newly acquired data (green points) taken at regular intervals since being awakened from sleep mode, in which it has been for 16 hours prior to the experiment. (The new data is discarded each time, so the plot comparisons are always with the same original data set.)

The largest differences were at 1 minute after wakeup, when the curve was shifted down by 0.2 ppm at the low end, and by 1 ppm at the high end. Over the course of 2 hours, the data slowly drifted toward the original data set.

Fortunately, the general shape of the curve was consistent. This suggests you can compensate for disequilibrium by performing a point match (to shift the curve fit), rather than by remeasuring range match data.

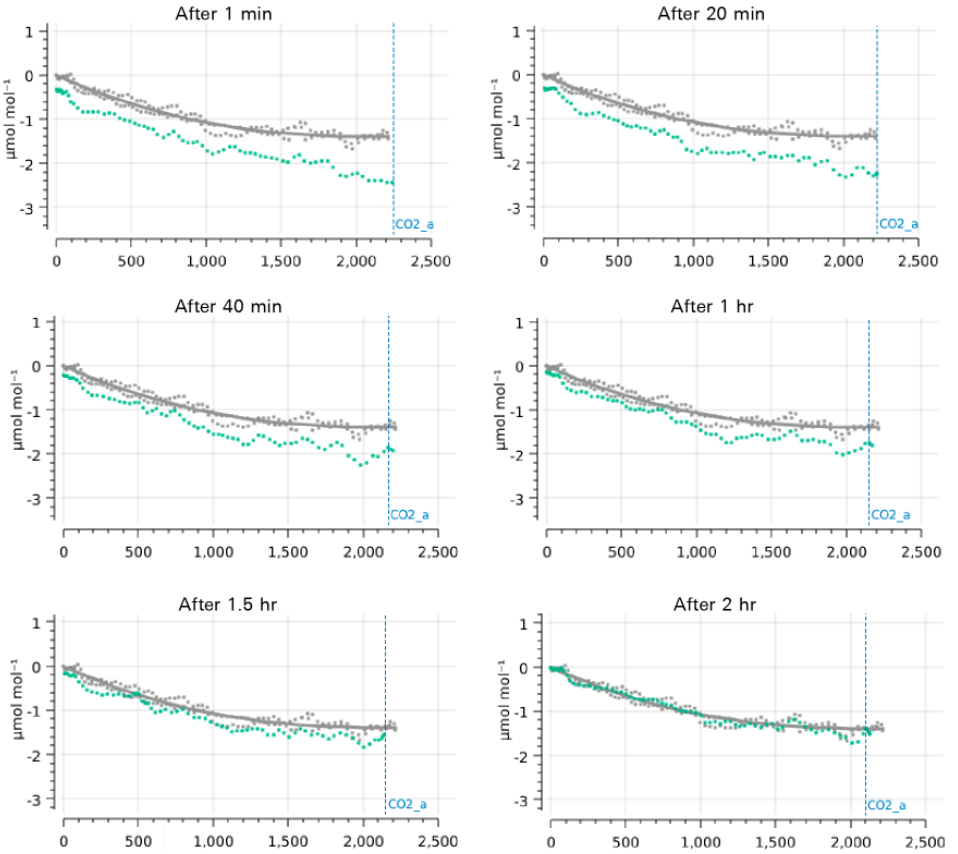


Figure 1-47. An illustration of the effect of warm up on range match data. The time label above each plot is the time since the instrument was waked up after a 16 hour sleep. The gray data points (same in each plot) are the original range match data from a previous measurement.

New match options

The Match Options available when logging have changed, allowing independent control of CO_2 and H_2O matching (*Figure 1-48* below). These settings only pertain to whether or not a match is triggered and performed as part of a log event; they do not apply to matching initiated by tapping Auto or Manual in the match screen.

Figure 1-48. The new Matching Options *screen.*

When a log file is open, the bottom line of the Log button indicates if a match will happen at the next log (**Yes** or **No**). **C** or **c** indicates if CO_2 will be matched (**C** is yes, **c** is no), and **H** (yes) or **h** (no) indicates if an H_2O match will occur. If conditional matching (**Match only if**) is enabled, there will be up to three code letters following the **C/c** and **H/h**, one for each item checked. Δ for ΔCO_2 or ΔH_2O if true (δ if false), **R** for reference if true (**r** if false), and **T** for time if true (**t** if false). Examples:

No c h - No match is happening, because both CO_2 and H_2O are set to **Never match**.

Yes C h - A CO_2 match will occur, because it is set to **Always match**.

Yes CΔt h - CO_2 is conditional on ΔCO_2 (true) and time (false). H_2O is conditional on ΔH_2O (false).

Yes cõrt HõRt - Both CO_2 and H_2O are conditional based on all three options. There will be an H_2O match, triggered by the reference change (**R**).

When a match is triggered because of only one gas (CO_2 or H_2O), only that gas will be matched.

Match information in data files

Version 1.4 has some changes to what is stored in data files to accommodate the new matching infrastructure:

- The group *Match* has been replaced by *MchEvent* ("match event").
- New group: *MchStatus* ("match status").
- *MchStatus* and *MchEvent* are always in data files, whereas the old *Match* group was optional.
- The variables *CO2_a* and *H2O_a* have moved from group *Meas2* to *Meas*, so are always present in data files.

Additions to *Meas*

as	Meas	Meas	Meas	Meas	Meas	Meas	Meas	Meas	Mea
1E	CO2_s	CO2_r	H2O_s	H2O_r	CO2_a	H2O_a	Flow	Pa	ΔPch
	µmol mol⁻¹	µmol mol⁻¹	mmol mol⁻¹	mmol mol⁻¹	µmol mol⁻¹	mmol mol⁻¹	µmol s⁻¹	kPa	kPa
56E+09	593.447	593.723	19.02	18.9405	593.735	19.06	610.04	97.7251	0.
56E+09	593.559	593.744	19.0133	18.9534	593.848	19.053	610.074	97.7213	0.0
56E+09	438.441	430.666	13.8224	13.4445	438.817	13.8691	610.04	97.7128	0.1

MchEvent - the most recent Match Event (manual or automatic)

MchEvent	MchEvent	MchEvent	MchEvent	MchEvent	MchEvent	MchEvent	MchEvent	MchEvent	MchEvent	MchEvent	MchEvent	MchEvent
time	hhmmss	co2_t	h2o_t	count	co2_adj	h2o_adj	co2_match	h2o_match	co2_at	h2o_at	co2_cv	h2o_cv
secs		s	s		µmol/mol	mmol/mol	µmol/mol	mmol/mol	µmol/mol	mmol/mol	%	%
1.56E+09	10:45:51	1.56E+09	1.56E+09	1	-0.162	-0.01	-0.288	-0.04	594	19	0.63	0.17
1.56E+09	10:45:51	1.56E+09	1.56E+09	1	-0.162	-0.01	-0.288	-0.04	594	19	0.63	0.17
1.56E+09	10:48:19	1.56E+09	1.56E+09	2	-0.085	-0.01	-0.376	-0.04	431	19	0.28	0.17

MchStatus - The state of the match infrastructure at time of logging

MchStatus	MchStatus	MchStatus	MchStatus	MchStatus	MchStatus	MchStatus	MchStatus	MchStatus	MchStatus	MchStatus	MchStatus	MchStatus	MchStatus	MchStatus	MchStatus
MatchValve	MatchValve	MatchCO2	MatchH2O	cf_co2_a	cf_co2_b	cf_co2_c	cf_co2_d	cf_h2o_a	cf_h2o_b	cf_h2o_c	cf_h2o_d	co2_range	h2o_range	co2_elapse	h2o_elapse
%	%	µmol/mol	mmol/mol	mmol/mol				mmol/mol						min	min
100	100	-0.288	-0.04	-0.10817	-9.4E-05	1.04E-07	6.36E-12	-0.05471	0.003604	-0.00012	0	(0.0,1997.0	(2.0,24.0)	26039026	26039026
100	100	-0.289	-0.0397	-0.27031	-9.4E-05	1.04E-07	6.36E-12	-0.06449	0.003604	-0.00012	0	(0.0,1997.0	(2.0,24.0)	0.5	0.5
100	100	-0.376	-0.0377	-0.27031	-9.4E-05	1.04E-07	6.36E-12	-0.06449	0.003604	-0.00012	0	(0.0,1997.0	(2.0,24.0)	2.2	2.2

Valve pos. | *match()* | CO_2 fit coeffs | H_2O fit coeffs | Fit range | Elapsed time

Figure 1-49. Match information as shown in an Excel data file.

Suggested match protocol

Now that we've covered the important details regarding matching, here is a recommended match protocol.

1. Acquire range match data for CO_2 and H_2O.

   If the values are not small, or if there is a significant slope to the data, zero and span as necessary and check again. Doing this will minimize the need for matching. The range match values should be as small as possible.

2. Take care of whatever residual corrections there are by implementing range matching.

   This should eliminate the need to rematch because of the concentration changes (i.e., any slope in the range match data).

3. Consider setting the H_2O matching log option to **Never**.

   Here's why: During a measurement, it is often the case that the reference air is fairly dry, and the sample air wet. The proper match correction is the one at the sample concentration, not the reference. Range match provides the right correction, point match doesn't. Further, a point match is not only at the "wrong" concentration, but getting there and back can involve some long equilibration times for the sample cell, and not waiting long enough will give you the wrong correction at the wrong concentration. Avoid all that and use range matching.

4. For CO_2, implement range matching, and periodically do a point match if temperatures are changing.

Section 6. **Soil chamber**

User interface updates

Version 1.4 has some done away with the **Controls** page, and moved the items that were there to either the **Settings** page or the **Environment > Flow** page.

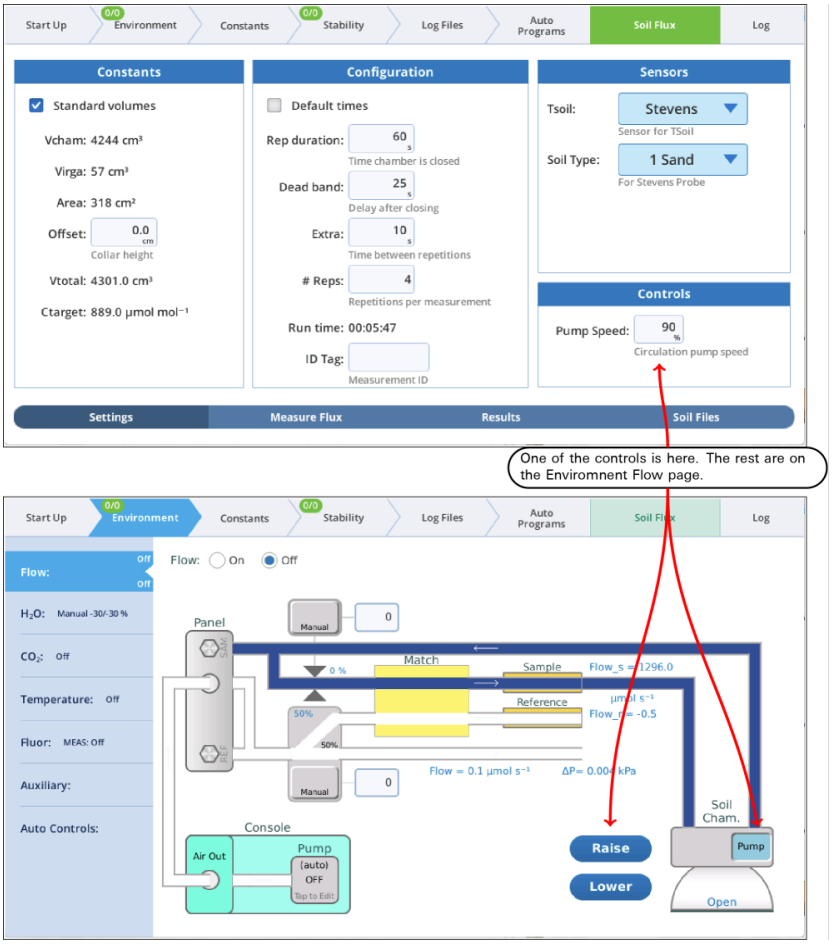


Figure 1-50. An example setup screen for soil.

Another change is that the figures and tables on the **Results** page will now update after each rep during a measurement. The update used to do all the reps at once at the end of the measurement.

Updating the soil chamber firmware

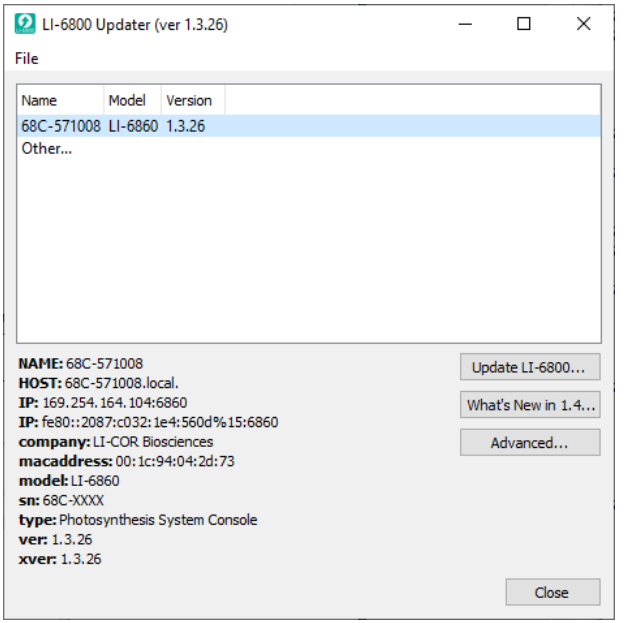
The soil chamber embedded firmware is now updated through the LI-6800 firmware updater. Fortunately, the LI-6800 updater itself is updated, so that the console and any attached head, fluorometer, or soil chamber can be updated in a single click (some waiting is required).

To update the soil chamber firmware, be sure the soil chamber is attached to a head, and follow the normal update procedure:

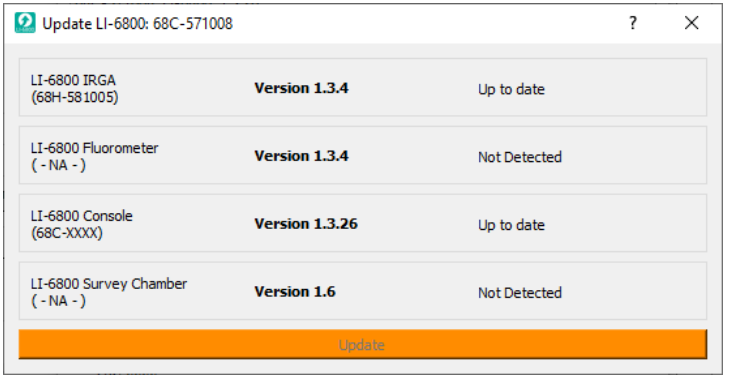
1. Install the updater to your computer.

   It is called li6800-win-updater-1.x.x.exe (Windows) or li6800-mac-updater-1.x.x.app.zip (macOS).
2. Connect the LI-6800 to your local network or your computer using the RJ-45 network cable.
3. Launch the application after it is installed.

   You'll see a list of all LI-6800s on your network, including the installed software version and the new software version. If the versions are the same, that component of your instrument is up-to-date.
4. Select the console (68C-xxxxxx; LI-6860) and click **Update LI-6800**.



The updater will display the instrument and attached components that need to be updated.



5 Click **Update** to proceed.

The updater will install the software on each component and notify you when it is done.

Section 7. Other changes

Balanced flow

Having sample and reference flow rates balanced can be advantageous for eliminating potential errors, and it is now easier to achieve. For every pump speed, there is one flow rate that will match sample and reference flows (to within 5 mol s^{-1}). To quickly get to that flow rate, simply tap the Pump button on the **Flow** control page to bring up the **Pump Speed** dialog (*Figure 1-51* below). Tap one of the four flow rate possibilities presented on the right side.

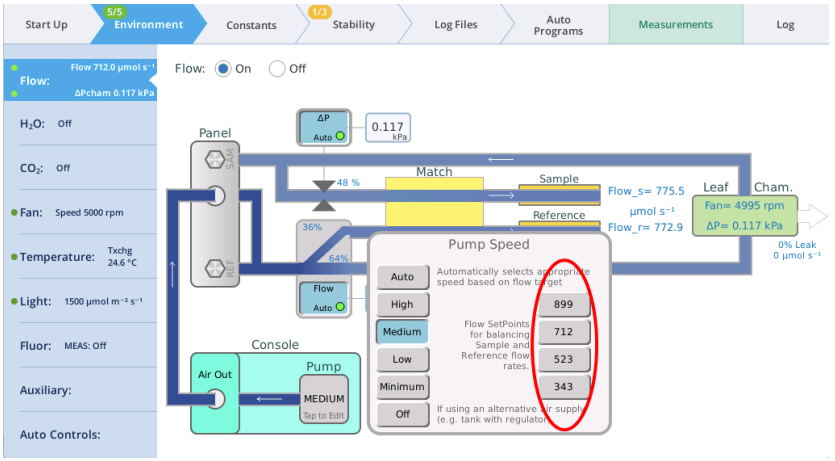


Figure 1-51. Balanced flow.

There are two Background Programs that deal with balanced flow:

- When you tap one of the balanced flow setpoint buttons, a BP (/home/utility/apps/system/balance_flow.py) is launched (no opening dialog) a few seconds later to check on the result, and fine-tune the flow if needed. That fine-tuning will automatically update the balanced flow setpoint for that pump speed. (Note: the chamber must be closed, of course, for the flows to match. If the chamber is open, then the BP won't attempt to adjust the flow rate.)

- The BP /home/utility/apps/utilities/Balance_Flow.py has an opening dialog that lets you pick what pump speed to use (*Figure 1-52* below), then balances the flow for that speed. (Cycling through all four pump speeds is also an option.) Running this program also updates the balanced flow setpoints shown in *Figure 1-51* on the previous page.

There is also a hidden shortcut: If you tap the flow rate set point edit box (the one you normally use to enter a new flow rate), and enter an E instead of a value, the balance_flow.py BP will be launched. If the pump is in Auto mode, it will change to the non-automatic version of its current speed, and the flows will be balanced.

Figure 1-52. The BalanceFlow utility program can be run manually to determine (and automatically update) balanced flow set points.

Boundary layer conductance

The chamber (and aperture)-based coefficients for computing BLC as a function of area and fan speed are now explicit in log les (*Figure 1-53* below). The coefficients are held in a new group (ChambConst) that appears in the log file header. The constants include chamber type and aperture, which used to be combined into one entry in the SysConst group.

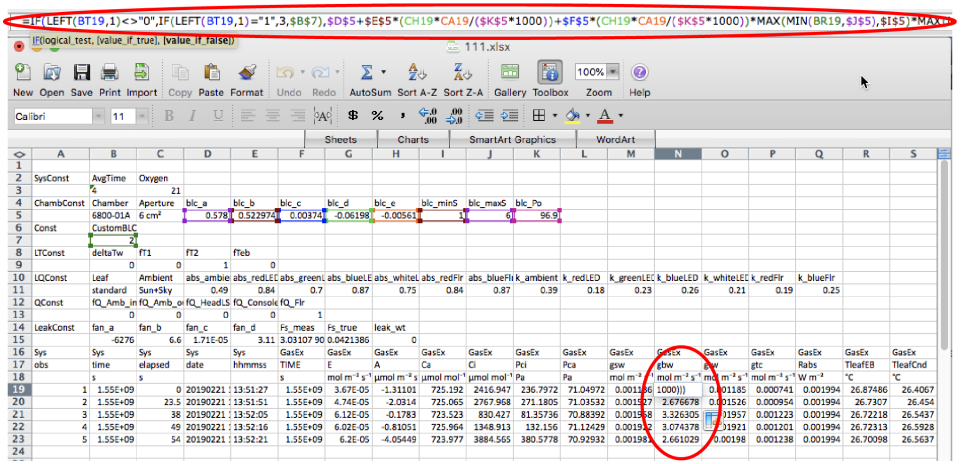


Figure 1-53. The boundary layer equation is now in the Excel file.

The one sided boundary layer conductance to water vapor g_{bw} for a broadleaf is a function of fan speed G (rpm) and leaf area S (cm^2).

$$g_{bw}(f,s) = c_o + c_1 f + c_2 f s^2 + c_3 s f + c_4 f^2 \qquad 1\text{-}5$$

where f is

$$f = \frac{GP_a}{1000P_o} \qquad 1\text{-}6$$

and s is forced to be

$$S_{min} >= s <= S_{max} \qquad 1\text{-}7$$

The empirical coefficients $c_o...c_4$, reference pressure P_o, and leaf area limits S_{min} and S_{max} depend on chamber type.

Table 1-3. Values for boundary layer conductance for chamber types.

Chamber	co	c1	c2	c3	c4	Po	Smin	Smax
6800-01 Flr	0.250	0.35860	-4.01816E-3	0.00451074	-0.0044762	96.9	1	6
6800-01A 6cm^2	0.578	0.5229739	3.740252E-3	-6.197961E-2	-5.608586E-3	96.9	1	6
6800-01A 2cm^2	0.572	0.3872742	-1.870584E-2	0.0	-7.37389E-3	96.9	1	2
6800-12 3x3	0.500	0.44869569	1.9000035E-3	-4.26088781E-2	-3.456516E-3	96.7	2	9
6800-12A 9cm^2	0.579	0.3210639	-1.109987E-3	5.106816E-3	-3.283688E-3	96.7	2	9
6800-12A 6cm^{2}FB	0.345	0.552336	-4.7985e-3	0.0	-7.3557e-3	96.7	1	6
6800-12A 6cm^{2}SS	0.418	0.5145466	-2.5106E-3	0.0	-8.1206E-3	96.7	1	6
6800-12A 3cm^{2}FB	0.188	0.5795409	-1.15295E-2	0.0	-9.7259E-3	96.7	1	3
6800-12A 3cm^{2}SS	0.141	0.5263354	-1.27376E-2	0.0	-1.10157E-2	96.7	1	3
6800-13 6x6	0.430	0.267827	-1.164018E-4	2.248202E-3	-5.109462E-3	96.8	6	36

Light control changes

Using multiple light sources

Suppose you are using the 6800-12A 3×3 chamber with a 6800-02 3×3 light source attached to the top (and connected to the LS sensor on the sensor head), and another 3×3 light source attached to the chamber bottom (remove lower plate, add Propafilm, attach light source). The bottom light source is attached to the light source connector on the console.

How to set this up? *Figure 1-54* on the facing page illustrates the first part of the process—getting the light sensors attached and enabled.

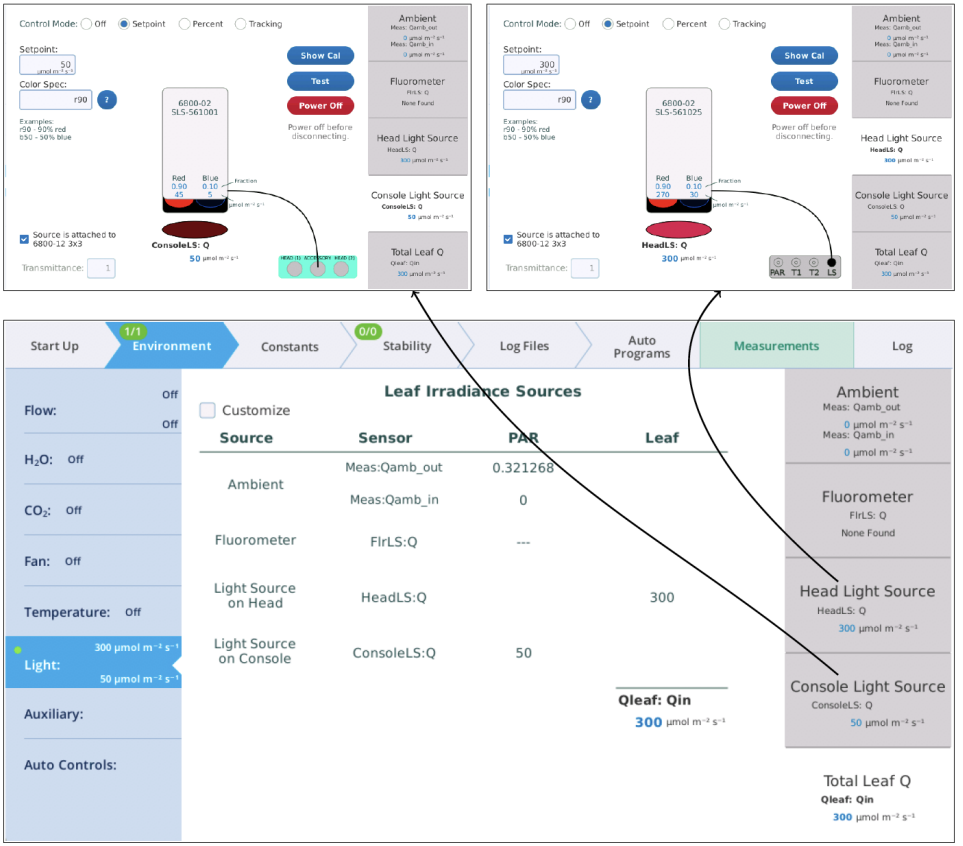


Figure 1-54. When initially configured, only one light source will be contributing to the leaf.

In *Figure 1-55* on the next page, there are two active light sources, but the software is not yet configured to use both of them when computing the total light on the leaf. *Figure 1-55* on the next page shows how to accomplish that.

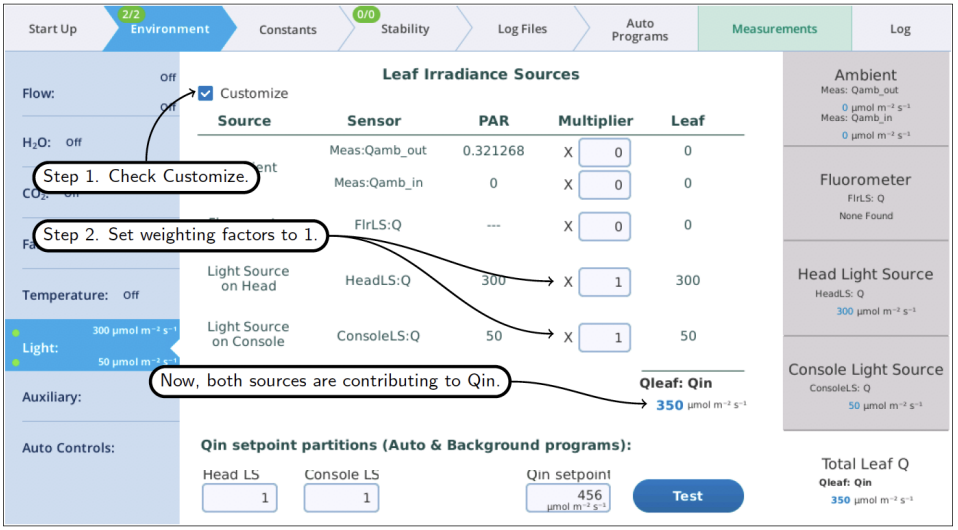


Figure 1-55. Getting two sources to contribute to the leaf.

Response check test program

We have added a Test button to light source control screens that launches a background program that checks some of the calibration coefficients (*u*1; *u*2; *u*3). This test is only available to light sources that attach to the head or console (not the MPF fluorometer).

The values in *u*0 are found by determining each color control's on/off threshold. The other values (*u*1; *u*2) relate control setting to color output, and are important for determining color mix to achieve the specified value. These values should be fairly stable with time, but are easily checked. The test that is launched (/home/licor/apps/tech/LightSourceCal.py) is best done with the light source in the dark; if the light source is attached to a chamber, then clamping the chamber onto something very unreflective (black felt, for example) is recommended.

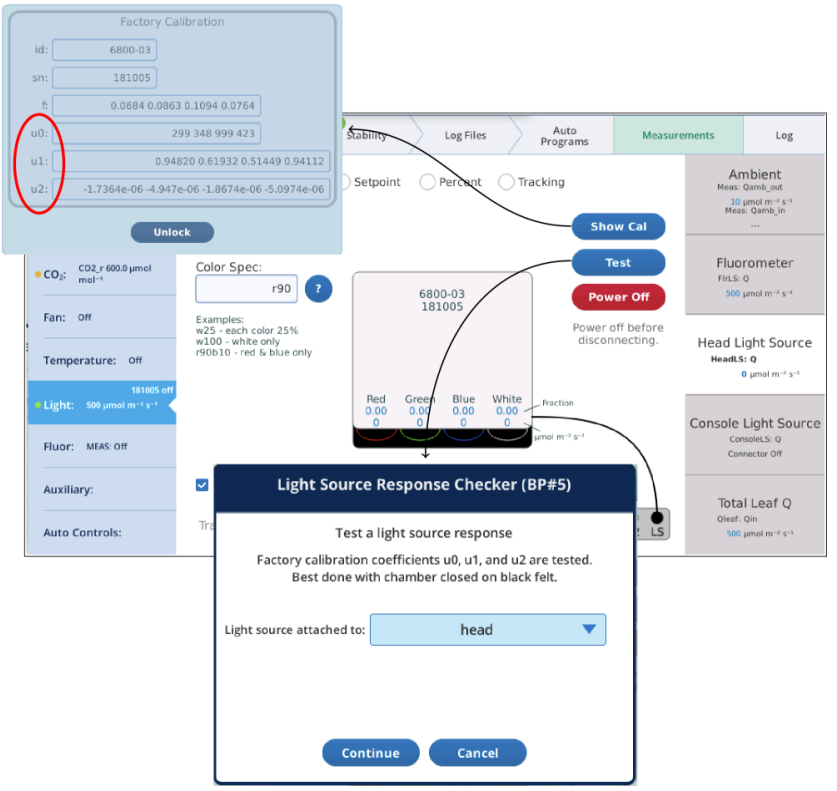


Figure 1-56. The test button will launch a BP that checks a light source.

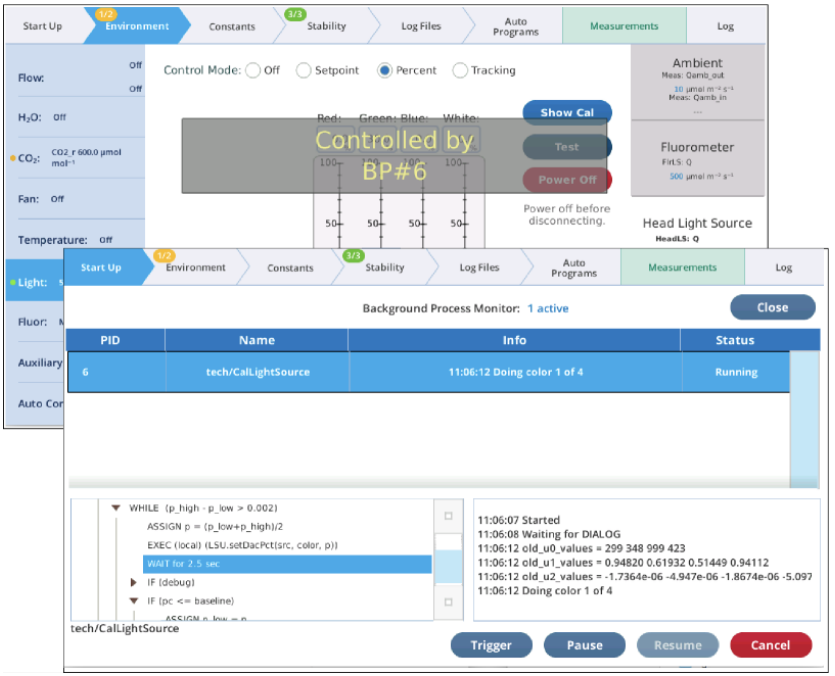


Figure 1-57. While the program is running, progress can be monitored in the Monitor screen, or on the light control panel screen.

When it is done, another dialog is presented showing the results. Tapping Install will update the coefficients with those that were just calculated.

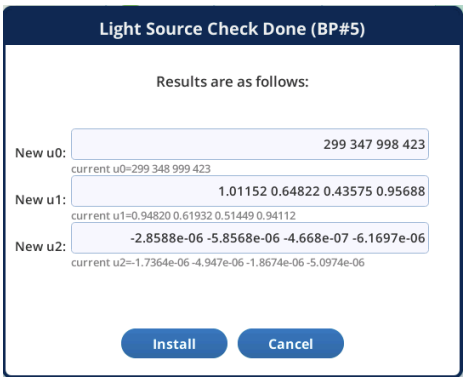


Figure 1-58. LightSourceCal closing dialog.