

# LabView Sequence Manager Program

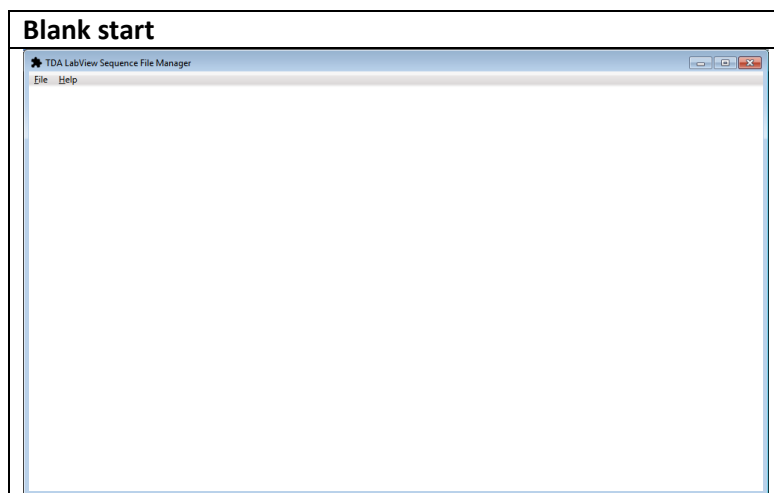
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## Introduction

This is a program that was put together to manage the sequence and other files associated with a LabView configuration. The program is a multi-pane text editor that has some features that are custom tailored to the structure and use of the specific files used.

## Getting Started

The program opens to a blank screen.



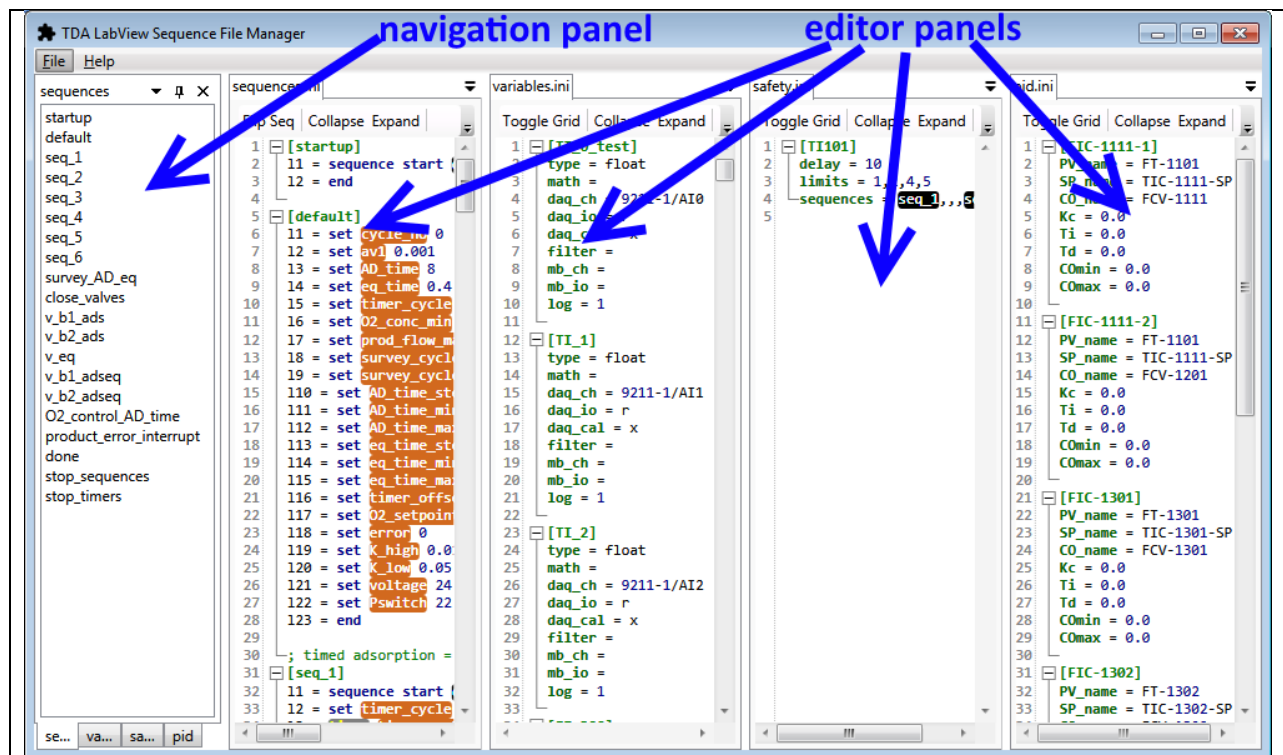
To get things going, go to File->Load Data to select a folder that contains the configuration files. The program will load up to 4 files with the following names:

- Sequences.ini
- Variables.ini
- Safety.ini
- PID.ini

The first two files are required, while the second two are optional.

Once the program has loaded the files, you will get a multi-pane editor that provides text editors along with a navigation panel.

## General Overview



The program will load all of the files that it finds side-by-side. The editor windows feature the following:

- Syntax highlighting based on the available commands
  - This also includes the available variable, sequence, and other names defined in the files. These update as you type if you add more.
- Hold control and click on a label in order to jump to the definition of the label.
- Code folding allows for all of the labels to be collapsed to their headers.
- CTRL+F allows for finding and navigating results
- Save/revert options
  - Save will copy the previous file to a “backup” folder and will save the current file over the previous one.
  - Revert will reset the editor to the file as it was originally loaded (saving will reset this)
- (For non-sequence files)
  - Import/export to Excel via the clipboard. Copies the data as tab separated or imports tab separated data.
  - View the data in a grid format. Edits to this grid will be brought back into the flat file. Be sure to hit ENTER after making a change to avoid losing the change.
- (For sequence files)
  - The syntax of the file will be changed to make it easier to edit. See below.

In addition to the editors, there is also the navigation panel. It features:

- Double click on any of the labels to cause the editor window to navigate to that label's definition.
- Note that all 4 files have tabs in that panel.

All of the document and tool panels feature:

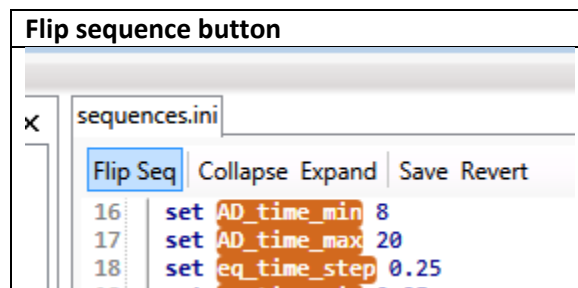
- Drag the tab title/header and you can rearrange/dock the various windows.

## Specific instructions

There are a couple items that are worth explaining in more detail.

### Editing sequence files

Sequence files have a specific syntax that LabView expects to see. In particular, the files are INI files which means they need to have section headers [like this] and also key = value pairs. When writing sequences, it's these key value pairs that can become cumbersome. In particular, they are difficult when dealing with goto statements that jump to a specific line.



To alleviate those concerns, the editor can switch the format of the sequence file. It does the following:

- Removes all of the key line numbers and “=” signs.
- Adds new labels “|1|” inside vertical pipes at the front of each line that is reference by a goto statement.
- Replaces the line number in the goto to use the label “goto 1” -> “goto |1|”.

These changes allow you to then make changes to the file including adding/removing lines without having to worry about breaking goto references.

Once you are done editing, you can switch back to the original format which will:

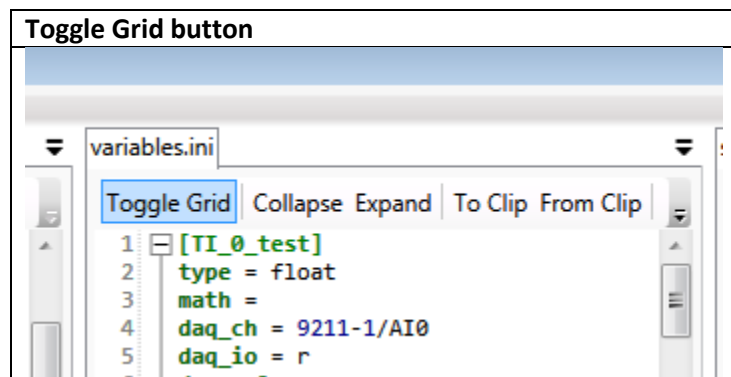
- Remove all of the |labels| at the start of the lines
- Replace the goto |1| with the correct line number
- Add the “|XX” line numbers back to the start of the lines

Note that when saving, the file will ONLY be saved in the LabView syntax, not the intermediate one. If you hit save while editing the modified format, the file will be switched back for saving.

Original	Modified
<pre> 29 30 ; timed adsorption = desorption and 31 [seq_1] 32 11 = sequence start close_valves 33 12 = set timer_cycle 0 34 13 = timer timer_cycle start 35 14 = set cycle_no cycle_no + 1 36 15 = set timer_cycle 0 37 16 = sequence start v_b1_ads 38 17 = set SL_purged 0 39 18 = set AL_purged 0 40 19 = wait AD_time 41 110 = sequence start v_eq 42 111 = wait eq_time 43 112 = sequence start v_b2_ads 44 113 = wait AD_time 45 114 = sequence start v_eq 46 115 = wait eq_time 47 116 = goto 4 48 117 = end 49 </pre>	<pre> 30 ; timed adsorption = desorption and 31 [seq_1] 32 sequence start close_valves 33 set timer_cycle 0 34 timer timer_cycle start 35 [4] set cycle_no cycle_no + 1 36 set timer_cycle 0 37 sequence start v_b1_ads 38 set SL_purged 0 39 set AL_purged 0 40 wait AD_time 41 sequence start v_eq 42 wait eq_time 43 sequence start v_b2_ads 44 wait AD_time 45 sequence start v_eq 46 wait eq_time 47 goto [4] 48 end 49 </pre>

## Flipping to the Grid View

When editing a non-sequence file, you can flip the file over to a grid view.



Before

variables.ini

Toggle Grid

Collapse

Expand

To Clip

From Clip

1

[TI\_0\_test]

2

type = float

3

math =

4

daq\_ch = 9211-1/AI0

5

daq\_io = r

6

daq\_cal = x

7

filter =

8

mb\_ch =

9

mb\_io =

10

log = 1

11

After

variables.ini

Toggle Grid

Collapse

Expand

To Clip

From Clip

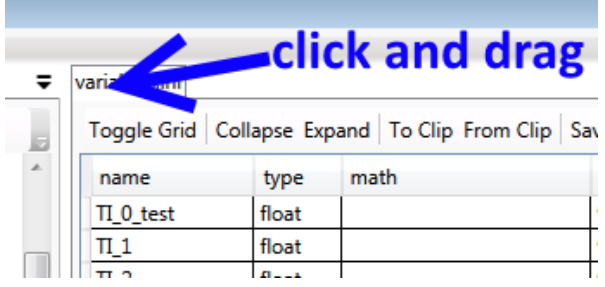
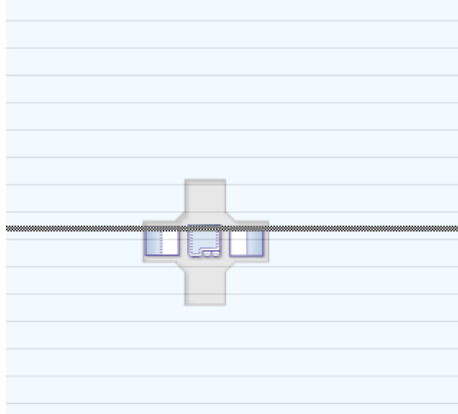
Save

Revert

name	type	math	daqch	daqio	daqcal	filter	mbch	mbio	log
TI_0_test	float		9211-1/AI0	r	x				1
TI_1	float		9211-1/AI1	r	x				1
TI_2	float		9211-1/AI2	r	x				1
FI_300	float		9205-2/AI12	r	50*x				1
PI_300	float		9205-2/AI13	r	32*x				1
FI_1	float		9205-2/AI0	r	0.9390*x^3-5.8189*x^2				1
FI_3	float		9205-2/AI1	r	(x>1.0141979)?0.1327*				1
FI_4	float		9205-2/AI2	r	(x>1.0097534)?0.1051*				1
av1	float								0
FI_4_avg	float	FI_4_avg*(1-av1)+FI_4*av1							1
PI_1	float		9205-2/AI3	r	10*x				1

## Moving Panels around

You can click and drag the different tab headers to drag the panels around. They can be combined into tabs or split or left side by side.

How to move things	When dragging												
 <p>The screenshot shows a software interface with a table. A blue arrow points to the 'name' column header with the text 'click and drag'. The table has the following data:</p> <table border="1"><thead><tr><th>name</th><th>type</th><th>math</th></tr></thead><tbody><tr><td>TI_0_test</td><td>float</td><td></td></tr><tr><td>TI_1</td><td>float</td><td></td></tr><tr><td>TI_2</td><td>float</td><td></td></tr></tbody></table>	name	type	math	TI_0_test	float		TI_1	float		TI_2	float		 <p>The screenshot shows a horizontal line with a small icon in the center, representing a dragging operation.</p>
name	type	math											
TI_0_test	float												
TI_1	float												
TI_2	float												