LUC Image Analysis in Fiji



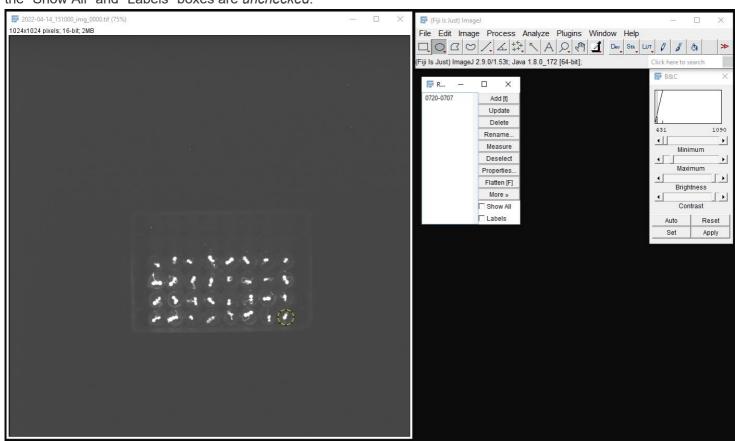
FIJI

CRITICAL: The images must be 16-bit type.

- 1. Open reference image on Fiji (ImageJ). Adjust brightness by going to Image → Adjust → Brightness/Contrast.
- 2. Select rectangle or oval tool on Fiji, depending on whether you have plates or wells, and select your "model" region of interest. Hit "Command + T". This will add your selection to your "ROI Manager".

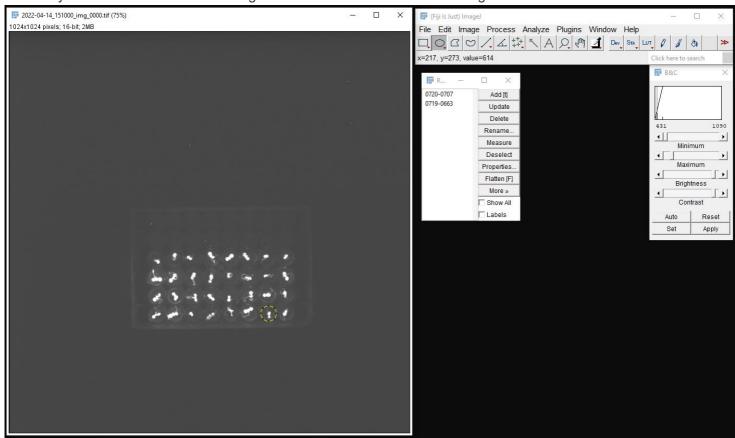
CRITICAL: You must do this on an image that is not part of the stack, else when you measure, your values will all be the same.

- 3. Save your "model" region of interest by hitting File > Save As > Selection
- 4. In your ROI Manager, highlight your first selection. Your box or circle will also be highlighted. **CRITICAL:** Make sure the "Show All" and "Labels" boxes are *unchecked*.



Selection of initial ROI

5. Move your box or circle to the next region of interest. Hit "Command + T" again.

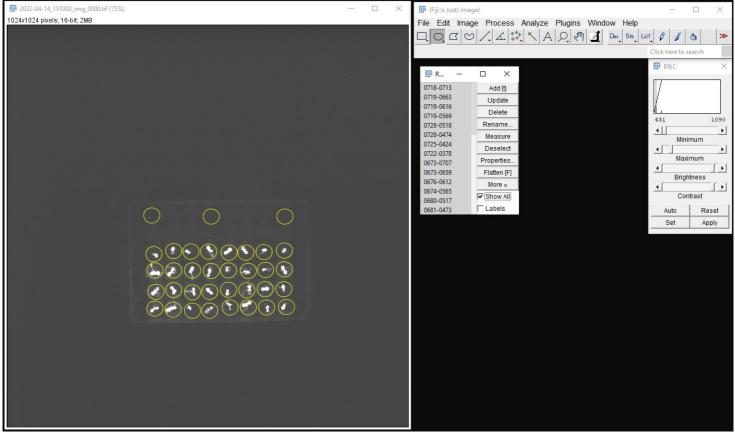


Moving the ROI circle to choose the next ROI

6. Repeat this until all your regions of interest are selected.

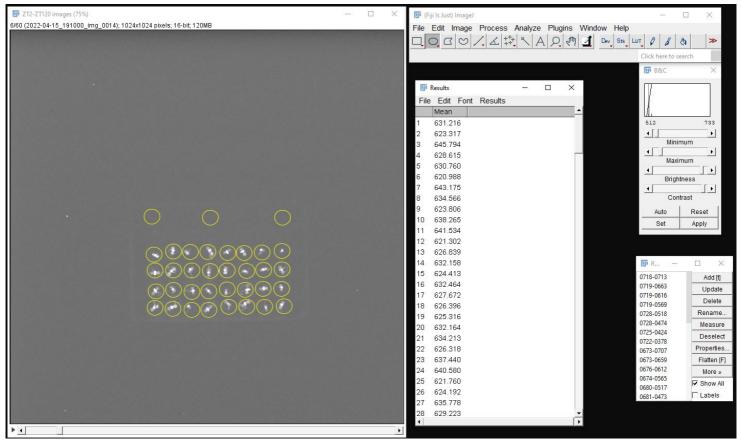
IMPORTANT: Make sure that your ROIs are in order and all grouped within one genotype!

NOTE: In addition to choosing all regions of interest, it is a good idea to also select 3-5 "blank" spaces (empty wells, empty pots or even empty space in the image). During analysis, these values can be averaged and subtracted from the experimental ROIs to control for background noise. **CRITICAL**: Select these regions last so that they are always the last measurements taken for each image.



Reference image with all ROIs selected - 32 wells containing plants, and three blank wells used to correct for background noise.

- 7. Open your LUC stack image in Fiji by <u>dragging the folder</u> containing your image sequence to the ImageJ bar. (**CRITICAL:** When prompted, leave "Covert to RGB" and "Virtual Stack" boxes *unchecked*.)
- 8. Overlay your ROIs by checking "Show All" and check to see that all your selections fit your LUC signals. If you need to adjust some of them, highlight the ROI in the ROI Manager, move your box or circle, hit "Command + T", then delete the original. **IMPORTANT**: Doing this actually puts them out of order!
- 9. To save your ROI set, highlight all and hit "More > Save"
- 10. Go to "Analyze" in ImageJ and select "Set Measurements". In the pop-up window, select only "Mean Gray Value".
- 11. To measure, highlight all and hit "Measure" or "Control + M" on the ROI Manager. Switch to the next image using the mouse scroll.



Results after applying the ROIs to the image stack and getting mean gray value for each ROI at each image.

ADDITIONAL NOTES

When setting up for imaging, make sure that the plates are not too far from the center of the camera lens.

If using a strong reporter (eg: Arabidopsis *CCA1p:LUC*) and long exposure, note that signal from one well will bleed in to nearby wells. It is important to use either black plates or to use adequate spacing around plants. It is best not to image a strong and weak reporter together.

ARRANGING DATA FOR IMPORT INTO BIODARE2

NOTE: There are multiple ways to accomplish this. We have provided versions for Excel and R.

CRITICAL: It is essential that you know exactly which ROI corresponds to each replicate. It is possible to rename the ROIs if that makes it easier to keep track of them. The order of the data output by Fiji will correspond to the order of ROIs. Save a backup of the raw data before proceeding with any analyses.

EXCEL:

Copy the two columns of data from Fiji (the measurement serial number and the measurement (i.e. mean gray value)). Paste these into an Excel Spreadsheet.

In a new column (other than column C)), use the following formula: =INDEX(\$B\$1:\$B\$X,ROW(C1)+(Y*(COLUMNS(\$C\$1:C\$1)-1)))

where X is the last measurement serial number (for example, if you have 56 total measurements, this would be 56) and Y is the sample size of your experiment (for example if you measured 7 plants, this would be 7)

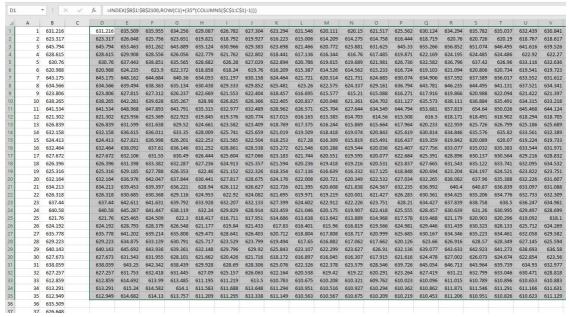
Critical: You must lock the data column in place using the dollar signs!

For the provided sample dataset, there are 32 plants and 3 blank wells, for a total of 35 observations per time point, and 60 total time points for a total of 2100 observations. Thus, the formula used is:

=INDEX(\$B\$1:\$B\$2100,ROW(C1)+(35*(COLUMNS(\$C\$1:C\$1)-1)))

Extend this formula into a grid where the number of rows is the sample size (ie, Y) and the number of columns is equal to the number of images you are analyzing. (Hint: an easy way to do this is to set up a grid beforehand by changing the color and using a guiding row/column and fill in the spots).

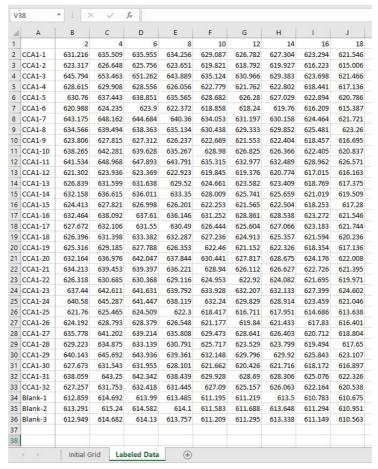
The data will be arranged into a grid.



Initial grid output using the provided excel formula.

To work with the data, select the newly arranged dataset and paste it into a new sheet, leaving the top row and first column empty, using 'Paste Special' -> 'Paste Values'. Name this sheet 'Labeled Data'.

Add the labels that correspond to each ROI. At this point, each column represents a time point, and each row represents an ROI.



Moving the grid to a new sheet and labeling rows and columns.

After entering the grid in a new sheet, separate the rows that correspond to the blanks by moving them down a row. Take the average blank value for the first time point using the AVERAGE command.

30	CCA1-29	640.143	645.692
31	CCA1-30	627.673	631.543
32	CCA1-31	638.059	643.25
33	CCA1-32	627.257	631.753
34			
35	Blank-1	612.859	614.692
36	Blank-2	613.291	615.24
37	Blank-3	612.949	614.682
38	Avg_blank	=Average(E	335:B37)

Finding the average blank value for the first timepoint.

Drag this across all the columns to get an average blank value for each time point.

28	CCA1-27	635.778	641.202	639.214	635.808	629.473	628.641	626.403	620.712
29	CCA1-28	629.223	634.875	633.139	630.791	625.717	623.529	623.799	619.494
30	CCA1-29	640.143	645.692	643.936	639.361	632.148	629.796	629.92	625.843
31	CCA1-30	627.673	631.543	631.955	628.101	621.662	620.426	621.716	618.172
32	CCA1-31	638.059	643.25	642.342	638.439	629.928	628.69	628.306	625.076
33	CCA1-32	627.257	631.753	632.418	631.445	627.09	625.157	626.063	622.164
34									
35	Blank-1	612.859	614.692	613.99	613.485	611.195	611.219	613.5	610.783
36	Blank-2	613.291	615.24	614.582	614.1	611.583	611.688	613.648	611.294
37	Blank-3	612.949	614.682	614.13	613.757	611.209	611.295	613.338	611.149
38	Average_blank	613.033	614.8713	614.234	613.7807	611.329	611.4007	613.4953	611.0753

Averaging blank values across all time points.

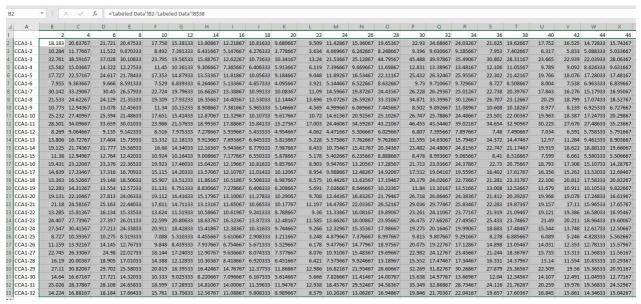
Open a new sheet and name it "Background Corrected Data". Paste in the top row and first column from the 'Labeled Data' sheet. Now, subtract the average blank value from each measurement at every timepoint. The formula for this

='Labeled Data'!B2-'Labeled Data'!B\$38

B	2	*	×										
A	Α	В		С	D	E	F	G	Н				
1			2	4	6	8	10	12					
2	CCA1-1	18.1	183										
3	CCA1-2		100										
4	CCA1-3												
5	CCA1-4												
6	CCA1-5												
7	CCA1-6												
8	CCA1-7		į.										
_													

Formula used to correct for average background for each ROI at each timepoint.

Now, drag it through the whole grid for all ROIs and timepoints (though you can disregard the blank rows). This should output a grid where each ROI mean gray value has the average background values subtracted from it.



Calculating background corrected values for the entire dataset.

Paste this grid into a new sheet called BCD Values using 'Paste Special' --> 'Values Only'. Then, make another new sheet labeled 'For Biodare'. Paste the grid from the BCD Values sheet into this grid using the 'Transpose' option.

1	Α	В	С	D	E	F	G	Н	1	J	k
1		CCA1-1	CCA1-2	CCA1-3	CCA1-4	CCA1-5	CCA1-6	CCA1-7	CCA1-8	CCA1-9	CCA1
2	2	18.183	10.284	32.761	15.582	17.727	7.955	30.142	21.533	10.773	25
3	4	20.63767	11.77667	38.59167	15.03667	22.57167	9.363667	33.29067	24.62267	12.94367	27.4
4	6	21.721	11.522	37.028	14.322	24.617	9.666	30.45	30.45 24.129		25
5	8	20.47533	9.870333	30.10833	12.27533	21.78433	8.591333	26.57933	21.35333	12.45633	21.4
6	10	17.758	8.492	23.795	11.45	17.353	7.529	22.724	19.109	11.34	17
7	12	15.38133	7.391333	19.56533	10.36133	14.87933	6.839333	19.79633	17.93233	10.15233	15.4
8	14	13.80867	6.431667	15.88767	9.306667	13.53367	6.264667	16.66267	16.35667	8.908667	12.8
9	16	12.21867	5.147667	12.62267	7.365667	11.81867	5.133667	13.38867	14.40567	7.381667	11.3
10	18	10.81633	4.276333	10.73633	6.406333	10.05633	4.657333	10.99133	12.53033	5.965333	10.1
11	20	9.680667	3.778667	10.34167	5.913667	9.184667	4.095667	10.08367	12.14467	5.146667	9.61
12	22	9.509	3.634	13.24	6.119	9.048	3.921	11.09	13.696	4.569	1
13	24	11.42867	4.669667	21.53667	7.396667	11.89267	5.144667	14.59667	19.07267	4.999667	14.6
14	26	15.36067	6.242667	35.12867	9.669667	16.53467	6.522667	19.87267	26.59267	6.069667	20.9
15	28	19.65367	8.248667	44.79567	11.69867	22.11167	8.632667	24.43567	33.31067	7.445667	25.1
16	30	22.93	9.396	45.488	12.831	25.432	9.73	26.228	34.871	8.502	26
17	32	24.68667	9.630667	39.97867	13.38967	26.32467	9.710667	26.29367	33.39967	9.892667	25.7
18	34	24.03267	9.185667	35.49067	13.48167	25.95567	9.729667	25.01267	30.12667	11.08967	24.4
19	36	21.625	7.953	30.802	12.106	22.302	8.727	22.738	26.707	10.608	23
20	38	19.62667	7.402667	28.31167	11.05567	21.42167	8.508667	20.39767	23.12667	10.18267	22.0
21	40	17.752	6.317	23.665	9.789	19.766	8.004	17.843	20.29	8.977	19
22	42	16.525	5.833	22.939	9.092	18.076	7.538	16.276	18.799	8.139	18
23	44	14.72833	5.088333	22.03933	8.624333	17.28033	6.963333	15.17933	17.07433	6.925333	17.2
24	46	15.74367	5.033667	28.06367	9.631667	17.48167	6.839667	16.95067	18.52767	6.727667	20.2
25	48	18.70133	5.851333	46.34533	12.00533	21.65133	7.731333	22.18833	23.75733	6.768333	28.5
26	50	24.74867	7.480667	68.84467	15.38967	30.38667	9.816667	30.23567	32.59767	7.200667	37.8
27	52	32.796	9.285	80.852	17.226	36.454	11.95	38.507	40.109	8.243	47
28	54	38.831	11.363	81.579	19.663	40.924	13.394	45.296	43.244	10.757	5:
29	56	40.25067	12.80267	74.09367	20.59267	41.26267	14.17167	47.47367	42.90967	12.66067	50.6
30	58	38.25933	13.69633	62.79033	20.51433	38.70233	14.36533	46.38433	39.77333	14.40333	46.0
31	60	34.9	13.381	50.9	19.567	36.058	13.851	43.123	35.668	15.066	42
32	62	31.71767	12.89067	44.29267	18.65267	34.31667	13.74267	40.49367	32.40667	14.64967	37.6
33	64	27.971	12.072	38.927	17.737	32.801	13.228	37.21	29.49	13.966	33
34	66	24.674	11.496	34.448	16.819	28.603	12.993	34.441	25.002	12.985	:
35	68	22.52967	11.29867	34.24967	16.47367	26.38367	12.34167	32.43467	21.97267	11.97867	29.9
36	70	23.76167	10.87167	44.77167	17.95267	28.68967	12.20967	32.82867	21.71667	11.31667	38.1
37	72	32.621	12.555	67.12	23.804	34.483	13.974	38.152	26.011	11.403	5
38	74	46.23233	14.68333	90.34733	28.93933	43.53933	17.23833	47.11533	32.17933	12.24933	74.8
4	>	Initial	Grid La	beled Data	Backg	round Corr	rected Data	BCD	(values)	For Bioda	re

Transposed values for analysis in BioDare.

Prior to uploading it to Biodare, paste the 'For Biodare' sheet in to a new excel file.

For Biodare to conduct analyses, all ROIs from the same genotype/treatment must have the same name, with no unique identifier. As a final step, ensure that all columns from a single genotype or treatment group have the same name. In the sample dataset, all plants are *CCA1p:LUC*, so all get the column name CCA1. (as an example, if we also had five wild type plants, we would name those five columns WT).

	CCA1																	
2	18.183	10.284	32.761	15.582	17.727	7.955	30.142	21.533	10.773	25.232	28.501	8.269	13.806	19.125	11.38	19.431	14.639	13.363
4	20.63767	11.77667	38.59167	15.03667	22.57167	9.363667	33.29067	24.62267	12.94367	27.40967	34.09667	9.064667	16.72767	21.74367	12.94967	23.22067	17.23467	16.52667
6	21.721	11.522	37.028	14.322	24.617	9.666	30.45	24.129	13.078	25.394	33.659	9.135	17.404	21.777	12.764	23.376	17.316	19.148
8	20.47533	9.870333	30.10833	12.27533	21.78433	8.591333	26.57933	21.35333	12.45633	21.48633	30.01033	9.142333	15.73933	19.56933	12.42033	22.36533	16.70933	18.50633
10	17.758	8.492	23.795	11.45	17.353	7.529	22.724	19.109	11.34	17.651	23.986	8.516	13.332	16.68	10.924	19.923	15.115	15.907
12	15.38133	7.391333	19.56533	10.36133	14.87933	6.839333	19.79633	17.93233	10.15233	15.42433	21.57633	7.975333	12.18133	14.34033	10.16433	17.46033	14.20333	13.51233
14	13.80867	6.431667	15.88767	9.306667	13.53367	6.264667	16.66267	16.35667	8.908667	12.87067	18.99367	7.278667	9.913667	12.16367	9.008667	15.04267	13.57067	11.86167
16	12.21867	5.147667	12.62267	7.365667	11.81867	5.133667	13.38867	14.40567	7.381667	11.32967	17.88667	5.939667	7.693667	9.943667	7.177667	12.19667	12.10767	10.51867
18	10.81633	4.276333	10.73633	6.406333	10.05633	4.657333	10.99133	12.53033	5.965333	10.10733	15.84133	5.433333	6.645333	8.779333	6.550333	10.81633	11.01433	9.506333
20	9.680667	3.778667	10.34167	5.913667	9.184667	4.095667	10.08367	12.14467	5 146667	9 617667	15 27367	4 954667	5.813667	7 987667	5 878667	9.857667	10 12067	8 987667

Changed column names for analysis.

Data Transformation in R:

Copy the two columns of data from Fiji (the measurement serial number and the measurement (i.e. mean gray value)). Paste these into an Excel Spreadsheet and save as a .csv file.

Download the R script 'FormattingFijiDataOutput.R' from github: https://github.com/GreenhamLab/CCD_Imaging

We have also provided the images, ROIs, and Raw Data output from Fiji as a test sample.

Run the script on the Fiji output data to format it for BioDare.

Note: At this time, Biodare adds quotation marks (" ") around the sample names when using a file output by R. This can be fixed by opening the output in excel and saving it as a csv. If we find a solution for this, we will update the script on our github page.

