

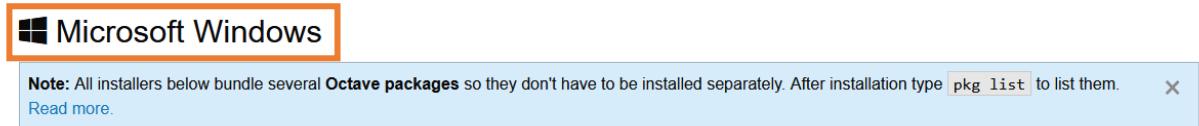
# How to run ClinCirc

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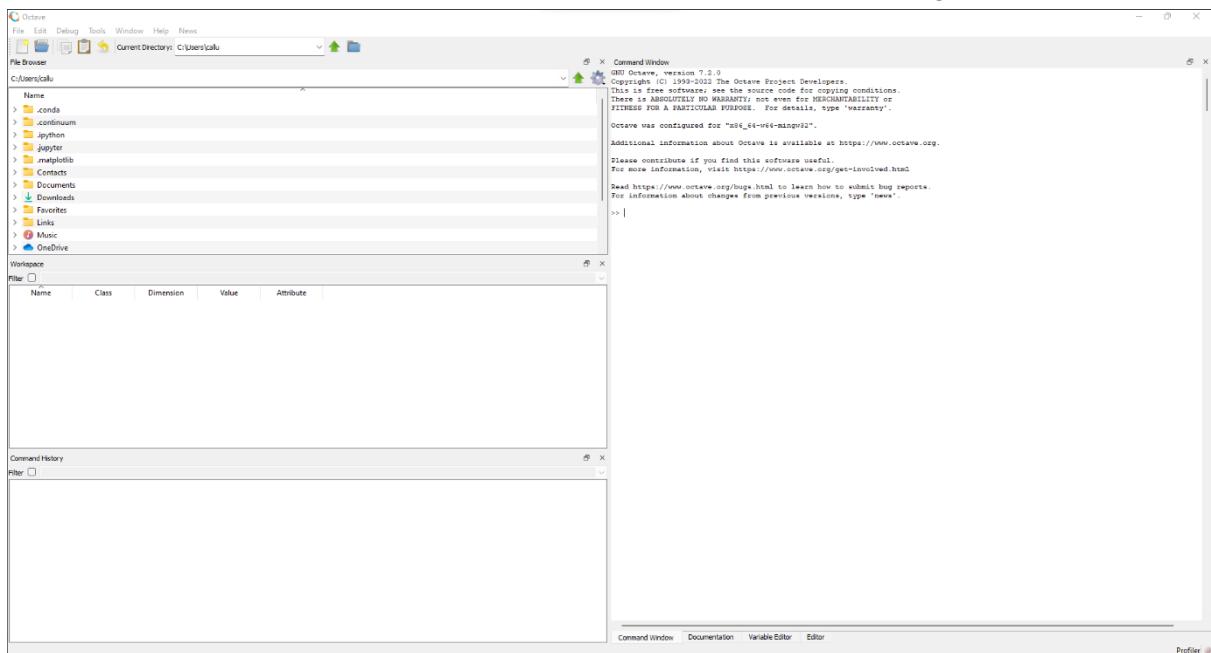
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# Installing GNU Octave for Microsoft Windows

1. Navigate to <https://octave.org/download>
2. Scroll down to the Microsoft Windows section. Download the file that ends in “-installer.exe”.



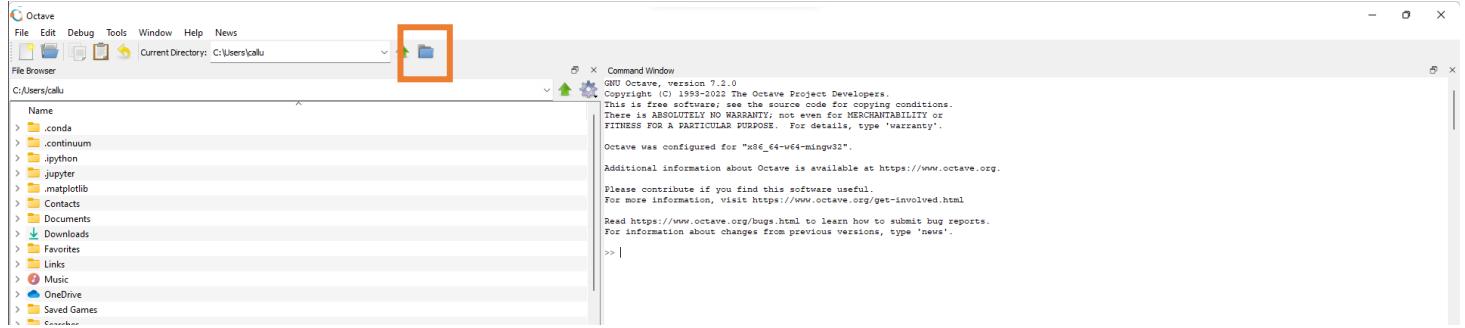
3. Once the file has downloaded, run the installer (you can accept all the default options in the installer).
4. GNU Octave is now installed and can be opened by running the programme GNU Octave (GUI). Once opened, it should look similar to the image below:



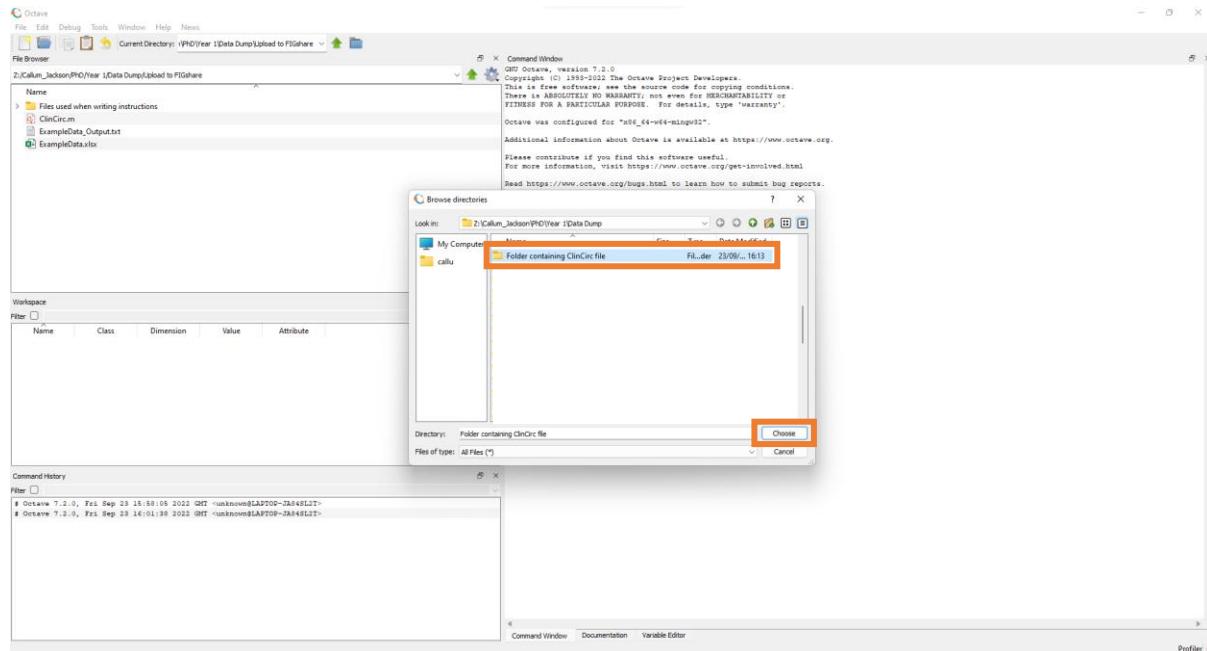
# Running ClinCirc in GNU Octave

## Analysing example data 1 (basic example)

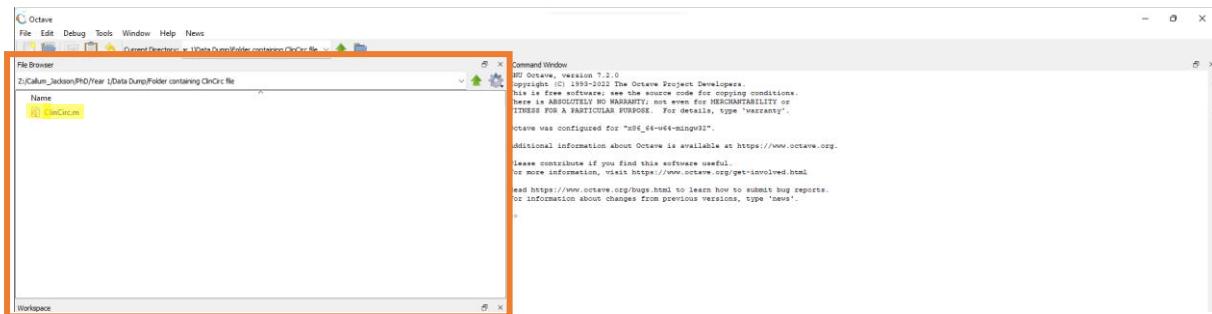
1. Download the ClinCirc.m file and ExampleData1.xlsx from [Figshare link](#) (take a note where you have saved the file to).
2. From within GNU Octave (GUI), select the blue folder on the top ribbon.



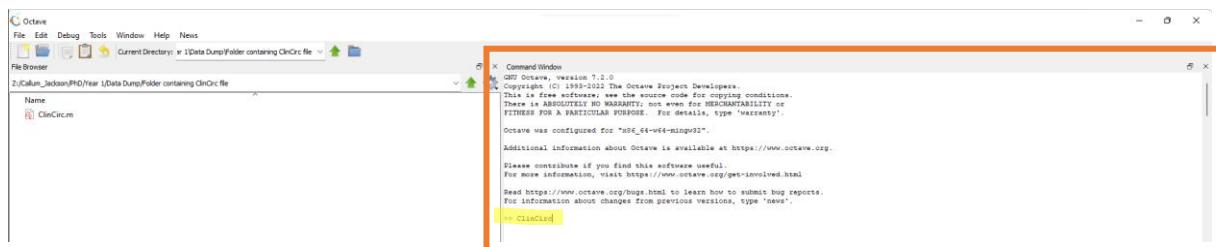
3. This will open a file browser. Use this to navigate to the folder that contains your ClinCirc.m file. Highlight the folder by clicking it once, and then press "Choose".



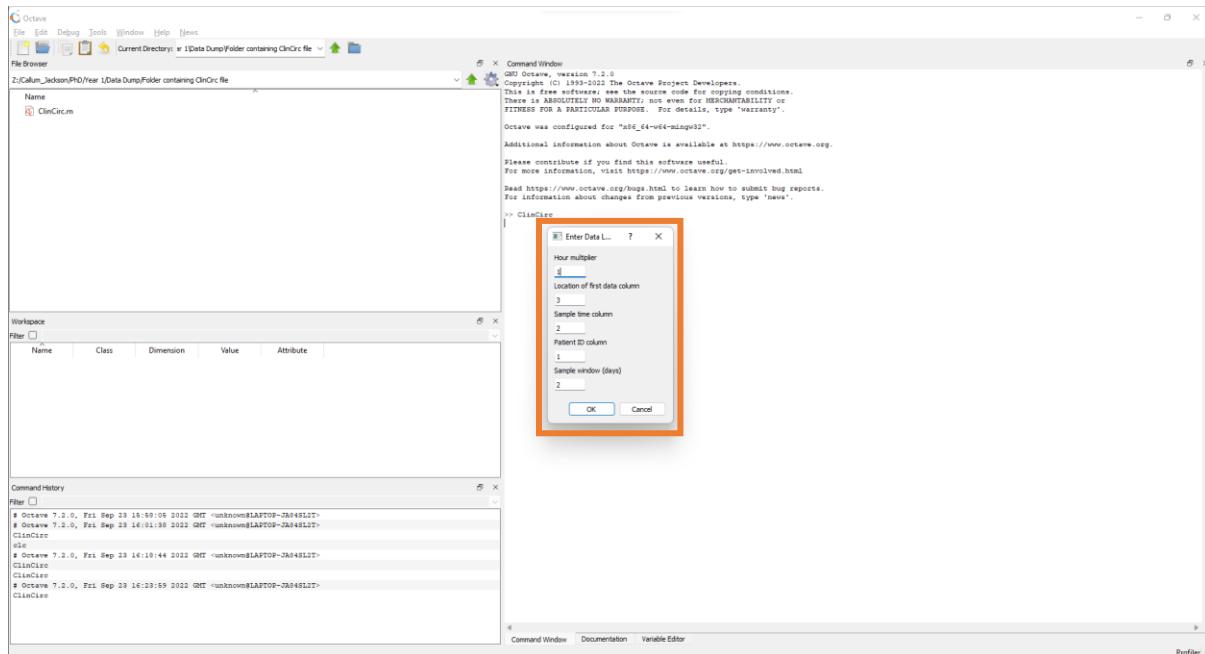
4. You should now see the file `ClinCirc.m` in the upper right box of GNU Octave.



5. To run ClinCirc, type “`ClinCirc`” into the command window on the right, next to the “`>>`” symbols and press enter.



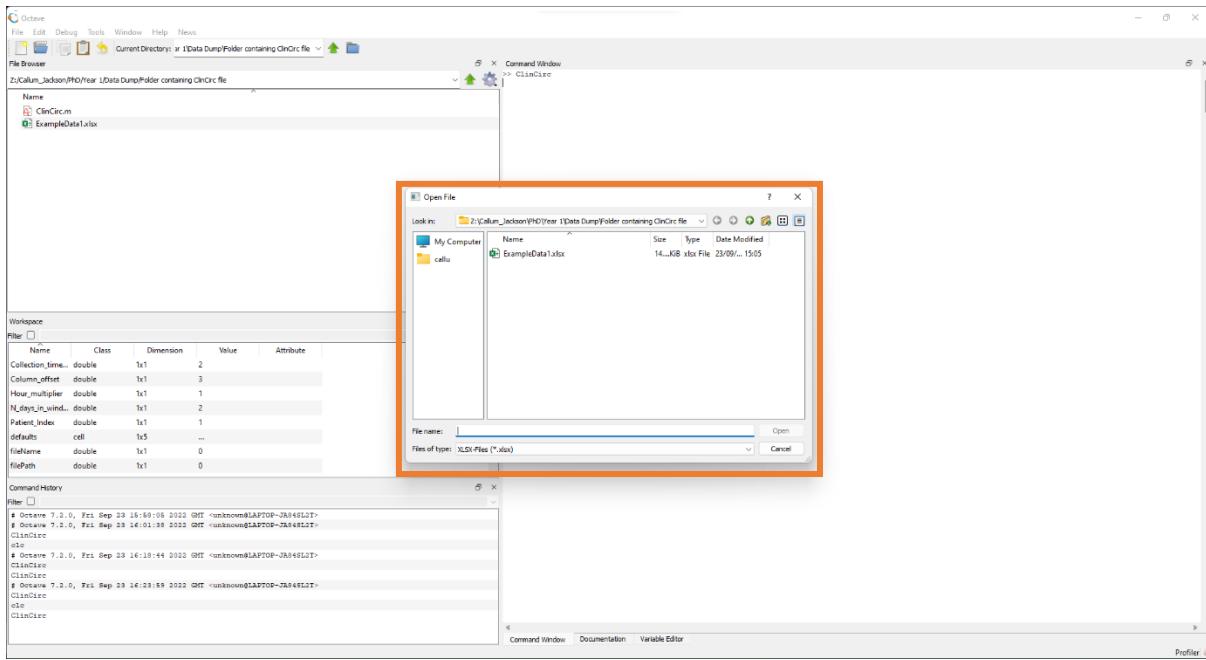
6. This will open the first dialogue box where we choose some of the analysis parameters. There are five numbers that can be changed. For ‘example data 1’, the default options do not need to be changed so press “OK”.



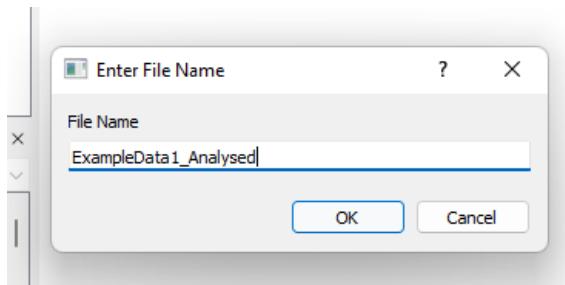
- Aside: Looking at a screenshot of ‘example data 1’, we can see what each value corresponds to

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1	ID	Sample time	Gene_1	Gene_2	Gene_3	Gene_4	Gene_5	Gene_6	Gene_7	Gene_8	Gene_9	Gene_10				
2	P1	0	3.596393358	-3.975089505	4.384113943	-1.397730864	1.949115889	4.987625513	-0.866812993	5.00063945	1.847240671	3.572085575				
3	P1	4	-0.095516503	-3.740841408	0.227231803	7.042053864	5.755327042	3.809006399	-3.219451948	3.493498976	-1.591129767	1.87260064				
4	P1	8	5.895039377	1.201672293	-2.746833778	2.453365195	5.447719085	1.254223956	1.962770413	-0.801162218	-0.693072877	4.380035427				
5	P1	12	-3.491445979	3.324465935	-2.334718981	5.356312275	-0.840440402	0.624134449	2.358083856	-1.995357539	-1.787100319	-2.205376721				
6	P1	16	0.982894615	2.980249473	-1.68201606	-4.298864608	-4.587694774	-4.029848256	8.918315252	-1.456566168	2.108418493	-4.994261361				
7	P1	20	4.935609979	-3.050887544	-1.377258314	0.384995196	-3.930950858	-1.172892354	-3.624567336	1.445799653	2.803567574	-4.084320648				
8	P1	24	4.416772464	-3.350474553	3.05741158	-0.610236217	3.1688916	3.682323405	-2.408401485	3.084798448	3.565990817	-1.931368173				
9	P1	28	1.98112345	-0.301866228	0.19003875	3.653723781	5.460100191	3.553291763	2.637374004	5.107625542	0.880350892	3.582445389				
10	P1	32	-2.007255838	-0.919053924	3.513836041	7.12813599	5.4331131	-4.156740041	5.773931152	-2.518270376	1.587900012	6.191909481				
11	P1	36	4.838295235	-0.70039757	0.870707809	2.035442823	2.089643164	1.839843331	3.510314936	-2.82170427	-3.38047097	0.233053546				
12	P1	40	1.60076061	4.42717809	-1.469942089	0.933729541	-2.893723521	4.490339822	5.215085819	0.569767319	1.442090467	-0.508257197				
13	P1	44	4.183612525	0.850057319	2.043352053	-4.228977837	3.060391726	3.642044753	0.949770055	4.034041584	6.49329333	-0.996250053				
14	P2	12	5.135803932	5.132480298	2.32070021	4.46743897	3.675791567	4.755467666	4.280710489	2.751336415	2.016505117	-3.636841764				
15	P2	16	3.458037318	3.94082748	-1.074252337	0.584443376	4.727663958	-0.788522091	2.521798689	2.968851254	-3.782749854	-1.469000092				
16	P2	20	-5.585961329	-0.302403713	-4.495741005	1.347723547	2.46469555	-3.493643664	-0.992311281	-0.00394911	3.179285262	2.131043007				
17	P2	24	-2.554728662	-4.6525054	-2.86796598	0.933162694	4.45885475	-4.221208116	4.927968298	4.671826677	5.560196256	5.37751417				
18	P2	28	-2.768325448	0.23549802	7.22213951	0.761037577	-3.363268238	3.042501704	5.427169563	3.313206061	7.351894187	2.642700866				
19	P2	32	-1.153488864	-0.428996088	-0.715750346	4.397332889	2.123706989	3.570800873	2.821799562	4.858646717	-3.64129433	0.888389138				
20	P2	36	5.272569519	2.782795607	1.354743047	3.451178943	-3.78201602	3.698719619	2.698845298	-1.600035512	2.640962602	-1.633800815				
21	P2	40	4.34590732	-1.277254421	4.142041501	5.307976304	4.296355459	3.940586135	2.919291513	-2.664515501	-1.8257772981	2.438099515				
22	P2	44	-1.615200628	4.274443412	3.267853366	3.132248536	2.935686736	-4.884842605	-4.609048256	5.317886084	-1.90296523	3.915976447				
23	P2	48	-0.00288548	-2.151845742	5.590204813	0.946519504	-2.404101124	-2.770868507	-1.097842358	-2.45114475	2.910302478					
24	P2	52	-2.976956316	0.554278865	-4.188918488	1.703730167	-3.314873036	-2.542050918	-2.472849628	4.904180564	1.427779246	-5.431448508				
25	P2	56	1.657991509	-1.126431433	2.688482357	-0.153345274	-2.952852556	5.608253304	0.328555494	2.86137769	4.34308387	-0.005870391				
26	P3	8	2.198629332	-2.53193956	-3.45165944	6.29283622	6.642136558	0.240829304	1.325409731	2.736430335	-0.136995967	5.301606976				

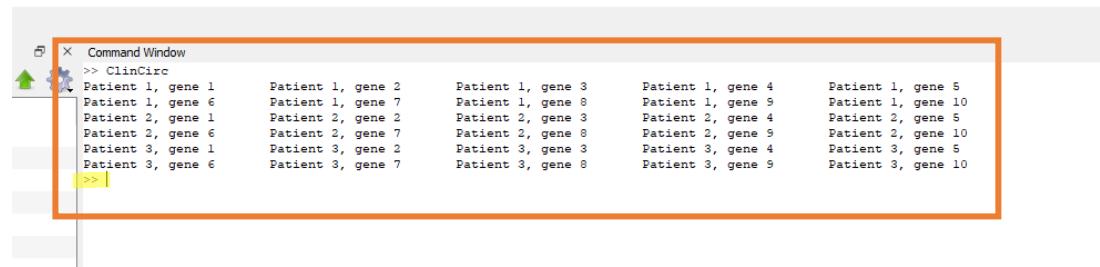
- The ‘Hour multiplier’ should typically be either 1 or 24. If the times associated with each sample are recorded in hours, then use the value 1. If the times associated with each sample are recorded in excel date format, then use the value 24.
    - In ‘Example Data 1’, the ‘Sample time’ column is recorded in hours (the second sample collected at 4am, second sample at 8am, etc.) hence the hour multiplier should be 1.
    - In Example Data 2, the “Sample time” column is recorded in Excel data format (hh:mm) and so the hour multiplier should be 24.
  - ‘Location of first data column’ tells ClinCirc which the first column is that contains the data we want to analyse. In the case of ‘Example Data 1’, the first column is an ID for each participant and the second column is the time each sample was collected. Therefore, the location of first data column is 3 to indicate the 3<sup>rd</sup> column.
  - ‘Sample time column’ tells ClinCirc which column contains the time each sample was collected at. In ‘Example Data 1’, we can see that this is column 2.
  - ‘Patient ID column’ tells ClinCirc which column to use to identify which samples are associated with which patient/participant. **This identifier must contain text.** For ‘Example Data 1’, the IDs are in column 1.
  - ‘Sample Windows (days)’ tells ClinCirc how long the samples were collected for. In ‘Example Data 1’ we can see the data was collected for 48h, and so we tell ClinCirc this was 2 days. Note that the number of days must be integer for the Lomb-Scargle process to work.
7. Now a second dialogue box will open. Use this to navigate to the folder where ‘Example Data 1’ is saved. Note that you do not have to store the ClinCirc.m file and your data in the same folder. Once you have found your data, click it and press “open”.



8. The final dialogue box will now open. This box allows you to rename the outputs of the analysis. By default, it will use the name of the file being analysed suffixed with “\_Analysed” but you can choose whatever you would like it to be.



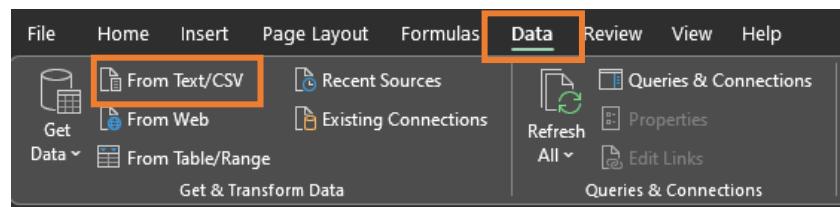
9. ClinCirc will now begin analysing the data, providing an update every time it finishes analysing a gene/patient. This should take ~30 seconds. Once the “>>” returns to the command window, it has finished running.



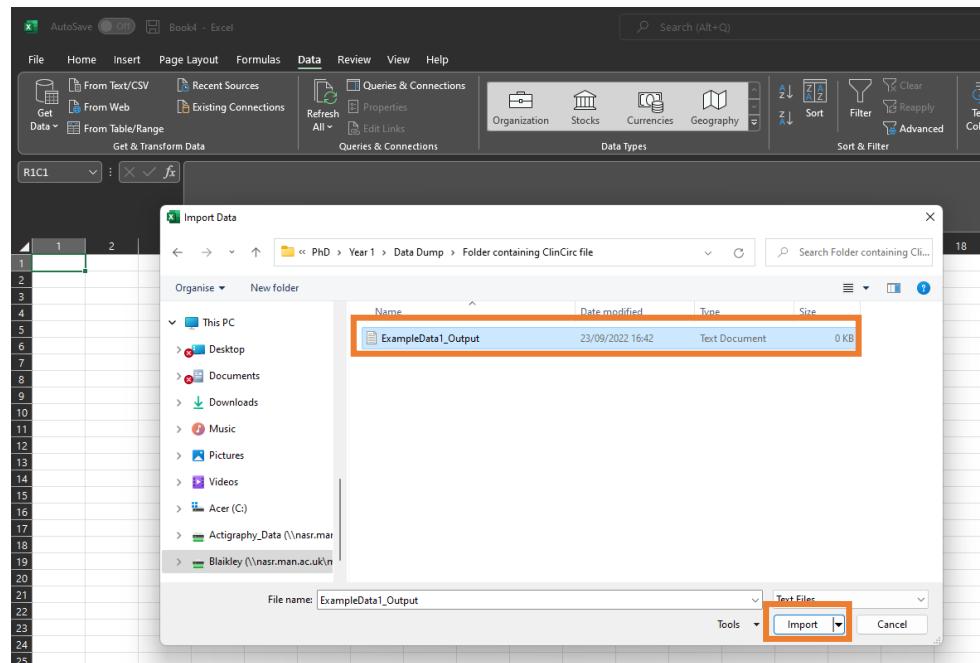
10. The numerical output of the analysis will be saved as a text file in the same folder as the data that was analysed with the suffix “\_Output”. The other file produced has the suffix “\_Graphs” and is a PDF which has a figure for every gene superimposing the fitted cosine over the raw data.

Name	Date modified	Type	Size
ClinCirc	23/09/2022 17:31	Wolfram Mathem...	34 KB
ExampleData1	23/09/2022 15:05	Microsoft Excel W...	15 KB
ExampleData1_Analysed_Graphs	23/09/2022 17:30	Microsoft Edge P...	14 KB
ExampleData1_Analysed_Output	23/09/2022 17:30	Text Document	2 KB

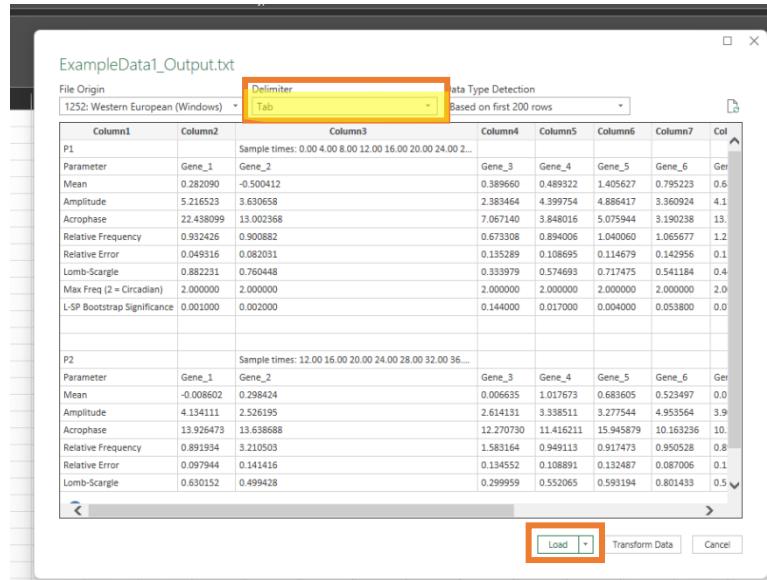
11. To import the numerical results into Excel, you can copy and paste the results. Alternatively, for improved formatting, open Excel and navigate to the “Data” tab. Then select the “From Text/CSV” option



12. This will open a dialogue box that you can use to navigate to the folder containing the analysis output. Select the analysis output and press “import”.



13. In the next pop-up, ensure the “Delimiter” is selected as “Tab”. Then press “Load”.



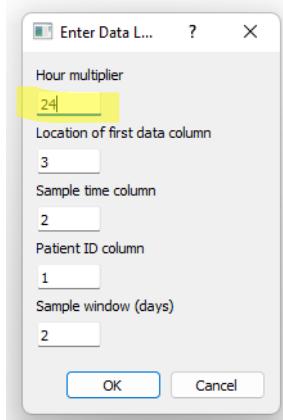
14. You can now explore the results! To check you completed the steps correctly, you can compare your results to the file “ExampleData1\_Output.xlsx” which can be downloaded from [Figshare link](#).

## Analysing example data 2 (Excel date format times & missing data)

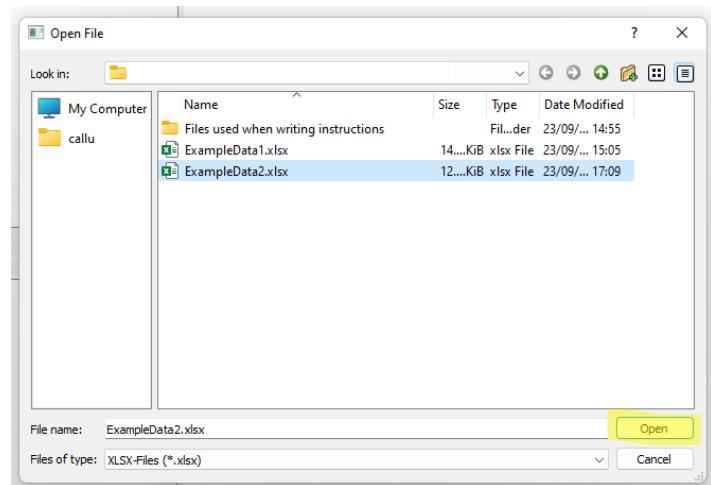
- Example Date 2 contains (i) sample time in Excel data format, (ii) missing data, (iii) samples for genes 1-5 being collected at different times to genes 6-10, and (iv) participant 2 had samples collected at uneven intervals. None of this is an issue to ClinCirc, and only feature (i) of the data requires us to set up the analysis differently.

The screenshot shows an Excel spreadsheet titled 'Book5 - Excel'. The table has 13 columns labeled 1 through 13. Column 1 is 'ID', column 2 is 'Sample time' (containing times like 02:00:00, 04:00:00, etc.), and columns 3 through 13 are 'Gene\_1' through 'Gene\_10'. The data for participant P1 spans from row 2 to 24, and for participant P2 from row 26 to 37. The 'Sample time' column in Excel uses a specific date/time format where 0=0:00:00 and 0.99=23:59.

- As in Example 1, load GNU Octave (GUI), navigate to the folder containing the ClinCirc.m file and run ClinCirc.
- From the screenshot of Example Data 2 above, we note that the participant identifiers are in column 1, the 'Sample time' column is still column 2, the data starts in column 3 and the data was collected over a 48h sample window. So, the only parameter that needs changing is the 'Hour multiplier'; since the times are saved in Excel data format, this now needs to be 24. This is because Excel saves time such that 0=0:0 and 0.99=23:59.



4. We now use the second dialogue box to navigate to the folder containing Example Data 2 and “open” it for analysis.



5. Name the output files whatever you would like and then the analysis will progress as normal.