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# CTG SIGNAL VIEWER USER GUIDE

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## Introduction

This is a brief guide to using the CTG Signal Viewer web application available at : <https://ctgviewer.infantresearchcentre.com>

This guide will cover getting set up, using the tool and exporting the data created.

If you have any issues that are not covered in this guide you can email me at [118363156@umail.ucc.ie](mailto:118363156@umail.ucc.ie) for more help.

This tool was developed for use in annotating CTG signals for the “*Detection of a baby in distress during labour using the CTG (Fetal Heart Rate) signal*” project

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## Accessing the Signal Viewer for the first time

On first accessing the website from a new device, you will be prompted to get a login code for security reasons.

Only your @ucc.ie or @umail.ucc.ie account will work for this, other email addresses must be manually added.

This step will have to be completed for each new device you use and there is no limit to the amount of codes you can request.

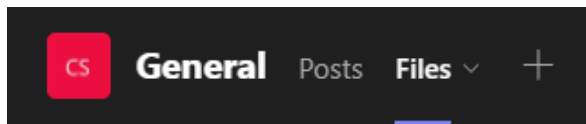
The image displays two sequential screenshots of the 'ctgviewer' login interface. The left screenshot shows the initial step where a user is prompted to 'Get a login code emailed to you'. It features an email input field with the placeholder 'example@email.com' and a blue button labeled 'Send me a code'. The right screenshot shows the subsequent step where the user must 'Enter code'. It includes a code input field with '000000', a 'Back' button, a blue 'Sign in' button, and links for 'Resend email' and 'Didn't receive an email?'. Both screens are branded with 'infantcentre.cloudflareaccess.com' and 'ctgviewer'.

## Accessing the data

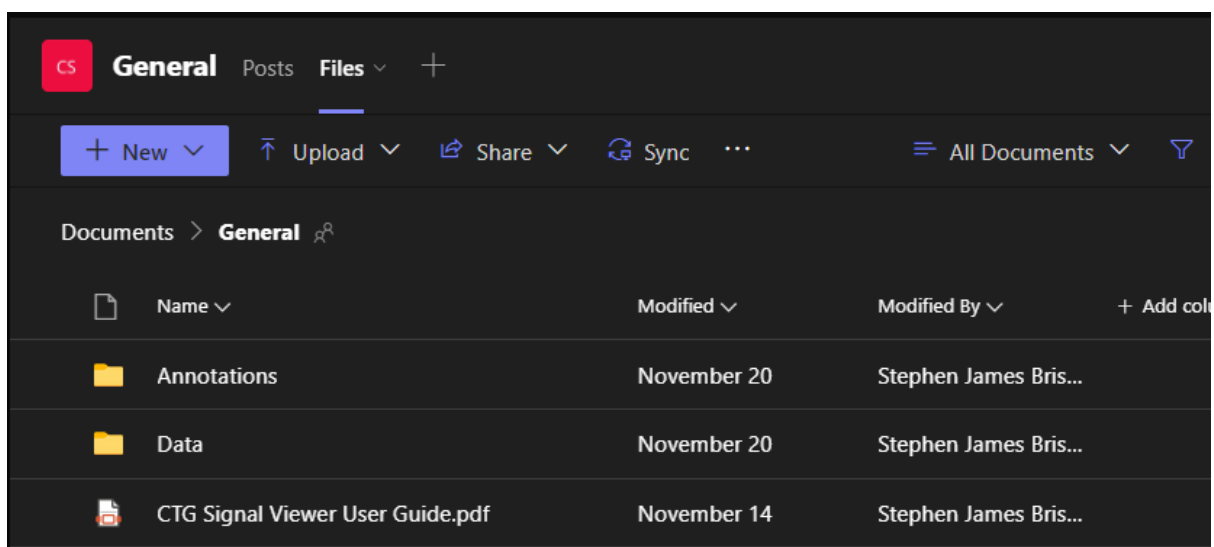
You can access all the data from the Microsoft Teams channel named CTG Signal Viewer.



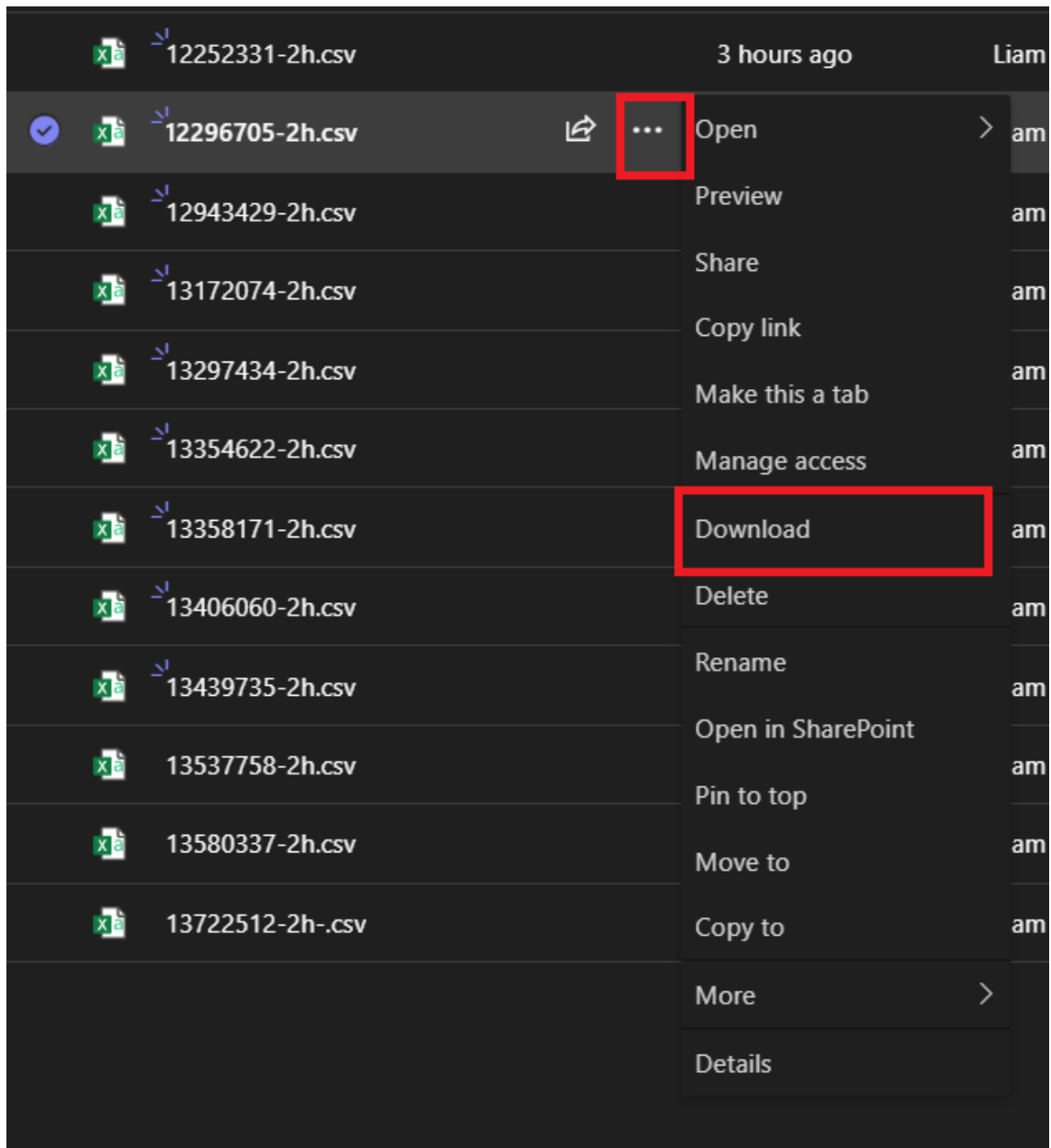
All the data will be contained in the Files section at the top.



The Files section will contain the **Annotations** folder, where completed annotation files are kept, the **Data** folder where the data files are kept (split into the *Completed Files* and the *Files to Annotate*) as well as this **User Guide**.



To download the files, simply click on the 3 dots next to the filenames, and click download:



**Important:** This will automatically add the file to the “Downloads” section in your computer, please ensure you have a folder to move this file to for ease of use.

# Uploading and viewing the signal data

Once you enter your security code you will be greeted with the following display:

## CTG Signal Viewer

Drag and Drop or [Select Files](#)

Epoch Number

0

Width

Height

EXPORT

Epoch	Baseline	Variability	Accels.	Decels.	FIGO	Notes
0						
1						
2						
3						
4						
5						
6						
7						
8						
9						

« < 1 / 2 > »

Baseline	Variability	Accels.	Decels.	FIGO
0 - None	0 - Normal	0 - Normal	0 - None	0 - Normal
1 - Tachycardia	1 - Abnormal	1 - Abnormal	1 - Intermittent	1 - Suspicious
2 - Bradycardia	-	-	2 - Early / Recurrent	2 - Pathological
-	-	-	3 - Variable	-
-	-	-	4 - Late	-

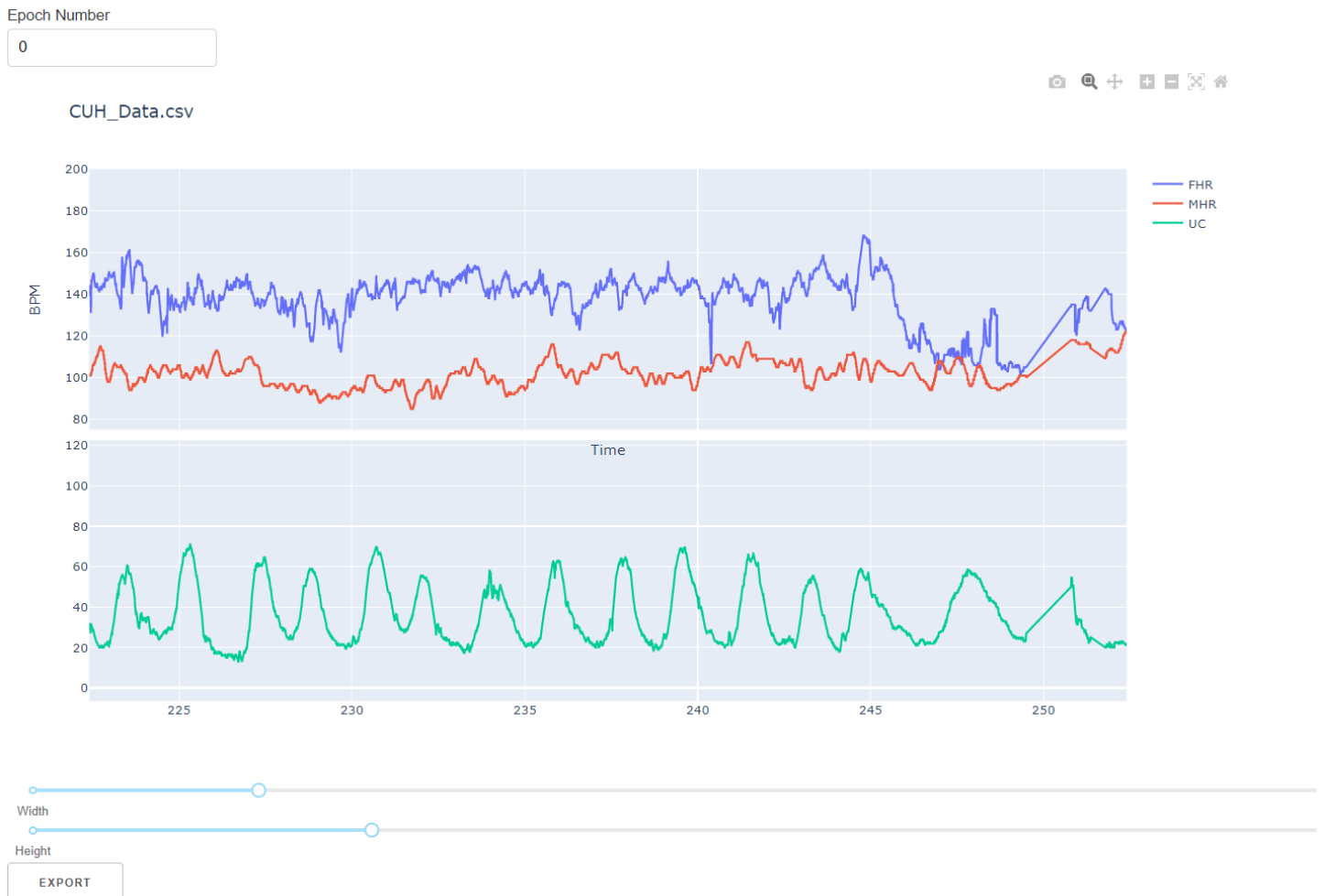
## Uploading

To upload a signal for viewing, simply click on “Select Files” and upload the relevant CTG file, or just drag and drop the file.

Drag and Drop or [Select Files](#)

# Signal Viewing

Once you have your signal set and your epoch selected you can view the graphed CTG signal



## Adjusting the size:

This signal can be interacted with to provide a better view for sections of interest.

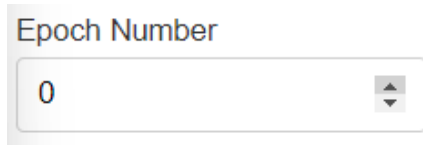
The width should be adjusted to a scale of 10 cm / 10 minutes.

The height can be adjusted also to get a better view of the signal.

## Progressing through the data

The signal viewer is setup to display 30 minute segments at a time.

You can advance through the signal by using the Epoch Number selector.



This will advance to the next epoch of the signal.

Each epoch is 30 minutes with a 20 minute overlap (i.e. Epoch 0: 0-30 min, Epoch 1: 10-40 min, Epoch 2: 20-50 min, etc...)

## Graph Interaction

The graph can be interacted with using the Epoch Selector to advance in time.

There are also multiple tools available in the toolbar:

Using the toolbar:



The toolbar has many useful tools to manipulate the CTG signal for viewing:

**1: Download plot as PNG:** This saves the current view of the CTG signal as an image to the PC. This is particularly useful when combined with the draw tool

**2: Zoom:** This is the default zoom tool. This allows you to zoom into an area by selecting it with the mouse

**3: Pan:** This allows you to pan across the signal, shifting it up, down, left or right.

**4: Zoom In:** Zooms into the signal

**5: Zoom Out:** Zooms out of the signal

**6: Auto-scale:** Zooms out to view the entire CTG signal

**7: Reset Axes:** Returns to the default zoom and view for the epoch

## Annotating

For each epoch, you will need to annotate the signal using the table.

EXPORT	Epoch	Baseline	Variability	Accels.	Decels.	FIGO	Notes
	0						
	1						
	2						
	3						
	4						
	5						
	6						
	7						
	8						
	9						

« < 1 / 2 > »

Baseline	Variability	Accels.	Decels.	FIGO
0 - None	0 - Normal	0 - Normal	0 - None	0 - Normal
1 - Tachycardia	1 - Abnormal	1 - Abnormal	1 - Intermittent	1 - Suspicious
2 - Bradycardia	-	-	2 - Early / Recurrent	2 - Pathological
-	-	-	3 - Variable	-
-	-	-	4 - Late	-

A look up table can be seen below the annotations table with references for numerical values.

Please only use the numerical values in the table.

A notes section is also present on the right most column if required.

Look up table:

	BASELINE	VARIABILITY	ACCELERATION	DECELERATION	FIGO SCORE
0	Normal	Normal	Normal	None	Normal
1	Tachycardia	Abnormal	Abnormal	Intermittent	Suspicious
2	Bradycardia			Early / Recurrent	Abnormal
3				Variable	
4				Late	

Each feature should be annotated according to the FIGO and HSE guidelines. The HSE national clinical guidelines can be found [here](#).



On page 35, you can find the table outlining the FIGO Consensus Guidelines, with more detailed information on the evaluation of Basic CTG Features found on page 31-34.

	Normal ✓	Suspicious ?	Pathological !
<b>Baseline</b>	110-160 bpm	Lacking at least one characteristic of normality, but with no pathological features	<100 bpm >10 mins
<b>Variability</b>	5-25 bpm		<ul style="list-style-type: none"> <li>• Reduced variability &lt; 5bpm for &gt;50 minutes.</li> <li>• Increased variability &gt;25bpm for &gt;50 minutes.</li> <li>• Sinusoidal pattern for &gt;30minutes.</li> </ul>
<b>Decelerations</b>	No repetitive* decelerations		Repetitive* late or prolonged (>3minutes) decelerations for >30minutes (or >20minutes if reduced variability). Isolated deceleration >5minutes
<b>Interpretation</b>	No hypoxia/acidosis	Low probability of hypoxia/acidosis	High probability of hypoxia/acidosis
<b>Clinical Management</b>	No intervention necessary to improve fetal oxygenation state	Action to correct reversible causes if identified, close monitoring or adjunctive methods	Immediate action to correct reversible causes, adjunctive methods, or if this is not possible expedite delivery. In acute situations immediate delivery should be accomplished.

## Exporting the annotation table

Important:

Before exporting the annotation table, please ensure your download settings are correct.

You should ensure that you will be asked where to save each file when downloading.

Chrome: This can be found at: <chrome://settings/downloads> and make sure the option to “Ask where to save each file before downloading” is enabled:



Microsoft Edge: This can be found at: <edge://settings/downloads#All> and make sure the option to “Ask me what to do with each download” is enabled:



If you use another browser and don't know how to enable this, please email the author.

When you have finished your annotation work, you can download the table by using the “export” button at the top left of the table:

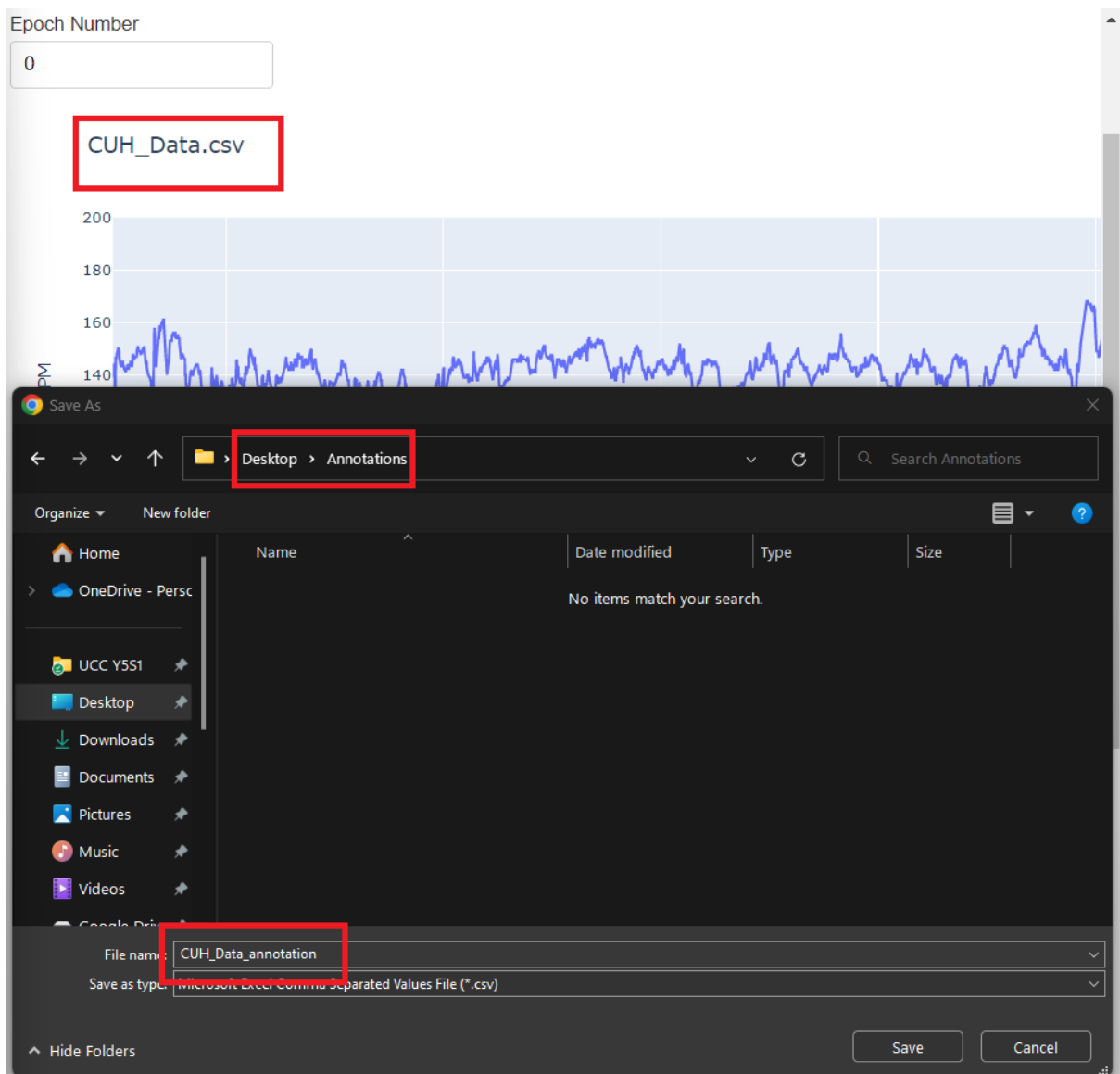
A screenshot of the annotation table interface. At the top left is a button labeled "EXPORT". Below it is a table with two columns: "Epoch" and "Baseline". The "Epoch" column has two rows with values "0" and "1". The "Baseline" column is empty.

EXPORT	
Epoch	Baseline
0	
1	

When you click “Export”, you should get a window asking you where you want to save the file.

Ensure you have an easily accessible folder on your computer to store all the annotations.

**Important:** The file must have the same name as the signal, with `_annotation` added at the end, i.e. for a file “CUH\_Data.csv” the annotation must be called “CUH\_Data\_annotation.csv”.



### Adding the file to MS Teams

Once the annotation file is on your computer, please ensure you upload it to the MS Teams “Annotations” folder.

Go to the teams channel as before, then into the “Annotations” folder and click upload and upload your file.

