



WE-LAB

We-Lab APP handbook

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Intro

The We-Lab APP is the essential tool used to operate the We-Lab portable laboratory, supporting the communication between the Smartphone/Tablet and the main module (based on Raspberry Pi®). The APP guides the user in a simple and intuitive manner during the execution of the experiences. At the moment, the We-Lab APP is only available for Android devices running OS version 4.2 or later, and is available free on the Google Play Store.

Once downloaded, the icon appears on your mobile device as illustrated by Figure 1.

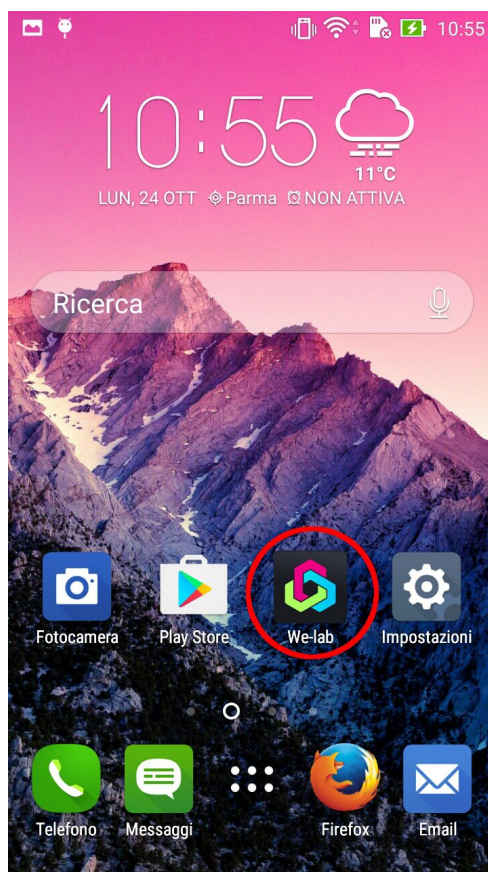


Figure 1. We-Lab APP icon.

Run the APP by clicking on the icon. Figure 2 shows the starting screen that allows you to connect the APP to the We-Lab Device (PAIR DEVICE), to access the main APP sections (SCIENCE NOTEBOOK and LAB AREA) and to display information on licenses and acknowledgements (INFO).

In addition, the upper right button allows you to turn off the We-Lab module.

WE SUGGEST YOU ALWAYS USE THE BUTTON TO TURN OFF THE WE-LAB MODULE. DO NOT UNPLUG THE POWER ADAPTER FROM THE MODULE BEFORE IT HAS BEEN SHUT DOWN. AFTER PRESSING THE BUTTON WAIT FOR ABOUT 20 SECONDS BEFORE UNPLUGGING THE POWER ADAPTER.

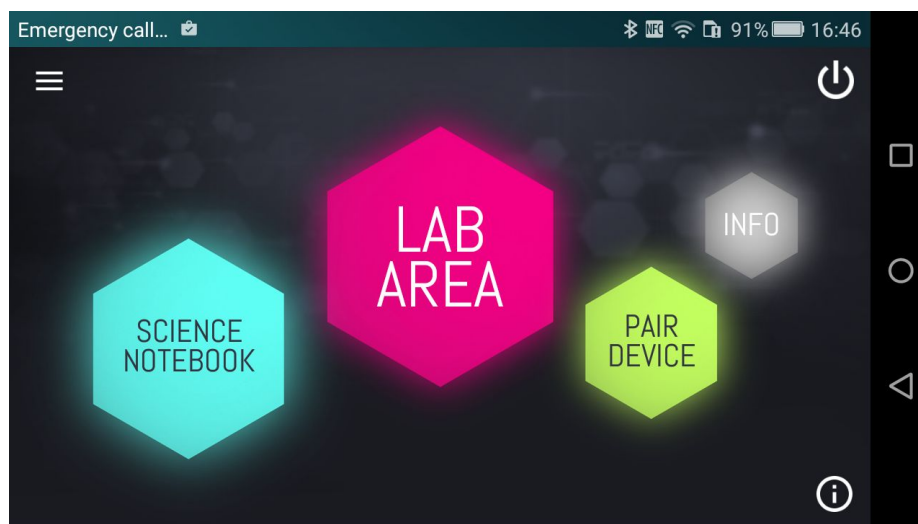


Figure 2. APP Main menu, providing an easy access to all sections.

1. Connecting to your mobile device

Connect the We-Lab main module to the power supply through the micro USB port. **It takes about 2 minutes to start the device.** Next, pair your mobile device to the main module of the We-Lab. Before doing so, please open the smartphone/tablet settings, go to the Wi-Fi management setting, and check that the We-Lab network has been generated. Such a network has the name reported on the QR code included in the kit.

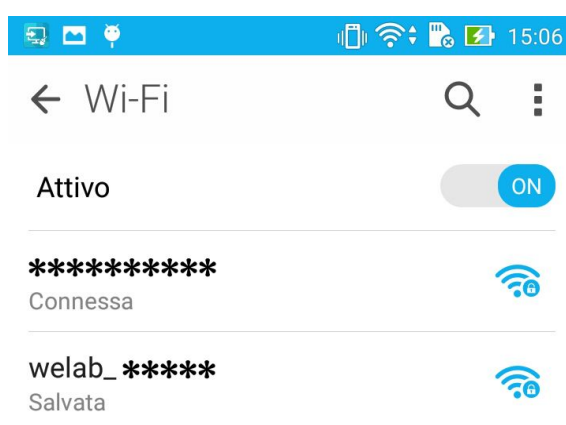


Figure 3. Android wi-fi setting, where the second network in the list is the one generated by the We-Lab.

After checking the network availability, press the PAIR button on the main menu as presented by Figure 2.

Next you have to scan the QR code included in the We-Lab kit, as presented by Figure 4. You need to grant the access to the device camera to capture images and video through a popup that appears on the screen.

Connection Failure: in the event that the message “connection failed” appears on the screen, open the Wi-Fi settings of your device and check that the network of your We-Lab is still available and proceed to select it. If your smartphone/tablet asks for a password press CANCEL, then return to the APP and repeat the QR code scanning process. If instead your smartphone/tablet does not ask for a password and connects to the network, it means the pairing has been successful so you can get back to APP and proceed without scanning the QR code again.

WARNING: Devices running Android 6 or later will ask you to give permission to modify system settings and enable Location Services before you can scan the QR code. Such a procedure is due to a policy required by the Android connectivity manager and does not depend on the APP. Allowing access to location services is therefore mandatory for the APP to communicate with We-Lab’s Main Module. *DNAPhone srl does not collect any data relating to your position during the connection process.*

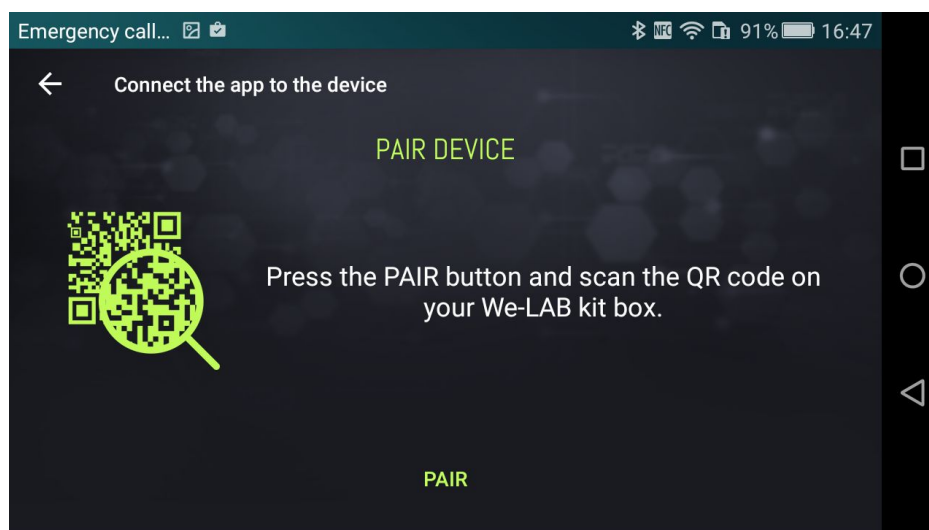


Figure 4. To connect to the device scan the QR code after you have clicked PAIR on the main screen.

2. How to begin a laboratory experience: the LAB AREA

To start building an experiment, you have to press the "LAB AREA" button in the main menu of the APP (Figure 2). Once pressed, you have to choose whether to use the Microscope or the Photometer (as shown by Figure 5). At the moment, these are the available functional modules.

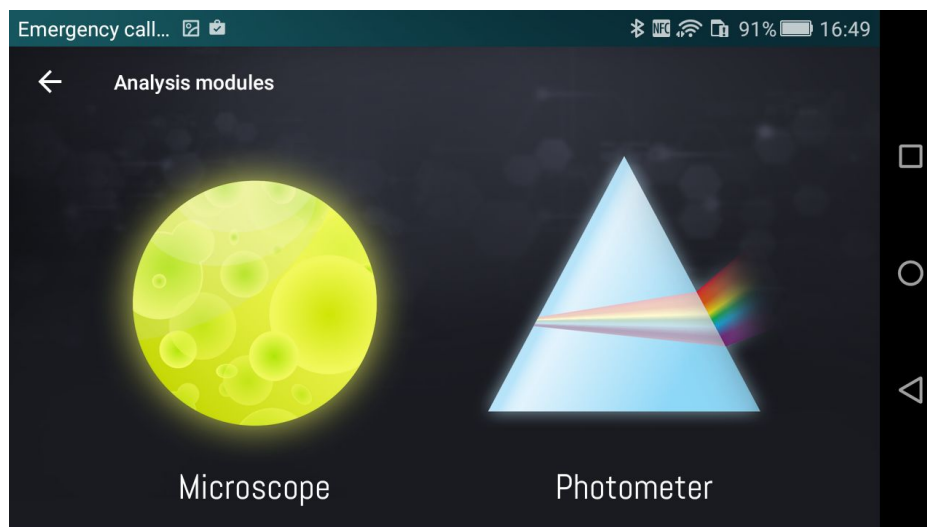


Figure 5. Screen presenting the LAB AREA sub-module selection.

2.1 Microscope

In this section the user will work with the **Microscope**, while having the opportunity to save high resolution images and video of the displayed samples. These samples can be either slides already prepared and included in the We-Lab kit, or samples that you can prepare using blank slides (also available in the kit).

Figure 6 presents the main menu of the Microscope section.

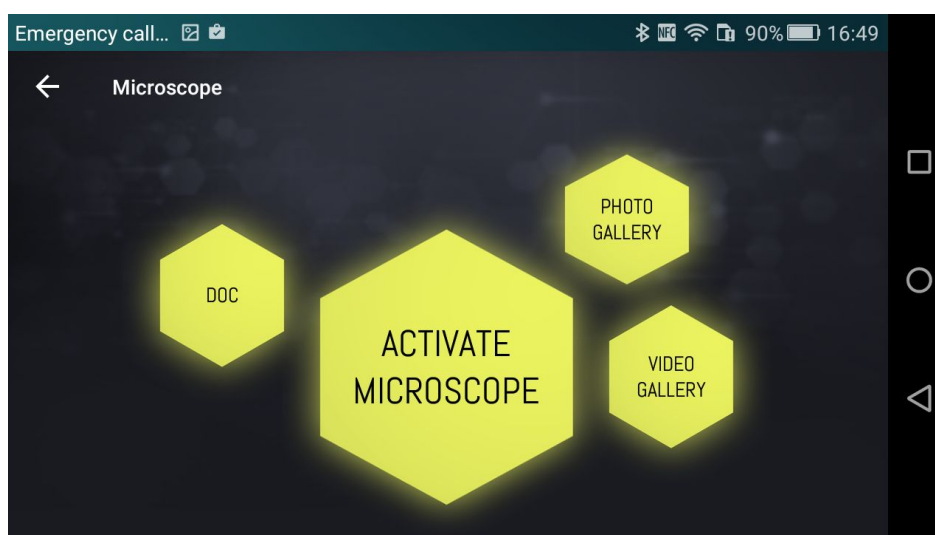


Figure 6. Microscope section.

The **Microscope** section has 4 subsections: DOC, ACTIVATE MICROSCOPE, PHOTO GALLERY and VIDEO GALLERY. When you press the ACTIVATE MICROSCOPE button, the system asks you to check you have plugged the proper lens. By confirming, you activate the LED that lights the sample and starts the

microscope video streaming on the monitor of your mobile device (as shown by Figure 7). Some devices require a few extra seconds to start the streaming during which the screen of the device appears gray.

The top right button is used to access the video settings, which allows you to change the sharpness, contrast, brightness, saturation and intensity of the LED (please refer to Figure 8). In addition, you can save video or pictures through the **video camera** and **photo camera** icons.

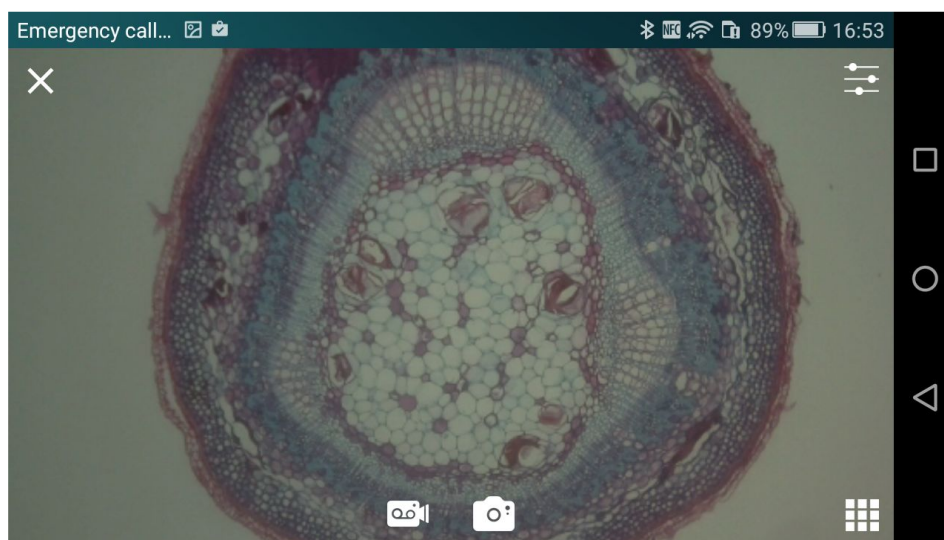


Figure 7. Sample observation using the Microscope module.

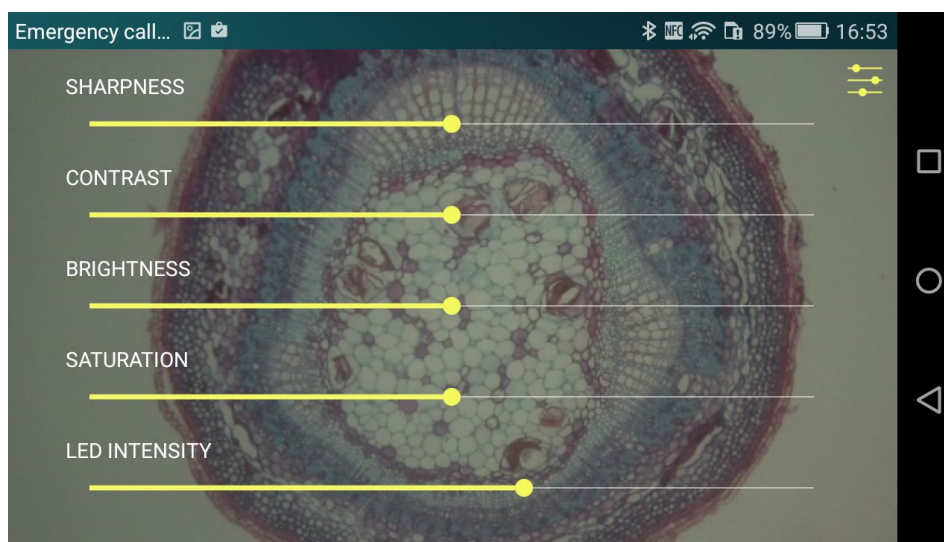


Figure 8. Video Settings.

Please note the **circle** engraved on the microscope surface. Such a circle is the **viewfinder** you should use to center the sample before connecting the microscope to the main module.

You can access all saved videos and images through the VIDEO GALLERY and PHOTO GALLERY sections. Another way of accessing such files is through the streaming video screen, by clicking on the icon at the bottom right of the screen, as shown in Figure 7.

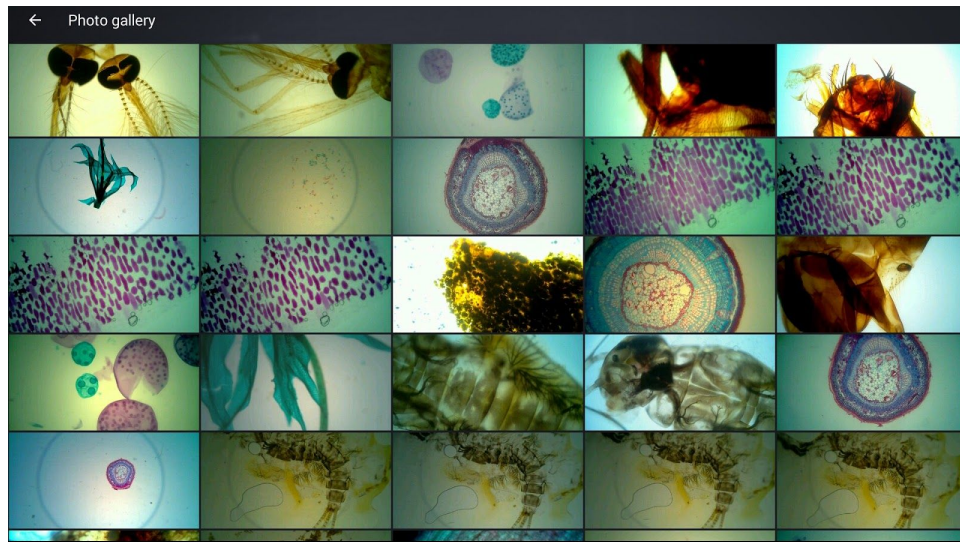


Figure 9. Photo Gallery.

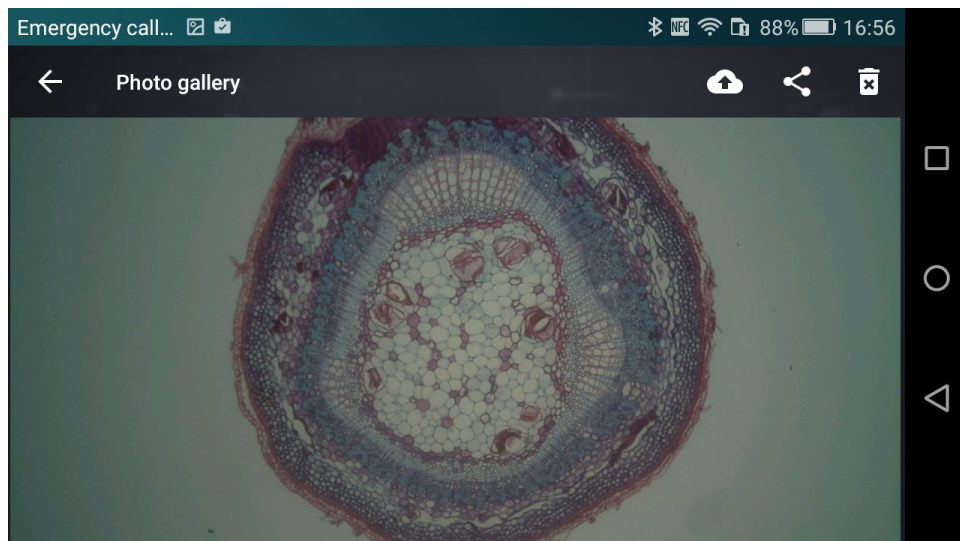


Figure 10. Details of an image selected in the Photo Gallery.

As seen in the Figure 10, the top menu bar contains 3 icons on the right which provide the following functions (from left to right):

- upload the picture on your We-Lab community profile;

- share the image (email, Dropbox, ...);
- delete the image.

In order to upload the image to your profile on the We-Lab community, the APP requires you to provide the name of the image (required), a description (optional), the master's name (required) and the name of the students who took the photo (optional). If you use the We-Lab privately (*i.e.*, not as part of a school activity), the master and the group will match your profile. In case the We-Lab is used by a school, the master is the username of the professor. The image is loaded as private on the master's web page. The master can make it public after checking the information included. Such a process is described by section 4.1.

Using the DOC icon, accessible from the menu presented by Figure 6, the user can compile reports of the experiences and add images and videos previously saved. Figure 11 shows the screen with a user-fillable form. Saved reports are accessible from the laboratory notebook and can be exported in PDF using the button at the top right of the screen.

Figure 11. Elaborate Reports following an experiment using the Microscope.

2.2 Photometer

This section, which is accessed by selecting the icon of the Photometer presented by Figure 5, allows the user to make experiments involving colorimetric analysis on liquids. By default, the APP presents a set of experiments that will be enriched over time. Following the instructions described in the following, you can choose among listed experiments. In addition, you may modify or delete any of these experiments by clicking on the three dots found at the right of each item on the list, or create a new one using the tool called Composer. Such a tool is accessed by pressing the + button at the bottom right of the screen. If you wish to restore deleted default experiment, you can use the button at the top right. Please note this only

works with default experiments, and not with the ones created by the user and then deleted. Figure 12 shows the list of available experiments.

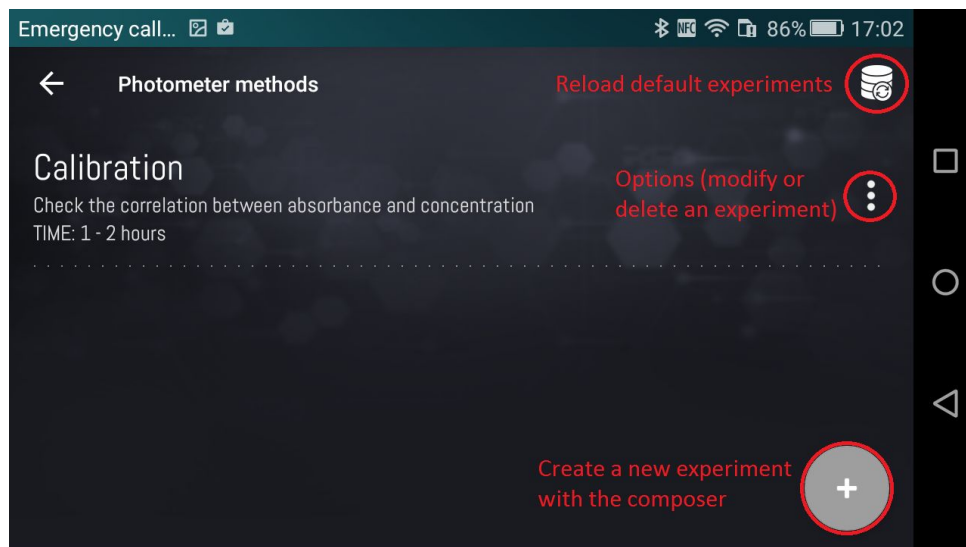


Figura 12. Photometer main screen.

2.2.1 Executing a default experiment

At the beginning of each experiment, the APP presents a form you can fill to specify information about the experiment itself, including the name, the method and materials used, as well as a brief description, as presented by Figure 13. All such information is optional and can be modified or added at the end of the experiment or in the laboratory notebook.

Figura 13. Form to be completed with the experiment's details.

Once all the information has been filled in the form, press the OK button at the bottom of the page to proceed to the first screen of the experiment. In the upper right corner of each screen you will find a group of hexagons indicating the progress of the experiment. Completed steps are represented by color filled hexagons, the current step is an empty hexagon with a colored border and all next steps are empty hexagons with a gray border (when we describe the **composer**, the meaning of each step will become clear). Each analysis that uses the photometer requires the selection of the light source and you can choose among blue, green or red, by tapping the icon above the representation of the visible spectrum (Please use Figure 14 for reference).

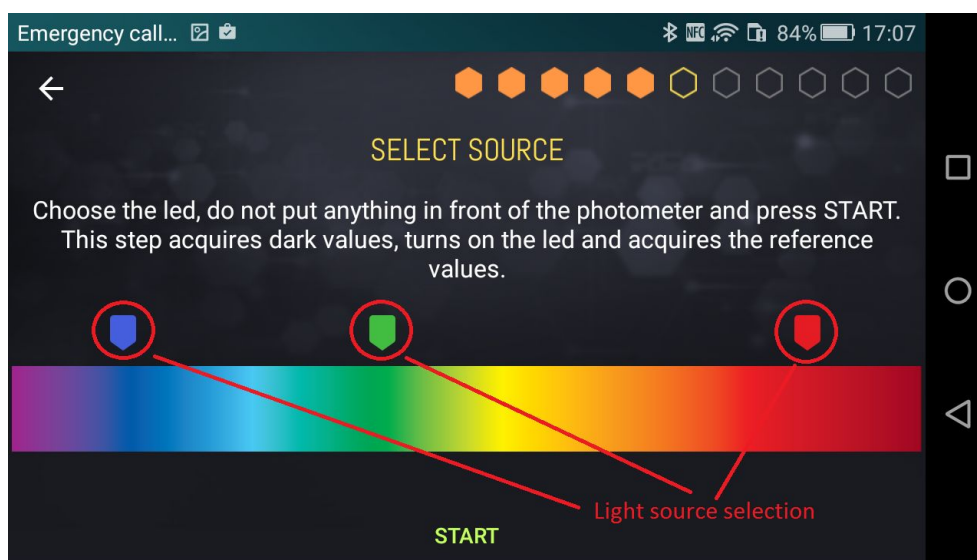


Figura 14. Screen indicating the selection of the light source.

The source selection depends on the type of molecule/substance to be analyzed. To perform the analysis in a proper way, it is necessary to activate the correct lighting. For example, if an analysis is performed using the amaranth food colorant, you must select the green LED source, since such a dye has an absorption peak centered in the green spectral region (wavelength of 525 nm approximately).

After the source has been selected, press the START button to proceed. The device acquires the signals with the LED off and then with the LED on. When finished, the system proceeds to the second screen of the experiment, which prompts the user to read the solvent, as shown in Figure 15.

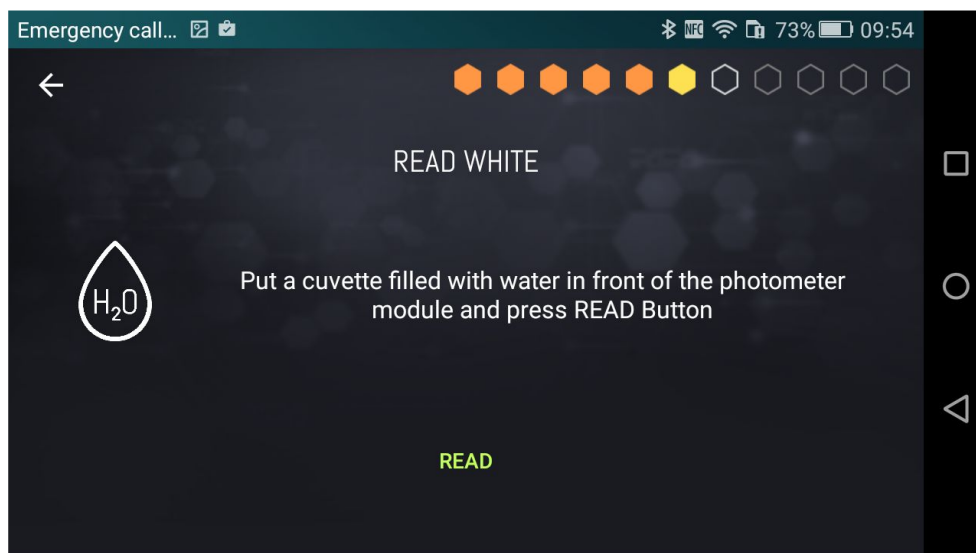


Figure 15. Blank reading.

The solvent is where the substance/molecule is diluted for the analysis. If you think again at the food colorant example, you dilute it in water, thus the solvent is a cuvette containing only water. In order to minimize the exposure to environmental light entering the photometer module, it is very important to cover the reading cell with the cap found inside the consumable box of the kit.

Once the reading of the solvent has been completed, proceed reading the samples, as presented by Figure 16. The bottom right + button is used to enter the number of samples to be analyzed (Figure 17). The APP asks to provide the name of each sample, as shown by Figure 18. In case the user decides not to assign a name to the current sample, or to any of the next samples, by pressing **OK**, the APP assigns default names (Sample 1, Sample 2, etc.).

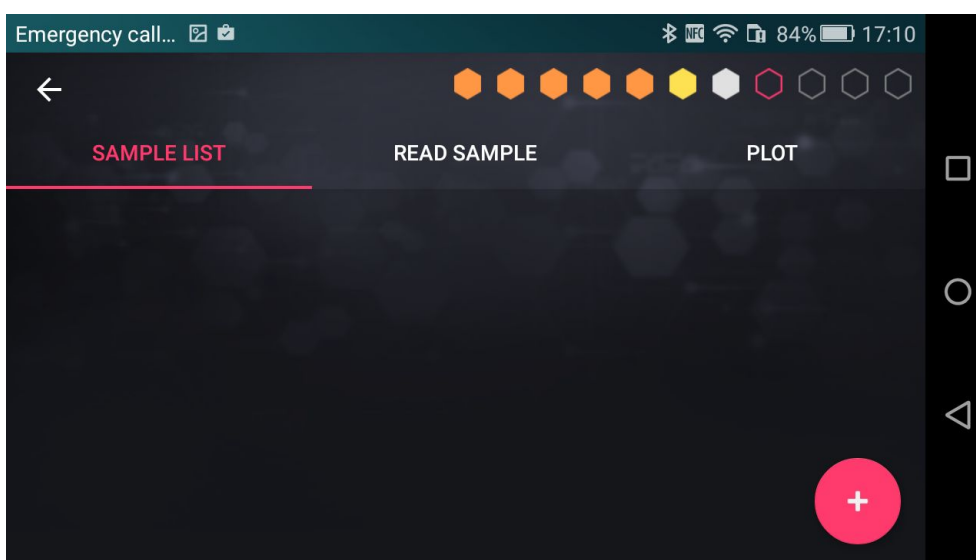


Figure 16. Samples definition.

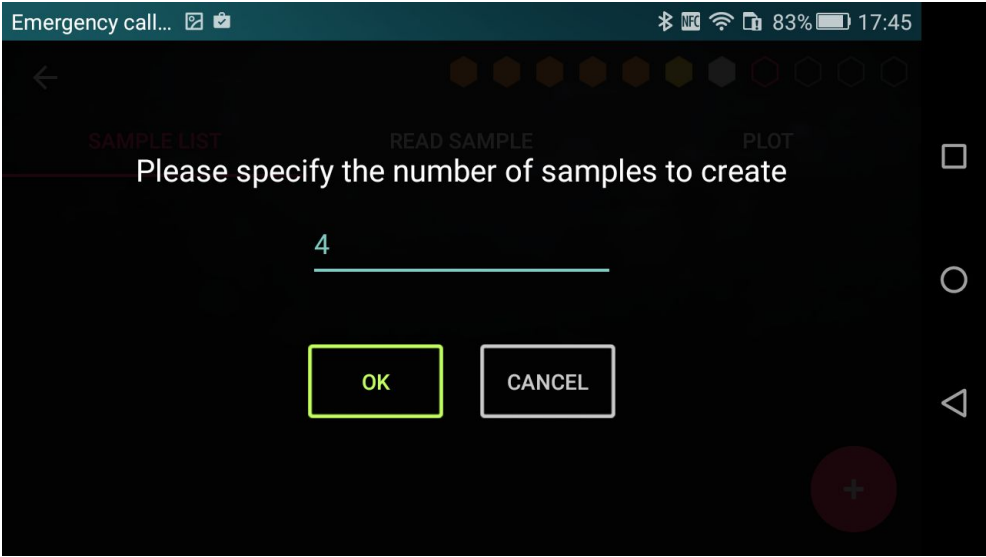


Figure 17. Providing the number of samples to be analyzed.

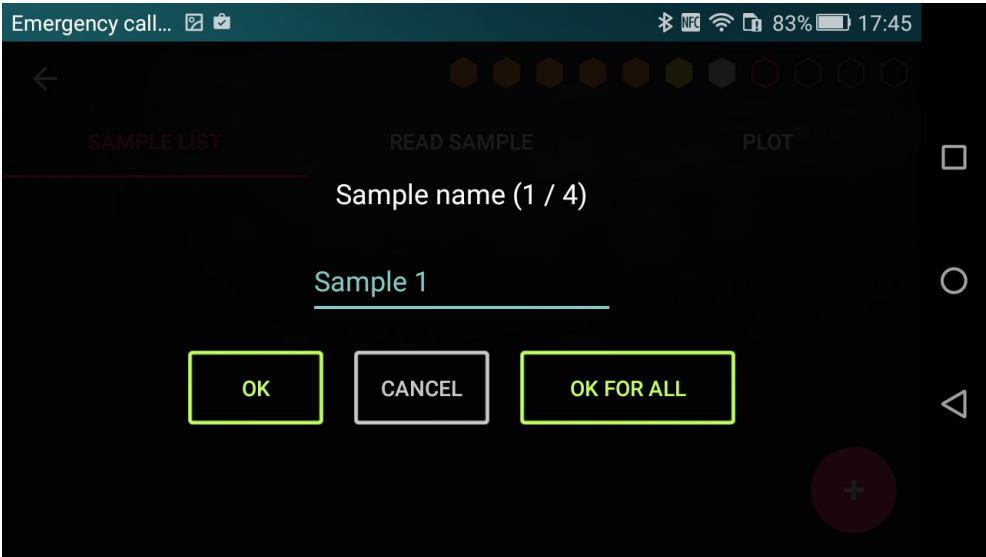


Figure 18. Specification of the samples names.

The reading of the samples can start when the user has created the complete sample list.

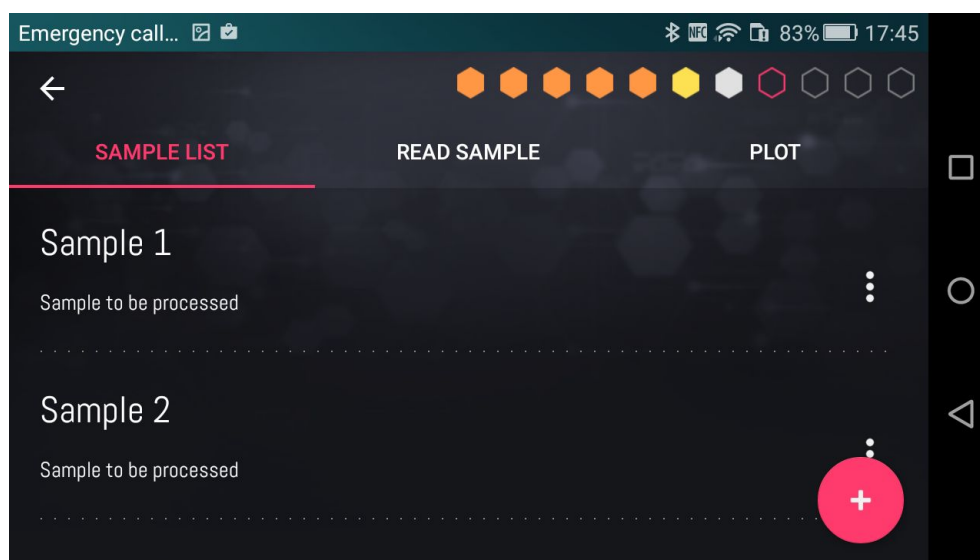


Figura 19. Samples list.

To read samples, the user must click on the READ SAMPLE tab provided by the top bar. Figure 20 shows the corresponding subsection describing the first step to be carried out, which is to insert the sample in the slot of the photometer module. Remember to always put the cap on the cuvette. Once the sample has been inserted, the user presses OK and provides the parts of the colorant and solvent (*e.g.*, water) which form the test solution. Proceed by pressing the button PARTS to display the settings shown in Figure 22. It is fundamental to include the appropriate amounts of solvent and dye to the solution, since incorrect amounts will lead to an incorrect calculation of the calibration curve. After inserting the parts, press the READ button that appears on the screen.

Example: let's assume that the total liquid volume used for the analysis is 3 ml, out of which 0.3 ml is colorant and 2.7 ml is water: the concentration of the colorant is 0.1 ($0.3/3$), while the concentration of the water is 0.9 ($2.7/3$). Consequently, the cuvette contains **1 part of colorant and 9 parts of water, as shown in Figure 22. The recommended volumes to be used in an analysis ranges between 2 ml to a maximum of 4.5 ml.**

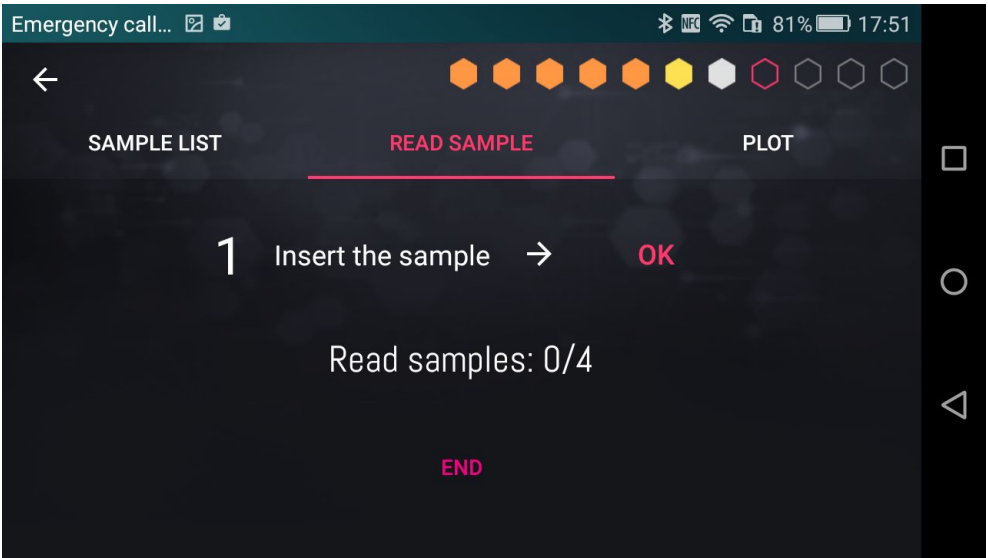


Figure 20. Insert the cuvette in the Photometer.

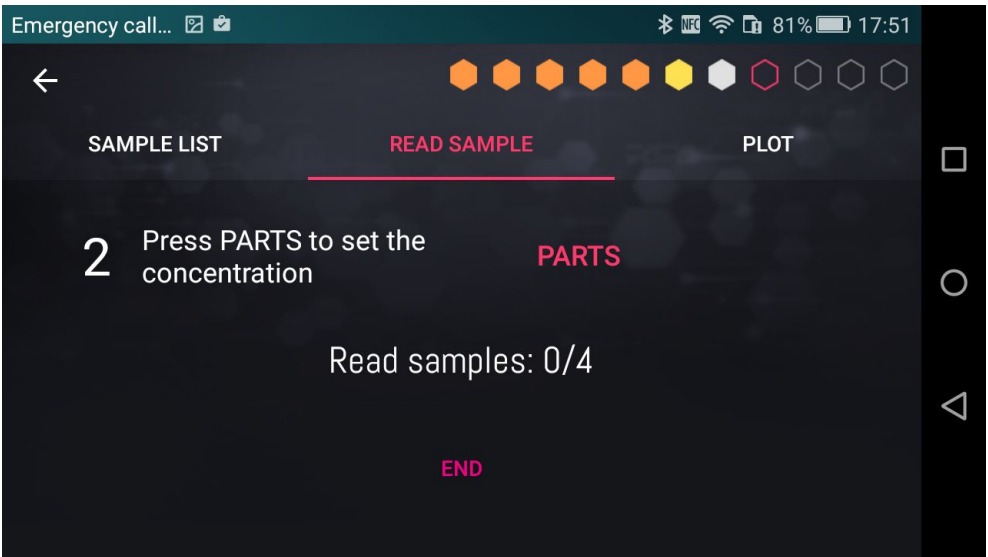


Figure 21. Press PARTS to specify the concentration of the sample.

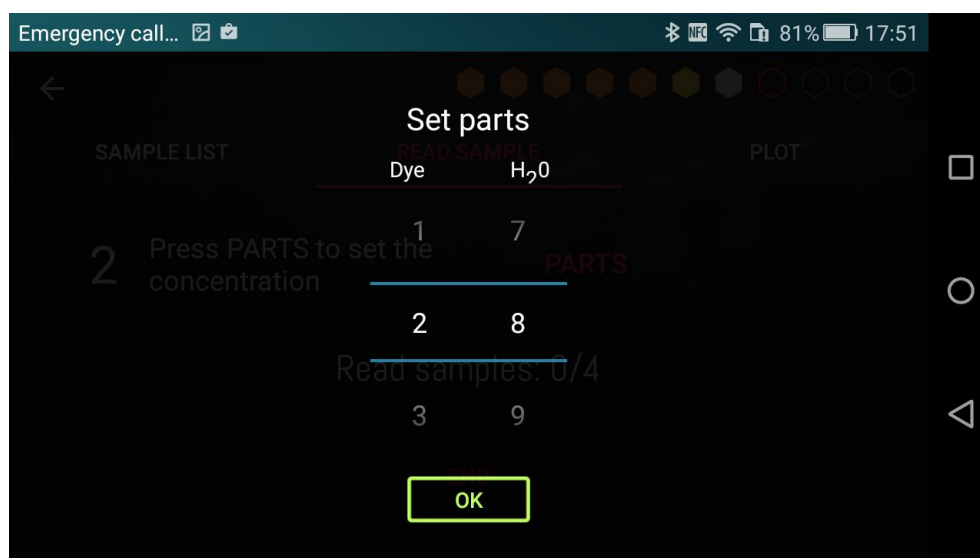


Figure 22. Specify the sample's concentration.

Once the reading of the first sample is complete, proceed to read the next sample, following the steps described above. After reading the last sample, the user can end the experiment by pressing the END button at the bottom of the screen. Note that you can add samples at any time or end the experiment before you have read them all. However, to generate a straight line is necessary to read at least 2 samples. If you click on the SAMPLES LIST tab on the top bar, you can go back to the starting subsection and see that each sample in the list has an icon with the shape of three dots at the right end. Such a button allows you to rename, read and delete the sample, as shown in Figure 23.

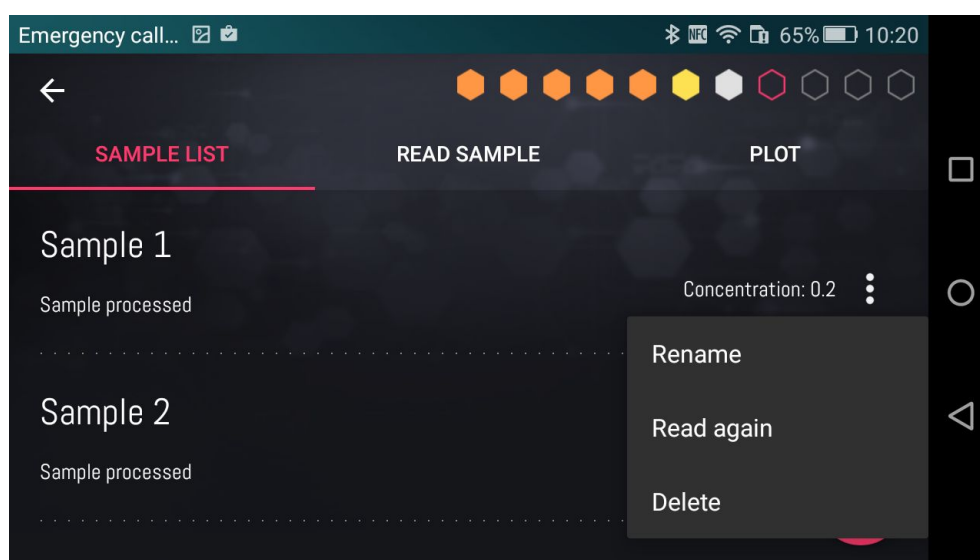


Figura 23. Sample's options menu.

The third sub-activity screen can be displayed at any time, to display the samples' absorbance based on their respective dilution. To access such a screen please select the PLOT button on the top bar. As seen in

Figures 24a and 24b, the graph is available in two types of representations: dots and bars, identified by the two icons located to the right of the diagram.

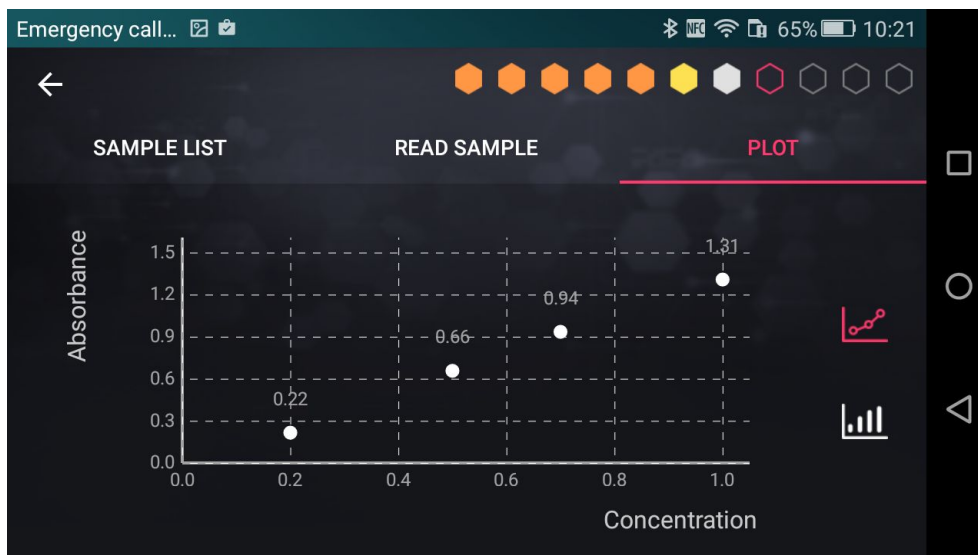


Figure 24a. Scatter plot representing the absorbances vs the dilution.



Figure 24b. Bar plot representing the absorbances vs the dilution.

When you press the END button to finish an experiment, you access the summary presenting the obtained results (as shown in Figure 25a and 25b). From here you can store results in the laboratory notebook by pressing the SAVE button at the top right of the screen.

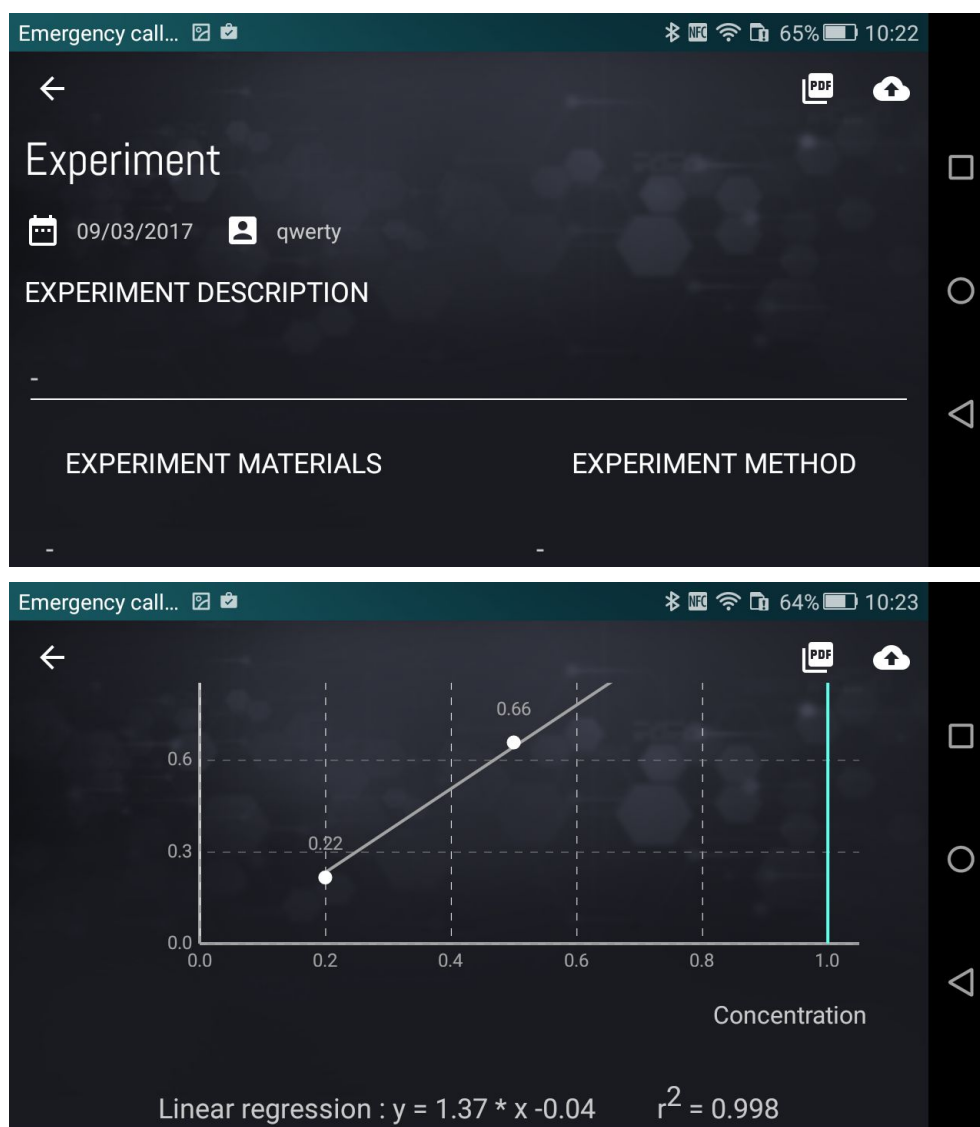


Figure 25. Summary.

As can be seen in Figure 25 (top), there are two buttons at the upper right side of the screen that allow:

- (left) to export results in PDF format (available in the `/storage/emulated/0/welab_docs` folder);
- (right) to upload results to the We-Lab community.

In order to upload the results to the We-Lab community, it is required to specify a name for the experiment (mandatory), a description (optional), the username of the Master (mandatory) and the name of the Group that run the experiment (optional). If the We-Lab is used for educational purposes within a school, the Master is the username of the teacher. If the use of We-Lab is personal, Master and Group match the username of the user. Results are uploaded to the Master profile and labelled as *private*. The Master can make them *public* after checking the contents. See section 4.1 for details.

2.2.2 The Calibration block

The **Calibration** block allows i) to create a calibration function or ii) to select a stored calibration function, to be used within the **Read Sample** block. Figure 26 shows the welcome screen of the block.

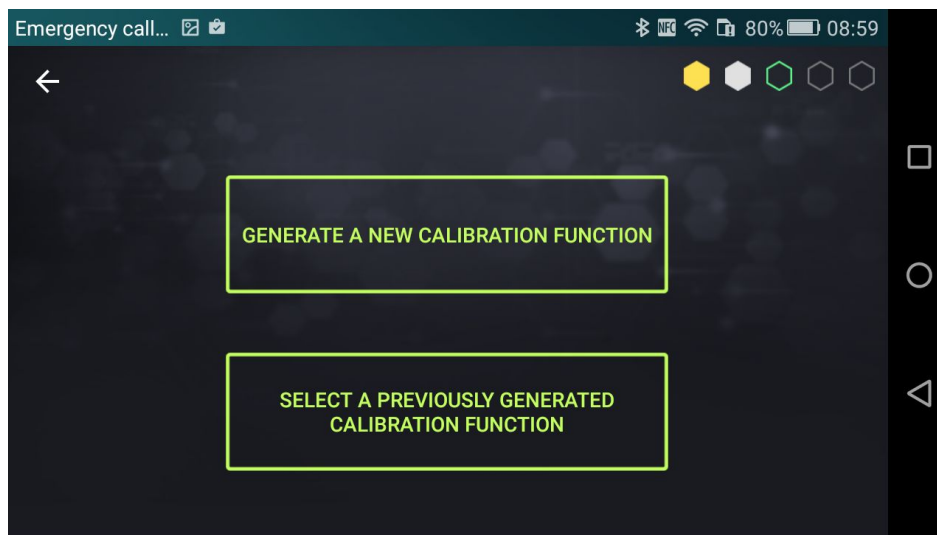


Figure 26. Main menu of the Calibration block.

The GENERATE A NEW CALIBRATION FUNCTION button allows the creation of a new calibration function through a wizard similar to the one described by section 2.2.1. On the screen presented by figure 27 you can specify the number, name and known concentration of samples to be analyzed by clicking on the + button (see Figure 28 and 29).

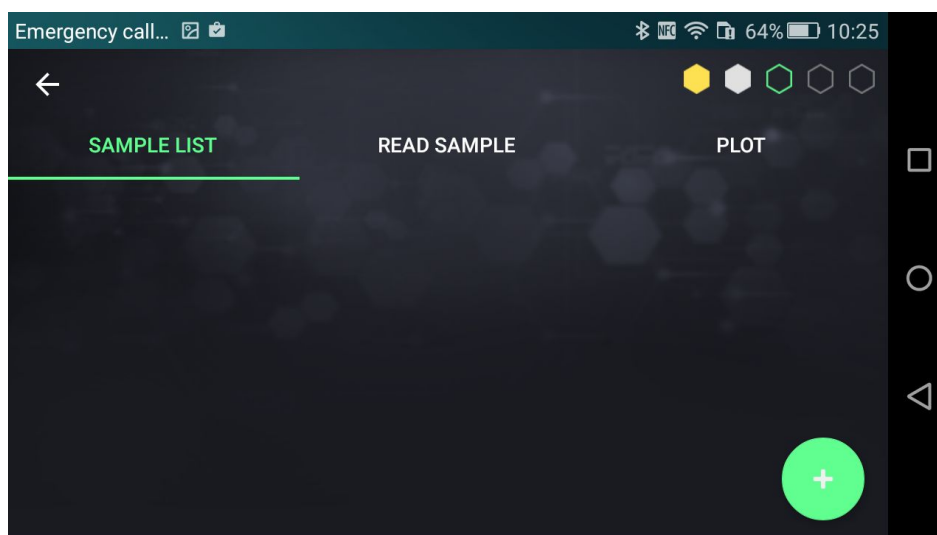


Figure 27. Click the “+” button to create a list of samples to be analyzed.

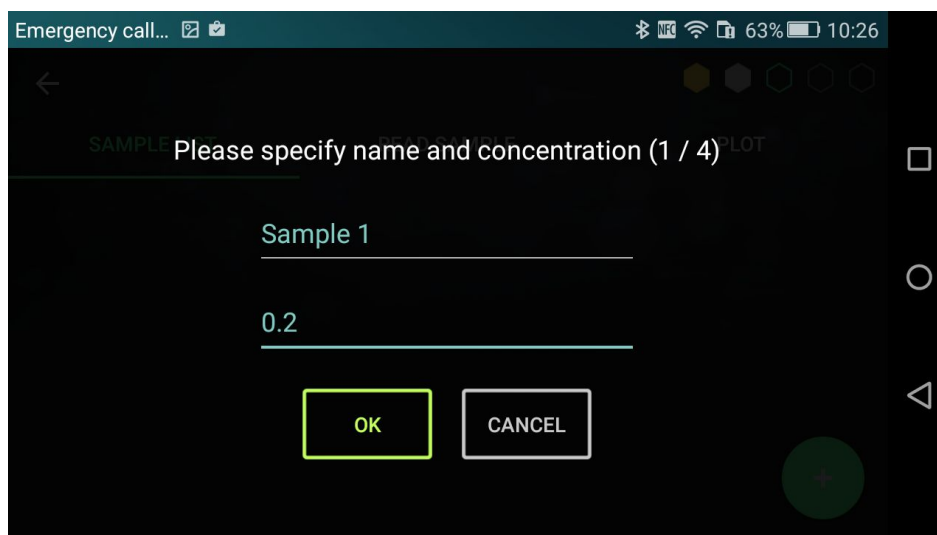


Figure 28. Definition of the name and concentration of a sample.

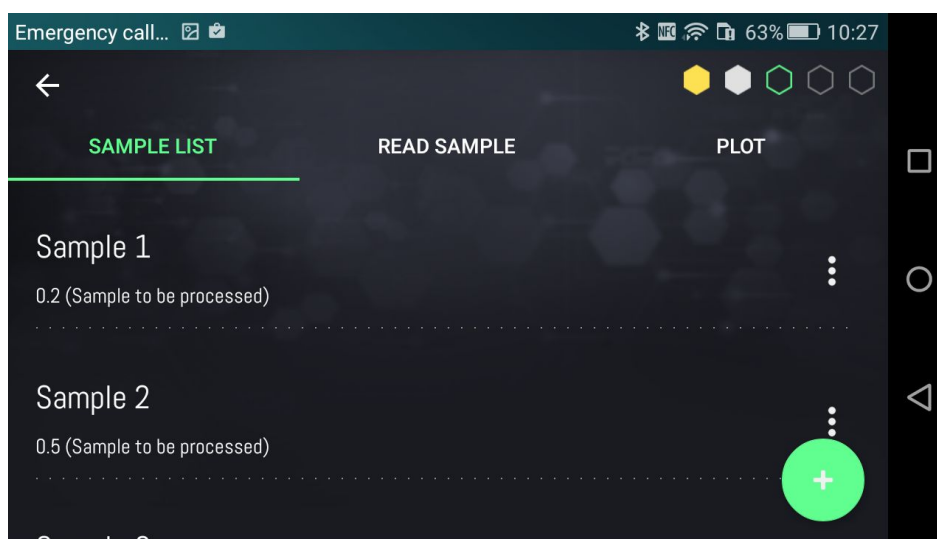


Figure 29. List of samples to be analyzed.

In order to obtain the absorbance of each sample, click on the READ SAMPLE tab on the top bar. A wizard similar to the one described in section 2.2.1 (with no need to specify the concentration of the sample, as shown by Figure 22) will guide you until the end of the analysis.

2.1.3 The Composer

The **Composer** is a We-Lab APP tool allowing the user to edit a preloaded experiment method or to create a new one. To edit a preloaded method click on the three dots visible on the right side of the experiment name, as shown in Figure 12. To create a new experiment click the + button available on the bottom right side of the screen shown in Figure 12. The user interface of the **Composer** is presented by Figure 30.

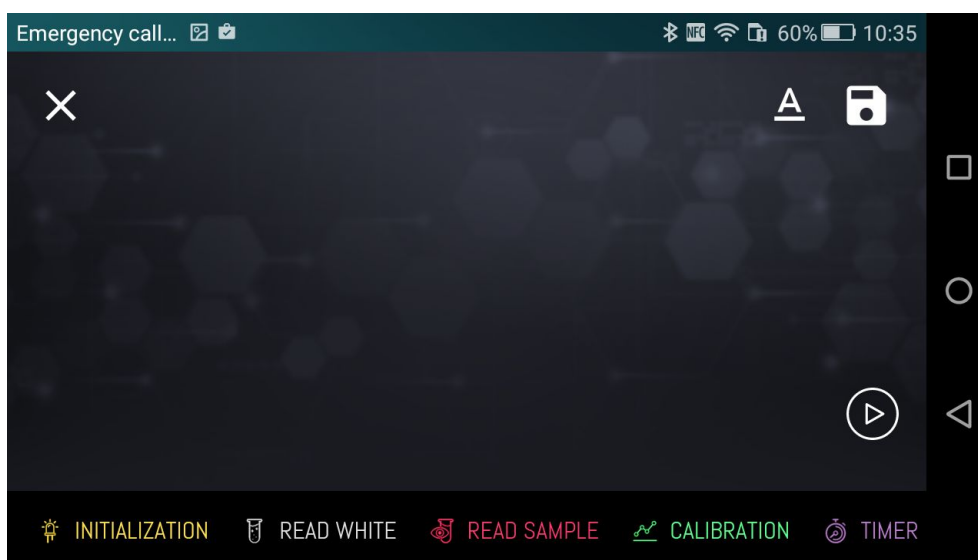


Figura 30. Schermata del compositore.

The scrollbar at the bottom of the screen shows all the logical blocks that can be used to build an experiment method. Each block has a specific function and represents a step of the experiment.

- **Initialization:** select the source and acquire the “dark” (source OFF) and the “reference” (source ON) intensity.
- **Read blank:** read the absorbance of the “blank”, *i.e.*, the absorbance of a cuvette filled with a buffer solution (*e.g.*, water).
- **Calibration:** allows to create a calibration function or to select a stored calibration function, to be used within the **Read sample** block.
- **Read sample:** read the absorbance of the samples to be analyzed.
- **Timer:** set a time sleep (*e.g.*, you can use it to wait for the completion of a chemical reaction).
- **Note:** add a note reporting useful information for the user.
- **Math:** perform mathematical operations on sample data (*e.g.*, absorbance sum and/or subtraction).
- **Graph:** plot sample data in a graph.

In order to add a block to the experiment, click the name of that block.

As an example, Figure 31 shows an experiment method composed by the following logical blocks: **Initialization**, **Read blank**, **Calibration**, **Read sample** and **Graph**.

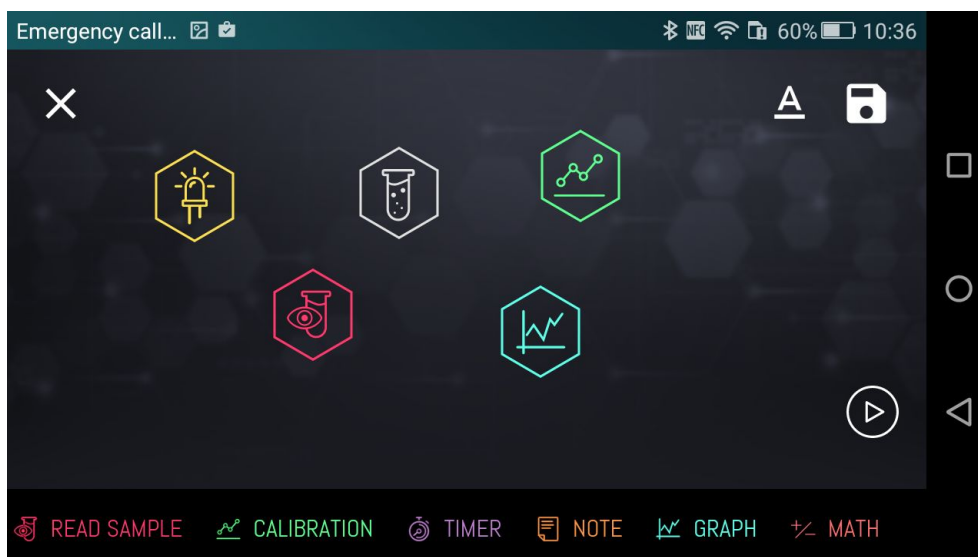


Figure 31. Set of blocks selected to compose the experiment.

Since each block represents a step of the experiment, it is important to set up the workflow in a proper way, *i.e.*, to define the order in which the operations of each block have to be executed. Each experiment method must start with the **Initialization** block followed by the **Read blank** block. In order to set the execution order, drag the **Read blank** block over the **Initialization** block. A line connecting the two block appears, including a dot displayed near the **Initialization** block. For every connecting line, a dot is placed near the first block of the segment (see Figure 32). All blocks must be connected in the same way to define the workflow of the experiment. As an example, Figure 32 presents an experiment method made of the following operation: **Initialization** → **Read blank** → **Calibration** → **Read sample** → **Graph**. Each logical block is represented by an hexagon in the upper right side of the screen during the execution of the experiment, as shown by Figure 14.

Note: not all blocks can be connected with each other. It depends on the function of each block. For example, you cannot add the **Initialization** block after a **Read blank** or a **Read sample** block since the led source must be selected before reading. The Initialization block can be preceded only by a Note block.

Once the workflow is defined, you can edit the name of the method along with a brief description and a duration indication by clicking the **A** icon available on the upper right side of the screen, as shown in Figures 32 and 33.

Then, the experiment method can be saved by clicking the icon on the upper right side of the screen having the shape of a floppy disk. The experiment method is then added to the list shown in Figure 12. It is possible to tap each block to delete it or to set its options. As an example, by clicking the **Read sample** block the settings shown by Figure 34 appear.

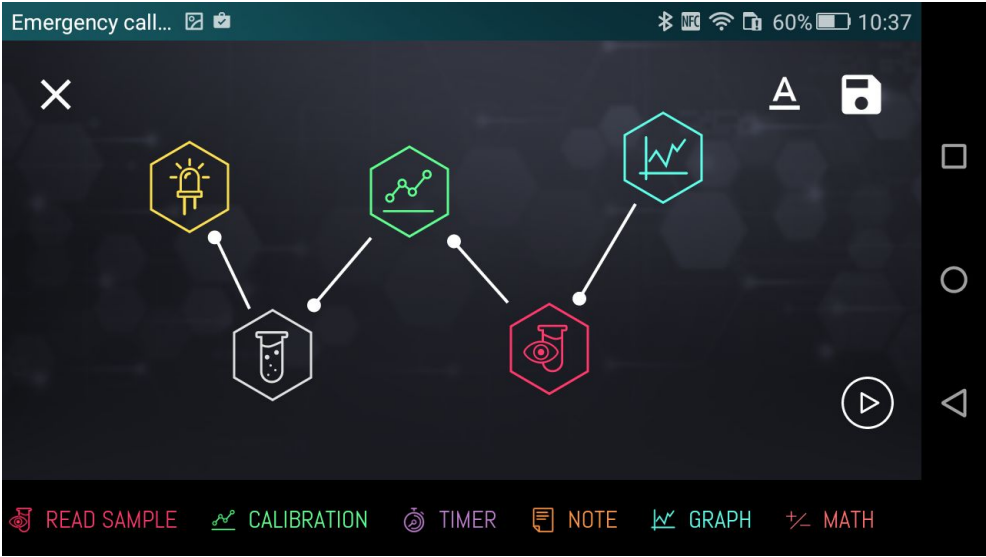


Figure 32. Sequence of blocks composing an experiment method.

Figure 33. Setting the method information: name, description and duration.

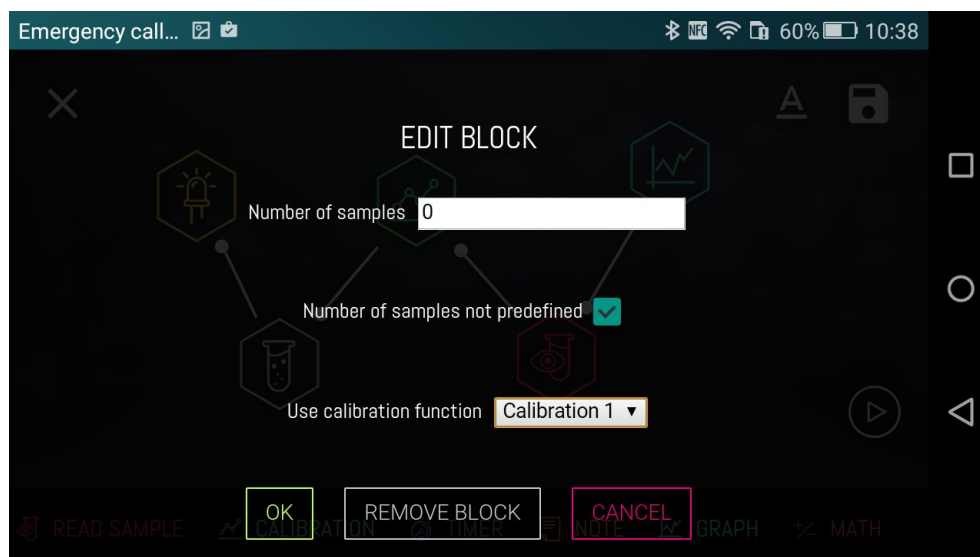


Figure 34. Read sample block settings.

As you can see in Figure 34, the **Read sample** block has 3 parameters that can be set. The first parameter is “number of samples” and allows you to set the number of samples that can be analyzed by the method. **Note that the minimum number of samples that can be analyzed is 2.** To analyze an arbitrary number of samples, the second parameter “number of samples not predefined” must be checked. In this case, the user selects the number of samples through the + button visible in the screen shown by Figure 16. Note that when you check such an option, the “number of samples” parameter is set to 0. **It must be remembered that it is necessary to insert at least two samples.**

The third parameter, “Use calibration function”, allows you to choose whether to use a calibration function obtained from a **Calibration** block previously inserted in the blocks sequence. By clicking on the drop-down menu, the available Calibration blocks list appears. In this case there will be just two items: i) **None** – that means no calibration functions - ii) **Calibration 1** – that is the block inserted before **Read Sample** in the sequence. Select the latter and when during the execution you get to the **Read Sample** block, you won’t have to specify the parts of the samples since such will be retrieved from the calibration curve obtained from the previous block. If you instead set the parameter to “none”, even if the method includes a **Calibration** block and you use it to create or select a function, the **Read Sample** block will not use it.

At this point we can save and execute the experiment. The execution can be started either by tapping the PLAY button at the bottom right of the **composer** section or by going back to the list presented by Figure 12 (you can close the composer by tapping the top left button).

3. Notebook

The NOTEBOOK section represents the lab notebook and is presented by Figure 35. Such a section lists all the experiments previously saved and allows you to access them to display results, write reports and share them on the We-Lab Community.

The experiments are listed in chronological order. To make the search easier, the user is able to filter the experiments based on the module, by clicking on the module's name on the top bar.

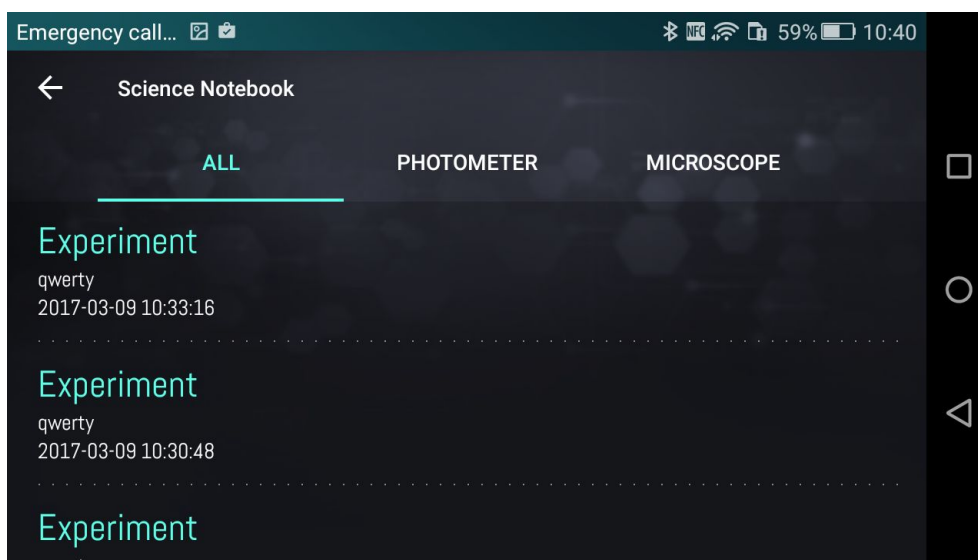


Figura 35. Notebook main screen.

If you select an experiment, its results are shown as presented by Figure 36. On the top right there is a set of buttons that let you (from left to right):

- edit the name, description, materials, method, comments and conclusions (the button turns yellow when the editing mode is *on*, and the edited information is stored when the Android back button or the top left arrow is pressed);
- export the results to PDF format;
- upload the results on your We-Lab Community profile;
- delete the experiment results;
- see the method generated by the **composer** used for the experiment.

In particular, the last button opens up the **composer** and displays the method blocks sequence. When the user deletes the used method, such a button is replaced by another one that asks the user whether to recover the method. In case of an affirmative answer, the method appears again in the screen presented by Figure 12.

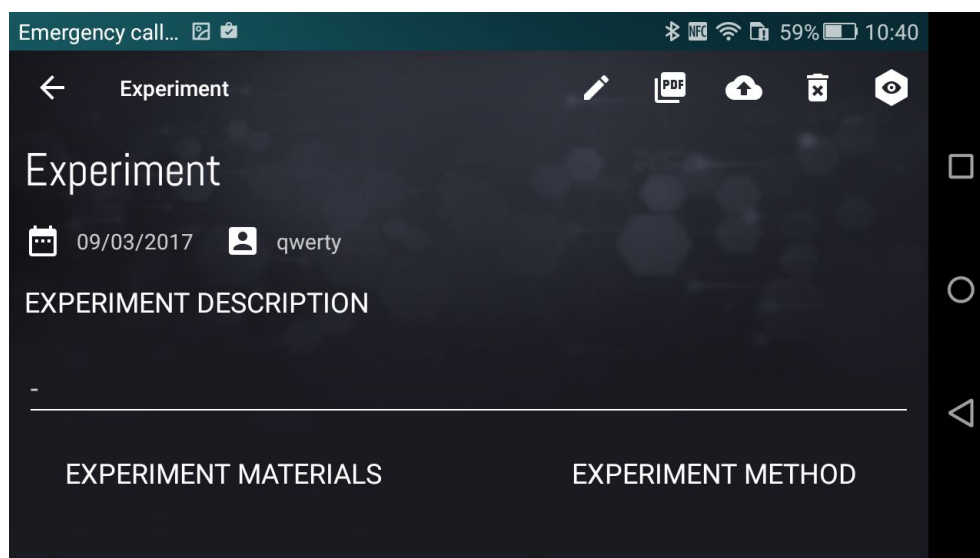


Figure 36. Details of a saved experiment.

To upload the results on your We-Lab Community profile, the APP asks you to provide a description (optional), the name of the master (mandatory) and the name of the group of students that made the experiment (optional). In case the We-Lab is used as a personal tool, the master and the group match the user's username. In case it is used in a school, the master is the teacher username. The results are uploaded as *private* on the master's web page. The master is then able to make them public after she/he checked the contents correctness. Such a process is described in details in section 4.1.

4. The We-Lab Community

The We-Lab Community is a scientific *social network*, that allows users to share their experiments results. The online community is accessible from the <https://www.we-lab.it/> page.

4.1 Edit elements and make them public or private

When experiment results or pictures captured using the microscope get uploaded from the APP, they appear as private on the page of the master. Thus, a teacher is able to check contents uploaded by students before making them public.

TO ACCESS THE COMMUNITY IT IS NECESSARY TO REGISTER WITH THE SAME CREDENTIALS (USERNAME, PASSWORD AND E-MAIL) USED ON THE APP.

When a user accesses the My DNA section by clicking the related link on the main bar of the website (see Figure 37), she/he sees the list of her/his own *public* experiments and images. An example is reported by Figure 38.

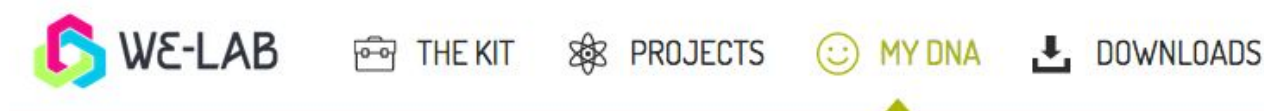


Figure 37. Access the My DNA section.

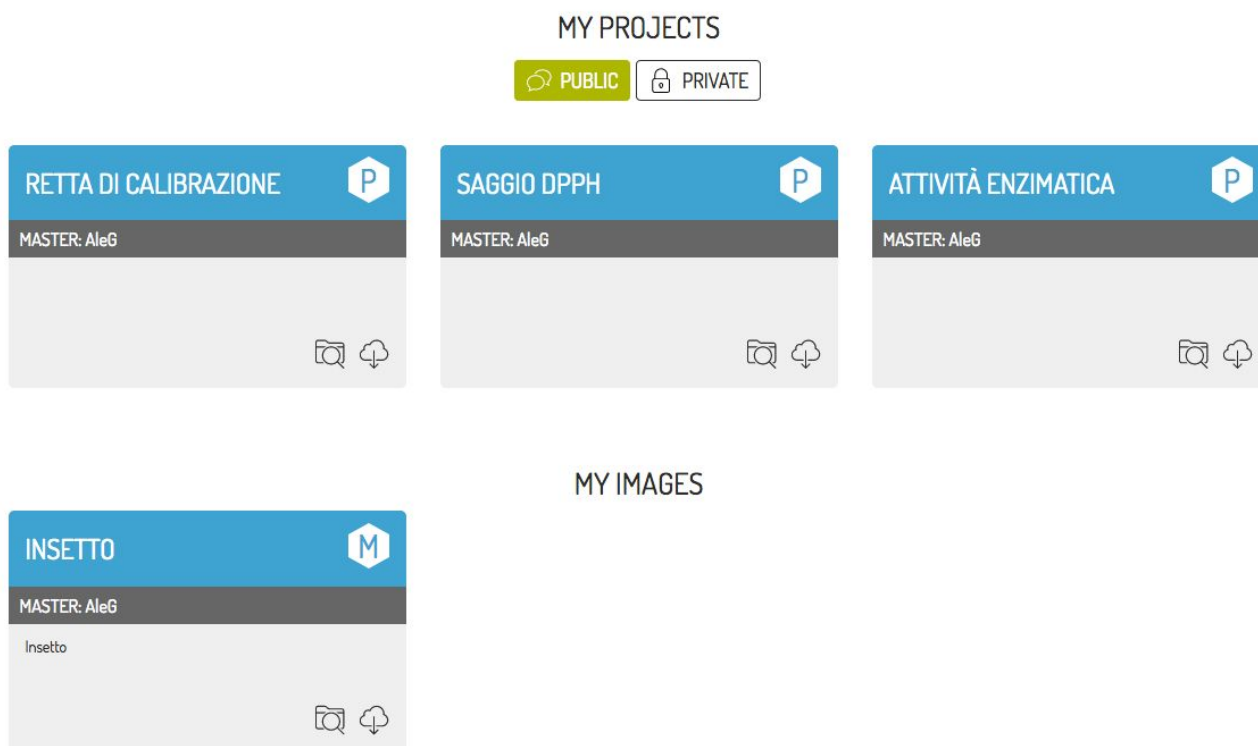


Figure 38. List of uploaded items.

By clicking on the PRIVATE button, the page displays instead the list of *private* experiments and images. To make a *private* experiment *public*, just move the mouse cursor over the bar with the title of the item you want to edit. On the top right corner the icon of a pencil appears as shown by Figure 39 (left). Click on such an icon to display the options that let you modify and delete the item, as shown by Figure 39 (right).



Figure 39. Item editing.

Select **Edit** to open a page the lets you modify the contents. Moreover, by using the **privacy** drop-down menu you can make *public* or *private* the item, as shown by Figure 40.

Edit Experiment Esperimento attività enzimatica

[View](#) [Edit](#) [Delete](#)

[Home](#) » [Esperimento attività enzimatica](#)

Language

privacy *

Private

Public

Private

password

groupName

participants

description

[Save](#) [Preview](#) [Delete](#)

Figure 40. Editing the properties of an item uploaded to the community.