

LabBook to DHIS2 Data Transfer

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Foreword

This manual is intended for medical biology laboratories (LBM) reporting aggregated data on DHIS2 (District Health Information System). The LabBook elements presented in this manual are accessible to biologist and administrator users. If you do not access any of the actions using your interface, contact your administrator.

DHIS2 export settings

LabBook offers two possibilities for transferring data to DHIS2. The first method is to get a csv data file from LabBook and import the file into the DHIS2 instance. The second is sending the data directly to the DHIS2 API. Both types of transfer require configuration.

a) DHIS2 API

This section allows you to add the DHIS2 instance identifiers. To add them, go to the " **Settings** " menu and click on " **DHIS2 Configuration** ", on the " **DHIS2 Export Settings** " page click on the " **Add** " button then fill in the fields. They are all mandatory.

DHIS2 API platform

Name

Login

Password

dhis2 platform address

By default Yes No

Cancel

Figure 1: Add DHIS2 Platform API

Name: designates the DHIS2 instance. For example, "DHIS2 ministry of health"

Identifiant: username on the DHIS2 instance.

Password: Password of the authorized user

DHIS2 platform address: Internet address of the DHIS2 instance.

Default: Allows you to set the default sending instance

The added instances are listed in the table. To edit or delete them, click on Action.

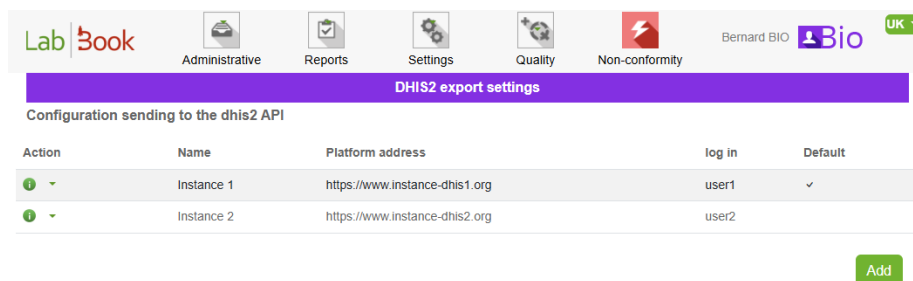


Figure 2: List of added DHIS2 APIs

b) Spreadsheets in LabBook

A spreadsheet is a csv file used to match the data retrieved from LabBook and those transferred to a DHIS2 instance. One spreadsheet is only dedicated to one DHIS2 form present in the instance. The configuration of the sheets is dedicated exclusively to experts and administrators. Details are provided in the upcoming chapter.

LabBook comes with two spreadsheets. Please note that these sheets are templates and should not be used in data transfer.

To add your spreadsheet templates, go to the **"Settings" menu and click on the "DHIS2 Configuration"** tab.

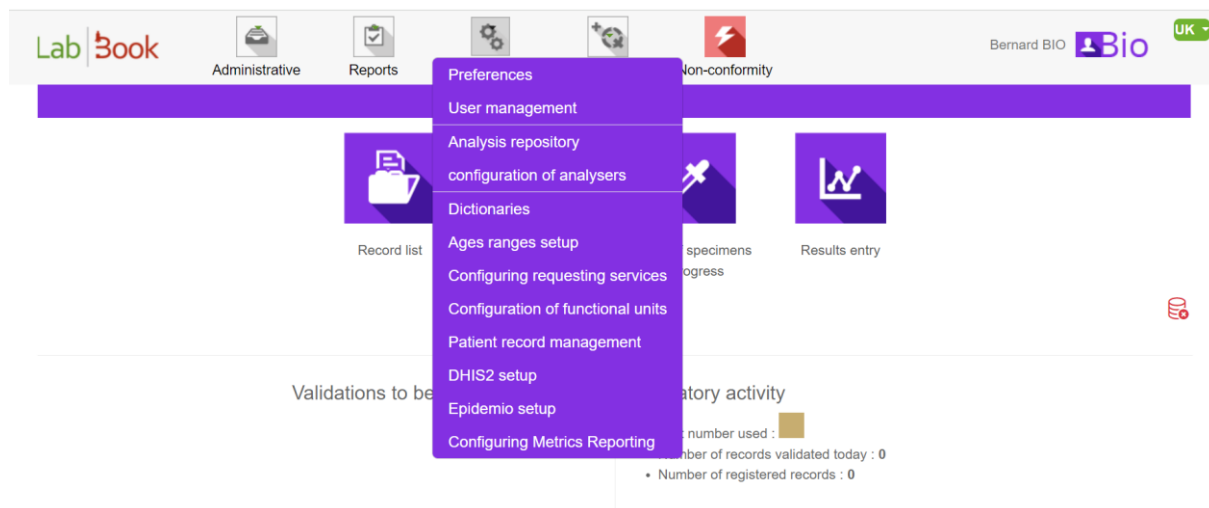


Figure 3: DHIS2 configuration

You will be redirected to the **"DHIS2 Export Settings"** page. This page allows you to add your spreadsheets. To do this, first select the spreadsheet by clicking on the **"Choose a file"** button, then click on **"Save spreadsheet"**. A **"Save successful"** notification will be sent to you if the action was successful.

All your saved spreadsheets are listed on the page. You can download or delete them.

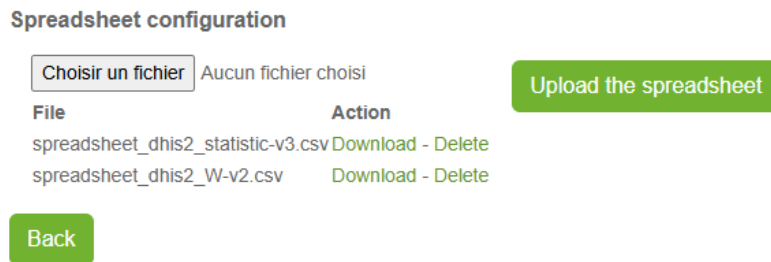


Figure 4: DHIS2 export settings

Transferring data to DHIS2

Data recovery and import

a) Data recovery

Data extraction is done from the “**DHIS2 Export**” page. To access it, click on the “**Reports**” *menu, then on the “DHIS2 Export”* tab.

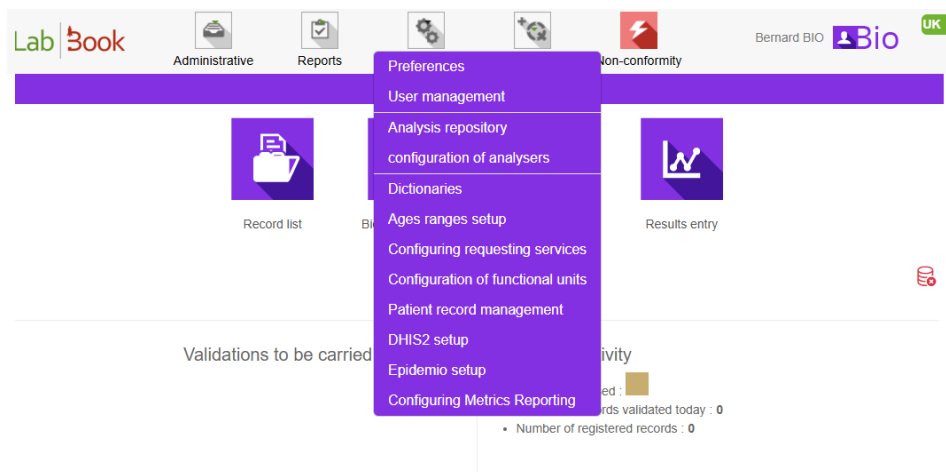


Figure 5: DHIS2 Export tab

(1) Select period:

Weekly spreadsheet: Monday and Sunday should be the start and end dates of the period.

Monthly spreadsheet: Start date must be the 1st of the month and end date must be the last day of the selected month.

Example:

Notification of weekly data for the 14th and 15th week of the year 2022: the start and end dates of the period are April 14 and April 17, 2022.

Report monthly data for the months of April and May 2022: period start, and end dates are April 1 and May 31, 2022.

(2) Select Period Type: Weekly or Monthly

(3) Select the worksheet

From the drop-down list, select the desired spreadsheet.

(4) Click on “Recover Data”

The data file is downloaded by clicking on the “**Retrieve Data**” button. The file is automatically downloaded and placed in the “**Downloads**” folder on your computer. The name of the downloaded file contains three parts A_B_C: A => DHIS2, B => name of the spreadsheet and C => start date of the period.

In our example we have selected the periods from 01/04/2022 to 17/04/2022, the spreadsheet is named DHIS2_MADO. The name of the downloaded data file is DHIS2_DHIS2_MADO_2022-04-04-2022-04-17.

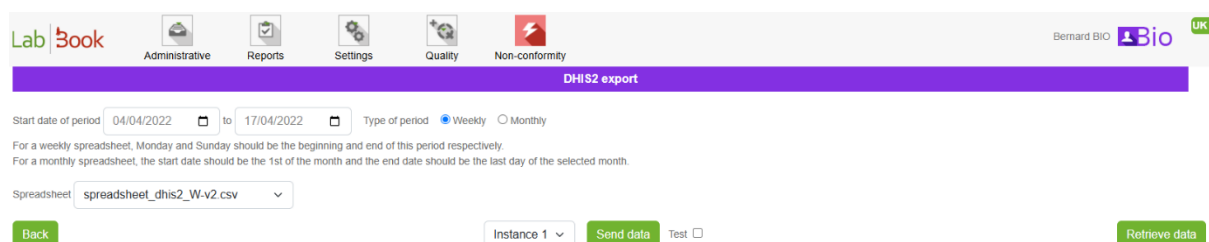


Figure 6: DHIS2 Export page

b) Importing data into DHIS2

This section is for users who have access to the DHIS2 Import/Export application.

Click on the red framed icon in Figure 7 “**Import/Export**” to launch the DHIS2 Import/Export module.

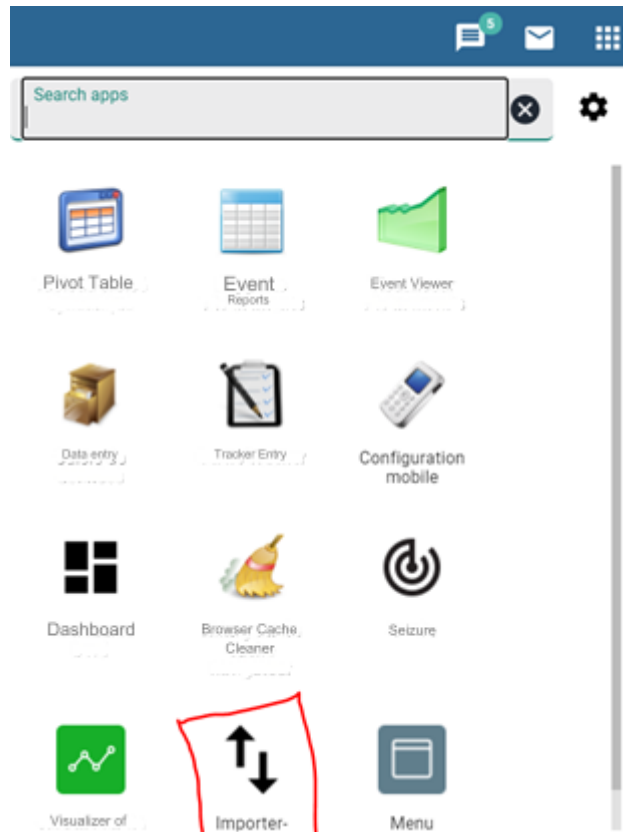


Figure 7: DHIS2 applications

You will be redirected to the Import/Export page. Then click on Data Import.

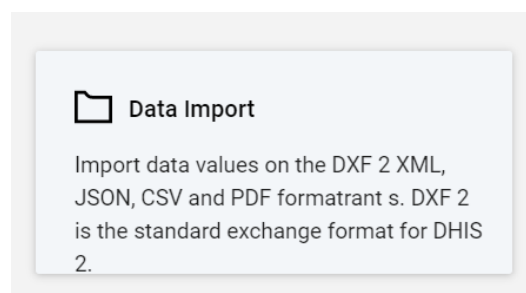



Figure 8: DHIS2 Data Import Module

A new page is presented to you. Leave the default settings and change as indicated on the items highlighted in red.

(1) Select your data file by clicking on the icon  .

In our example we selected the file DHIS2_RAM_2021-08-02.

(2) Select CSV format.

- (3) Select Name from the proposed “Data Element Schema” list.
- (4) Select Name from the list provided by “Organizational Unit Schema”.
- (5) Click the “Import” button.

Data Import

↑ dhis2_RAM_2021-08-02.csv

FORMAT

JSON XML ADX PDF CSV

DRY RUN

Yes No

FIRST ROW IS HEADER

Yes No

STRATEGY

New and updates New only Updates only Delete

PREHEAT CACHE

Yes (faster for large imports) No

— **MORE OPTIONS**

Data element id scheme
Name

Org unit id scheme
Uid

Id scheme
Uid

SKIP EXISTING CHECK

Skip check (fast) Check (safe, recommended)

Importer

Figure 9: Importing CSV data into DHIS2

After clicking the “Import” button, the summary gives an overview of the operation:

Import Summary

SUMMARY				
Créé le	Deleted	Ignored	Updated	Total
679	0	0	0	679

Figure 10: DHIS2 import summary

- Created: Number of data elements imported. If all items in your data file are imported, the total number is displayed.
- Deleted: Number of data items deleted.
- Ignored: Number of data elements ignored. If the contents of a cell in your data file are not recognized, then the corresponding row is ignored.

- Updated: Number of data items updated. If you import data items more than once for the same period, organizational unit, and user, the old values of these data items are replaced by the new ones.
- Total: Number of data items imported.

Figure 10 shows the successful import of a file with 679 data elements.

If you encounter any difficulties while importing data, you can contact the DHIS2 administrator.

Sending data

The " **Send Data** " button allows you to send data directly to the DHIS2 server. This is done using the spreadsheet and the DHIS2 API settings. This option requires the LabBook server to be connected on internet.

The process of sending data is the same as retrieving LabBook data, the difference is that no data files are downloaded. The data is directly uploaded to the server.

- 1) Select a period
- 2) Select a worksheet
- 3) Choose a DHIS2 instance from the proposed list (the default instance is positioned)
- 4) Click on "**Send data**"

A dialog box is displayed and informs about the sending status. A success message is shown if the data is successfully sent.

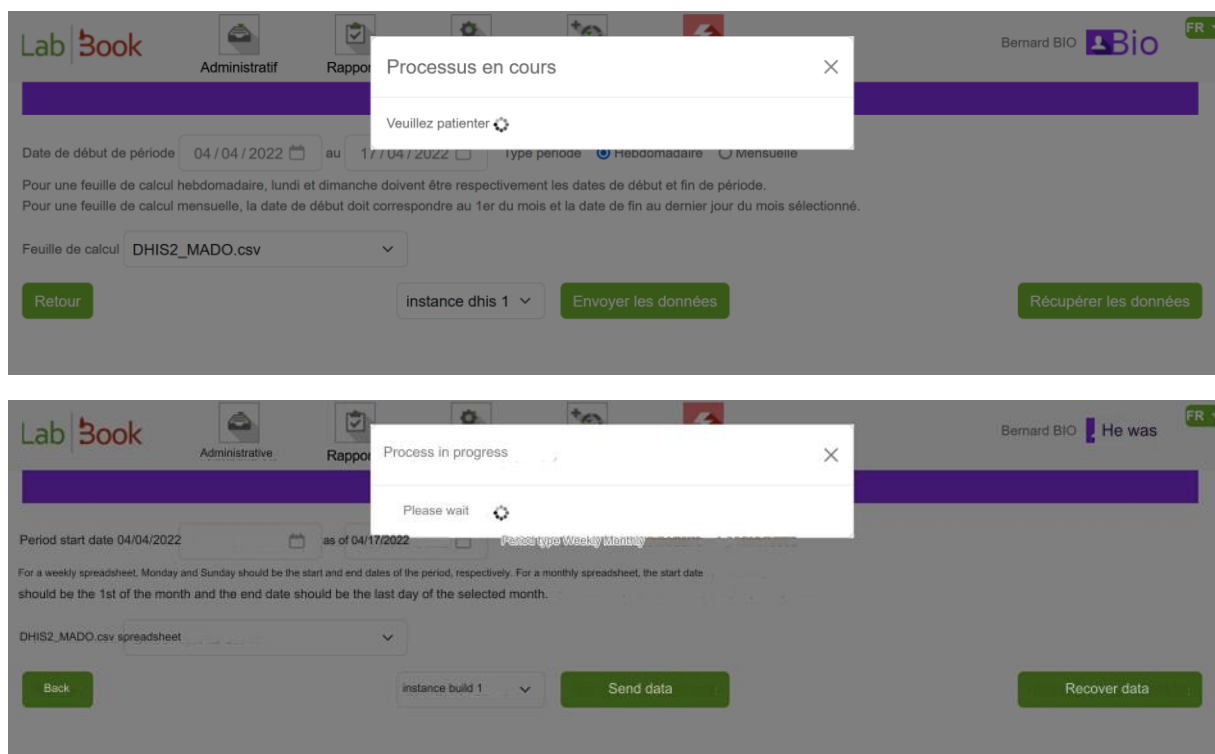


Figure 11: Sending data via the DHIS2 API

Developing spreadsheets

This section is intended for administrators responsible for developing DHIS2 spreadsheets.

a) Spreadsheets Overview

Extracting DHIS2 data from LabBook is done with spreadsheets. The spreadsheet is a file in CSV format. The values are separated by semicolons (;), the encoding used is UTF-8. It contains eight (8) columns:

- **dhis2_label:** label that will be exported (data element name, data element code for direct transfer)
- **version:** intended to distinguish the developments that could occur on this export service (currently v3)
- **filter:** formula used by LabBook to calculate the value of the data element.
- **type_sample:** Sample Id corresponding to the type of sample. If you do not want to filter by sample, then put 0
- **categoryoptioncombo:** property taken from DHIS2
- **attributeoptioncombo:** property taken from DHIS2
- **orgunit:** DHIS2 associated organization unit code)
- **storedby:** DHIS2 associated username

b) Syntaxes recognized by the “filter” column

Example 1:

Syntax:	$\\$_{IDVARIABLE} = [DICTIONARY_NAME.CODE]$
Details:	Selects analyses where one of the results matches the specified value.
Example:	Counting gram negative bacilli, the syntax is: $\$_{333} = [gram.2]$

- 333 corresponds to the variable ID in LabBook.

To find the variable identifier:

Log in to LabBook with the “Biologist” profile.

Search for the corresponding analysis in the analysis repository and click on edit.

The screenshot shows the LabBook interface with a navigation bar at the top containing icons for Administrative, Reports, Settings, Quality, and Non-conformity. The user is logged in as Bernard BIO. Below the navigation bar is a purple header for the 'Analysis repository'. A search form is visible with the following fields: 'Designation of the act' (B248), 'Analysis family' (dropdown), 'Type of specimen' (dropdown), and 'Active analysis' (Yes). A green 'Search' button is on the right. Below the search form, it indicates 'Total number of lines : 1' and provides navigation links 'First Previous 1 Next Last'. A table displays the search results:

Action	Code	Designation	Abbreviation	Family	Status	Bio. product
	B248	Urine analysis: microscopy, culture and sensitivity (fresh state, coloring cytology)		Bacteriology	Activated	PB3 : Urine sampling

Figure 12: Search for analysis B248 in the Analysis Repository

At the bottom of the analysis page, you will find the list of variables related.

Click on the edit icon. For our example click on Gram stain.

The screenshot shows the LabBook interface with a navigation bar at the top. Below the navigation bar is a purple header for the 'Analysis' page. A table displays the list of variables for the analysis:

Action	Name	Unit	Min	Max	Num. var	Position
	Parasites					
	Other					10
	Bacterial flora					20
	Gram staining					30
	Macroscopic appearance					40
	Epithelial cells					50
	Leukocytes	/ml				60
	Red blood cells	/ml				70
	Yeasts					80
	Crystal					90
	Cylinders					100

Version : 3.3.11 | Contributors

Figure 13: List of variables in the B248 analysis

The elements of the variable are positioned in their respective fields. The variable identifier "333" is in the grayed-out Id field.

The screenshot shows the 'Analysis' form in LabBook. The 'Variables' section includes a search bar with the text 'Search for a variable' and a dropdown menu. Below the search bar, there are input fields for 'Label *' (Gram staining), 'Var. code' (333), and 'Id' (333, highlighted with a red box). Other fields include 'Result type *' (Gram), 'Normal value min.', 'Normal value max.', and 'Underline' (Yes/No).

Figure 14: Variable Gram stain

- Gram corresponds to the name of the dictionary.

Find the list of dictionaries (choice of answers) by clicking on the "Settings" menu then on the "Dictionaries" tab. It is possible to search for an element of the dictionary by its name/label/code.

The screenshot shows the 'List of dictionaries (choice of answers)' page. A search bar at the top contains the text 'gram'. Below the search bar, there is a table with columns for 'Action', 'Name', and 'Description'. The table contains one row with 'gram' in the 'Name' column. A dropdown menu is open over the 'gram' row, showing options: 'Edit', 'Export dictionary', 'Delete', and 'Back'. At the bottom of the page, there are buttons for 'Dictionary import', 'Export dictionary', and 'Add a dictionary'.

Figure 15: Search for Gram-negative bacilli in the Dictionary

In our example, searching for the gram-negative bacilli element returns the name gram. Click Edit, the "Dictionary" page displays the values that "gram" can take with the label, code, short label and position of the element.

The screenshot shows the LabBook interface for editing a dictionary. At the top, there is a navigation bar with icons for Administrative, Reports, Settings, Quality, and Non-conformity. The current page is titled 'Dictionary'. Below the navigation bar, there is a form for the dictionary name (set to 'gram') and a description field. A green 'Add a value' button is located to the right of the description field. Below this, a section titled 'Values' contains a table with the following data:

Action	Label *	Code *	Short label	Position	Formatting
Delete	absence of visible bacteria	1	1	10	No
Delete	Gram-negative bacilli	2	2	20	No
Delete	Gram-positive bacilli	3	3	30	No
Delete	rare Gram-negative bacilli	4	4	40	No
Delete	Gram-negative bacilli, Gram-positive bacilli	5	5	50	No
Delete	Gram-negative bacilli, Gram-positive cocci	6	6	60	No

At the bottom of the interface, the version '3.3.11' and 'Contributors' are listed.

Figure 16: Values taken by the "gram" dictionary

- 2 is the code for the value Gram-negative bacilli in the dictionary.

Figure 17: Code for the label "gram-negative bacilli"

Example 2:

Syntax	$\\$_{IDVARIABLE} = [DICTIONARY_NAME.CODE] ON ('ANALYSIS_CODE')$
Details	Selects analyses where one of the results matches the value specified for the specified analysis code.
Example	Count the number of times that RESISTANT was chosen as a result on the Meningococcal Antibiogram analysis with the DISK method for Penicillin, the syntax is: $\$_{571} = [resist_sensible.R] ON('B650')$

Follow the same process indicated in example 1 to find the corresponding values:

- 571 is the variable ID in LabBook.

The screenshot shows the 'Add variable' form in LabBook. The 'Label' field contains 'Penicillin', 'Var. code' is '571', and 'Id' is '571' (highlighted with a red box). The 'Result type' is set to 'Resistant/Sensitive'. Other fields like 'Normal value min.', 'Normal value max.', 'Min./max. display', 'Formula', 'Unit', and 'Accuracy' are empty.

Figure 18: Penicillin variable ID

- resist_sensible is the dictionary name.
- R is the code for the value "Resistant".

The screenshot shows the 'Dictionary' configuration page. The 'Dictionary name' is 'resist_sensible' (highlighted with a red box). Below, a table lists the values for this dictionary:

Action	Label *	Code *	Short label	Position	Formatting
Delete	Resistant	R	R	10	No
Delete	Intermediate	I	I	20	No
Delete	Sensitive	S	S	30	No
Delete	Not performed	NE	NE	40	No

The 'Code' 'R' for 'Resistant' is highlighted with a red box. Buttons for 'Back' and 'Save' are visible at the bottom.

Figure 19: resist_sensible dictionary

650 corresponds to the code for the "Meningococcal Antibiogram" analysis using the DISK method.

The screenshot shows the 'Analysis repository' page in LabBook. The search filters are: Designation of the act: Meningococcal antibiogram; Analysis family: (empty); Type of specimen: (empty); Active analysis: Yes. The results table has columns: Action, Code, Designation, Abbreviation, Family, Status, Bio. product. Two rows are shown: B650 (Meningococcal antibiogram [DISK]) and B670 (Meningococcal Antibigram [CAM]). The B650 row is highlighted with a red box. Below the table are navigation buttons: Back, Import the repository, Export the repository, List of variables, Add an analysis.

Figure 20B650 Analysis

A complete list of recognized syntaxes is attached in the appendix.

c) Values taken by the “type_sample” column

Type_sample takes an identifier number corresponding to the type of sample (see table below). It also allows you to filter on the type of sample. If you do not want to filter on the sample, then put 0.

type_sample	label
34	Joint puncture fluid
35	Ascites puncture fluid
38	Biopsy
50	Spit
56	Broncho Alveolar Washing
75	Throat swab
99	Cerebrospinal fluid
100	Bronchial puncture fluid
102	Alveolar puncture fluid
104	Pleural puncture fluid
138	Blood
141	Stool
152	Urethral swab
153	Urine
162	Vaginal swab
163	Other
1000	Genital swabbing
1014	Drinking water

1015	Wastewater
1016	Surface water
1189	Pus sampling

Example of a spreadsheet:

1	dhis2_label	version	filter	type_sample	categorieoptioncombo	attributeoptioncombo	orgunit	storedby
2	Other species	v3	\$_614 = [especepalu others]					138
3	Other shigellae		\$_344 IN ([bacterium.26], [bacterium.27], [bacterium.28])					141
4	Gram (-) polymorphic bacilli		\$_333 = [gram.2]					99
5	Curved polar motile bacilli a Gram (-) 6 Candida albicans (Vaginal Sample)		\$_636 = [yorn.1] AND \$_637 = [yorn.1]					141
6	Candida albicans (Prelevement Uretral)		\$_361 [bacterium.33]					162
7	Chlamydia trachomatis direct (Prelevement Vaginal)		\$_344 [bacterium.33]					152
8	Chlamydia trachomatis direct (Prelevement Uretral)		\$_212 = [absent.present]					162
9	D - S. mansoni		\$_236 = [absent.present]					152
10	Diplocoq. in Gram (-) (Urethral Sampling)		\$_641 = [shisto2.S.mansoni]					141
11	Diplocoq. a Gram (-) (Prelevement Uretral)		\$_353 = [absent.present]					152
12	Diplocoq. a Gram (-) (Prelevement Vaginal)		\$_353 = [absent.present]					162
13	Diplocoque a Gram (-)		\$_333 = [gram.21]					99
14	Diplocoque a Gram (+)		\$_333 = [gram.20]					99
15	Hib		\$_344 = [bacteria.15]					99
16	Levures (Urethral Sampling)		\$_356 IN ([nombre.3], [nombre.4], [nombre.5])					152
17	Levures (Prelevement Vaginal)							162

Figure 21: Spreadsheet read Excel view

```

1 dhis2_label;version;filter;type_sample;categorieoptioncombo;attributeoptioncombo;orgunit;storedby
2 Autres especes;v3;$_614 = [especepalu autres];138;;;
3 Autre shigelles;;$_344 IN ([bacterie.26], [bacterie.27], [bacterie.28]);141;;;
4 Bacilles a Gram (-) polymorphes;;$_333 = [gram.2];99;;;
5 Bacilles mobiles polaires incurves a Gram (-);$_636 = [yorn.1] AND $_637 = [yorn.1];141;;;
6 Candida albicans (Prelevement Vaginal);$_361 = [bacterie.33];162;;;
7 Candida albicans (Prelevement Uretral);$_344 = [bacterie.33];152;;;
8 Chlamydia trachomatis direct (Prelevement Vaginal);$_212 = [absent.present];162;;;
9 Chlamydia trachomatis direct (Prelevement Uretral);$_236 = [absent.present];152;;;
10 D - S. mansoni;;$_641 = [shisto2.S.mansoni];141;;;
11 Diplocoq. a Gram (-) (Prelevement Uretral);$_353 = [absent.present];152;;;
12 Diplocoq. a Gram (-) (Prelevement Vaginal);$_353 = [absent.present];162;;;
13 Diplocoque a Gram (-);$_333 = [gram.21];99;;;
14 Diplocoque a Gram (+);$_333 = [gram.20];99;;;
15 Hib;;$_344 = [bacterie.15];99;;;
16 Levures (Prelevement Uretral);$_356 IN ([nombre.3], [nombre.4], [nombre.5]);152;;;
17 Levures (Prelevement Vaginal);$_356 IN ([nombre.3], [nombre.4], [nombre.5]);162;;;

```

Figure 22: Spreadsheet read in Notepad view

d) data file extracted from LabBook

The DHIS2 data file retrieved from LabBook is in CSV format. The values are separated by commas (,) and the encoding used is UTF-8. The sheet contains eleven (11) columns:

- **data element:** name or code of the data element
- **period:** Weekly (eg. 2021W25) or Monthly (eg. 202106)
- **orgunit:** name of the organizational unit
- **categoryoptioncombo:** Property obtained from DHIS2
- **attributeoptioncombon:** Property obtained from DHIS2
- **value:** value of the data element
- **storedby:** username
- **lastupdated:** date of last modification
- **comment:** your comment

- **followup:** (leave blank)
- **deleted:** (leave blank)

NB: Make sure that:

- The values in the “orgunit” column correspond to an organizational unit in DHIS2.
- storedby " column correspond to a DHIS2 username authorized to access the data elements in column A.

dataelement	period	organ	categoryoptioncombo	attributeoptioncombo	value	storedby	lastupdated	comment	followup	deleted
Other species	2023W17	Name of the laboratory	2xCFaze87145	2xCFaze87145	0	User	2023-05-02T14:11:42		FALSE	
Other shigellae		2023W17 Lab Name	2xCFaze87146	2xCFaze87146	5	User	2023-05-02T14:11:42		FALSE	
Gram (-) polymorphic bacilli	2023W17	Name of the laboratory	2xCFaze87147	2xCFaze87147	4	User	2023-05-02T14:11:42		FALSE	
Gram (-) curved polar motile bacilli	2023W17	Name of the laboratory	2xCFaze87148	2xCFaze87148	2	User	2023-05-02T14:11:42		FALSE	
Candida albicans (Prelevement Vaginal)	2023W17	Name of the laboratory	2xCFaze87149	2xCFaze87149	1	User	2023-05-02T14:11:42		FALSE	
Candida albicans (Prelevement Uretral)	2023W17	Name of the laboratory	2xCFaze87150	2xCFaze87150	0	User	2023-05-02T14:11:42		FALSE	
Chlamydia trachomatis direct (Prelevement Vaginal)	2023W17	Name of the laboratory	2xCFaze87151	2xCFaze87151	0	User	2023-05-02T14:11:42		FALSE	
Chlamydia trachomatis direct (Prelevement Uretral)	2023W17	Name of the laboratory	2xCFaze87152	2xCFaze87152	1	User	2023-05-02T14:11:42		FALSE	
D - S. mansonii	2023W17	Name of the laboratory	2xCFaze87153	2xCFaze87153	0	User	2023-05-02T14:11:42		FALSE	
Diplocoq. to Gram (-) (Urethral Sampling)	2023W17	Name of the laboratory	2xCFaze87154	2xCFaze87154	0	User	2023-05-02T14:11:42		FALSE	
Diplocoq. to Gram (-) (Vaginal Sampling)	2023W17	Name of the laboratory	2xCFaze87155	2xCFaze87155	0	User	2023-05-02T14:11:42		FALSE	
diplococci on Gram (-)	2023W17	Name of the laboratory	2xCFaze87156	2xCFaze87156	0	User	2023-05-02T14:11:42		FALSE	
Diplococcus on Gram (+)	2023W17	Name of the laboratory	2xCFaze87157	2xCFaze87157	0	User	2023-05-02T14:11:42		FALSE	
Hib		2023W17 Lab Name	2xCFaze87158	2xCFaze87158	0	User	2023-05-02T14:11:42		FALSE	
Yeasts (Urethral Sampling)			2xCFaze87159	2xCFaze87159	0	User	2023-05-02T14:11:42		FALSE	
Yeasts (Vaginal Sample)	2023W17	Name of the laboratory	2xCFaze87160	2xCFaze87160	0	User	2023-05-02T14:11:42		FALSE	
Meningo A	2023W17	Name of the laboratory	2xCFaze87161	2xCFaze87161	0	User	2023-05-02T14:11:42		FALSE	
Meningo B	2023W17	Name of the laboratory	2xCFaze87162	2xCFaze87162	0	User	2023-05-02T14:11:42		FALSE	
Meningo C	2023W17	Name of the laboratory	2xCFaze87163	2xCFaze87163	0	User	2023-05-02T14:11:42		FALSE	
Meningo W135	2023W17	Name of the laboratory	2xCFaze87164	2xCFaze87164	0	User	2023-05-02T14:11:42		FALSE	
Neisseria gonorrhoeae (Prelevement Uretral)	2023W17	Name of the laboratory	2xCFaze87165	2xCFaze87165	0	User	2023-05-02T14:11:42		FALSE	

Figure 23: Extract from DHIS2 LabBook data file

Annex

Example of syntaxes taken by the “filter” column

Formula	Definition
\$_IDVARIABLE = [DICTIONARY_NAME.CODE]	Selects the analyses where one of the results corresponds to the indicated value
\$_IDVARIABLE > NUMERIC_VALUE	Selects the analyses where one of the results is greater than the NUMERIC_VALUE
\$_IDVARIABLE = [DICTIONARY_NAME.CODE] AND \$_IDVARIABLE > VALUE_NUMERIC	Selects the analyses where one of the results corresponds to the indicated value and is higher than the NUMERIC_VALUE
\$_IDVARIABLE IN ([DICTIONARY_NAME.CODE1], [DICTIONARY_NAME.CODE2], [DICTIONARY_NAME.CODE3], ...)	Selects the analyses where one of the results corresponds to one of the indicated values
\$_IDVARIABLE NOT IN ([DICTIONARY_NAME.CODE1], [DICTIONARY_NAME.CODE2], [DICTIONARY_NAME.CODE3], ...)	Selects the analyses where one of the results does not correspond to the indicated values {IDVARIABLE1, IDVARIABLE2, IDVARIABLE3, ...} selects the analyses where the result contains one of the listed variables.
{IDVARIABLE1, IDVARIABLE2, IDVARIABLE3, ...}	Selects analyses whose results contain one of the listed variables.
CAT(SEX_M)	Selects analyses from patient files men
CAT(SEX_F)	Selects analyses from patient files women
CAT(AGE_1)	Selects analyses from patient records whose age is within range 1 (see age range settings in the menu Settings => Age ranges)
CAT(SEX_M, AGE_2)	Selects analyses from files concerning male patients whose age is within the range 2
NB_REC_SAVED	Number of records with at least administrative status in the period
NB_ANA_SAVED	Number of tests prescribed in the period
NB_SAMP_OUTSOURCED	Number of samples outsourced during the period
NB_STAFF	Number of employees
NB_SECRETARY_TYPE	Number of secretary and advanced secretary

NB_TECHNICIAN_TYPE	Number of technicians, senior technicians and quality technicians
NB_QUALITICIAN_TYPE	Number of quality controllers and quality control technicians
NB_BIOLOGIST_TYPE	Number of biologists
NB_EQUIPMENT	Number of equipment's
NB_EQP_BREAKDOWN	Number of broken equipment's in the period
NB_PROCEDURE	Procedure number
NB_PRODUCT_WITH_EXPIRY_WARNING	Number of products with expiry notices compared to the current date
NB_PRODUCT_WITH_EXPIRY_ALERT	Number of products with expiry alerts in relation to the current date
NB_PRODUCT_UNDER_SAFE_LIMIT	Number of products under the safety limit
NB_PRODUCT_OUT_OF_STOCK	Number of products on backorder
NB_OPEN_NON_CONFORMITY	Number of open non-conformities
NB_NON_CONFORMITY	Number of non-conformities (open and closed) in the period
NB_INTERNAL_QUALITY_CONTROL	Number of internal controls (even without results)
NB_INTERNAL_QUALITY_RESULT	Number of internal control results in the period
NB_EXTERNAL_QUALITY_CONTROL	Number of external audits (even without results)
NB_MEETING	Number of meetings in the period

Filter options

It is possible to associate filters with the above expressions.

\$_IDVARIABLE = [DICTIONARY_NAME.CODE] CAT(SEX_M)	Selects analyses where one of the results matches the specified value. regarding male patients
\$_IDVARIABLE = [DICTIONARY_NAME.CODE] CAT(SEX_F)	Selects analyses where one of the results matches the specified value. regarding female patients

<p>\$_IDVARIABLE = [DICTIONARY_NAME.CODE] CAT(AGE[min - m ax])</p>	<p>Selects analyses where one of the results matches the specified value. concerning patients whose ages are between min and max</p>
<p>\$_IDVARIABLE = [DICTIONARY_NAME.CODE] CAT(SEX_ M , AGE [min - max])</p>	<p>Selects analyses where one of the results matches the specified value. concerning patients whose male and ages are between min and max</p>