

## DHIS2 Data Recovery Manual

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## Foreword

This manual is intended for medical laboratories (MBL) that upload data to the District Health Information System (DHIS2). The LabBook elements presented in this manual are accessible to a user with "Biologist" and "Administrator" rights. If you do not have access to any of the actions via your interface, please contact your administrator so that these rights can be assigned to you.

**NB:** A spreadsheet is used to retrieve data from a DHIS2 form.

## Data export method

The data exchange consists of four (4) steps:

- Spreadsheet configuration ;
- Saving spreadsheets in LabBook ;
- Data recovery;
- Import of data into DHIS2.



Figure 1 Method of exchanging LabBook data to DHIS2

The configuration of the spreadsheets is dedicated exclusively to experts and administrators. It is detailed in the next chapter.

### a) Saving spreadsheets in LabBook

By default, LabBook has a spreadsheet based on data feedback related to notifiable diseases (MADO) from the Senegalese Laboratories Directorate.

To change the worksheet, go to the "**Settings**" menu and click on the "**DHIS2 Set up**" tab.

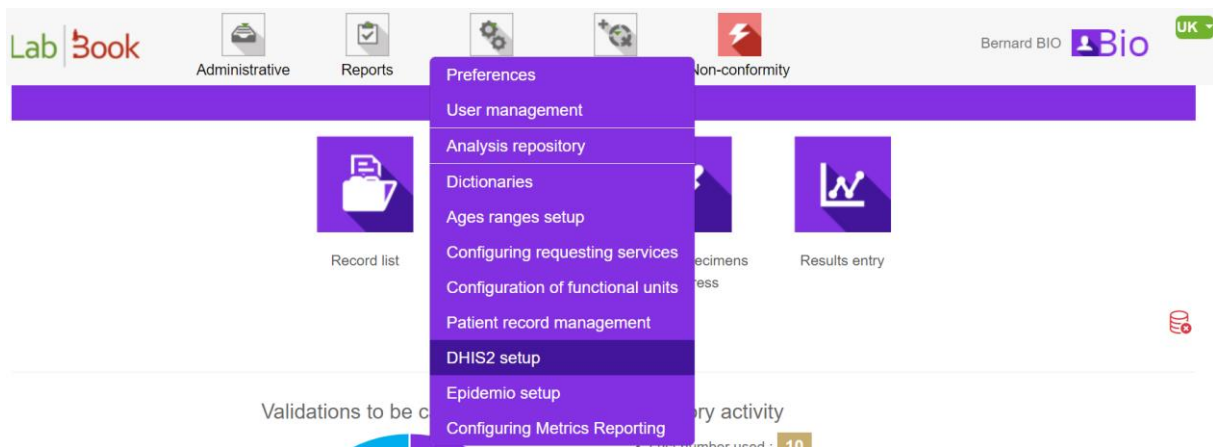


Figure 2 DHIS2 configuration

You will be redirected to the "**DHIS2 Export Settings**" page. This page allows you to save your spreadsheets. To do this, first select the spreadsheet by clicking on the "**Choose a file**" ("**Choisir un fichier**") button, then click on "**Upload the spreadsheet**". If the save was successful, you will receive a "**Save Successfully**" notification.

All your saved spreadsheets are listed on the page. You can download or delete them. The page below shows one (1) saved spreadsheet: DHIS2\_MADO.

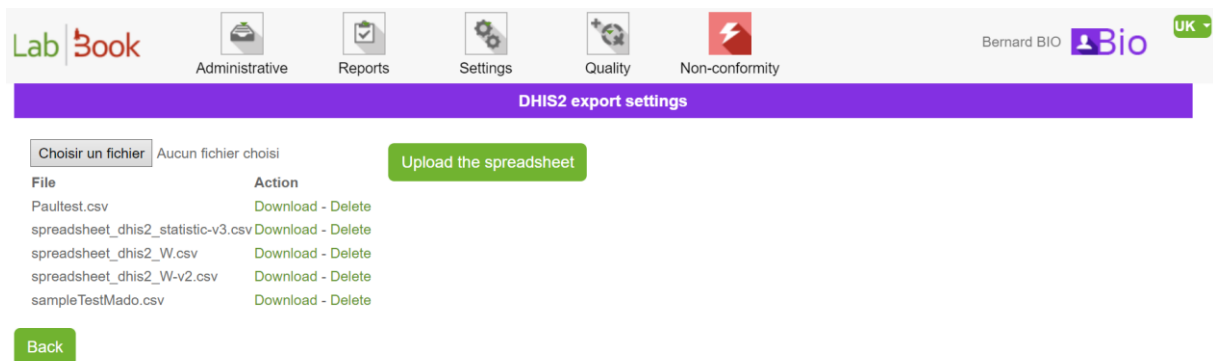


Figure 3 DHIS2 export settings

## b) 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.

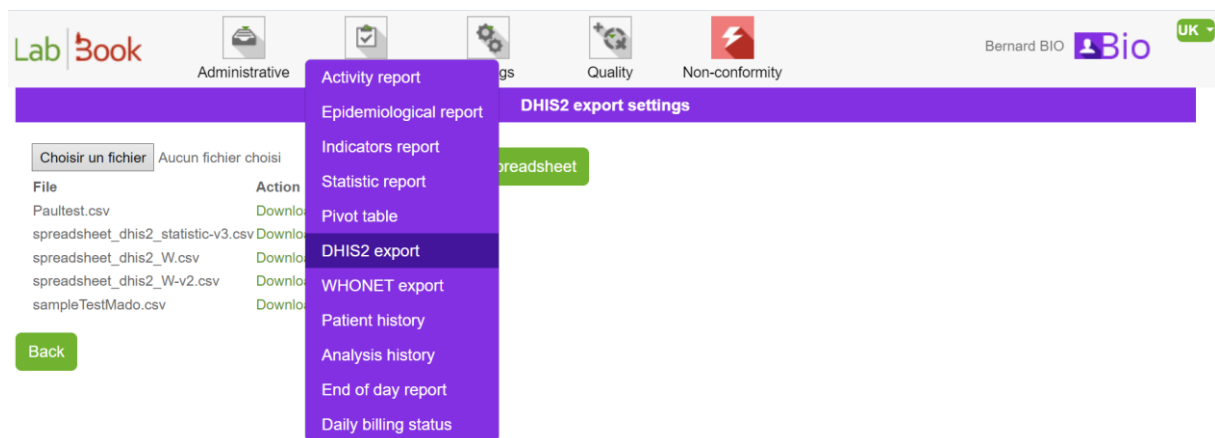


Figure 4 DHIS2 Export Tab

**(1) Select the start date of the period:**

For a weekly spreadsheet, Monday and Sunday must be the start and end dates of the period respectively.

For a monthly spreadsheet, the start date must correspond to the 1st of the month and the end date to the last day of the selected month.

For example, if you report weekly data on the 14th<sup>ème</sup> and 15th<sup>ème</sup> week of the year 2022, the start and end dates of the period are April 4th and April 17th 2022 respectively.

If you are reporting monthly data for the months of April and May 2022, the start and end dates are 1<sup>er</sup> April and 31 May 2022 respectively.

**(2) Select the worksheet : weekly or monthly**

**(3) Select the spreadsheet : from the drop-down list, select the desired worksheet**

**(4) Click on "Retrieve data":**

The data file is downloaded by clicking on the "**Retrieve Data**" button. The file is automatically downloaded and placed in the "**Downloads**" folder of 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.

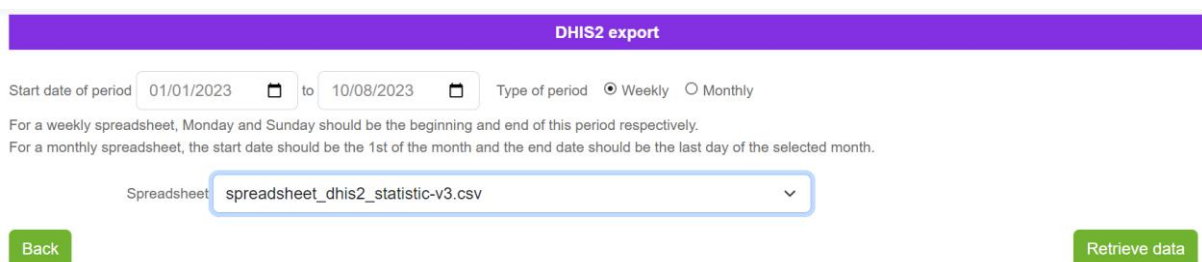


Figure 5 DHIS2 Export" page

## c) Importing data into DHIS2

This section is for users who have access to the DHIS2 Import/Export application. Those who do not have access can share the previously downloaded data file by email with the contact person responsible for importing the data in DHIS2.

Click on the red-framed icon in Figure 6 "**Import/Export**" to launch the DHIS2 Import/Export module.

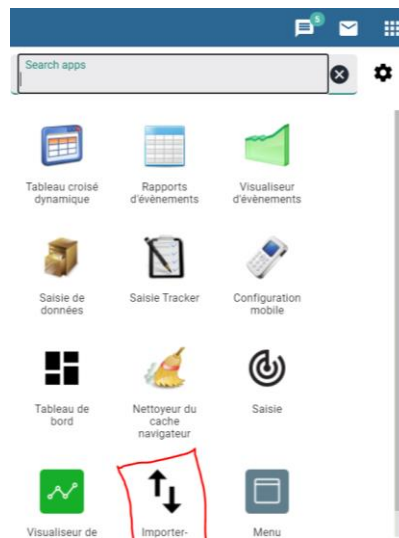


Figure 6 DHIS2 Applications

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

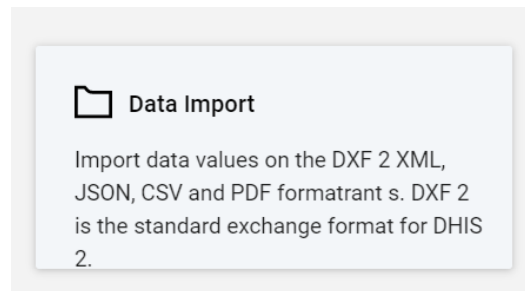



Figure 7 DHIS2 Data Import Module

A new page has been created. 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 have selected the file dhis2\_RAM\_2021-08-02.

- (2) Select the CSV format.
- (3) Select Name from the proposed list "Data Element Schema".
- (4) Select Name from the list proposed by "Organization unit diagram".
- (5) Click on 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 8 Importing CSV data into DHIS2

After clicking on 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 9 DHIS2 Import Summary

- Created on: number of imported data elements. If all the elements of your data file are imported, the total number is displayed.
- Deleted: number of data elements deleted.
- Ignored: number of data elements ignored. If the content of a cell in your data file is not recognized then the corresponding line is ignored.
- Updated: number of updated data elements. If you import data elements more than once for the same period, the same organizational unit and the same user, then the old values of these data elements are replaced by the new ones.
- Total: number of imported data elements.

Figure 9 shows the successful import of a data file with 679 data elements. If you encounter any difficulties importing the data, you can contact the DHIS2 administrator.

## Spreadsheets at the heart of data extraction

This chapter is intended for administrators who are responsible for developing DHIS2-compliant spreadsheets.

### a) Presentation of the spreadsheets

The extraction of DHIS2 data from LabBook is done with the help of a spreadsheet. The spreadsheet is a file in CSV format. The values are separated by semicolons (;), the encoding used is UTF-8. It contains five (5) columns:

- **dhis2\_label** : The label that will be exported (name of the data element)
- **version**: v1, intended to distinguish the evolutions that they could have on this export service
- **filter**: filter to refine the calculation of the expected result
- **type\_sample**: identification number corresponding to the type of sampling. If you don't want to filter on the sample then put 0
- **categoryoptioncombo** : Property obtained from DHIS2
- **attributeoptioncombon** : Property obtained from DHIS2
- **orgunit**: Property obtained from DHIS2 (Organization Unit Code)
- **storedby**: Property obtained from DHIS2 (associated user name)

### b) Syntaxes recognized by the "filter" column

Example 1:

Syntax:	<b><math>\\$\_IDVARIABLE = [DICTIONARY\_NAME.CODE]</math></b>
Explanation:	Selects the analyses where one of the results corresponds to the indicated value.
Example:	Count the gram negative bacilli, the syntax is: $\$\_333 = [gram.2]$

- 333 is the variable identifier in LabBook.

To find the identifier of the variable :

Log on to LabBook with the "Biologist" profile;

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

Lab Book | Administrative | Reports | Settings | Quality | Non-conformity | Bernard BIO | Bio | US

**Analysis repository**

Search

Designation of the act:

Analysis family:

Type of specimen:

Active analysis:

Total number of lines : 1  
First Previous 1 Next Last

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 10 Searching for the B248 test in the Test Repository

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

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

Lab Book | Administrative | Reports | Settings | Quality | Non-conformity | Bernard BIO | Bio | US

**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 11 List of variables in the B248 analysis



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

The screenshot shows the 'Analysis' form in Lab Book. The 'Variables' section includes a search bar with 'Click to start a search' and a '+' button. Below the search bar, the 'Label' is 'Gram staining', 'Var. code' is '333', and 'Id' is '333' (highlighted with a red box). Other fields include 'Result type' (Gram), 'Normal value min.', 'Normal value max.', and 'Underline' (Yes/No).

Figure 12 Gram stain variable

- Gram is the name of the dictionary.

Find the list of dictionaries (answer choices) by clicking on the "Settings" menu and then on the "Dictionaries" tab. It is possible to search for an item in the dictionary by its name/word/code.

The screenshot shows the 'List of dictionaries (choice of answers)' page. The search results table has columns for 'Action', 'Name', and 'Description'. The 'Name' column contains 'gram'. A dropdown menu is open over the 'gram' entry, showing options: 'Edit', 'Export dictionary', 'Delete', and 'Back'. There are also buttons for 'Dictionary import', 'Export dictionary', and 'Add a dictionary'.

Figure 13 Search for gram-negative bacilli in the Dictionary

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

Dictionary name:  Description:

[Add a value](#)

Values

Action	Label *	Code *	Short label	Position	Formatting
<a href="#">Delete</a>	absence of visible bacteria	1	1	10	No <input type="text" value="v"/>
<a href="#">Delete</a>	Gram-negative bacilli	2	2	20	No <input type="text" value="v"/>
<a href="#">Delete</a>	Gram-positive bacilli	3	3	30	No <input type="text" value="v"/>
<a href="#">Delete</a>	rare Gram-negative bacilli	4	4	40	No <input type="text" value="v"/>
<a href="#">Delete</a>	Gram-negative bacilli, Gram-positive bacilli	5	5	50	No <input type="text" value="v"/>
<a href="#">Delete</a>	Gram-negative bacilli, Gram-positive cocci	6	6	60	No <input type="text" value="v"/>

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Figure 14 Values taken by the "gram" dictionary

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

Dictionary name:  Description:

[Add a value](#)

Values

Action	Label *	Code *	Short label	Position	Formatting
<a href="#">Delete</a>	absence of visible bacteria	1	1	10	No <input type="text" value="v"/>
<a href="#">Delete</a>	Gram-negative bacilli	2	2	20	No <input type="text" value="v"/>
<a href="#">Delete</a>	Gram-positive bacilli	3	3	30	No <input type="text" value="v"/>
<a href="#">Delete</a>	rare Gram-negative bacilli	4	4	40	No <input type="text" value="v"/>
<a href="#">Delete</a>	Gram-negative bacilli, Gram-positive bacilli	5	5	50	No <input type="text" value="v"/>
<a href="#">Delete</a>	Gram-negative bacilli, Gram-positive cocci	6	6	60	No <input type="text" value="v"/>

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Figure 15 Code for the wording "gram-negative bacilli".

Example 2:

Syntax	<b><math>\\$\_IDVARIABLE = [DICTIONARY\_NAME.CODE] ON ('CODE\_ANALYSIS')</math></b>
Explanation	Selects the tests where one of the results matches the specified value for the specified test code.
Example	Count the number of times that RESISTANT was chosen as a result on the Meningococcal Antibigram analysis with the DISK method for Penicillin, the syntax is: $\$\_571 = [resist\_sensible.R] ON('B650')$

Follow the same procedure as in Example 1 to find the corresponding values:

- 571 is the identifier of the variable in LabBook.

The screenshot shows the LabBook interface. The top navigation bar includes 'Administrative', 'Reports', 'Settings', 'Quality', and 'Non-conformity'. The main content area is titled 'Analysis' and contains several input fields: 'Code' (B650), 'Designation of the act' (Meningococcal antibiogram [DISK]), 'Abbreviation' (ABG Méningocoques), 'Analysis family' (Bacteriology), 'Type of specimen', 'Rating unit' (B), 'Quotation value' (0), 'Active analysis' (Yes/No), and 'Whonet export' (Yes/No). A 'Comments' field contains '[WHONET]'. Below this is the 'Variables' section, which includes a search bar, a dropdown for 'Label' (Penicillin), a dropdown for 'Result type' (Resistant/Sensitive), and input fields for 'Var. code' (571) and 'Id' (571). The 'Id' field is highlighted with a red border. At the bottom, there are fields for 'Normal value min.', 'Normal value max.', and 'Underline' (Yes/No).

Figure 16 Id of the variable Penicillin

- resist\_sensible is the name of the dictionary.
- R is the code for the value "Resistant".

The screenshot shows the 'Dictionary' section of the Lab Book interface. The 'Dictionary name' is 'resist\_sensible'. Below it, there is a table of values with columns: Action, Label, Code, Short label, Position, and Formatting. The 'Code' column has a red box around the value 'R' in the first row.

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

Figure 17 : resist\_sensible dictionary

650 corresponds to the code of the "Meningococcal antibiogram" analysis with the DISK method.

The screenshot shows the 'Analysis repository' section. A search filter for 'Designation of the act' is set to 'Meningococcal antibiogram'. The search results table has columns: Action, Code, Designation, Abbreviation, Family, Status, and Bio. product. The first row has a red box around the 'Code' 'B650' and the 'Designation' 'Meningococcal antibiogram [DISK]'.

Action	Code	Designation	Abbreviation	Family	Status	Bio. product
+	B650	Meningococcal antibiogram [DISK]	ABG Méningocoques	Bacteriology	Activated	
+	B670	Meningococcal Antibiogram [CMI]	ABG Méningocoques	Bacteriology	Activated	

Figure 18 :B650 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). If you don't want to filter on the sample type 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 rows in a spreadsheet :

A	B	C	D	E	F	G	H	I
dhis2_label	period	version	filter	type_sample	categorieoptioncombo	attributeoptioncombo	orgunit	storedby
Autres especes	W	v2	\$ 614 = [especepalu.autres]	138	cat12345	attrb12345	testOrgunit	testUser
Autre shigelles			\$ 344 IN ([bacterie.26], [bacterie.27], [bacterie.28])	141	cat12346	attrb12346	testOrgunit	testUser
Bacilles a Gram (-) polymorphes			\$ 333 = [gram.2]	99	cat12347	attrb12347	testOrgunit	testUser
Bacilles mobiles polaires incurves a Gram (-)			\$ 636 = [yorn.1] AND \$ 637 = [yorn.1]	141	cat12348	attrb12348	testOrgunit	testUser
Candida albicans (Prelevement Vaginal)			\$ 361 = [bacterie.33]	162	cat12349	attrb12349	testOrgunit	testUser
Candida albicans (Prelevement Uretral)			\$ 344 = [bacterie.33]	152	cat12350	attrb12350	testOrgunit	testUser
Chlamydia trachomatis direct (Prelevement Vaginal)			\$ 212 = [absent.present]	162	cat12351	attrb12351	testOrgunit	testUser
Chlamydia trachomatis direct (Prelevement Uretral)			\$ 236 = [absent.present]	152	cat12352	attrb12352	testOrgunit	testUser

Figure 19 Spreadsheet read with Excel

```

dhis2_label;period;version;filter;type_sample;categorieoptioncombo;attributeoptioncombo;orgunit;storedby
Autres especes;W;v2;$ 614 = [especepalu.autres];138;cat12345;attrb12345;testOrgunit;testUser
Autre shigelles;;; $ 344 IN ([bacterie.26], [bacterie.27], [bacterie.28]);141;cat12346;attrb12346;testOrgunit;testUser
Bacilles a Gram (-) polymorphes;;; $ 333 = [gram.2];99;cat12347;attrb12347;testOrgunit;testUser
Bacilles mobiles polaires incurves a Gram (-);;; $ 636 = [yorn.1] AND $ 637 = [yorn.1];141;cat12348;attrb12348;testOrgunit;testUser
Candida albicans (Prelevement Vaginal);;; $ 361 = [bacterie.33];162;cat12349;attrb12349;testOrgunit;testUser
Candida albicans (Prelevement Uretral);;; $ 344 = [bacterie.33];152;cat12350;attrb12350;testOrgunit;testUser
Chlamydia trachomatis direct (Prelevement Vaginal);;; $ 212 = [absent.present];162;cat12351;attrb12351;testOrgunit;testUser
Chlamydia trachomatis direct (Prelevement Uretral);;; $ 236 = [absent.present];152;cat12352;attrb12352;testOrgunit;testUser
D - S. mansoni;;; $ 641 = [shisto2.S.mansoni];141;cat12353;attrb12353;testOrgunit;testUser

```

Figure 20 Spreadsheet read with Notepad

## d) DHIS2 data file 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:

- **dataelement** : name of the data element
- **period**: Weekly (e.g. 2021W25) or Monthly (e.g. 202106)

- **orgunit** : name of the organization unit
- **categoryoptioncombo** : Property obtained from DHIS2
- **attributeoptioncombos** : Property obtained from DHIS2
- **value** : value of the data element
- **storedby**: username
- **lastupdated**: date of last modification
- **how** : 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.
- The values in the "storedby" column correspond to a DHIS2 user name authorized to access the data elements in column A.

A	B	C	D	E	F	G	H	I	J	K
dataelement	period	orgunit	categoryoptioncombo	attributeoptioncombo	value	storedby	lastupdated	comment	followup	deleted
Autres especes	2022W14	testOrgunit	cat12345	attrb12345	0	testUser	2022-04-07T12:51:56		FALSE	
Autre shigelles	2022W14	testOrgunit	cat12346	attrb12346	0	testUser	2022-04-07T12:51:56		FALSE	
Bacilles a Gram (-) polymorphes	2022W14	testOrgunit	cat12347	attrb12347	1	testUser	2022-04-07T12:51:56		FALSE	
Bacilles mobiles polaires incurves a Gram (-)	2022W14	testOrgunit	cat12348	attrb12348	0	testUser	2022-04-07T12:51:56		FALSE	
Candida albicans (Prelevement Vaginal)	2022W14	testOrgunit	cat12349	attrb12349	0	testUser	2022-04-07T12:51:56		FALSE	
Candida albicans (Prelevement Uretral)	2022W14	testOrgunit	cat12350	attrb12350	0	testUser	2022-04-07T12:51:56		FALSE	
Chlamydia trachomatis direct (Prelevement Vagine)	2022W14	testOrgunit	cat12351	attrb12351	0	testUser	2022-04-07T12:51:56		FALSE	
Chlamydia trachomatis direct (Prelevement Uretra)	2022W14	testOrgunit	cat12352	attrb12352	0	testUser	2022-04-07T12:51:56		FALSE	
D - S. mansoni	2022W14	testOrgunit	cat12353	attrb12353	0	testUser	2022-04-07T12:51:56		FALSE	

Figure 21 Excerpt from DHIS2 LabBook data file

## Appendix

Example of syntaxes recognized by the "filter" column

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

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