

➤ Phenotyping data management tools

Michael Alaux, Cyril Pommier & Vanita Haurheeram



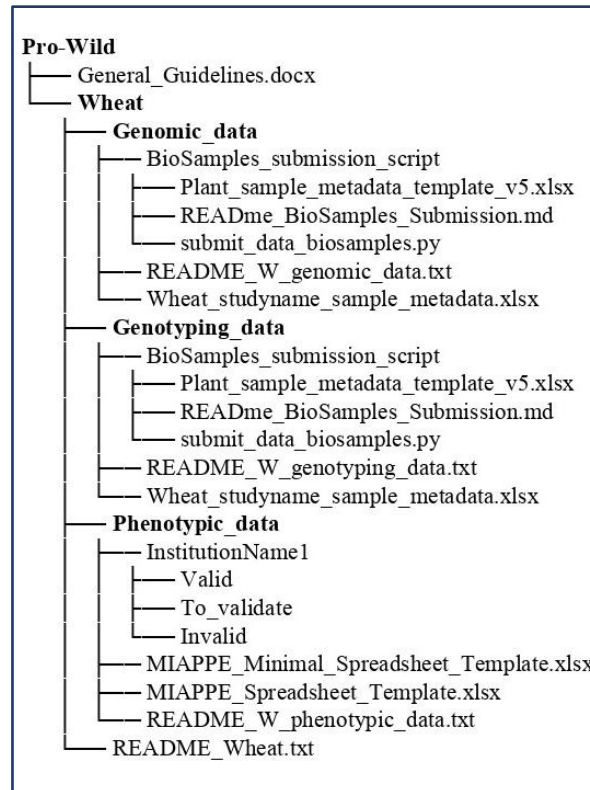
➤ Data management space

How it works

Creation of an online storage space using the collaborative platform Nextcloud to :

- Share and manage data files still under curation
- Collect and validate metadata before submission to international archives

Available during the project period and for project members' internal use only.



➤ Data management space

Navigation

Root folder

Species folders

Guidelines document describing how data collected and produced by the Pro-Wild project is organized

Type	Modified	People	Name	Size	Modified
Folder			Oilseed_rape	341 KB	yesterday
Folder			Sugar_beet	341 KB	yesterday
Folder			Wheat	341 KB	yesterday
File			General_Guidelines.docx	50 KB	September 9

1 file · 3 folders 1 MB



➤ Data management space

Navigation

Root folder

Species folders

Guidelines document describing how data collected and produced by the Pro-Wild project is organized

Type	Modified	People	Name	Size	Modified
Folder		Shared VH	Oilseed_rape	341 KB	yesterday
Folder		Shared VH	Sugar_beet	341 KB	yesterday
Folder		Shared VH	Wheat	341 KB	yesterday
File		Shared VH	General_Guidelines.docx	50 KB	September 9

1 file · 3 folders 1 MB



➤ Data management space

Navigation

Root folder

Species folders

Guidelines document describing how data collected and produced by the Pro-Wild project is organized

Type	Modified	People	Name	Size	Modified
Folder		Shared VH	Oilseed_rape	341 KB	yesterday
Folder		Shared VH	Sugar_beet	341 KB	yesterday
Folder		Shared VH	Wheat	341 KB	yesterday
File		Shared VH	General_Guidelines.docx	50 KB	September 9

1 file · 3 folders 1 MB



➤ Data management space

Navigation

Root folder

Species folders

Guidelines document describing how data collected and produced by the Pro-Wild project is organized

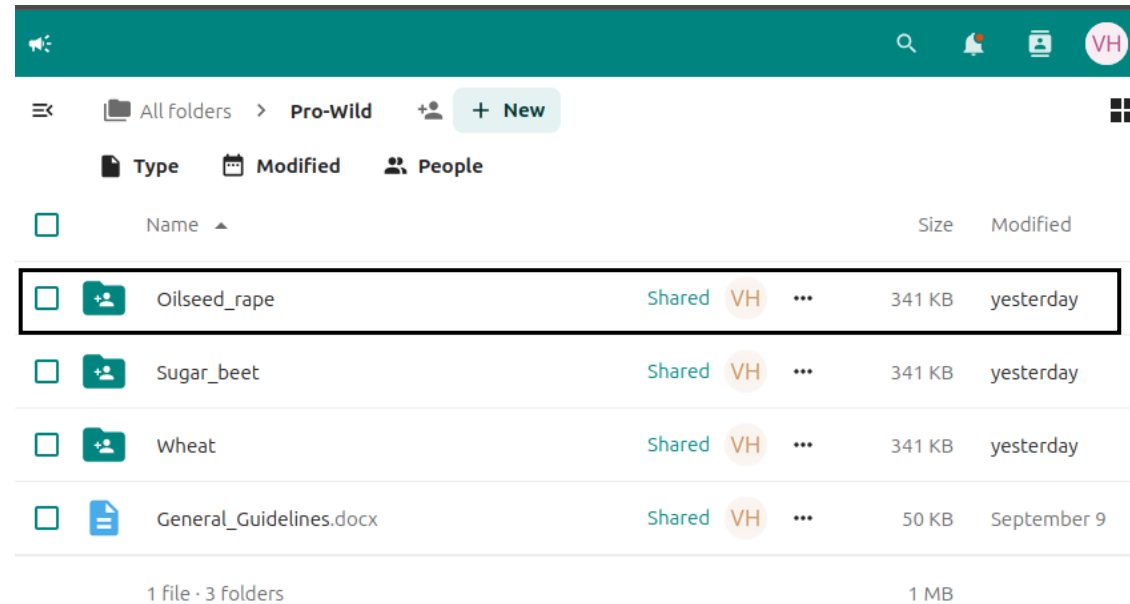
Name	Size	Modified
Oilseed_rape	341 KB	yesterday
Sugar_beet	341 KB	yesterday
Wheat	341 KB	yesterday
General_Guidelines.docx	50 KB	September 9

1 file · 3 folders 1 MB



➤ Data management space

Navigation



➤ Data management space

Navigation

The screenshot shows a OneDrive file explorer interface. The breadcrumb path is 'All folders > Pro-Wild > Oilseed_rape'. The file list is as follows:

Type	Modified	People	Name	Size	Modified
Folder		Shared VH	Genomic_data	89 KB	yesterday
Folder		Shared VH	Genotyping_data	89 KB	yesterday
Folder		Shared VH	Phenotypic_data	161 KB	yesterday
File		Shared VH	README_Oilseed_rape.txt	3 KB	September 9

Annotations on the image:

- A box labeled "Data types folders" with a bracket pointing to the three subfolders: Genomic_data, Genotyping_data, and Phenotypic_data.
- A box labeled "README file describing folder architecture" with an arrow pointing to the README_Oilseed_rape.txt file.

Summary: 1 file · 3 folders, 341 KB

➤ Data management space

Navigation

The screenshot shows a OneDrive interface for a folder named 'Oilseed_rape' under 'Pro-Wild'. The folder contains three subfolders and one file:

Type	Modified	People	Name	Size	Modified
Folder		Shared VH	Genomic_data	89 KB	yesterday
Folder		Shared VH	Genotyping_data	89 KB	yesterday
Folder		Shared VH	Phenotypic_data	161 KB	yesterday
File		Shared VH	README_Oilseed_rape.txt	3 KB	September 9

Annotations on the image:

- A box labeled "Data types folders" with a bracket pointing to the three subfolders: Genomic_data, Genotyping_data, and Phenotypic_data.
- A box labeled "README file describing folder architecture" with an arrow pointing to the README_Oilseed_rape.txt file.

➤ Data management space

Navigation

The screenshot shows a OneDrive file explorer interface. The breadcrumb path is 'All folders > Pro-Wild > Oilseed_rape'. There is a '+ New' button and a user profile icon 'VH'. The file list is as follows:

<input type="checkbox"/>	Type	Name	Shared	Modified	Size	Modified
<input type="checkbox"/>	Folder	Genomic_data	Shared VH	...	89 KB	yesterday
<input type="checkbox"/>	Folder	Genotyping_data	Shared VH	...	89 KB	yesterday
<input type="checkbox"/>	Folder	Phenotypic_data	Shared VH	...	161 KB	yesterday
<input type="checkbox"/>	File	README_Oilseed_rape.txt	Shared VH	...	3 KB	September 9

Summary: 1 file · 3 folders, 341 KB



➤ Data management space

Navigation

The screenshot shows a OneDrive folder view for 'Phenotypic_data'. The breadcrumb path is 'All folders > Pro-Wild > Oilseed_rape > Phenotypic_data'. The folder contains the following items:

Type	Modified	People	Size	Modified
Folder				
Folder				
File				
File				

Callouts in the image:

- Partners folders**: Points to the 'INRAE' and 'UNIPA' folders.
- MIAPPE template**: Points to the 'MIAPPE_Minimal_Spreadsheet_Te... .xlsx' file.
- README file describing folder architecture**: Points to the 'README_OR_phenotypic_data.txt' file.

➤ Data management space

Navigation

The screenshot shows a OneDrive folder view for 'Phenotypic_data'. The breadcrumb path is 'All folders > Pro-Wild > Oilseed_rape > Phenotypic_data'. The folder contains three files and two sub-folders. Callouts point to the 'INRAE' and 'UNIPA' folders, the 'MIAPPE_Minimal_Spreadsheet_Te... .xlsx' file, and the 'README_OR_phenotypic_data.txt' file.

Type	Modified	People	Name	Size	Modified
Folder		Shared VH	INRAE	0 KB	yesterday
Folder		Shared VH	UNIPA	0 KB	yesterday
File		Shared VH	MIAPPE_Minimal_Spreadsheet_Te... .xlsx	68 KB	September 9
File		Shared VH	README_OR_phenotypic_data.txt	< 1 KB	yesterday

3 files · 2 folders 161 KB

➤ Data management space

Navigation

The screenshot shows a OneDrive interface for a folder named 'Phenotypic_data'. The breadcrumb path is 'All folders > Pro-Wild > Oilseed_rape > Phenotypic_data'. The folder contains three items: two sub-folders, 'INRAE' and 'UNIPA', and two files, 'MIAPPE_Minimal_Spreadsheet_Te... .xlsx' and 'README_OR_phenotypic_data.txt'. A summary bar at the bottom indicates '3 files · 2 folders' and a total size of '161 KB'. Three callout boxes with arrows point to specific elements: 'Partners folders' points to the 'INRAE' and 'UNIPA' folders; 'MIAPPE template' points to the 'MIAPPE_Minimal_Spreadsheet_Te... .xlsx' file; and 'README file describing folder architecture' points to the 'README_OR_phenotypic_data.txt' file.

Type	Modified	People	Name	Size	Modified
Folder			INRAE	0 KB	yesterday
Folder			UNIPA	0 KB	yesterday
File			MIAPPE_Minimal_Spreadsheet_Te... .xlsx	68 KB	September 9
File			README_OR_phenotypic_data.txt	< 1 KB	yesterday

➤ Data management space

First time access (3 steps procedure)

1. Create an account which is required to access this storage space

- This account service is a virtual identity provider. It is supported by RENATER (French research network) which can be used to access certain services as Nextcloud.
- To create an account, you must fill out an account creation request form : <https://cru.renater.fr/sac/>. The required fields are :
 - last name,
 - first name,
 - and email address.

COMPTES CRU

CREATE ACCOUNT ACTIVATE YOUR ACCOUNT USE PASSWORD? FORGOT CRU ACCOUNT?

Account creation

Fill this form to create your profile. The * tag means mandatory input. Test or disposable or temporary email addresses are forbidden. If you wish to do tests, please set up your own identity provider or use the testing tools registered in the test Federation.

EMAIL ADDRESS *

LAST NAME *

FIRST NAME *

CHOOSE THE ACCOUNT LANGUAGE

English

Submit Cancel

Click here to see the English version of this page

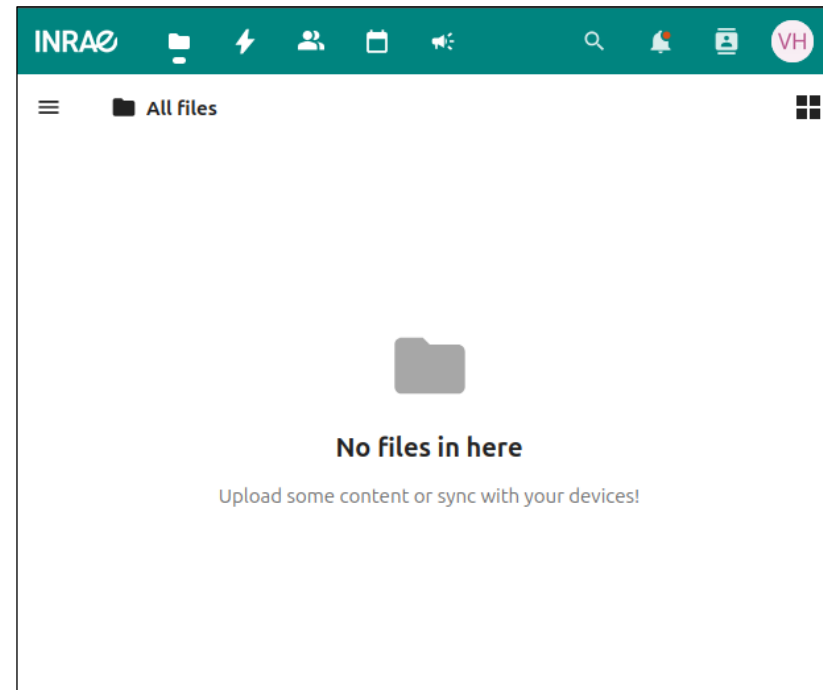


➤ Data management space

First time access (3 steps procedure)

2. Initialize your Nextcloud account

- Log in to Nextcloud <https://nextcloud.inrae.fr> and search for “Comptes CRU” from the drop-down menu.

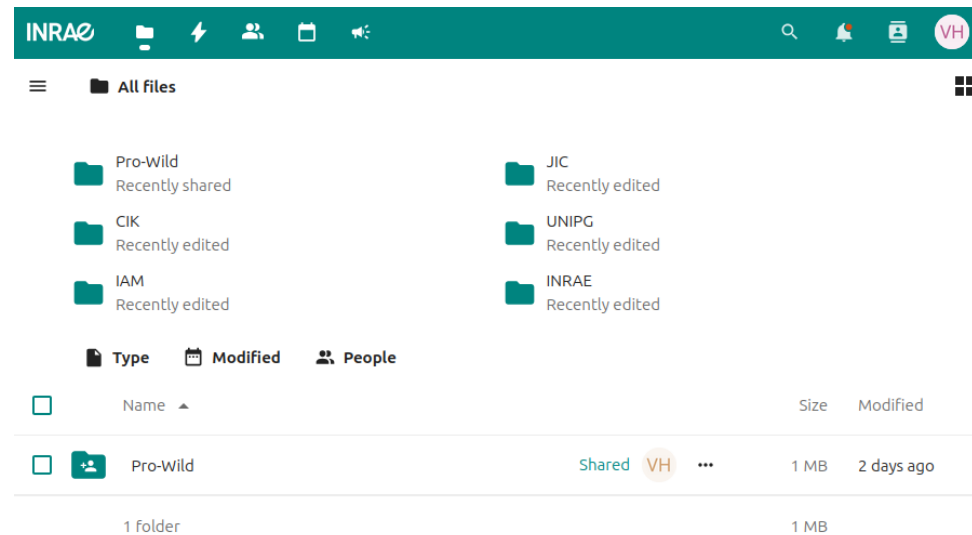


➤ Data management space

First time access (3 steps procedure)

3. Contact pro-wild-data@inrae.fr

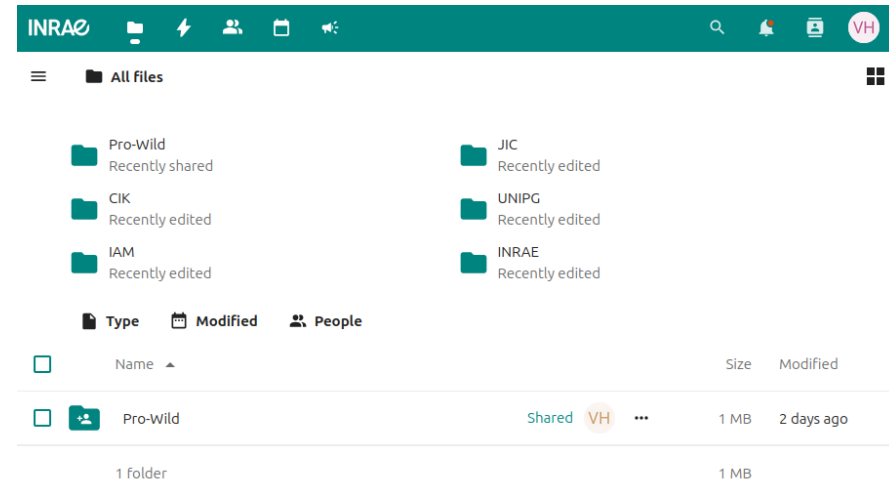
- Send an email to pro-wild-data@inrae.fr with the email address you used to create your CRU account to be added to the access group.
- You will receive an email when your account is added and the Pro-Wild folder will appear on your Nextcloud interface.



➤ Data management space

Daily access

- Log in to Nextcloud <https://nextcloud.inrae.fr> and search for “Comptes CRU” from the drop-down menu with the CRU account credentials you have created.



➤ Data management space

Nextcloud

There are two methods for uploading data.

- For small data use the web client and for large data use the desktop client.
- For phenotyping data, the web client is usable, but for genome/genotyping data (e.g., 1GB), use the desktop client.



➤ MIAPPE validator

General principles

- The purpose of the MIAPPE validator is to verify that MIAPPE Excel files are filled out appropriately according to the MIAPPE schema.
- In case of validation errors it produces a biologist-friendly detailed report.
- Available on Nextcloud to automatically validate files uploaded in the data management space.
- You can also use the MIAPPE validator here : <https://urgi.versailles.inrae.fr/excel-validator/mimiappe>



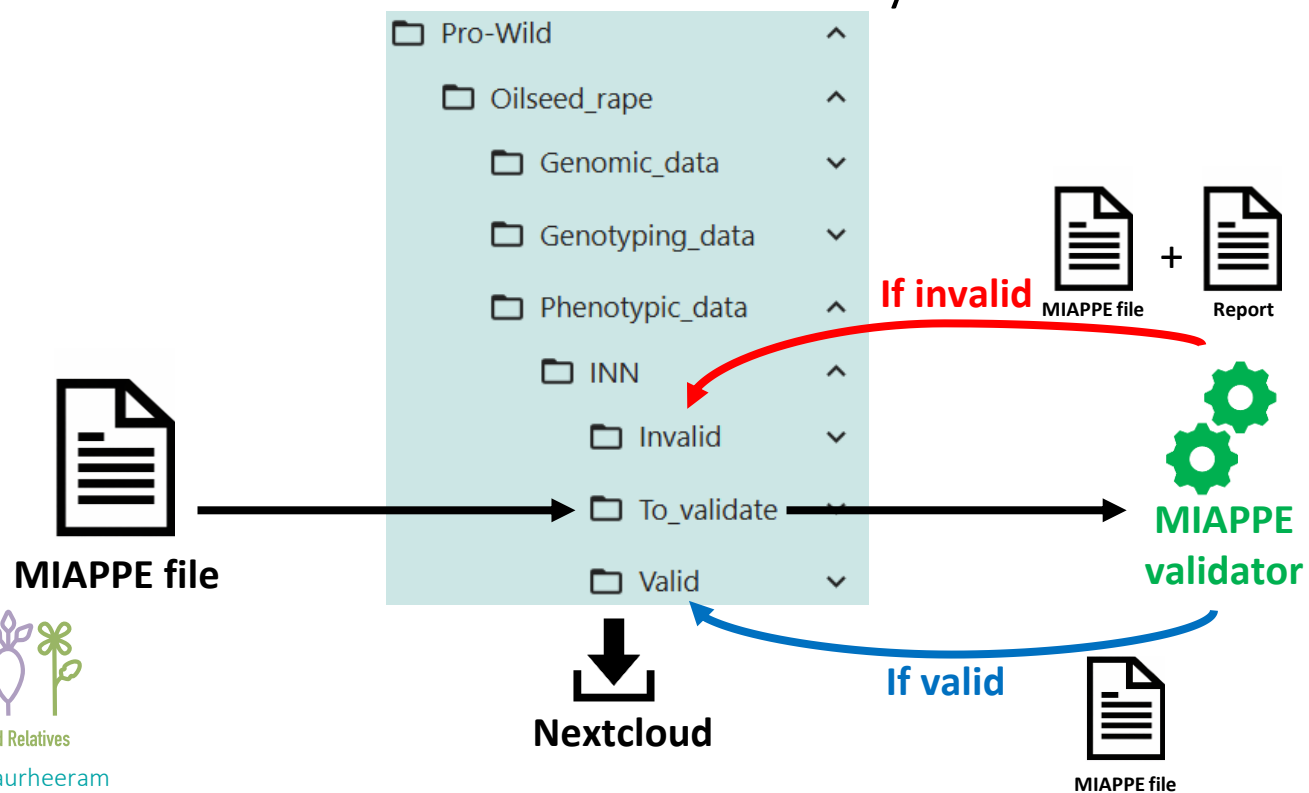
[matthijsbrouwer/excel-validator](https://github.com/matthijsbrouwer/excel-validator)



➤ MIAPPE validator

Where to upload

- To validate a MIAPPE file you need to download it from the Phenotypic_data folder, fill it and upload it in the **To_validate** folder. Each partners folder contains one To_validate folder.
- Once it has been validated, the file will be moved either to the valid folder if it is correct or to the invalid folder if it contains errors and in this case you will also find containing the explaining alid.



➤ MIAPPE validator

Report file error examples

The MIAPPE validator does not validate the data but only the format. If a mandatory field is not filled, or if anything has been changed from the template.

Example 1:

Problem with sheet 'Investigation' ←

Sheet containing the error

- 1x 'Constraint Error' ←

Type of error

A field value does not conform to a constraint.

- B2 (investigationTitle 'None'): constraint "required" is "True"

Field containing the error

=> The validator has checked the values in the Investigation sheet and found that the investigationTitle field is mandatory but has been left empty in the file.



> MIAPPE validator

Report file error examples

The MIAPPE validator does not validate the data but only the format. If a mandatory field is not filled, or if anything has been changed from the template.

Example 2:

Problem with sheet 'Study'

Sheet containing the error

- 1x 'Type Error'

Type of error

The value does not match the schema type and format for this field.

- D2 (studyStartDate '2025'): type is "date/default"

Field containing the error

=> The validator has checked the values in the Study sheet and found that the the studyStartDate field must be filled with a date but has only been filled with a year.



➤ MIAPPE validator

Report file error examples

The MIAPPE validator does not validate the data but only the format. If a mandatory field is not filled, or if anything has been changed from the template.

Example 3 :

Problem with sheet 'Person'

Sheet containing the error

- 1x 'ForeignKey Error'

Type of error

Values in the foreign key fields should exist in the reference table

- for "studyId": values "Study2" not found in the lookup table "study" as "studyId"

Field containing the error

	A	B	C	D	E	F
1	studyId	personName	personEmail	personId	personRole	personAffiliation
2	Study1	Vanita			Data manager	INRAE
3						

Investigation Study Person Data file Biological Material Observation Unit Observ ...

	A	B	C	D	E	F
1	studyId	studyTitle	studyDescription	studyStartDate	studyEndDate	contactInst
2	Study2	Study2		01/02/2024	01/06/2025	INRAE
3						

10 March README Investigation Study Person Data file Biological Material Observation Uni ...

> MIAPPE validator

Report file error examples

The MIAPPE validator does not validate the data but only the format. If a mandatory field is not filled, or if anything has been changed from the template.

Example 3 :

Problem with sheet 'Person'

Sheet containing the error

- 1x 'ForeignKey Error'

Type of error

Values in the foreign key fields should exist in the reference table

- for "studyId": values "Study2" not found in the lookup table "study" as "studyId"

Field containing the error

=> The validator has checked that the studyId value in the Person sheet matches an existing studyId in the Study sheet.



> MIAPPE validator

Report file error examples

The MIAPPE validator does not validate the data but only the format. If a mandatory field is not filled, or if anything has been changed from the template.

Example 4 :

Problem with sheet 'Study'

Sheet containing the error

- Missing Columns: 'studyTitle'

- Unrecognized Columns: 'studytitle'

Type of error

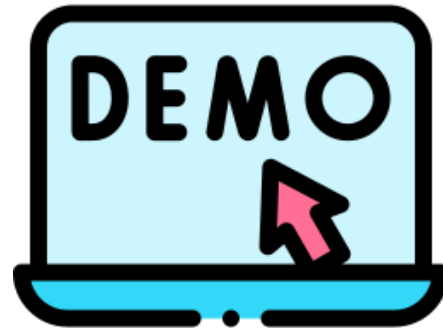
=> The validator has checked the field names in the Study sheet and found that the studyTitle field name has been changed in the file.

Errors such as 'Unrecognized column' should be ignored if you have added the field yourself and have not modified existing fields.



➤ MIAPPE validator

Step by step test



➤ Acknowledgements

MIAPPE validator : Matthijs Brouwer with the help of Erwan Le Floch, Cyril Pommier, Paul Kersey, Michael Alaux, Matthias Lange, Stephan Weise, and the AGENT Bioinformatic team

URGI team





All files >

Pro-Wild >



INRAE >

To_validate

+ New



Drag and drop files



Upload

Type

Modified

+ Copier





No files in here



☰ All files > Pro-Wild > ... > INRAE > To_validate

Files uploaded successfully ✕

 **Type**  **Modified**  **People**

Name ▲

 MIAPPE_file_upload_test.xlsx ...

1 file



=== INVALID 'MIAPPE_file_upload_test.xlsx' (version 0.9.4) ===

Problem with sheet 'Investigation'

- 1x 'Type Error'

The value does not match the schema type and format for this field.

- H2 (associatedPublication '10.15454/1.4489666216568333E12'): type is "string/uri"

Problem with sheet 'Person'

- 1x 'Type Error'

The value does not match the schema type and format for this field.

- C3 (personEmail '0000-0003-1858-1897'): type is "string/email"

Problem with sheet 'Biological Material'

- 1x 'Unique Error'

This field is a unique field but it contains a value that has been used in another row.

- B3 (biologicalMaterialId 'Barok'): the same as in the row at position 2

- 1x 'PrimaryKey Error'

Values in the primary key fields should be unique for every row

- row 3: the same as in the row at position 2

Problem with sheet 'Observed Variable'

- 1x 'Constraint Error'

A field value does not conform to a constraint.

- O3 (scaleName 'None'): constraint "required" is "True"

	A	B	C	D	E	F	G	H	I
1	investigationId	investigationTitle	investigationDescription	submissionDate	publicReleaseDate	license	miappeVersion	associatedPublication	
2	https://doi.org/10.15454	INRA Small Grain Cereals	Winter wheat phenotypic	2015-12-01 0:00:00	2015-12-01 0:00:00	CC BY-SA 4.0	1.2	10.15454/1.4489666216568333E12	
3									

	A	B	C	I
4	Investigation			
5	Investigations are research programmes with defined aims. They can exist at various scales (for example, they could encompass a grant-funded programme of work, the various components comprising a peer-reviewed publication, or a single experiment). This section is mandatory.			
6	Field	Investigation unique ID	Investigation title	Associated publication
7	Abbreviation	investigationId	investigationTitle	associatedPublication
8	Definition	Identifier comprising the unique name of the institution/database hosting the submission of the investigation data, and the accession number of the investigation in that institution.	Human-readable string summarising the investigation.	An identifier for a literature publication where the investigation is described. Use of DOIs is recommended.
9	Example	EBI:12345678	Adaptation of Maize to Temperate Climates: Mid-Density Genome-Wide Association Genetics and Diversity Patterns Reveal Key Genomic Regions, with a Major Contribution of the Vgt2 (ZCN8) Locus.	doi:10.1371/journal.pone.0071377
10	Format	Unique identifier	Free text (short)	DOI

=== INVALID 'MIAPPE_file_upload_test.xlsx' (version 0.9.4) ===

Problem with sheet 'Investigation'

- 1x 'Type Error'

The value does not match the schema type and format for this field.

- H2 (associatedPublication '10.15454/1.4489666216568333E12'): type is "string/uri"

Problem with sheet 'Person'

- 1x 'Type Error'

The value does not match the schema type and format for this field.

- C3 (personEmail '0000-0003-1858-1897'): type is "string/email"

Problem with sheet 'Biological Material'

- 1x 'Unique Error'

This field is a unique field but it contains a value that has been used in another row.

- B3 (biologicalMaterialId 'Barok'): the same as in the row at position 2

- 1x 'PrimaryKey Error'

Values in the primary key fields should be unique for every row

- row 3: the same as in the row at position 2

Problem with sheet 'Observed Variable'

- 1x 'Constraint Error'

A field value does not conform to a constraint.

- O3 (scaleName 'None'): constraint "required" is "True"

	A	B	C	D	E	F
1	studyId	personName	personEmail	personId	personRole	personAffiliation
2	BTH_Champagne-céréale	Francois-Xavier OURY	Francois-Xavier.OURY@inrae.fr		Coordinator of experime	INRAE
3	BTH_Champagne-céréale	Arnaud GAUFFRETEAU	0000-0003-1858-1897		Scientific	INRAE
4	BTH_Champagne-céréale	Gilles CHARMET	charmet@inrae.fr		Coordinator of experime	INRAE
5	BTH_Champagne-céréale	Emmanuel HEUMEZ	emmanuel.heumez@inrae.fr		Coordinator of experime	INRAE
6	BTH_Champagne-céréale	Bernard ROLLAND	bernard.rolland@inrae.fr		Coordinator of experime	INRAE
7						

Navigation: **README** Investigation Study **Person** Data file Biological Material Observation Unit Observed Variable ... (+)

	A	B	C	D
18	Person			
19	A human involved in the investigation or specifically any of its studies. This section is mandatory.			
20	Field	Study unique ID	Person name	Person email
21	Abbreviation	studyId	personName	personEmail
22	Definition	Semicolon-separated list of (internal) study identifiers (cross-referencing to study worksheet) in which the person was involved	The name of the person (either full name or as used in scientific publications)	The electronic mail address of the person.
23	Example	study_1; study_2	Ines Chaves	ichaves@itqb.unl.pt
24	Format	List	Name	email address

Navigation: **README** Investigation Study **Person** Data file Biological Material Observation Unit Observed Variable ... (+)



=== INVALID 'MIAPPE_file_upload_test.xlsx' (version 0.9.4) ===

Problem with sheet 'Investigation'

- 1x 'Type Error'

The value does not match the schema type and format for this field.

- H2 (associatedPublication '10.15454/1.4489666216568333E12'): type is "string/uri"

Problem with sheet 'Person'

- 1x 'Type Error'

The value does not match the schema type and format for this field.

- C3 (personEmail '0000-0003-1858-1897'): type is "string/email"

Problem with sheet 'Biological Material'

- 1x 'Unique Error'

This field is a unique field but it contains a value that has been used in another row.

- B3 (biologicalMaterialId 'Barok'): the same as in the row at position 2

- 1x 'PrimaryKey Error'

Values in the primary key fields should be unique for every row

- row 3: the same as in the row at position 2

Problem with sheet 'Observed Variable'

- 1x 'Constraint Error'

A field value does not conform to a constraint.

- O3 (scaleName 'None'): constraint "required" is "True"

	A	B	C	D	E	F	G	M	N
1	studyId	biologicalMaterialId	biologicalMaterialExtId	organism	genus	species	infraspecificName	materialSourceId	materialSourceDoi
2	BTH_Clermont-Ferrand_2005_SetA2; BTH_Colmar_20 Barok				Triticum	aestivum	subsp. aestivum	FRA040:32101	doi:10.15454/Z3MNYF
3	BTH_Clermont-Ferrand_2005_SetA2; BTH_Colmar_20 Barok				Triticum	aestivum	subsp. aestivum	FRA040:32101	doi:10.15454/Z3MNYF
4	BTH_Champagne-céréales_2005_SetA1; BTH_Clermo Tremie				Triticum	aestivum	subsp. aestivum	FRA040:7043	doi:10.15454/9YBOHR
5	BTH_Clermont-Ferrand_2005_SetA2; BTH_Colmar_20 DI9714				Triticum	aestivum	subsp. aestivum	FRA040:20369	doi:10.15454/FRBOLL

	A	B	C	D
32	Biological Material			
	The biological material being studied (e.g. plants grown from a certain bag or seed, or plants grown in a particular field). The original source of that material (e.g., the seeds or the original plant cloned) is called the material source, which, when held by a material repository, should have its stock identified. This section is mandatory.			
34	Field	Study unique ID	Biological material ID	Biological material external ID
35	Abbreviation	studyId	biologicalMaterialId	biologicalMaterialExtId
36	Definition	Semicolon-separated list of (internal) study identifiers (cross-referencing to study worksheet) where the event was recorded.	Code used to identify the biological material in the data file. Should be unique within the Investigation. Can correspond to experimental plant ID, seed lot ID, etc... This material identification is different from a BiosampleID which corresponds to Observation Unit or Samples sections below.	One to many identifiers for the biological material. Can include EBI Biosamples ID. URI are recommended when possible.
37	Example	study_1; study_2	INRA-W95115_inra_2001 ; INRA:inra_kernel_2351 ; Rothamsted:rres_GK090847	AGENT_project:AGENT_ID; Kernel_ID; experimentalPlatformID; GERMP_LAS_M_DB_ID; Biosamples: SAMEA001234
38	Format	List	Unique identifier	Semicolon-separated list of unique identifiers, possibly prefixed by repository name



=== INVALID 'MIAPPE_file_upload_test.xlsx' (version 0.9.4) ===

Problem with sheet 'Investigation'

- 1x 'Type Error'

The value does not match the schema type and format for this field.

- H2 (associatedPublication '10.15454/1.4489666216568333E12'): type is "string/uri"

Problem with sheet 'Person'

- 1x 'Type Error'

The value does not match the schema type and format for this field.

- C3 (personEmail '0000-0003-1858-1897'): type is "string/email"

Problem with sheet 'Biological Material'

- 1x 'Unique Error'

This field is a unique field but it contains a value that has been used in another row.

- B3 (biologicalMaterialId 'Barok'): the same as in the row at position 2

- 1x 'PrimaryKey Error'

Values in the primary key fields should be unique for every row

- row 3: the same as in the row at position 2

Problem with sheet 'Observed Variable'









- 1x 'Constraint Error'


A field value does not conform to a constraint.






- O3 (scaleName 'None'): constraint "required" is "True"

	A	B	C	D	E	F	J	K	L	M	N	O	P
1	studyId	variableId	variableName	variableAccNumber	traitName	traitEntity	traitAccNumber	methodName	methodAccNumber	methodDesc	methodRef	scaleName	scaleAccNumber
2		rdt	Grain yield at 0%	CO_321:1000074	Grain yield	Grain	CO_321:0000013	Direct measure	CO_321:1020013	method:		e q/ha	CO_321:1030011
3		r	Yield	CO_321:1000217	Grain yield		CO_321:0000013	Reference varie	CO_321:1020029	expressed as			UO:0000187
4		ht	Height	CO_321:1000218	Plant height		CO_321:0000020	undefined	CO_321:1021009	method		cm	UO:0000015

	A	B	E	K	O
46	Observed Variable				
	An observed variable describes how a measurement has been made. It typically takes the form of a measured characteristic of the observation unit (plant or environmental trait), associated to the method and unit of measurement. Multiple variables with the same combination of trait, method and scale can be used in association with different plant parts (leaf 1, leaf 2), when this distinction is necessary for observations referring to different parts of the same observation unit.				
47	<i>This section is mandatory.</i>				
48	Field	Variable ID	Trait	Method	Scale
49	Abbreviation	variableId	traitName	methodName	scaleName
50	Definition	Code used to identify the variable in the data file. We recommend using a variable definition from the Crop Ontology where possible. Otherwise, the Crop Ontology naming convention is recommended: <trait abbreviation> <method abbreviation> <scale	Name of the (plant or environmental) trait under observation	Name of the method of observation	Name of the scale associated with the variable
51	Example	Ant_Cmp_Cday	Anthesis time; Reproductive growth time	Growing degree days to anthesis	°C day
52	Format	Unique identifier	Free text	Free text	Unique identifier

INRAE         2

☰ All files > Pro-Wild > Oilseed_rape > ... > INRAE > Valid + New 

 Type	 Modified	 People
<input type="checkbox"/> Name ▲		
<input type="checkbox"/>  MIAPPE_file_upload_test.xlsx		...
<input type="checkbox"/>  MIAPPE_file_upload_test.xlsx.report.txt		...

2 files



```
=== VALID 'MIAPPE_file_upload_test.xlsx' (version 0.9.4) ===  
Warnings:  
- Sheet 'Investigation':  
  - Incorrect Type: changed type for 1 entries from column  
  'miappeVersion'  
  - Empty Rows: removed 6 empty rows  
- Sheet 'Person':  
  - Empty Rows: removed 2 empty rows  
- Sheet 'Data file':  
  - Empty Columns: removed 20 empty columns  
  - Empty Rows: removed 7 empty rows  
- Sheet 'Biological Material':  
  - Incorrect Type: changed type for 75 entries from column  
  'materialSourceAccNumber'  
- Sheet 'Observation Unit':  
  - Empty Rows: removed 7 empty rows
```