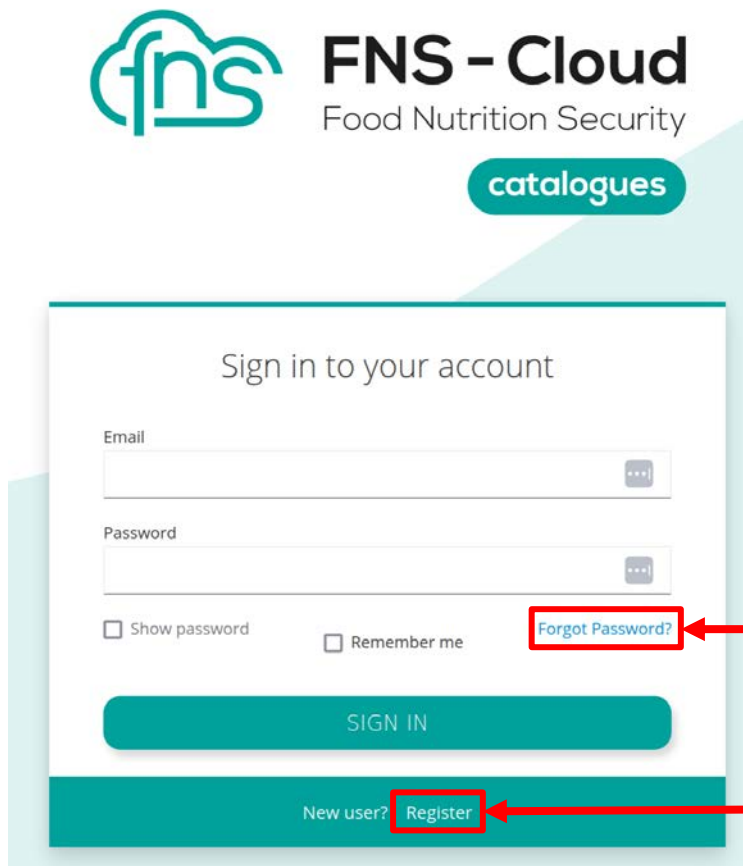



Fairspace demo session Brussels

This document contains a proposed workflow for the demo sessions.

FNS-Cloud access

Open the Fairspace demo page via <https://demo.fns-fairspace.app/> and log in with your credentials. In case you are not yet registered or forgot your password, click the “Forgot Password?” or “**Register**” links to proceed.



 **FNS - Cloud**
Food Nutrition Security

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Sign in to your account

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SIGN IN

New user? [Register](#)

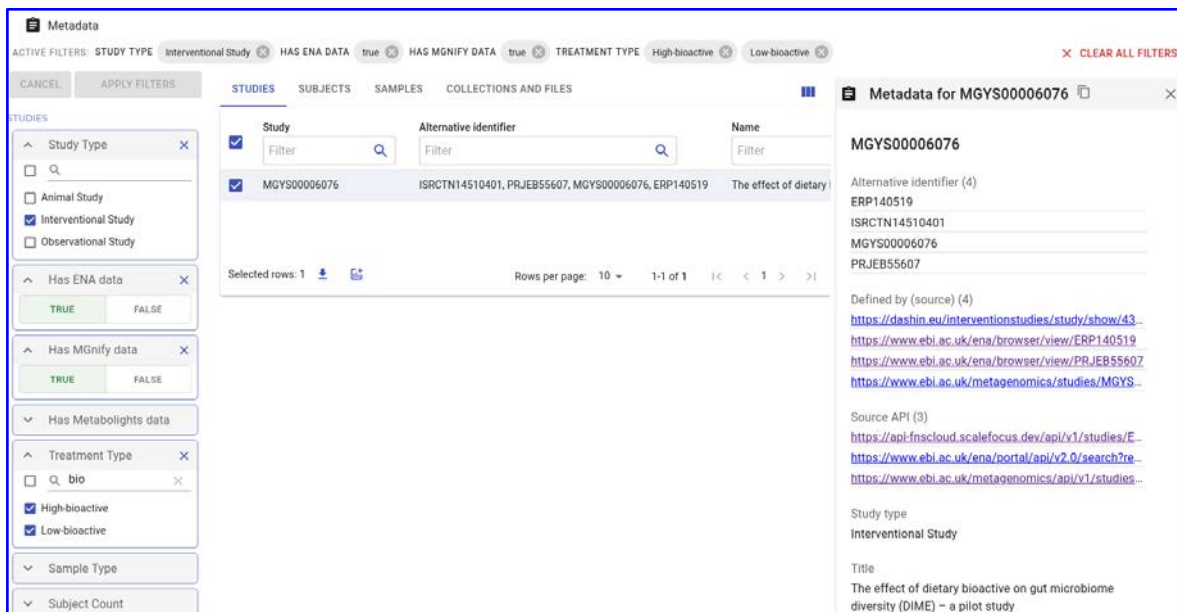


Demonstrator 1

Research question: Does a diet rich in plant bioactives affect our gut microbiome and how?

Steps:

- 1) Open Fairspace, log in with your credentials.
- 2) Go to the Metadata menu on the left side.
- 3) Enter text search for the name of the studies: “microbiome”
- 4) For the remaining studies, enter filters for
 - Study Type: “Interventional Study”
 - Set Has MGnify and Has ENA data filters to TRUE
 - Treatment Type: Start typing “bioactive” and select “High-bioactive” and “Low-bioactive”
- 5) In the STUDIES tab, click the title of the DIME study (MGYS00006076) to view the metadata.



The screenshot shows the 'Metadata' interface in FNS-Cloud. On the left, a sidebar contains filter panels for 'Study Type' (Interventional Study selected), 'Has ENA data' (TRUE), 'Has MGnify data' (TRUE), 'Treatment Type' (High-bioactive and Low-bioactive selected), 'Sample Type', and 'Subject Count'. The main area displays a table of studies with columns for 'Study', 'Alternative identifier', and 'Name'. The study 'MGYS00006076' is selected. On the right, a detailed view for 'MGYS00006076' is shown, including alternative identifiers (ERP140519, ISRCTN14510401, PRJEB55607), source information, and the title: 'The effect of dietary bioactive on gut microbiome diversity (DIME) - a pilot study'.

- 6) Navigate to the SUBJECTS tabs to show that subjects are all linked to this study and can therefore be found with the same filters.
- 7) Add a SUBJECTS Gender filter for “Female” and an Age filter of >30. Show that now a subset of the study subjects is shown. After this, remove the filters for Gender and Age.
- 8) Go back to the STUDIES tab and select the DIME study. Click the button to “Download as CSV”.

- 9) Open the `fairSPACE_export.csv` file that was downloaded in the previous step and explain the different columns. Also explain that the columns that are selected to show in FairSPACE are also the ones that are shown here.
- 10) Go back to FairSPACE and make sure that the DIME study is still selected. Then click the “Export to Jupyter Analysis” button.
- 11) In the left menu, click on Analysis (JupyterHub) to open a new window with Jupyter.
- 12) Go to the `fairSPACE-metadata-exports` folder to show that the metadata was imported.
- 13) Go to the `collections/[Demo03] Use Case 1` folder and explain the script(s).
- 14) Summarize the answer to the research question.
- 15) Mention additional scripts we have available, e.g. related to metabolomics and metagenomics from UM (`collections/[Demo03] Use Case 1/UM_analytical_workflows` folder)
- 16) Close the JupyterHub instance.

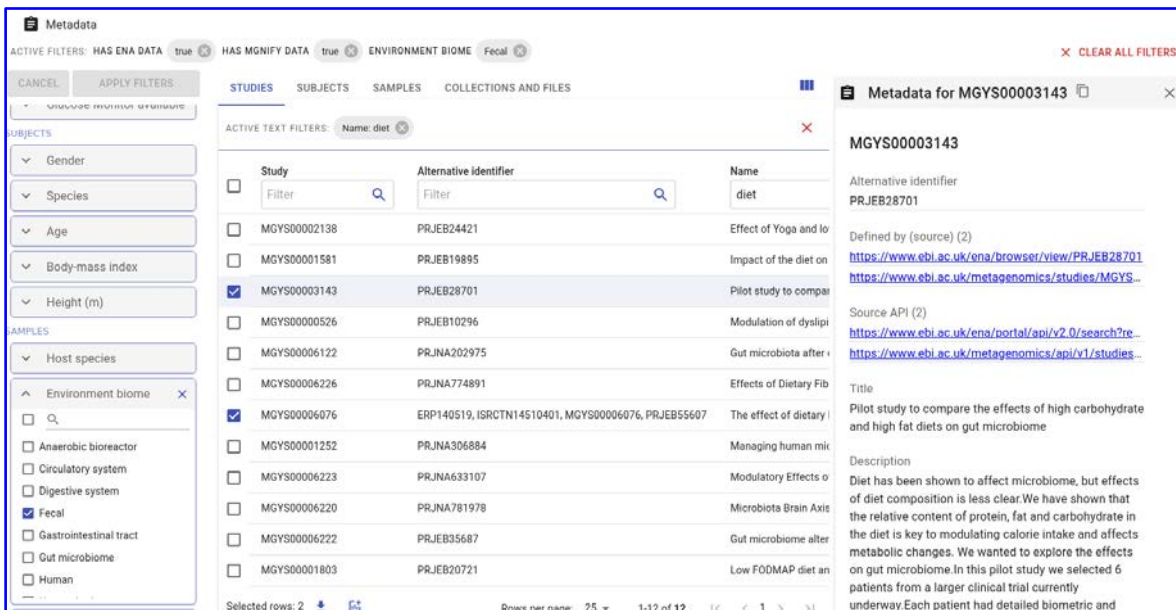


Demonstrator 2

Research question: Does our baseline gut microbiome define how species composition shifts upon dietary interventions? Does diet intervention lead to a similar reduction in strain persistence in independent cohorts?

Steps:

- 1) Go back to Fairspace and enter the Metadata menu.
- 2) Clear any existing filters.
- 3) Enter filters for
 - Set Has MGnify and Has ENA data filters to TRUE
 - Filter Samples > Environment biome for “Fecal”
 - Enter “diet” text filter for the study name
- 4) In the STUDIES tab, click on the title of the MGYS00003143 study to view the metadata.
- 5) Go back to Fairspace and select both MGYS00003143 (PRJEB28701) and MGYS00006076 (PRJEB55607; DIME). Click the “Export to Jupyter Analysis” button.

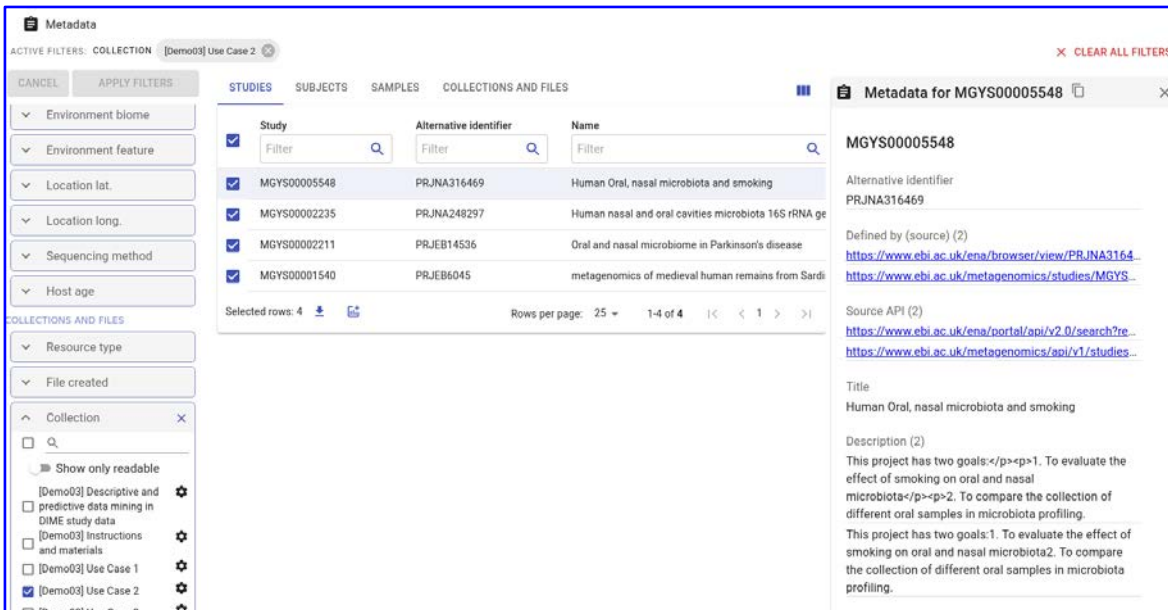


The screenshot shows the 'Metadata' view in the FNS-Cloud interface. The 'ACTIVE FILTERS' section includes 'HAS ENA DATA: true', 'HAS MGNIFY DATA: true', and 'ENVIRONMENT BIOME: Fecal'. The 'STUDIES' tab is active, displaying a table of studies with columns for 'Study', 'Alternative identifier', and 'Name'. A text filter 'Name: diet' is applied. The table lists several studies, with MGYS00003143 (PRJEB28701) and MGYS00006076 (ERP140519, ISRCTN14510401, MGYS00006076, PRJEB55607) selected. A detailed metadata view for MGYS00003143 is shown on the right, including its alternative identifier (PRJEB28701), source information, and a description of the pilot study comparing high carbohydrate and high fat diets.

Study	Alternative identifier	Name	
<input type="checkbox"/>	Filter	Filter	
<input type="checkbox"/>	MGYS00002138	PRJEB24421	Effect of Yoga and lo
<input type="checkbox"/>	MGYS00001581	PRJEB19895	Impact of the diet on
<input checked="" type="checkbox"/>	MGYS00003143	PRJEB28701	Pilot study to compar
<input type="checkbox"/>	MGYS00000526	PRJEB10296	Modulation of dyslipi
<input type="checkbox"/>	MGYS00006122	PRJNA202975	Gut microbiota after r
<input type="checkbox"/>	MGYS00006226	PRJNA774891	Effects of Dietary Fib
<input checked="" type="checkbox"/>	MGYS00006076	ERP140519, ISRCTN14510401, MGYS00006076, PRJEB55607	The effect of dietary i
<input type="checkbox"/>	MGYS00001252	PRJNA306884	Managing human mic
<input type="checkbox"/>	MGYS00006223	PRJNA633107	Modulatory Effects o
<input type="checkbox"/>	MGYS00006220	PRJNA781978	Microbiota Brain Axis
<input type="checkbox"/>	MGYS00006222	PRJEB35687	Gut microbiome alter
<input type="checkbox"/>	MGYS00001803	PRJEB20721	Low FODMAP diet an

- 6) In the left menu, click on Analysis (JupyterHub) to open a new window with Jupyter.
- 7) Go to the “collections/[Demo03] Use Case 2” folder and explain the dietary intervention (script(s)).
- 8) Summarize the results.
- 9) Go back to Fairspace and enter the Metadata menu.
- 10) Clear any existing filters.

- 11) At the bottom of the filter panel, select the COLLECTIONS AND FILES > Collection > “[Demo03] Use Case 2” filter and apply.



The screenshot shows the 'Metadata' interface with the following components:

- ACTIVE FILTERS:** COLLECTION [Demo03] Use Case 2
- Navigation:** CANCEL, APPLY FILTERS, STUDIES, SUBJECTS, SAMPLES, COLLECTIONS AND FILES
- Filter Panel (Left):** Environment biome, Environment feature, Location lat., Location long., Sequencing method, Host oge, COLLECTIONS AND FILES, Resource type, File created, Collection (expanded), Show only readable, [Demo03] Descriptive and predictive data mining in DIME study data, [Demo03] Instructions and materials, [Demo03] Use Case 1, [Demo03] Use Case 2 (checked), [Demo03] Use Case 3.
- Table:**

Study	Alternative identifier	Name
<input checked="" type="checkbox"/>	Filter	Filter
<input checked="" type="checkbox"/>	MGYS00005548	PR/JNA316469 Human Oral, nasal microbiota and smoking
<input checked="" type="checkbox"/>	MGYS00002235	PR/JNA248297 Human nasal and oral cavities microbiota 16S rRNA ge
<input checked="" type="checkbox"/>	MGYS00002211	PR/JEB14536 Oral and nasal microbiome in Parkinson's disease
<input checked="" type="checkbox"/>	MGYS00001540	PR/JEB6045 metagenomics of medieval human remains from Sardi
- Selected rows:** 4
- Rows per page:** 25
- Page:** 1-4 of 4
- Metadata for MGYS00005548 (Right Panel):**
 - Alternative identifier:** PR/JNA316469
 - Defined by (source) (2):**
 - https://www.ebi.ac.uk/ena/browser/view/PR_JNA3164
 - <https://www.ebi.ac.uk/metagenomics/studies/MGYS>
 - Source API (2):**
 - <https://www.ebi.ac.uk/ena/portal/api/v2.0/search?re>
 - <https://www.ebi.ac.uk/metagenomics/api/v1/studies..>
 - Title:** Human Oral, nasal microbiota and smoking
 - Description (2):**
 - This project has two goals:1. To evaluate the effect of smoking on oral and nasal microbiota2. To compare the collection of different oral samples in microbiota profiling.
 - This project has two goals:1. To evaluate the effect of smoking on oral and nasal microbiota2. To compare the collection of different oral samples in microbiota profiling.

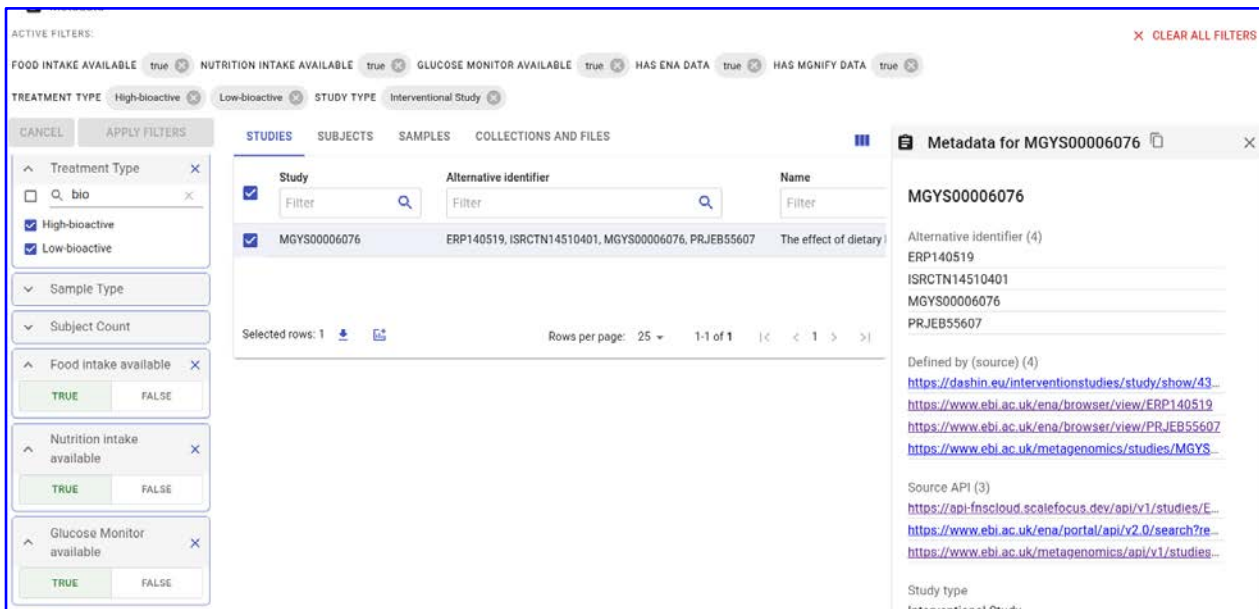
- 12) Select all 4 studies and export to Jupyter.
- 13) In the left menu, click on Analysis (JupyterHub) to open a new window with Jupyter.
- 14) Generalised scripts are available in the “[Demo 03] Use Case 2” folder. Will not run now, but they are available during the hands on time. The analysis is similar to the previous example, but less specific on what metadata is used.

Demonstrator 3

Research question: Does our gut microbiome contribute to our metabolic response to foods?
Can we predict metabolic responses to foods using microbiome data?

Steps:

- 1) Open Fairspace, log in with your credentials.
- 2) Go to the Metadata menu on the left side.
- 3) Enter text search for the name of the studies: “microbiome”
- 4) For the remaining studies, enter filters for
 - a) Study Type: “Interventional Study”
 - b) Set Has MGnify and Has ENA data filters to TRUE
 - c) Treatment Type: Start typing “bioactive” and select “High-bioactive” and “Low-bioactive”
 - d) Set ‘Food intake available’, ‘Nutrition intake available’, ‘Glucose Monitor available’ to TRUE
- 5) In the STUDIES tab, click the title of the DIME study (MGYS00006076) to view the metadata.



The screenshot displays the Fairspace interface with several active filters applied: FOOD INTAKE AVAILABLE (true), NUTRITION INTAKE AVAILABLE (true), GLUCOSE MONITOR AVAILABLE (true), HAS ENA DATA (true), and HAS MGNIFY DATA (true). The TREATMENT TYPE filter is set to High-bioactive and Low-bioactive, and the STUDY TYPE filter is set to Interventional Study. The STUDIES tab is active, showing a table with one row selected: MGYS00006076, with alternative identifiers ERP140519, ISRCTN14510401, and PRJEB55607. The study name is 'The effect of dietary'. A metadata window for MGYS00006076 is open on the right, showing alternative identifiers, source definitions, and source APIs.

- 6) Make sure that the DIME study is still selected. Then click the “Export to Jupyter Analysis” button.
- 7) In the left menu, click on Analysis (JupyterHub) to open a new window with Jupyter.
- 8) Go to the fairspace-metadata-exports folder to show that the metadata was imported.



- 9) Go to the “[Demo03] Use Case 3” folder **QIB takes over** and explains the script(s).
- 10) Close the JupyterHub instance.

Extra steps:

- 1) There is an extra scripts - machine learning provided by JSI (*collections/Descriptive and predictive data mining in DIME study data*)

