ELIXIR Food and Nutrition Community

Jildau Bouwman | FNS-Cloud meeting Brussels



ELIXIR: the offer



Guidelines Web portals Guidelines and best practices to help you Find the right software, training courses,
standards and more in our interlinked portals
to life science resources. Find c

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All resources

Find compute services, databases, and the full list of resources ELIXIR coordinates.



Partnerships with Industry and SMEs

Join events and projects that bring the private and public sectors together.



Opportunities to work together

Join a scientific group in ELIXIR or partner with us to apply for EC funding.



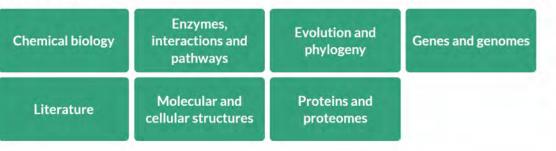
For ELIXIR members

If you work at an institute that is part of ELIXIR, then remember to take advantage of the benefits ELIXIR offers. ELIXIR

A Mark

ELIXIR: services

Scientific domain



Type of service

Compute	Data resources	Interoperability and standards	Software tools
Training			
Training service col	lections		

COVID-19 resources: ELIXIR provides a range of services that you can use for studying the SARS-CoV-2 coronavirus and the COVID-19 disease.

ELIXIR: communities

3D-BioInfo Helps to understand the 3D structure of macromolecules like proteins and DNA.



fin

Galaxy

training.

Biodiversity Aims to help us understand biodiversity, and how it responds to changing environmental pressures.

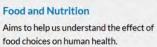
Fosters a Galaxy community in Europe,

together with Galaxy resources and

Develops a sustainable metagenomics

infrastructure to nurture research and innovation in the marine domain.

Marine Metagenomics



Intrinsically Disordered Proteins

Develops standards, tools and resources to help identify and characterise IDPs.



identification.

Provides the resources, analysis tools and infrastructure to help metabolite







Plant Sciences Develops an infrastructure to facilitate genotype-phenotype analysis for crop and tree species.



single-cell and spatial omics.



Toxicology Supports the integration of standards, tools and resources to aid toxicology research projects.



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Develops and maintains sustainable proteomics tools and data resources.

Proteomics

Systems Biology Aims to make systems biology modelling a

central pillar of research in biology.

Human Data Communities

Rare Diseases



Tİİİİ

Develops long-term strategies for managing and accessing sensitive human data.





Human Copy Number Variation Aims to make it easier to detect, annotate and interpret human Copy Number Variations (hCNVs).



Why a food and nutrition community?

ELIXIR focusses on Biomedical data on health (unhealthy subjects)

- Healthy citizens
- Social science
- Psychology
- Food composition
- Food preparation
- Effect food on health





ELIXIR F&N

Marine

70%

F&N community and the connection to ELIXIR

(FAIR) data Tools Interoperability Training

ELIXIR

 Specific application and translation of needs

Metabolomics

Food databases

F&N

Consumer behaviour tools

F&N data users

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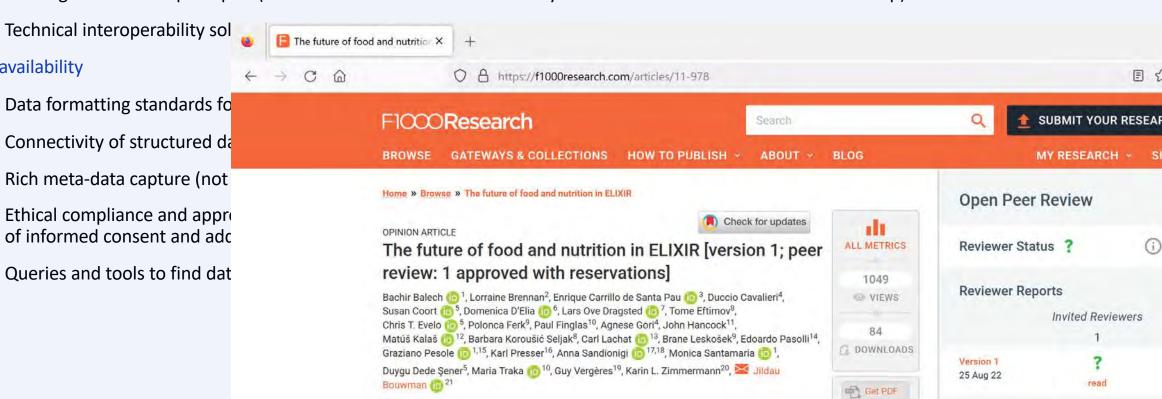
Data availability

Bioinformatics needs (1)

Standardization/Interoperability

- Terminology: ontology development (not all relevant ontologies for F&N are in place and managed) •
- Standardization of questionnaires (Questionnaires are hardly aligned) ٠
- Tools for standardization (Tools for standardization are not always available to F&N scientists) ۲
- Training on FAIR data principles (not all F&N scientists know how they are share FAIR data and where to find help) ۲

Author datalla

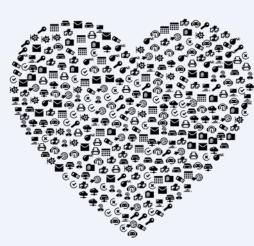


ELIXIR F&N F1000 paper

Bioinformatics needs (2)

Data reuse

- Complex data integration (including omics and personalization) with specific focus on metabolomics and microbiome
- Hardware for analysis
- Software and pipelines for analysis
- Interaction with consumers (onboarding and transparency)
- Training on data reuse





Bioinformatics needs (3)

Advocacy and training

- Researchers and governmental organizations publish research documents to spread knowledge but hardly publish data (raw or modified). Convincing arguments and incentives must be created to consider publication of documents of equal importance as publication of data.
- Training/Capacity Building on FAIR data and standards (not all F&N scientists know the FAIR principles and are aware of the standard's importance to align their data management plans with FAIR principles and where to find support)

Tool and service availability and interoperability

- Make also tools and services available with which data can be analyzed, visualized and manipulated
- Need for alignment of existing and new analysis software with ELIXIR existing ELIXIR efforts (e.g. microbiomics/GALAXY and similar dataflows)
- Public and private repositories must be integrated in such a way that it allows users to easily transfer data into existing tools for their data processing. This would lead to a landscape of repositories and tools where an arbitrary number of systems can be connected or chained to perform data analysis.

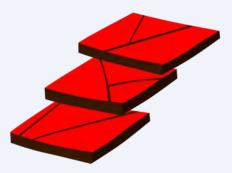
Networking actions

- Interaction with consumers (onboarding and transparency) and other stakeholders such as F&N researchers, policy makers, educators, industry, hospital and patients
- Alignment with European Open Science Cloud (EOSC) strategy for sustainable long term data reuse and other initiatives



Alignment with ELIXIR Platforms

- Data Platform \rightarrow DASH-IN: align with ELIXIR resources
- Tools Platform → tools provided and used by the F&N community will be registered in the bio.tools registry
- Interoperability Platform → F&N data must be interoperable in order to align with other data sources.
 Extension of the current metadata standards toward food and consumer science is needed
- Compute Platform → Computing power necessary for the analyses. The community should have a helpdesk that knows the access points for compute platforms
- Training Platform → Courses from the F&N community (e.g. FNS-Cloud, NuGO) can be registered in TeSS





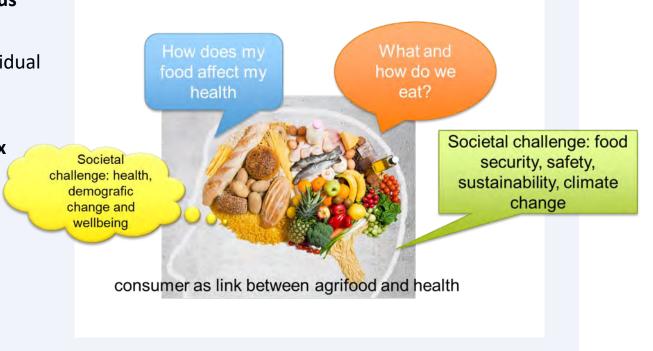
Alignment with ELIXIR communities

- The Federated Human Data community for long-term strategies for managing and accessing sensitive human data and connecting consumer and patient data
- The Rare Diseases community for privacy issues on the individual data and describing phenotypes.
- The Marine Metagenomics (Microbiome) community for the solutions in the area of microbiome/metagenome analysis.
- The Biodiversity focus group for the accessibility to taxonomic and molecular data (including other metadata) related to the species described so far (biodiversity catalogues).
- Plant Science community for the link between plant science in general and plants as food compounds.
- The metabolomics community for readouts of intake and health
- The toxicology (not yet an approved community) on describing phenotypes
- The newly developing Microbiome community and the Microbial Biotechnology community for two different microbiome approaches
- The Machine learning focus group for complex data integration (including omics and personalization) with specific focus on metabolomics and microbiome, and software and pipelines for analysis.
- (other Communities are Proteomics, Galaxy, 3D-Bioinformatics and Intrinsically Disordered Proteins)



Key F&N community challenges

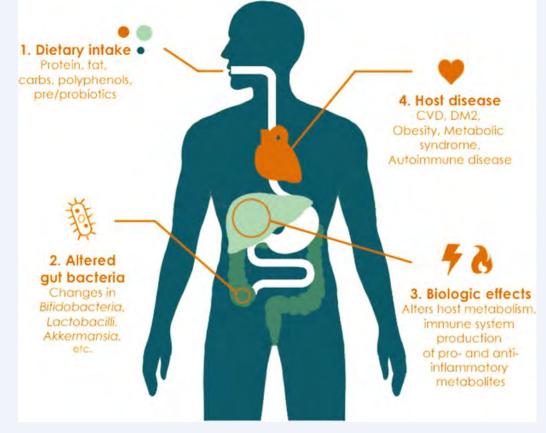
- Measure a health effect → Define **individual health status**
- Every individual has different dietary needs → Develop individual advice (e.g. what advice is needed for an individual at risk for a non-communicable disease)
- Quantify what individuals have eaten (standard is questionnaires but these are very unreliable → Complex dietary and food intake biomarkers





Implementation study: Food, microbiome & health

- FNS-Cloud (DIME study, ontology, FAIRspace)
- JPI INTIMIC Knowledge platform





F&N community

FAIR meta-data availability through PhenotypeDB

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Introduction The Phenotype Database is an application that can store any biological study. It contains templates which makes it possible to customize.	Study Microbion obese women w Study Diet, micr Study Stad Affe Induces Out Micr Citycemic Respon	Individual Studies					
In order to allow flexibility to capture all information you require within a study, and to make it possible to compare studies or study data, the system uses customizable templates and ontologies. It is especially designed to store complex study designs including. Read more	In Dep Licensi metabolism, ban	Show 25 \$ entries				Se	earch:
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Nutritional issues

- Large background on treatment (many measurements needed)
- Broad effect (many different processes)
- Seasonal effect (cross-over design essential)

\rightarrow Data integration essential

	Week	< 5 Week	x 10
Group 1	Placebo	Supplement mix	
Group 2	Supplement mix	Placebo	



Structured meta-data

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Diet intervention (switch)

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Route (Dropdown selection of terms)	
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JPI HDHL INTIMIC knowledge platform

INTIMIC has created a network of transnational and multidisciplinary collaboration to further develop and increase the impact of microbiome research in human health. It assembles 52 partners all over Europe (including Israel) and thus allows addressing the microbiome research community in a broad and comprehensive way. The consortium was generated by national and European funding organizations to reflect the local and international excellence in the best way.



Partner countries (alphabetical order):

- Austria (5 partners)
- Belgium (1 partner)
- France (5 partners)
- Germany (12 partners)
- Israel (3 partners)
- Italy (13 partners)
- The Netherlands (5 partners)
- Spain (3 partners)
- Sweden (4 partners)

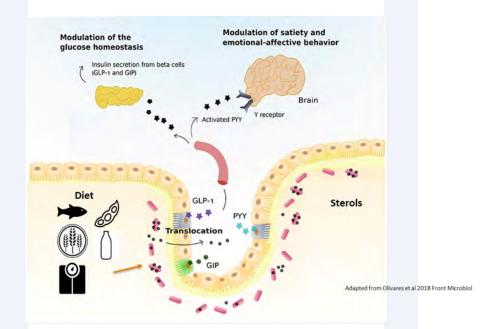
Learn more about our partners





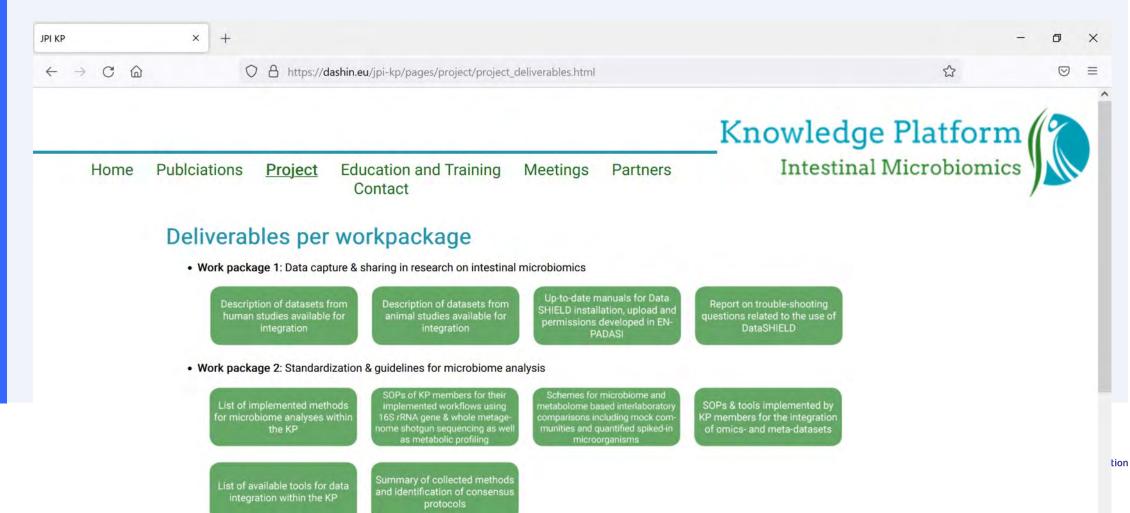
AIM of INTIMIC KP

 Foster transnational and multidisciplinary collaboration and networking in order to accelerate, further develop and increase the impact of intestinal microbiome research related to human health



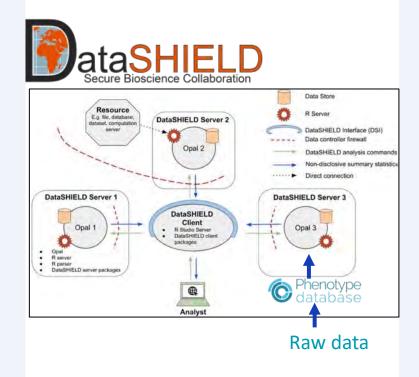


Deliverables of the KP (https://dashin.eu/jpi-kp)



Results: Data (https://dashin.eu)

- Expansions of the Phenotype database standards with (microbiome) standards
 - Observational study data
 - Intervention study data
 - Microbiome data
 - Other omics data (food, processing, fermentation, Food-Biomarker, physical activity, metagenomics, metabolomics)
- Many datasets available in a standardized way (also for studies focusing on prebiotic)
- Cleaned set from literature of infant studies download (on the KP website)
- Data of some open data sources is made FAIR

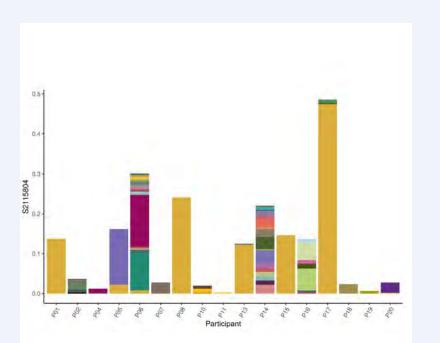






Results: ANALYSIS

- Better insight in the background of the variation in the measures \rightarrow needed for better and more standardization
 - Region for 16S PCR (please note that some species may not be detectable)
 - Databases/ bioinformatics pipeline
 - Sample preparation
- Shotgun metagenomics is the future, but standardization is even more challenging
- Population (biological) variance is often overwhelmed by the combined technical variance
- The core human microbiome is difficult to strictly define
- Functional microbiome is shared with other host species



Results of a ringtrial





INTIMIC KP

Results: Tools & other output

- SOP databank in place
- Definition of and list of functional foods
- Described connection food microbiome and gut microbiome
- Web-interface (easyPubmed) for literature review (will be on the KP website)
- Inventory of for models and model organisms (intimicdb.com registration needed) → including specimens, isolates
- Training material collected on the website





Impact

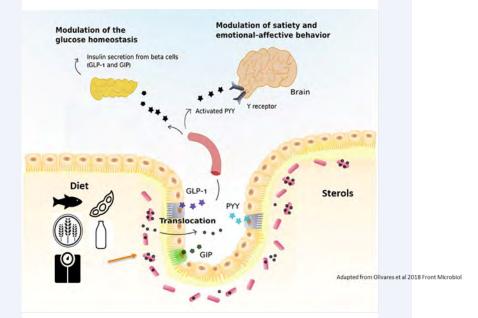
- False positives and negatives should be removed in the analysis for more societal impact
- The microbiome is heavily affected by the diet, including the food microbiome
- Definition of functional food
- Dysbiosis can be diagnosed
- The microbiome is clinically relevant to many diseases and from a diagnosis and intervention point of view
- The core human microbiome will help here, but the road is long



ELIXIR implementation study

This implementation study describes the integration of microbiome, metabolomics and dietary data of nutrition studies, as a first example how the F&N Community can benefit from ELIXIR and vice versa

- WP1 Collection of relevant datasets & training \rightarrow Workshop
- WP2 Development and implementation of microbiome standards \rightarrow Workshop
- WP3 Development and implementation of metabolomics standards → Workshop
- WP4 Integration of study (meta)data, microbiome and metabolome → Hackathon (starting tomorrow with DIME study)





Expected outcomes

- A better interaction between ELIXIR and the F&N Community
- Unify the RICHFIELDS, ENPADASI and FNS-Cloud requirements and ontologies
- Link standards and ontologies with other standardized ones (provided through ELIXIR).
- Standardization in consumer and human nutrition science (to be able to analyze food behavior)
- Show the modulating effect of food on the human gut microbiome and health



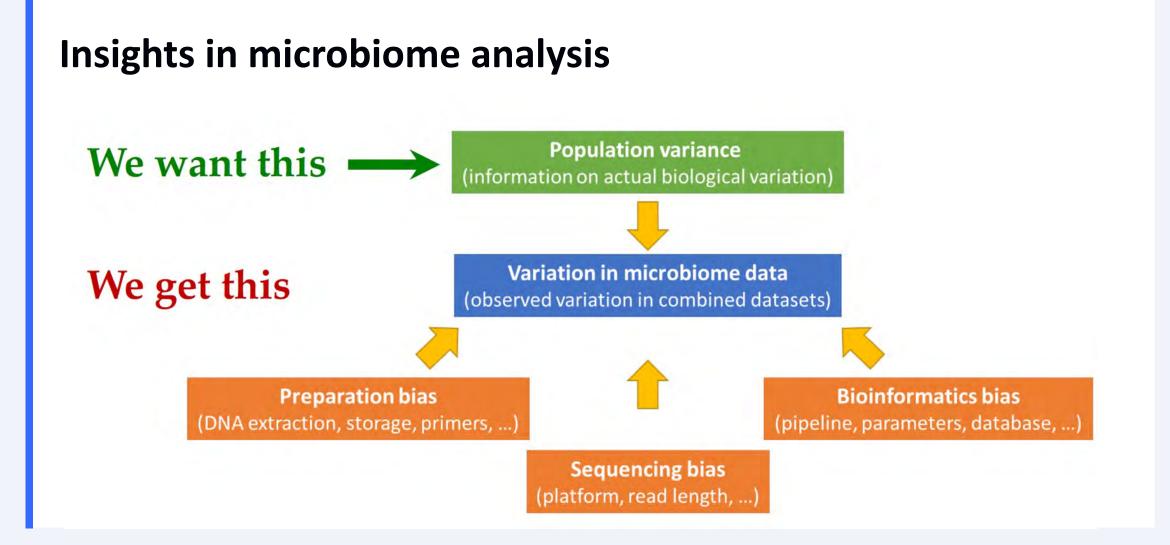


FNS –Cloud Brussels

Thank you!

Jildau.bouwman@tno.nl

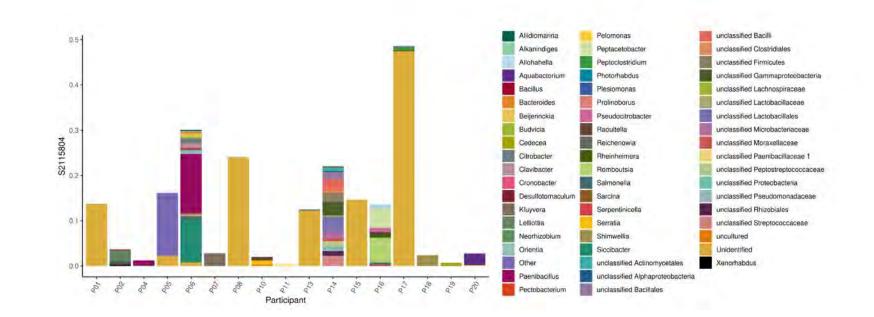








Many differences in ringtrial



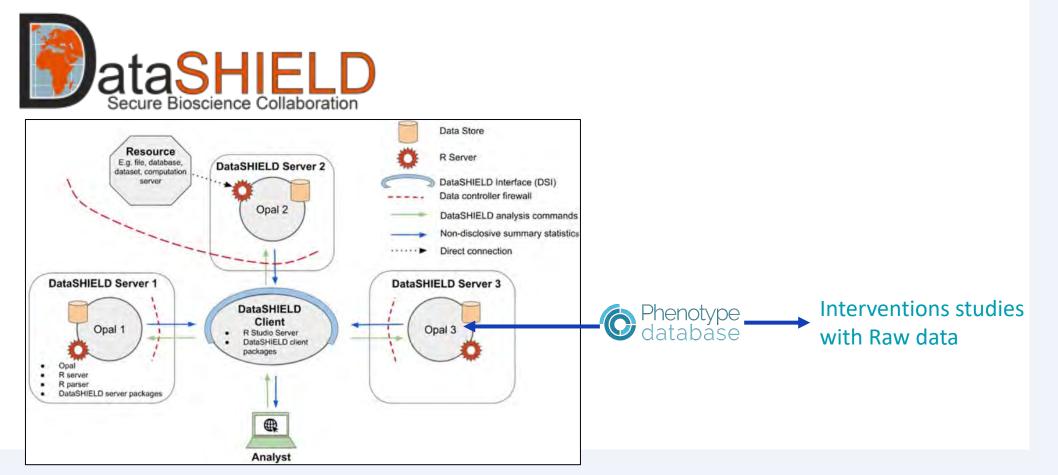




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Online trai	ning modules available within the KP consortium	
	KP partners (7 e-training modules)	
- 5 Austrian	(P partners (3 e-trainings)	
- 2 German H	partner (1 e-training module)	
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FAIR data availability through DASH-IN



Schematic diagram of a multi-site DataSHIELD infrastructure



SOP databank in place (collected via survey)

31 Workflows ana	lyzed
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Sample Types High Biomass: Stool (13), Skin (5), Saliva (3), Lower Respiratory (3), Nasal (1) Low Biomass: Tissue (3), Blood (1), Vaginal swab (1) Other: In vitro gut simulation fermenter (1), Indoor Environment (1)

Sample Stabilization

Commercial Kit (15), RNALater (11), NA (3), EDTA (1), Glycerol (1)

Sequencing

Illumina MiSeq (17), NovaSeq (2), NextSeq (2), HiSeq (1), IonTorrent GeneStudio S5 (1)

Controls

Negative Sample (29), Mock Community (11), Spike-in Control Cells (1) DNA Spike (2), NA (2).

Region

16S rRNA: V3-4 (9),V1-2 (1), V1-3 (3), V4-5 (3), V4 (5), all regions (6). Fungal ITS (6), Shotgun (7)

Clustering

dada2 Amplicon Sequence Variants (23), 97 % OTU (6), Self-developed (2)

16S Ref. Databases SILVA (8), Greengenes (6), Unite IST (2), RDP (1), Commercial (1).



A human core microbiome is hard to define

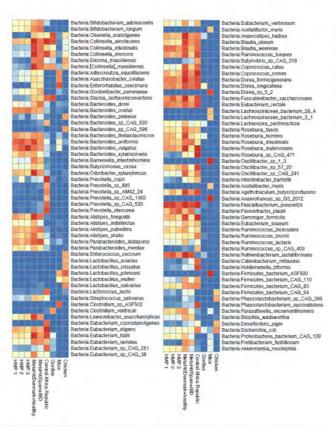
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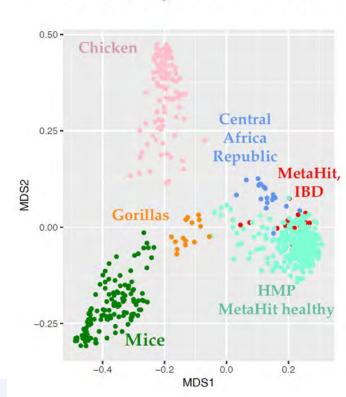
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Taxonomy: find a set of consistent taxa across populations

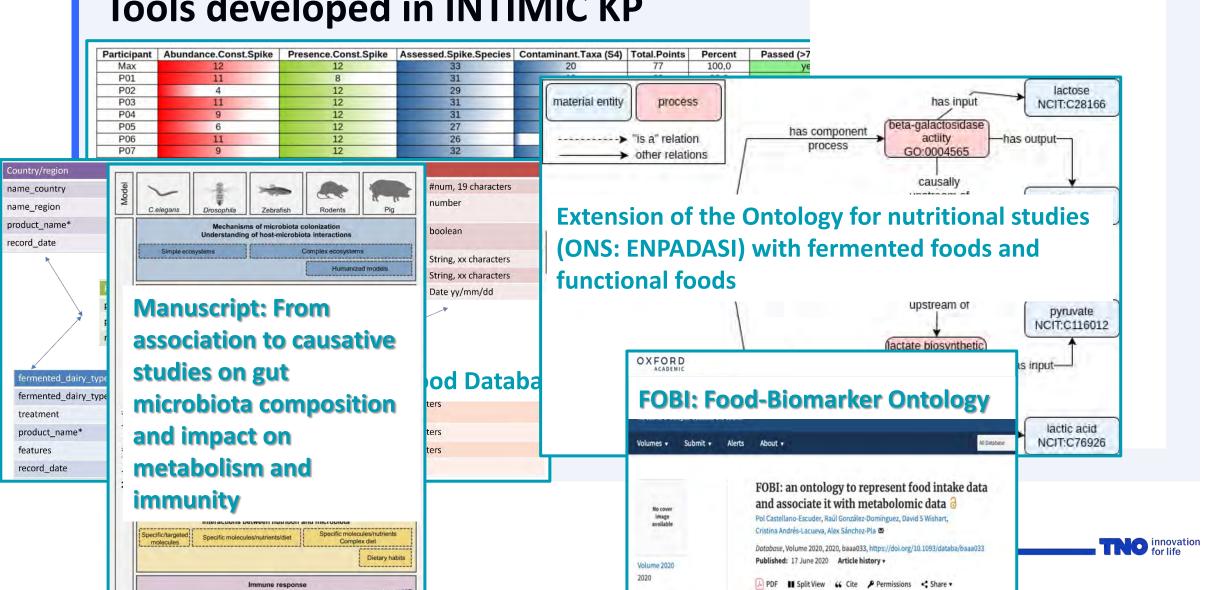
- We analyzed data from 9 cohorts
- Human samples clustered separately from animal samples

Unweighted UniFrac-based MDS analysis of 370 human and 277 animal samples

No species appeared in 90% or more of the samples of all human cohorts

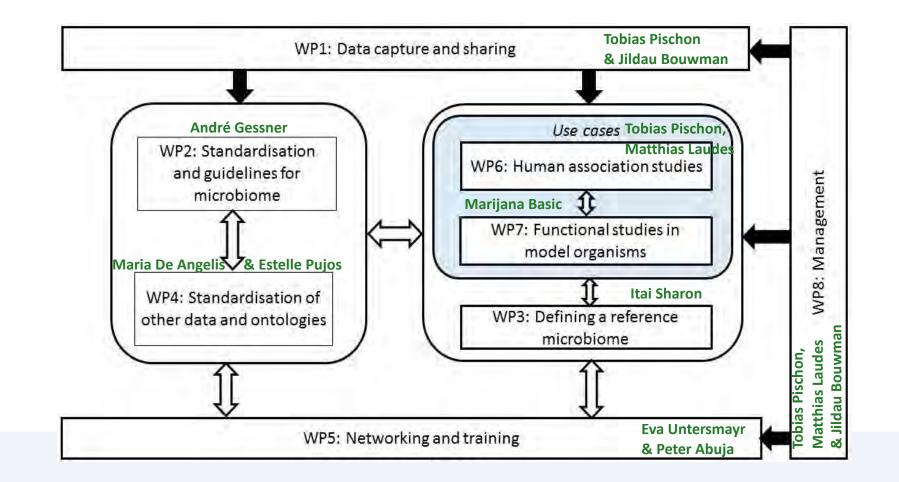


innovation



Tools developed in INTIMIC KP

Structure INTIMIC-PH





INTIMIC KP

Scientific Impact

- Presentations and publications (most open access):
 - 20 publications in the special issue of nutrients 'Connection between microbiome, lifestyle and diet'
 - 18 direct publications of the knowledge platform
 - Studies available via DASH-IN for future work
 - <u>https://dashin.eu/jpi-kp/pages/home/</u>



