

The 1st Microbiome CRO

Comprehensive microbiome research services

Atlas Biomed Group
R&D department

Atlas Biomed Group

Atlas Biomed

Global provider of DTC genetic and microbiome tests in 15+ countries (UK, EU, Japan, Asia, Russia/CIS)

Aimed to develop a cloud system for multisource data co-interpretation to diseases prevention

The head company of the group

Atlas rnd

Contract Research Organisation specialised in microbiome-focused clinical trials and research projects.

Knomics Biota – a proprietary microbiome data analysis SaaS

100+ publications

60+ completed projects

50+ partners

Oncoatlas

The leader of laboratory services providing and diagnostic kits development in the oncology field in Russia

The sole NGS-based diagnostic kit for tumors profiling registered in Russia

1000+ cases processed

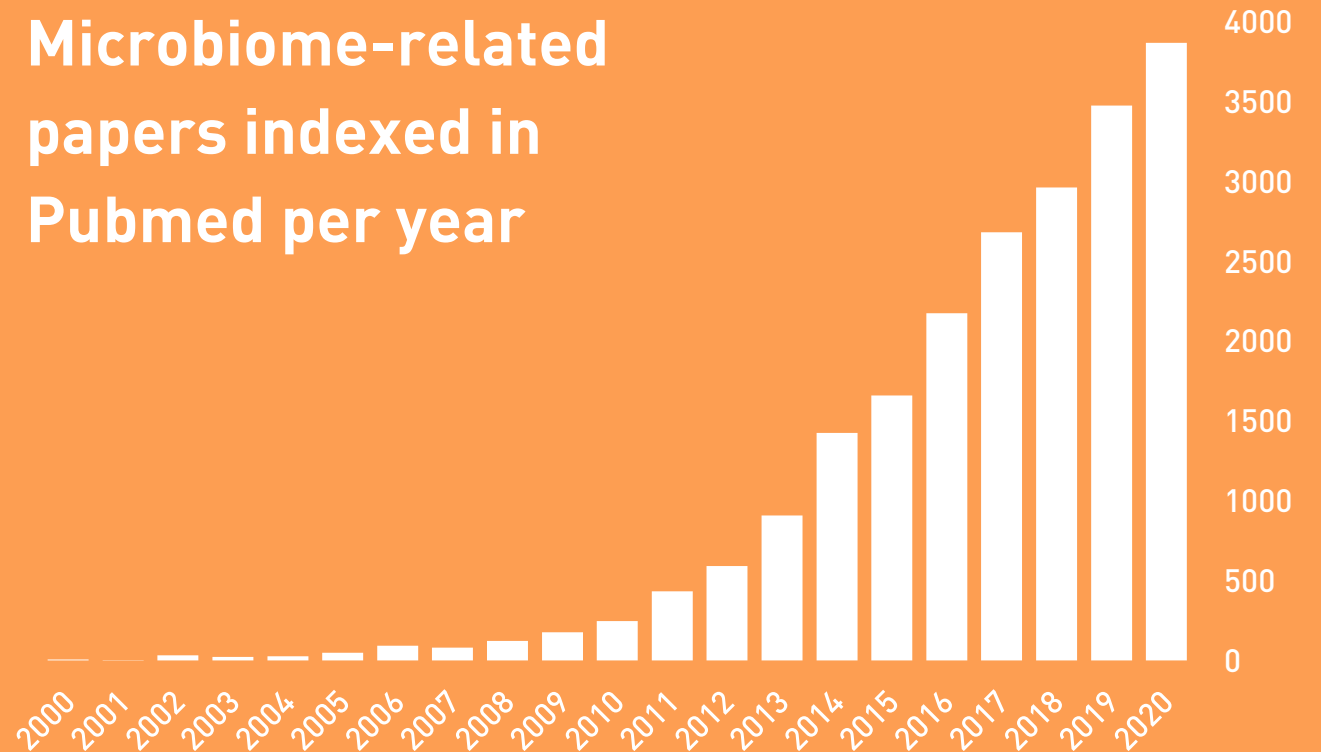
Microbiomics: a rapidly accelerating global research trend

The microbiome is a complex community of microbes inhabiting many niches. Numerous links between the microbiome and a wide variety of health conditions have been elucidated.

Top 5 topics

1. Gastrointestinal disorders
2. Oncological microbiomics
3. Autoimmune conditions
4. CNS + gut-brain axis
5. Metabolic disease

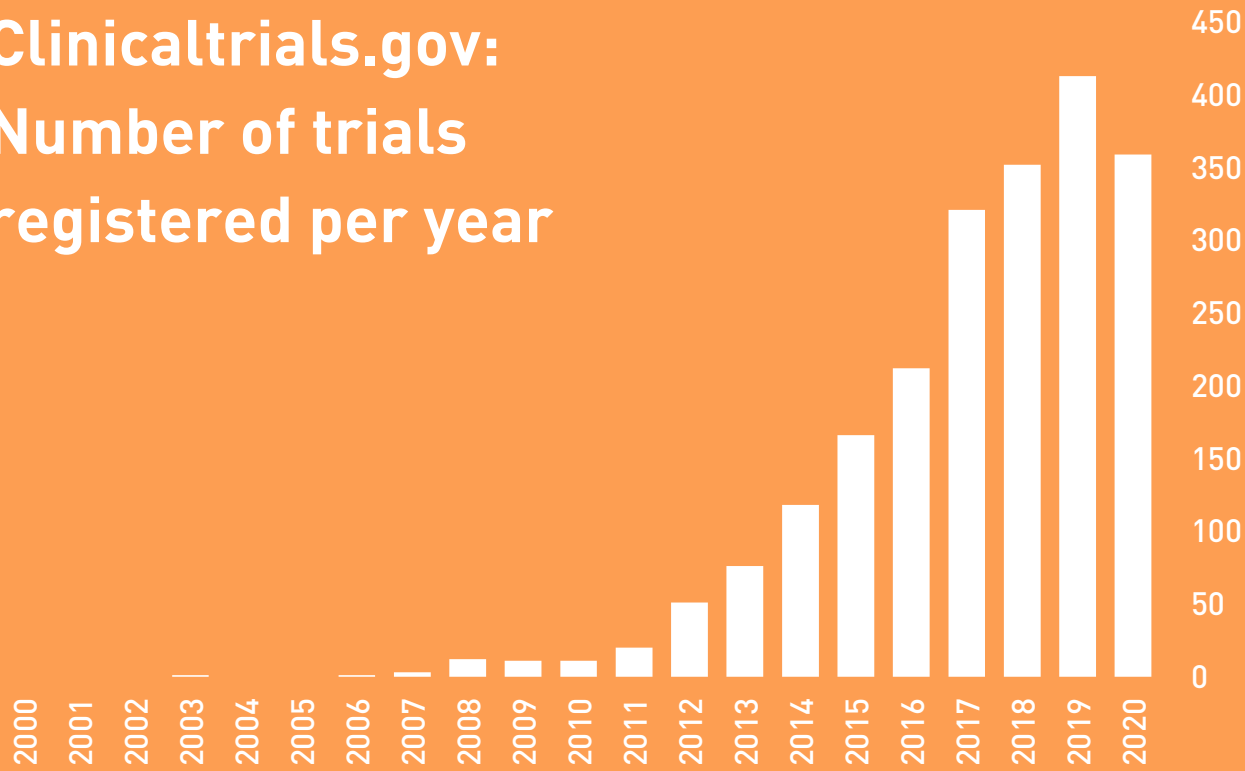
Microbiome-related papers indexed in Pubmed per year



Microbiome clinical trials market

Developments in microbiome-targeted therapies are a major driving force in market evolution. Efficacy of each such product has to be confirmed via in vitro experiments and well designed clinical trials.

**Clinicaltrials.gov:
Number of trials
registered per year**



Key market foci

1. Live biotherapeutic products
2. Specialised nutrition
3. Functional foods
4. Research projects
5. Pharmaceuticals

Atlas R&D: from idea to publication

What are we offering?

1. Microbiome services
2. Data analysis platform (SaaS)
3. Full-cycle CRO services

Project types

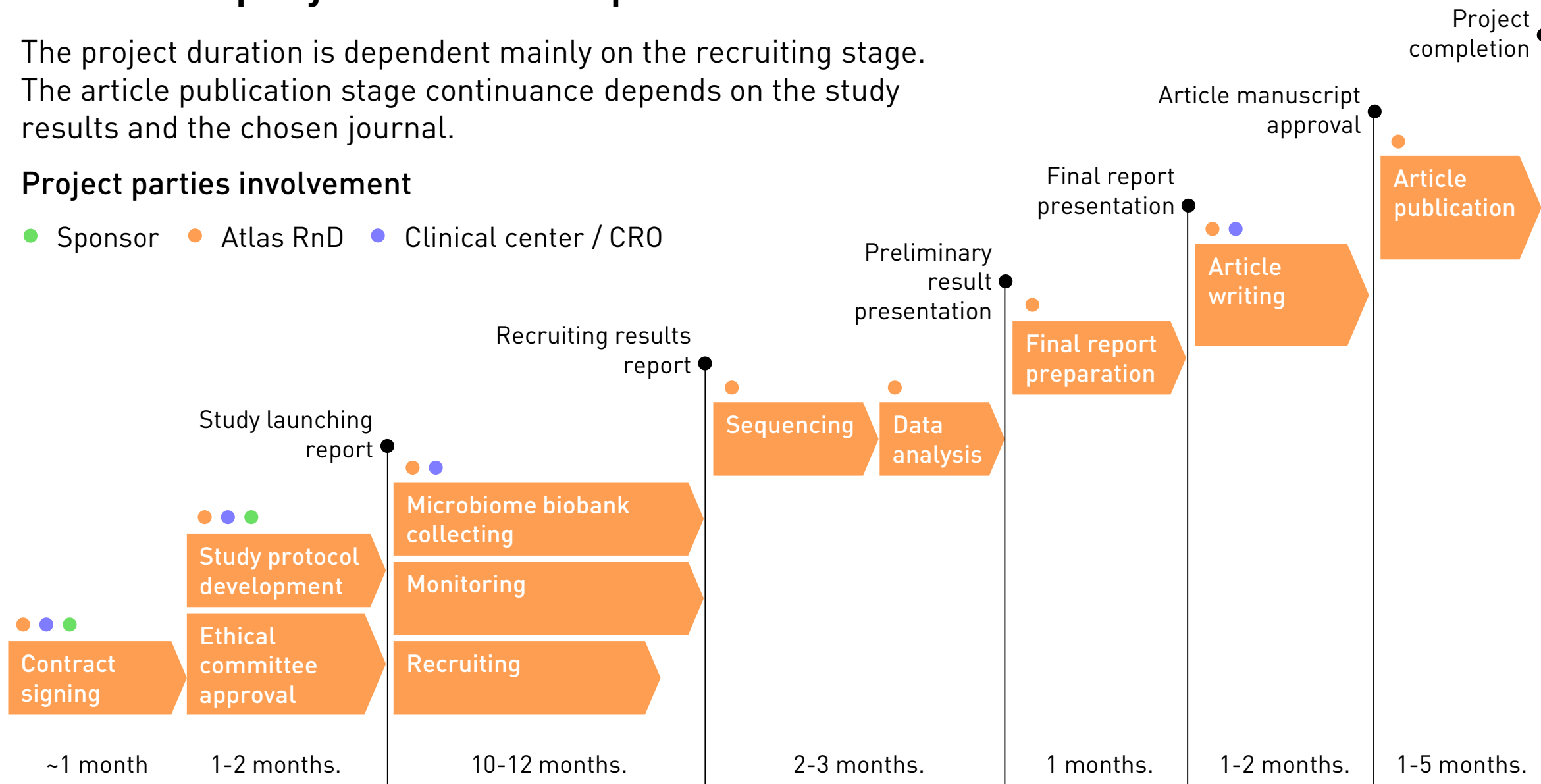
1. Research projects
2. Observational studies
3. Interventional clinical trials
4. Pharmacomicrobiomics

Standard project's roadmap

The project duration is dependent mainly on the recruiting stage.
The article publication stage continuance depends on the study results and the chosen journal.

Project parties involvement

● Sponsor ● Atlas RnD ● Clinical center / CRO



Project example

Description

Cohort

Healthy volunteers
18-40 years old
without immune
system diseases signs

Groups

- 1. Experimental group
(n = 60)
- 2. Placebo group
(n = 60)

Research participant's path

Operational part

Inform consent signing
Microbiome collection kits giving out

Clinical data collection

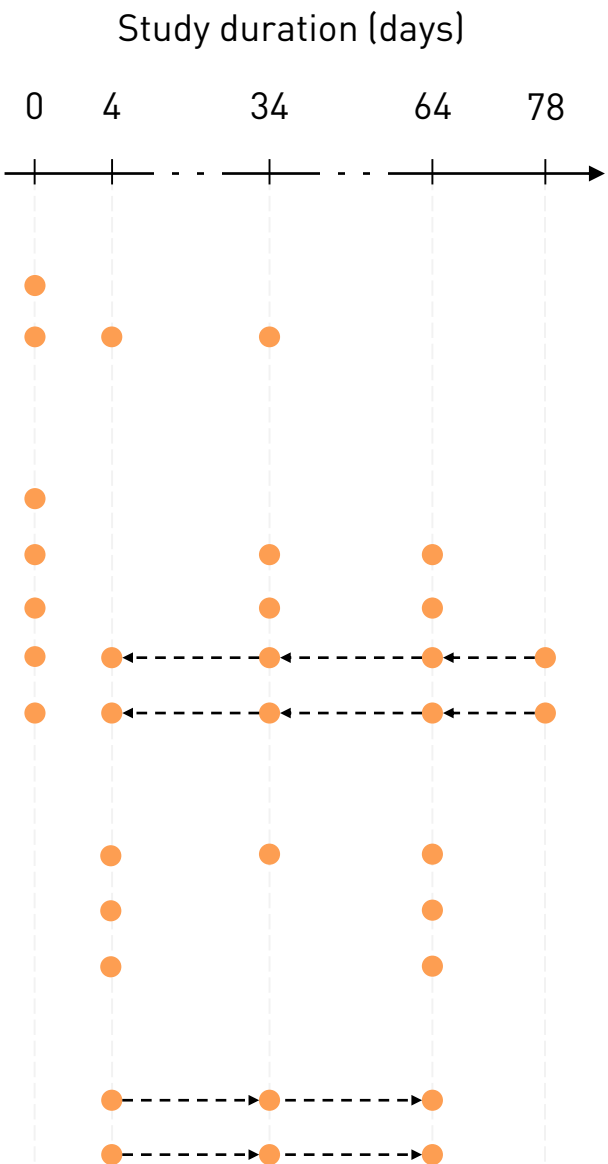
Inclusion / exclusion criteria compliance assessment
Clinical examination
Questionnaire
Incidence rate
Adverse events monitoring

Samples collection

Blood
Saliva
Feces

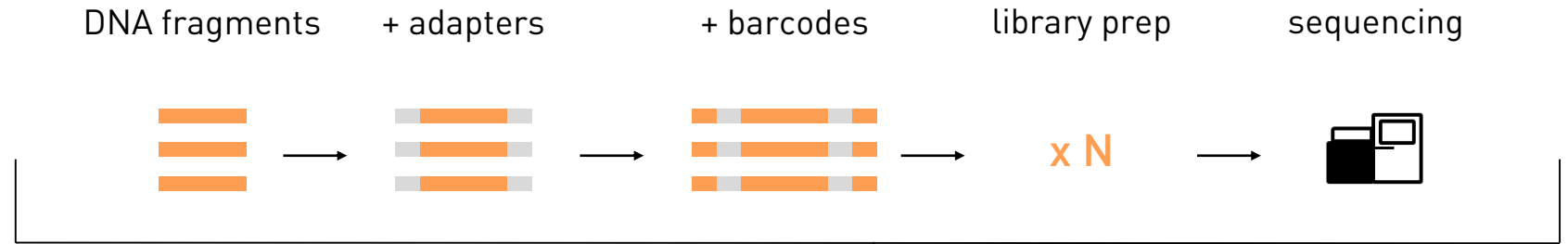
Intervention

Product intake
Placebo intake



Microbiome analysis: Sample processing

16S rRNA sequencing for
key taxa searching
in large-scale clinical
trials



Sample collection and stabilisation

Stabilization is an
essential stage for bias
avoiding
Specific kits for different
tissues

DNA isolation

Mechanical cell lysis
stage – the second key
point for relative
abundance retention
(Bead Beating)

High-throughput sequencing

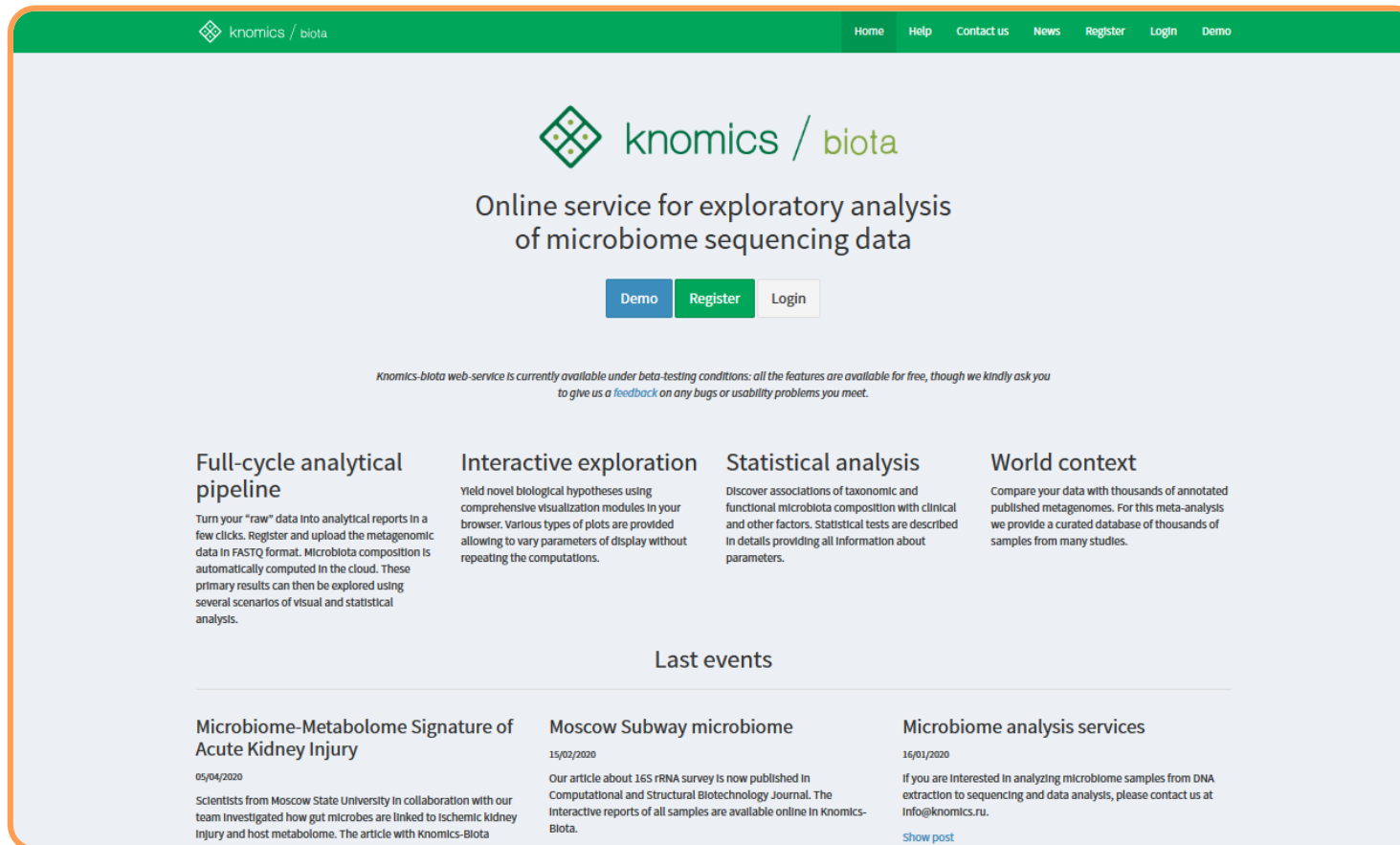
Any type of microbiome
NGS
Any sequencing
platform
Any covering rate

Data analysis

The most
significant stage,
not proposed by
lab services
providers

Microbiome data analysis

For microbiome data analysis and presentation, we propose our cloud platform Knomics-Biota. Push the logo at the right to explore the demo.



Options

1. Fully automatic analysis
2. Interactive visualisation
3. Collaborative mode
4. Large-scale data sets supported



Data analysis roadmap

1 Preprocessing

2 Taxa composition analysis

3 Functional potential analysis

4 Factor analysis

After receiving the sequencing data from the laboratory, the first step is to check the data quality and filter the low-quality reads.

Data analysis: quality control

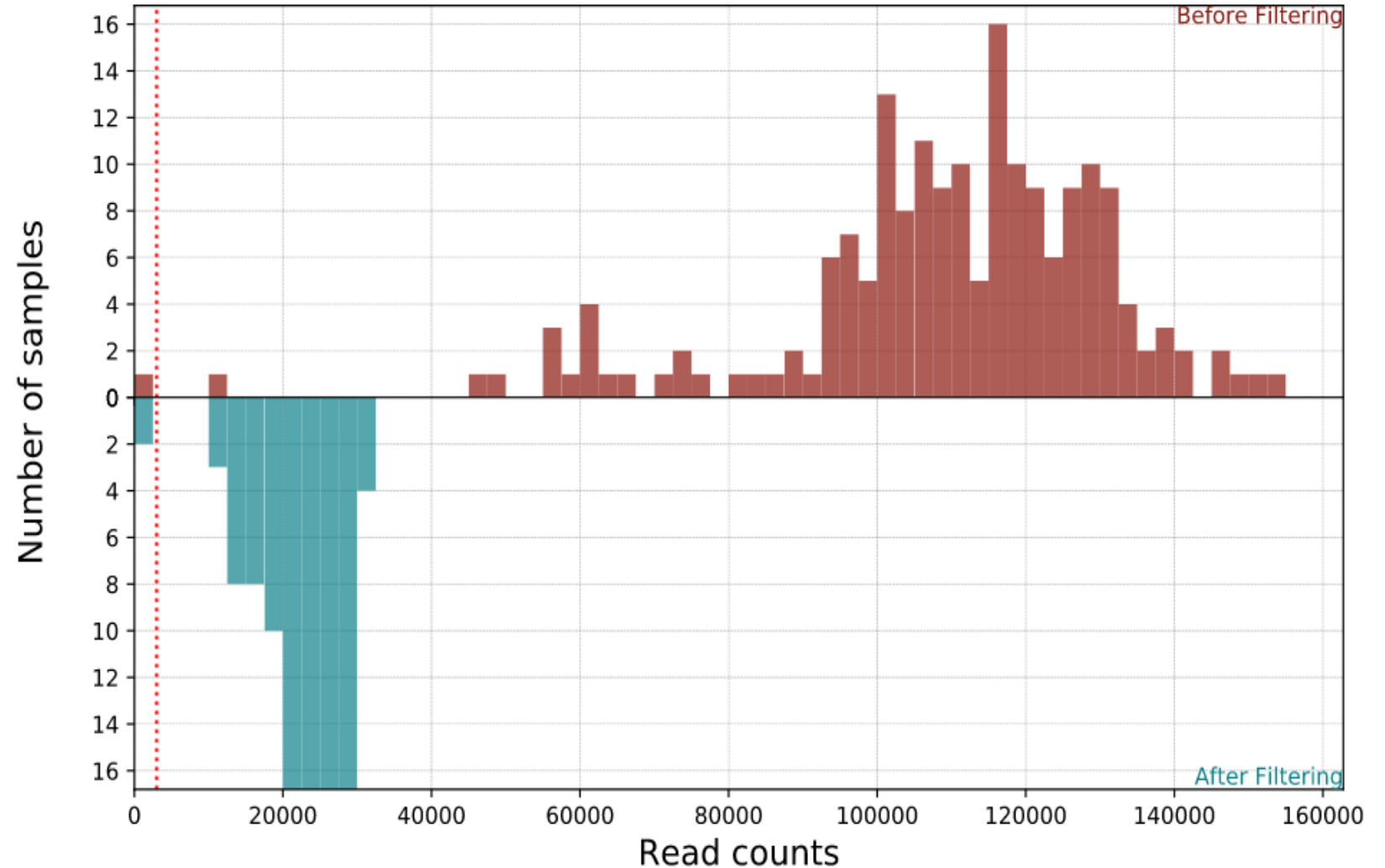


Purpose

Trimming of low-quality read ends, removing shot reads and denoising

Description

All reads on the right of the red dotted line are pass quality control examination. Samples not passed through QC are not reliable for further analysis





Data analysis roadmap

1 Preprocessing

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4 Factor analysis

The next step is identification of taxonomic composition. Reads are aligned against reference sequences databases. Based on the comparison results, we obtain a list of detected bacterial taxa along with their reads counts. It allows to assess community diversity and relative abundance of the identified taxa.

Taxonomy investigation: heat map

Purpose

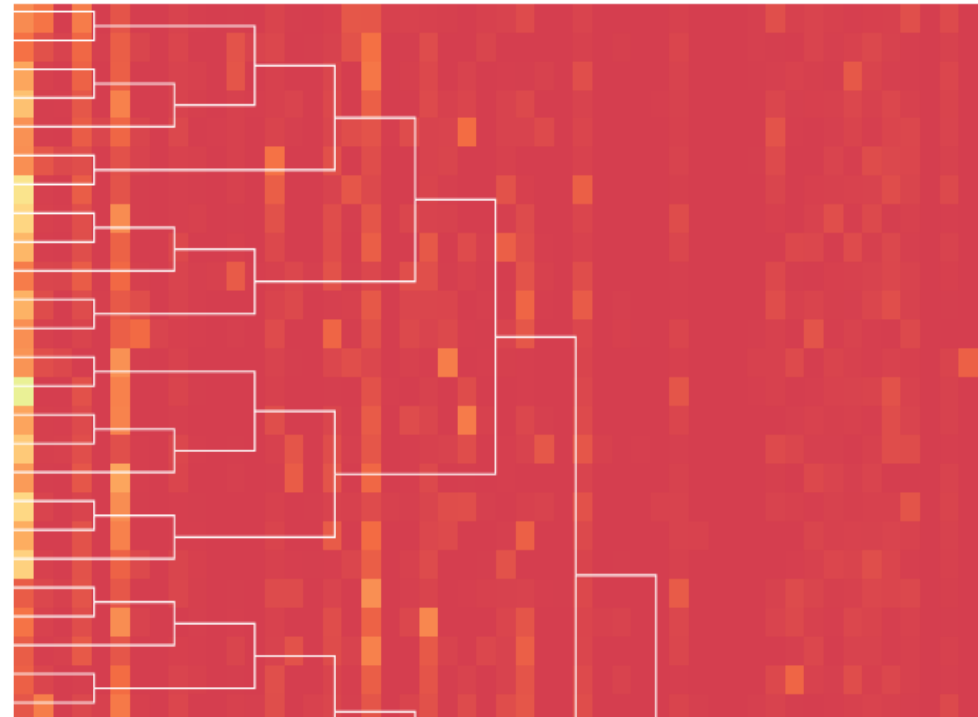
Samples and whole cohort taxonomy visualisation

Description

Samples placed horizontally, bacterial taxa vertically. Samples clustered based on microbial composition

All user data

DFI-2516
DFI-2468
DFI-2507
DFI-2386
DFI-2114
DFI-2242
A000-0578
DFI-2521
A000-1299
DFI-2309
DFI-2183
A000-1220
DFI-2371
DFI-2065
DFI-2662
DFI-2440
DFI-2235
DFI-2057
A000-1300
DFI-2182
DFI-2318
A000-1458
DFI-2115
DFI-2524
A000-1699

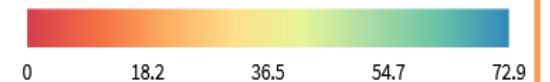


All samples

Top by all samples

Bacteroides	16.73%
Faecalibacterium	7.33
UCG-002	2.93
Alistipes	2.07
u(f__Lachnospiraceae)	1.63
[Eubacterium]_coprost...	1.2
Prevotella	1
Parabacteroides	1
Roseburia	0.93
Christensenellaceae_R...	0.77

Legend



Heatmap settings

Grouping

Bacteria by genus

✓ Show samples tree

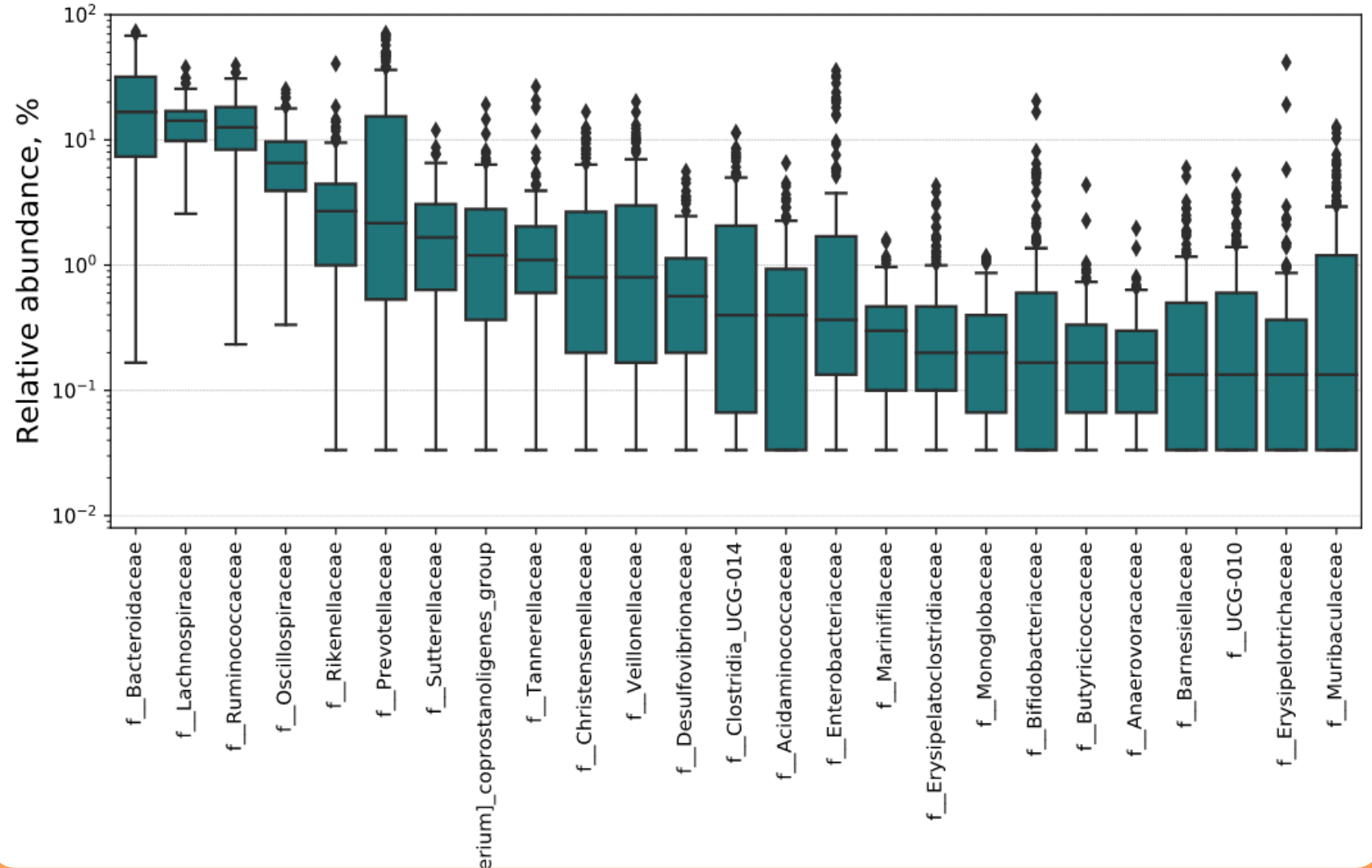
Cohort taxonomy description

Purpose

Description of taxa abundance in whole cohort

Description

Relative abundance of microbes on configurable taxonomy level.



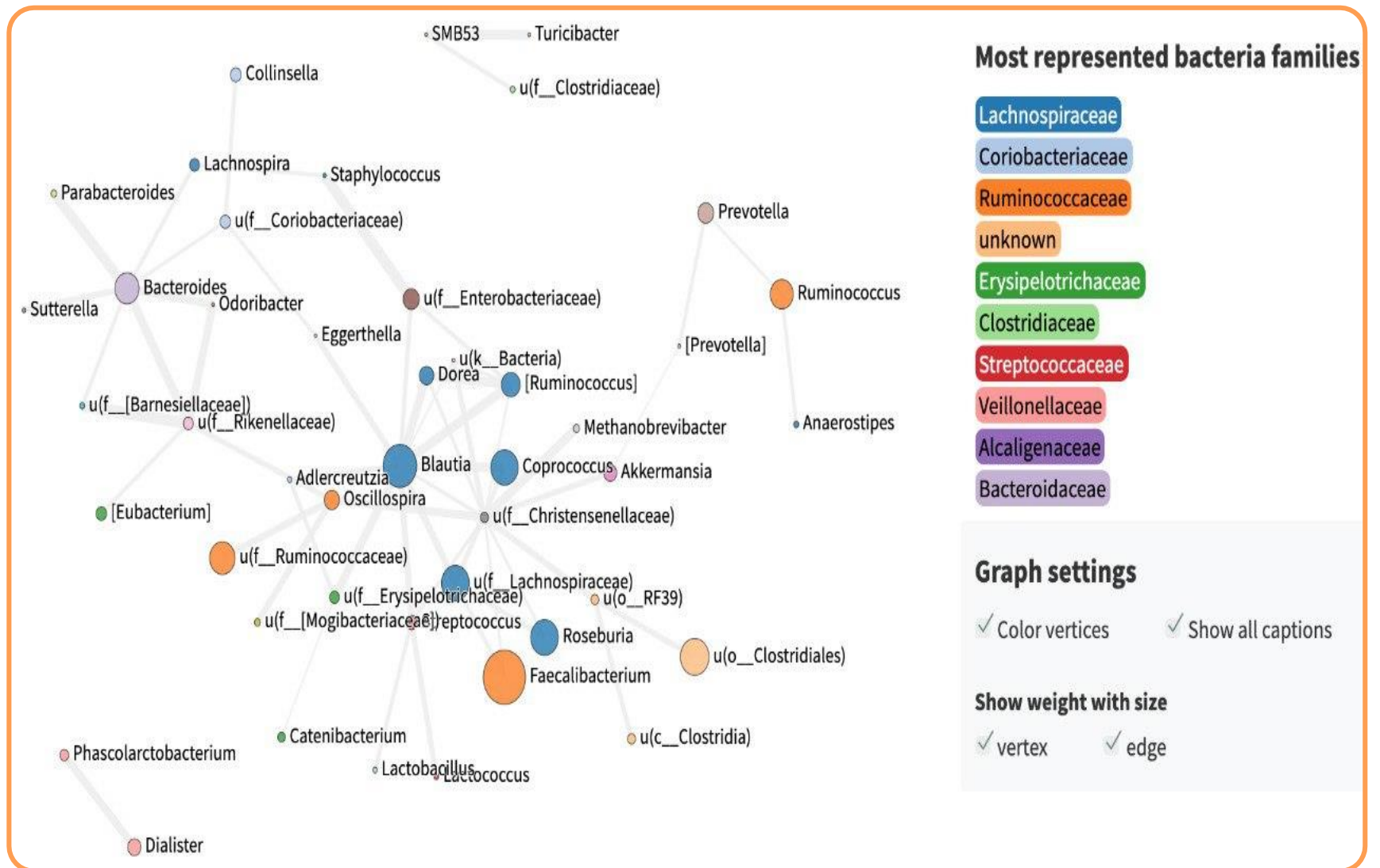
Microbial cooperatives visualisation

Purpose

Associated taxa
identification

Description

Clusters of co-occurring taxa which can be used for the analysis of microbial cooperation. Clusters can be also transmitted to statistical analysis.



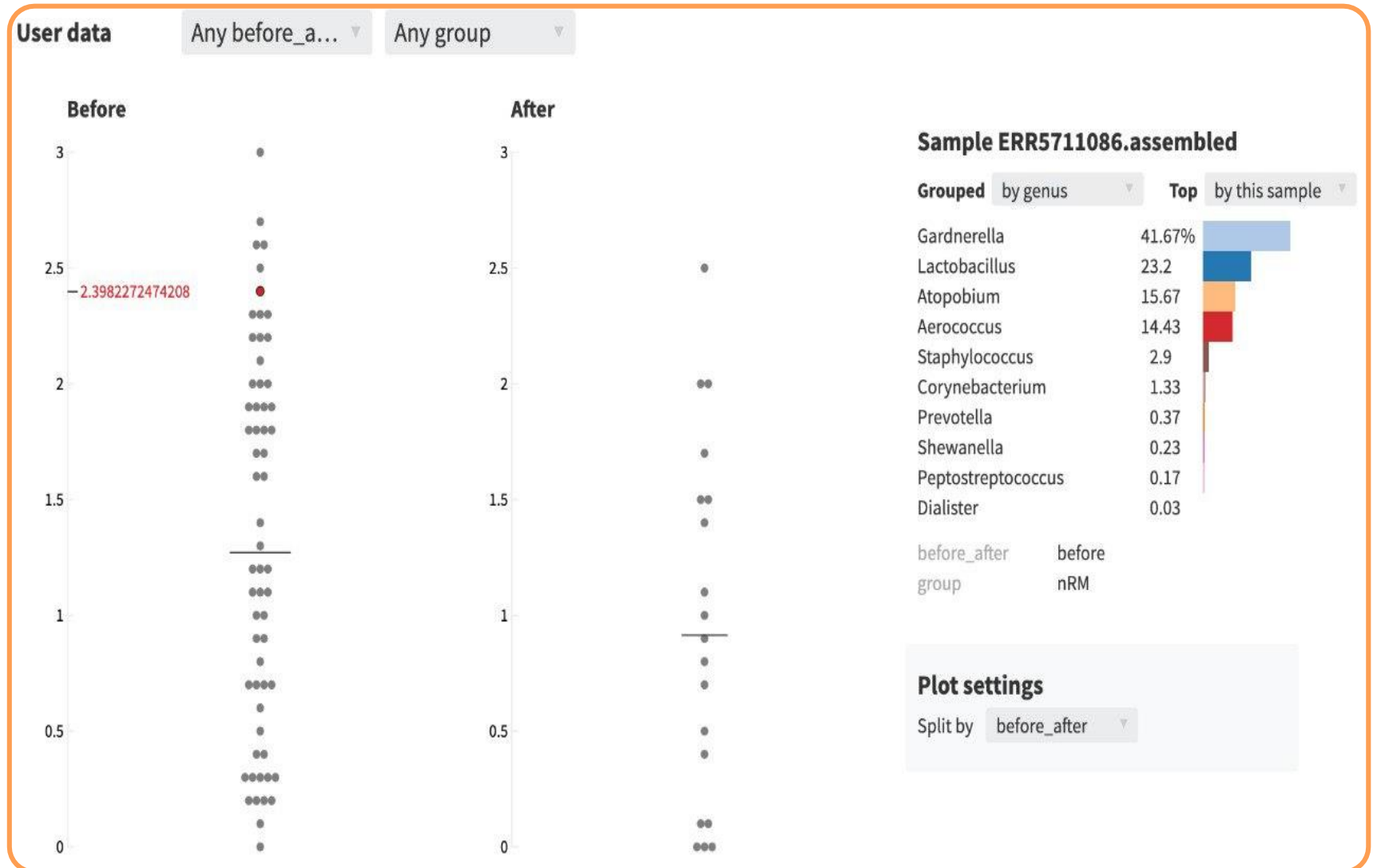
Integral index: Alpha diversity

Purpose

Microbiome richness visualisation

Description

Automatically calculating with two scores using (Chao and Shannon indexes).





Data analysis roadmap

1 Preprocessing

2 Taxa composition analysis

3 Functional potential analysis

4 Factor analysis

By knowing the taxonomic composition, it becomes possible to predict the microbiome metabolic potential. For this purpose, both publicly available and in-house metabolic pathway databases are used.

Metabolic potential prediction

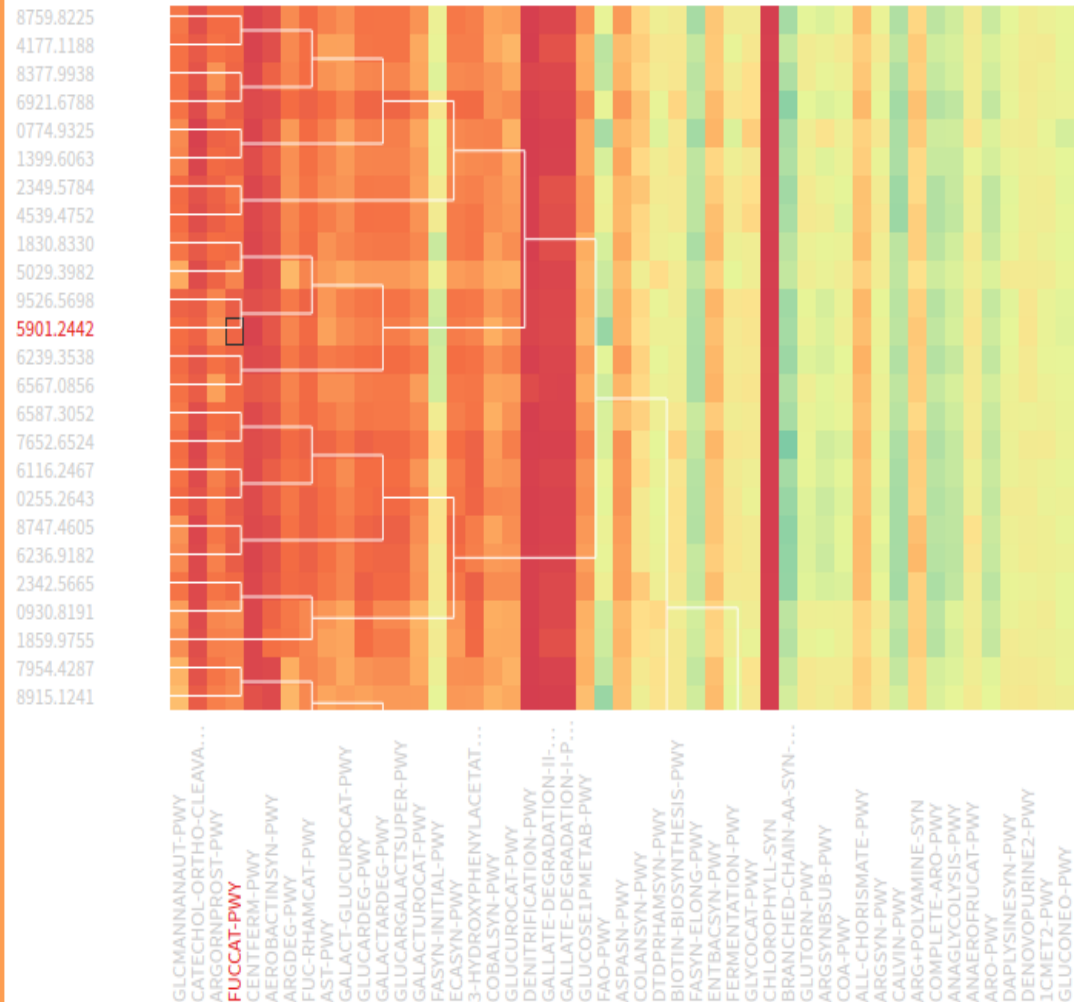
Purpose

Visualisation of whole microbiome metabolic potential

Description

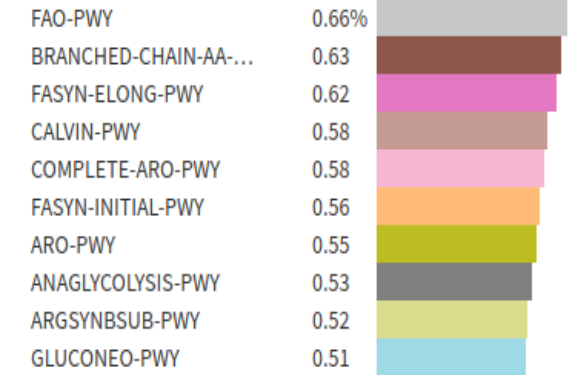
Samples placed horizontally, pathways vertically. Metabolic pathways relative abundance presented on the right

All user data

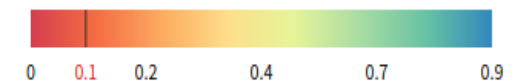


Sample 5901.2442

Top by this sample



Legend



Heatmap settings

Grouping

Bacteria by MetaCyc

☒ Show samples tree

Metabolic potential: specific pathways

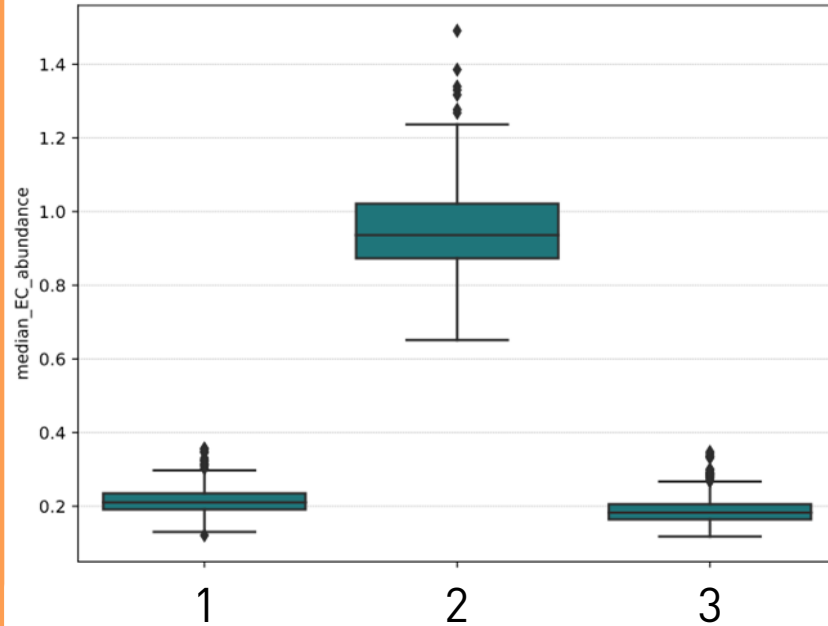


Purpose

Manually curated metabolic pathways for the most clinically-relevant pathways in human gut microbiome differentiation

Description

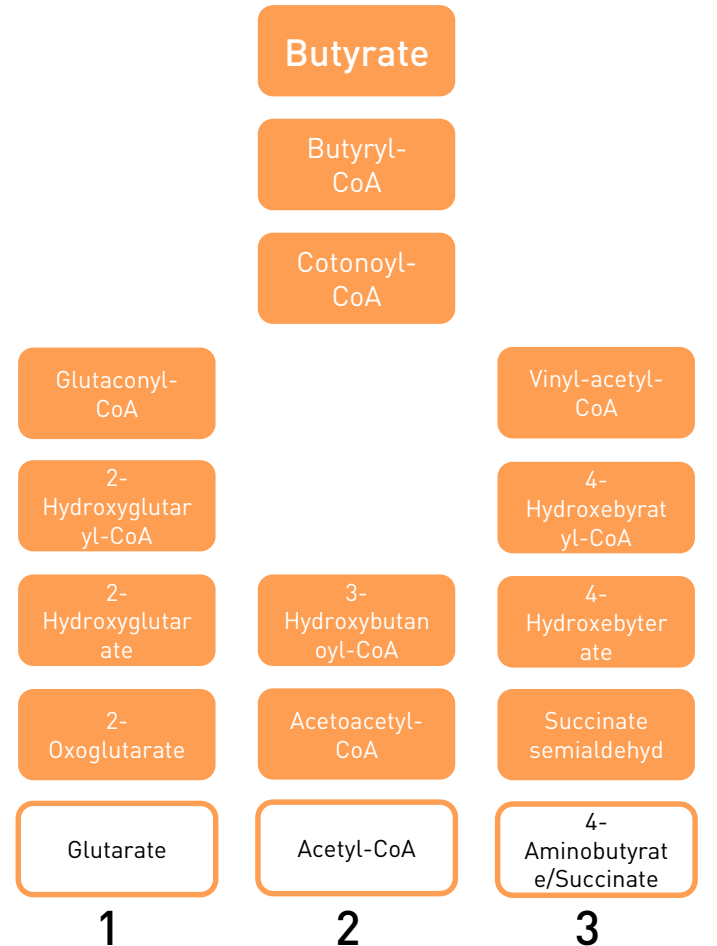
Pathways relative abundances are shown as boxplots and can be downloaded



Pathways curated

Right now curated pathways for SCFA and vitamins synthesis

Alternative butyrate synthesis pathways





Data analysis roadmap

1 Preprocessing

2 Taxa composition analysis

3 Functional potential analysis

4 Factor analysis

For the clinical trials, the crucial part is to identify the specific taxa and metabolic functions associated with clinical data. For this purpose, multiple modules of processing clinical data were integrated into our platform.

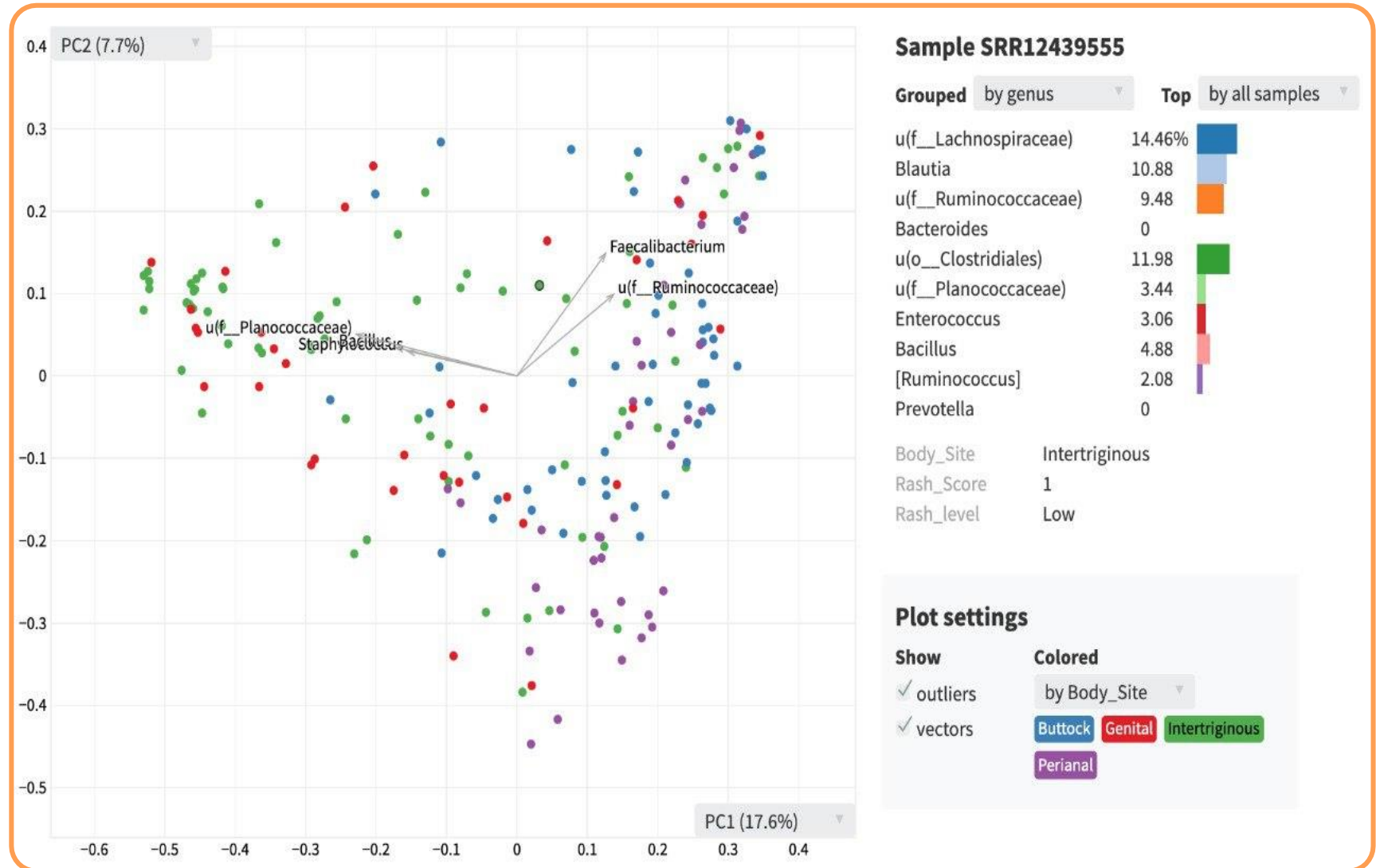
Beta diversity: Categorical factors

Purpose

Observational clinical trials, single time-points comparison

Description

Samples are shown in the space of microbes using relevant dimensionality reduction methods. Two options of visualisation available: color and form



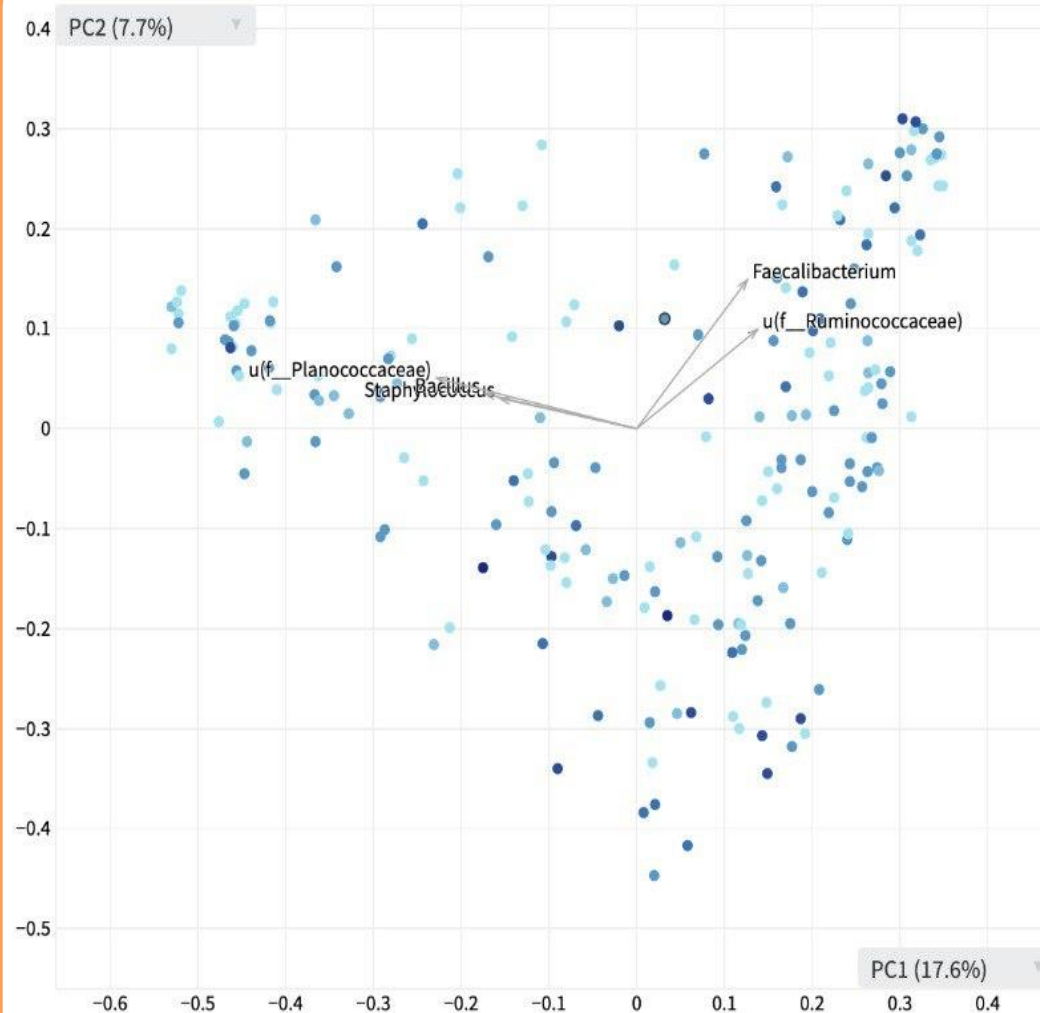
Beta diversity: Continuous factors

Purpose

Observational clinical trials, single time-points comparison

Description

Every point on the plot is a single sample.
The numerical factor visualized as a brightness of points.



Sample SRR12439555

Grouped by genus Top by all samples

u(f__Lachnospiraceae)	14.46%
Blautia	10.88
u(f__Ruminococcaceae)	9.48
Bacteroides	0
u(o__Clostridiales)	11.98
u(f__Planococcaceae)	3.44
Enterococcus	3.06
Bacillus	4.88
[Ruminococcus]	2.08
Prevotella	0

Body_Site Intertriginous
Rash_Score 1
Rash_level Low

Plot settings

Show

- ☒ outliers
- ☒ vectors

Colored

by Rash_Score

0 0.6 1.3 1.9 2.5

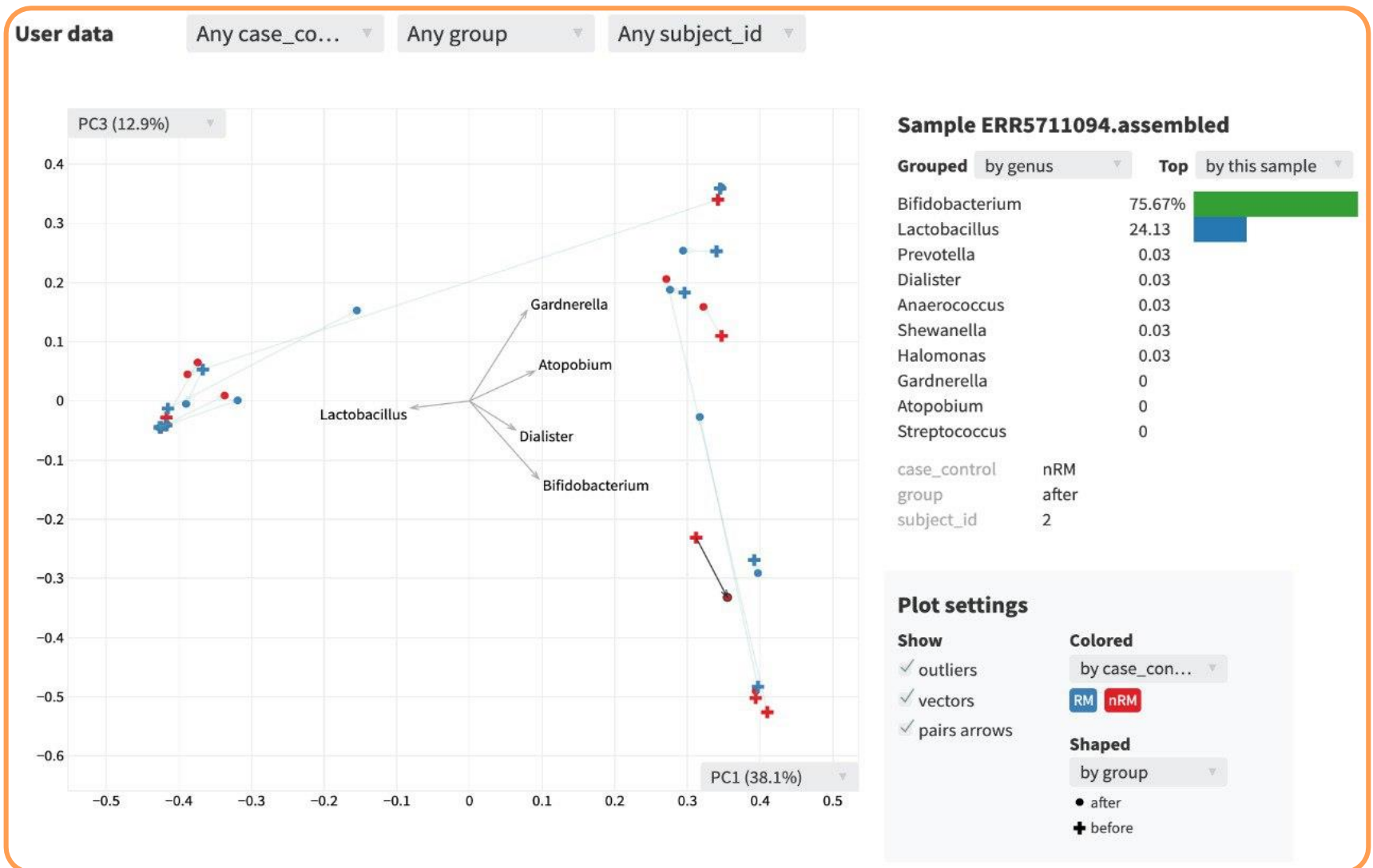
Beta diversity: Paired case-control study

Purpose

Classical interventional placebo - controlled clinical trial design

Description

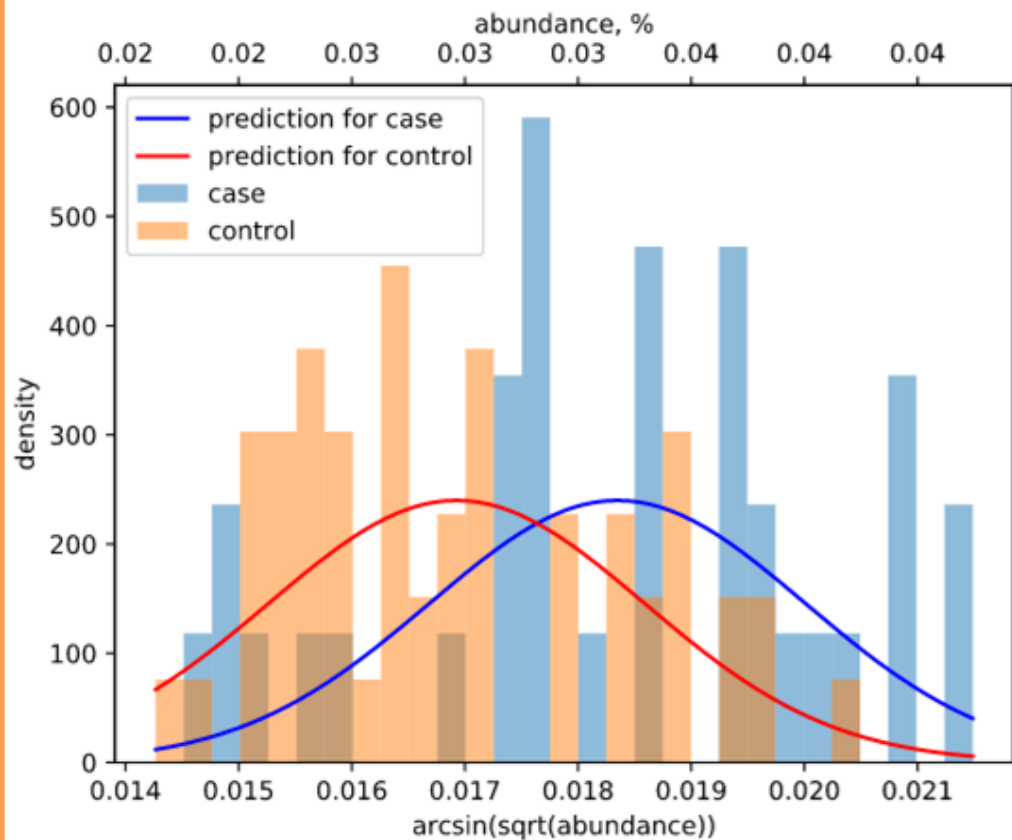
Paired samples are connected by lines. Before/after and placebo/control visulisation can be configured by user



Metabolic potential comparison

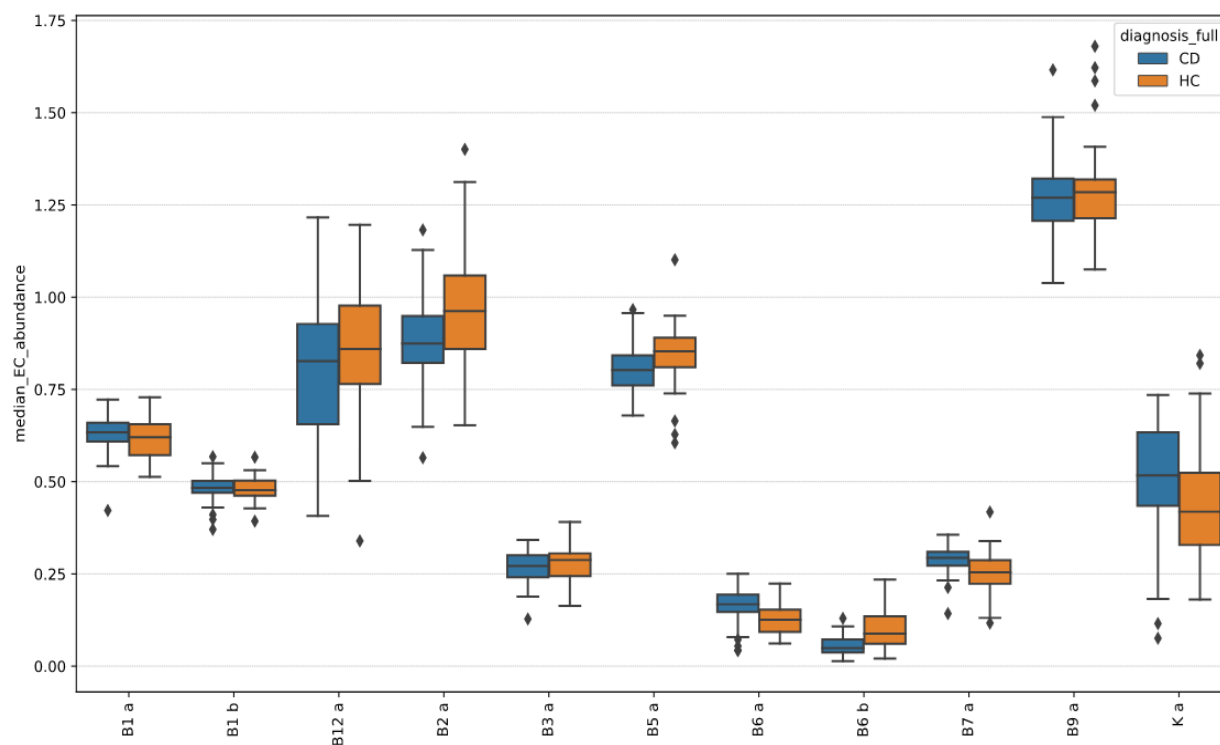


Standard metabolic pathways



Curated metabolic pathways

Bacterial vitamin synthesis pathways

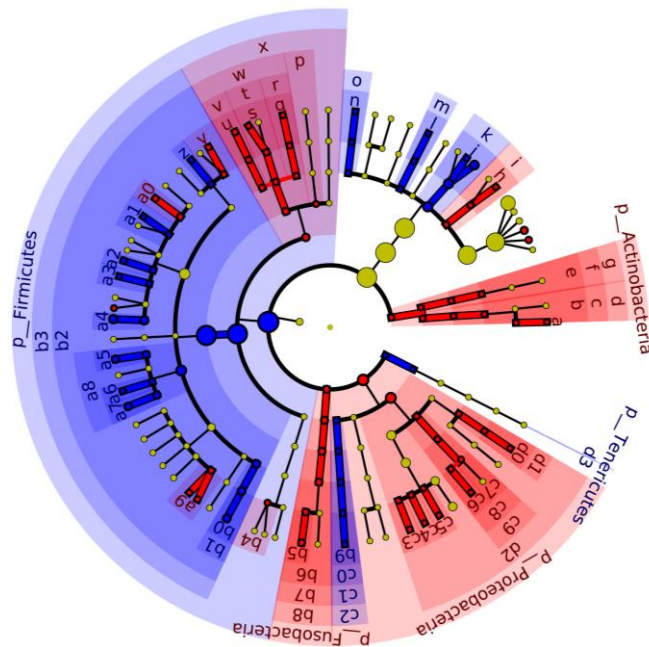


Key taxa discovering

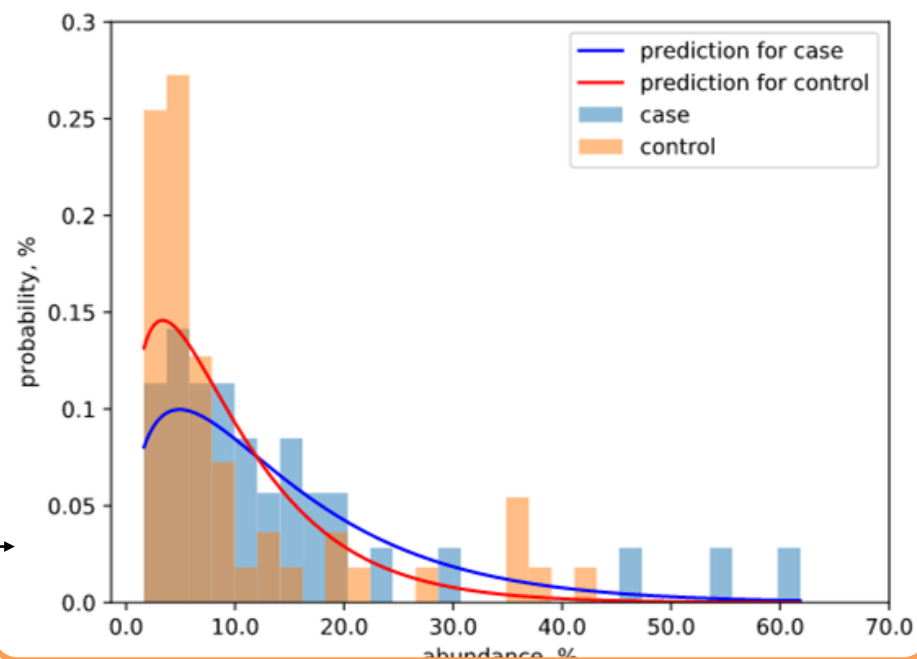
The main goal is to define statistically significant links between factors and microbes on the different taxonomic levels

■ increased in case
■ increased in control

1. Microbiome landscape



2. Single taxa abundance



taxon	taxa level	case mean, %	case sd, %	control mean, %	control sd, %	p-value	adjusted p-value	lda score	sample size
p__Fusobacteria	phylum	4.338	9.277	0.937	1.393	0.000	0.000	4.664	87
p__Actinobacteria	phylum	1.139	1.449	0.536	0.575	0.001	0.003	4.381	87
p__Proteobacteria	phylum	14.532	13.983	9.937	10.362	0.034	0.040	4.122	87

Publications

The platform is being applied in many microbiome studies conducted in house as well as by our customers. Some of results are presented on the slide

To see the list of publications with Knomics Biota in Google scholar ([Click here](#))



Journal of Functional Foods
Volume 83, August 2021, 104572



Yogurt fortified with vitamins and probiotics impacts the frequency of upper respiratory tract infections but not gut microbiome: A multicenter double-blind placebo controlled randomized study



Food Microbiology
Volume 94, April 2021, 103658



Characteristics of bacterial and yeast microbiomes in spontaneous and mixed-fermentation beer and cider



Acta Tropica
Volume 217, May 2021, 105835



The impact of *Opisthorchis felineus* infection and praziquantel treatment on the intestinal microbiota in children



Computational and Structural Biotechnology Journal
Volume 18, 2020, Pages 314-322



Co-occurrence patterns of bacteria within microbiome of Moscow subway



Serum and fecal profiles of aromatic microbial metabolites reflect gut microbiota disruption in critically ill patients: a prospective observational pilot study



Gut microbiome signature of Viliuisk encephalomyelitis in Yakuts includes an increase in microbes linked to lean body mass and eating behaviour

Open Access Article

Microbiome Responses to an Uncontrolled Short-Term Diet Intervention in the Frame of the Citizen Science Project

Open Access Article

Human Gut Microbiome Response Induced by Fermented Dairy Product Intake in Healthy Volunteers

Open Access Article

Subfractional Spectrum of Serum Lipoproteins and Gut Microbiota Composition in Healthy Individuals

Open Access Article

Host-Microbiome Interactions Mediated by Phenolic Metabolites in Chronically Critically Ill Patients

Open Access Article

Microbiome-Metabolome Signature of Acute Kidney Injury

Open Access Editor's Choice Article

Microbiological Activity during Co-Composting of Food and Agricultural Waste for Soil Amendment



nutrients



nutrients



microorganisms



metabolites



metabolites



agronomy



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