



# HoloFoodR

A statistical programming framework for holo-omics data  
integration workflow

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# Agenda

- What is HoloFood?
- What is HoloFoodR?
- Results and the case study
- Discussion and conclusions

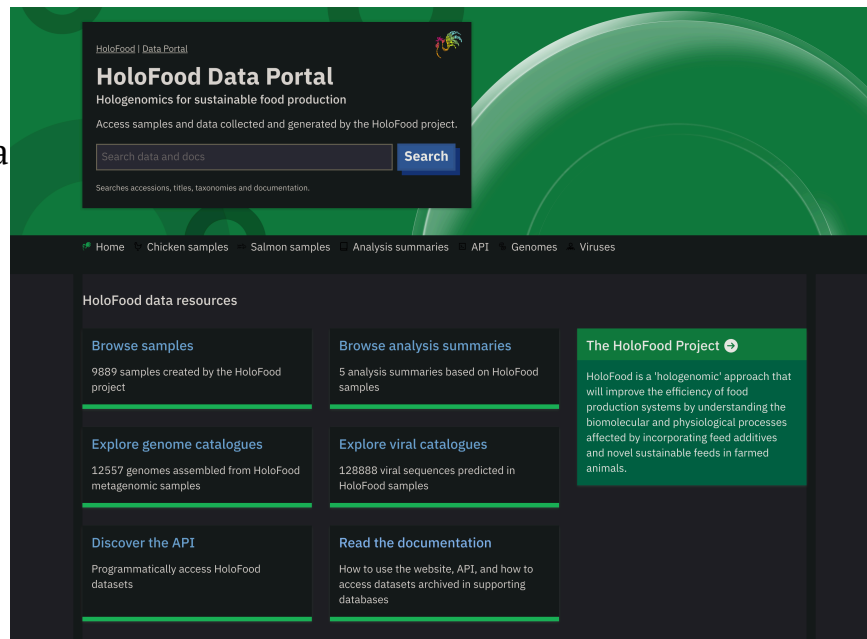


# What is HoloFood?

- Horizon 2020 funded project
- Aimed to study the modulation of animal gut microbiota via food additives
- Two animals were studied: salmon (*Salmo salar*) and chickens (*Gallus gallus*)
- More than 2000 individual specimen
- Biomolecular and physiological measurements are also available
- Hologenome: a set of genomes of the host and microbiota
- HoloFood encompassed more than genomes: metabolomics, transcriptomics, etc.
- Read more about HoloFood

# HoloFood Data Portal

- HoloFood Data Portal provides access to a lot of data
- You can **download** a lot of JSON data with Python...
- ...which you'll need to **transform** into tables...
- There should be an easier way to **download** such valuable data...
- ...and **transform** it into common Bioconductor formats



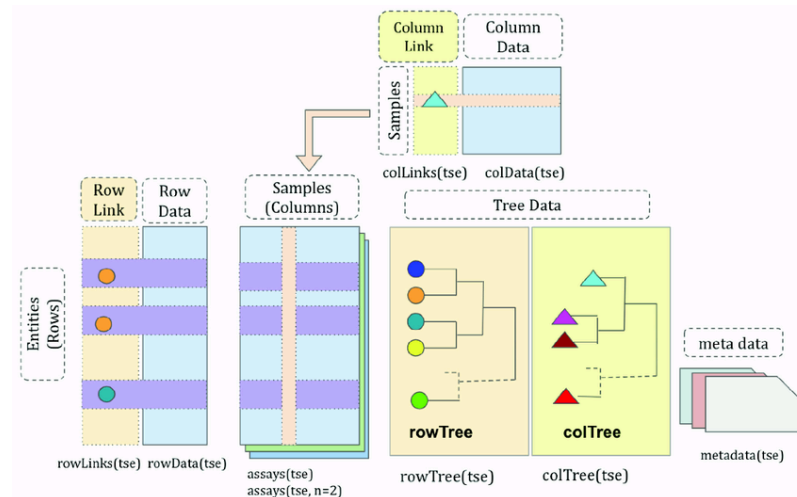
Rogers AB, Kale V, Baldi G, et al. HoloFood Data Portal: holo-omic datasets for analysing host-microbiota interactions in animal production. Database (Oxford). 2025;2025:baae112. doi:10.1093/database/baae112

# HoloFoodR

## ...and transform into common Bioconductor formats

These two formats are:

- TreeSummarizedExperiment
- MultiAssayExperiment



# HoloFoodR workflow

## Data retrieval

Fetch data from HoloFood database

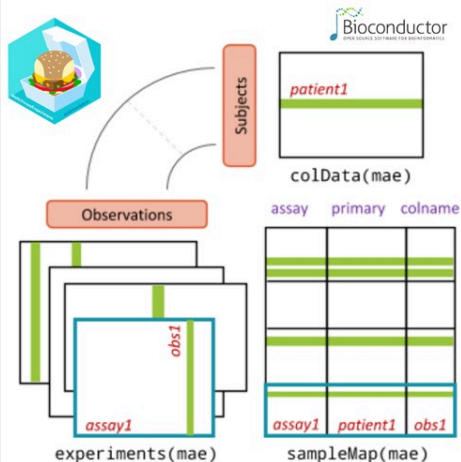


Available salmon and chicken data for in HoloFood database includes:

- Animal and sample metadata
- Host genomic and transcriptomic data
- Metagenomic and metatranscriptomic data
- Metabolomic data

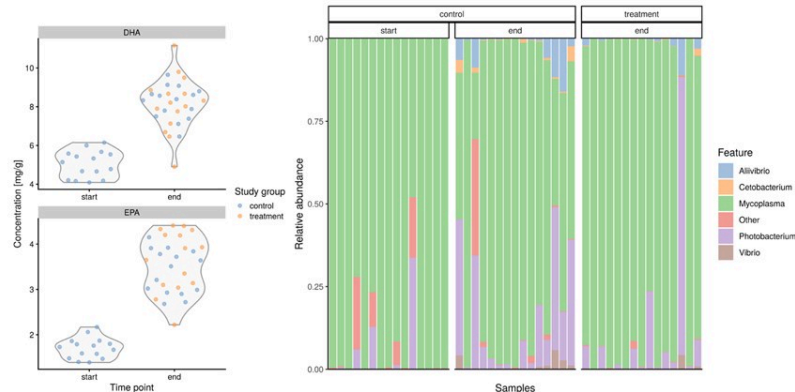
## Multi-omic data container

MultiAssayExperiment links samples across single omic datasets



## Data analysis & visualization

Older salmon have higher levels of omega-3 fatty acids  
Mycoplasma is a dominant species in salmon gut



# Available functions

Function	Description
<code>doQuery()</code>	Search HoloFood database.
<code>getResult()</code>	Retrieve sample-level data (e.g. metadata and measurements) from the HoloFood database in MultiAssayExperiment format.
<code>addMGnify()</code>	Integrate the results retrieved with <code>getResult()</code> with the metagenomic datasets
<code>getData()</code>	Similar to <code>getResult()</code> , more flexible, but returns unstructured data.
<code>getMetaboLights()</code>	Retrieve processed metabolomic data from MetaboLights.
<code>getMetaboLightsFile()</code>	Downloads raw metabolomic data files from MetaboLights.

# Results

- Package released on Bioconductor
- Case study with a formal analysis





# Case study

## Steps

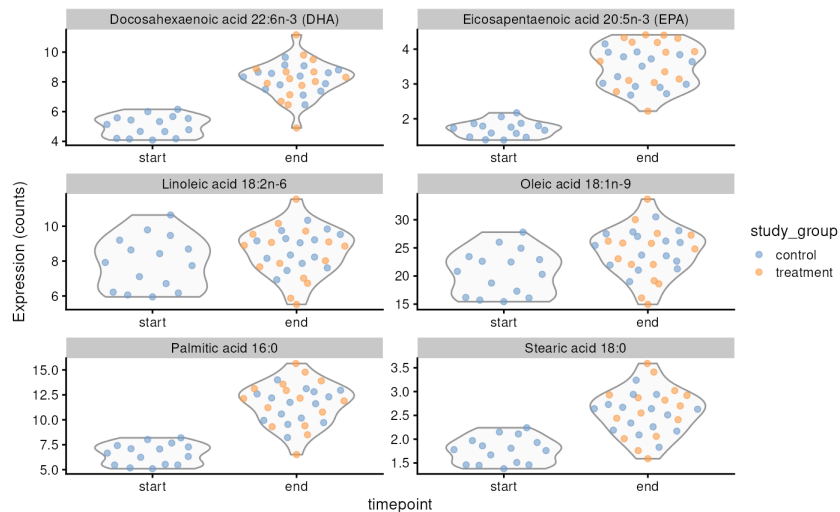
1. **Fetch and integrate** data from the HoloFood and MGnify databases.
2. **Filter, clean, and transform** data for analysis.
3. **Explore and summarize** the data.
4. **Test associations** between fatty acids, time, and treatment.
5. **Test associations** between microbiome composition, time, and treatment.
6. **Characterize the joint variation** between the parallel omics measurements.

# About the data

- Study of a fermented seaweed additive in the salmon diet
- The seaweed contains plenty of bioactive components and a diverse microbiota
- More info on HoloFood Salmon Experimental Design

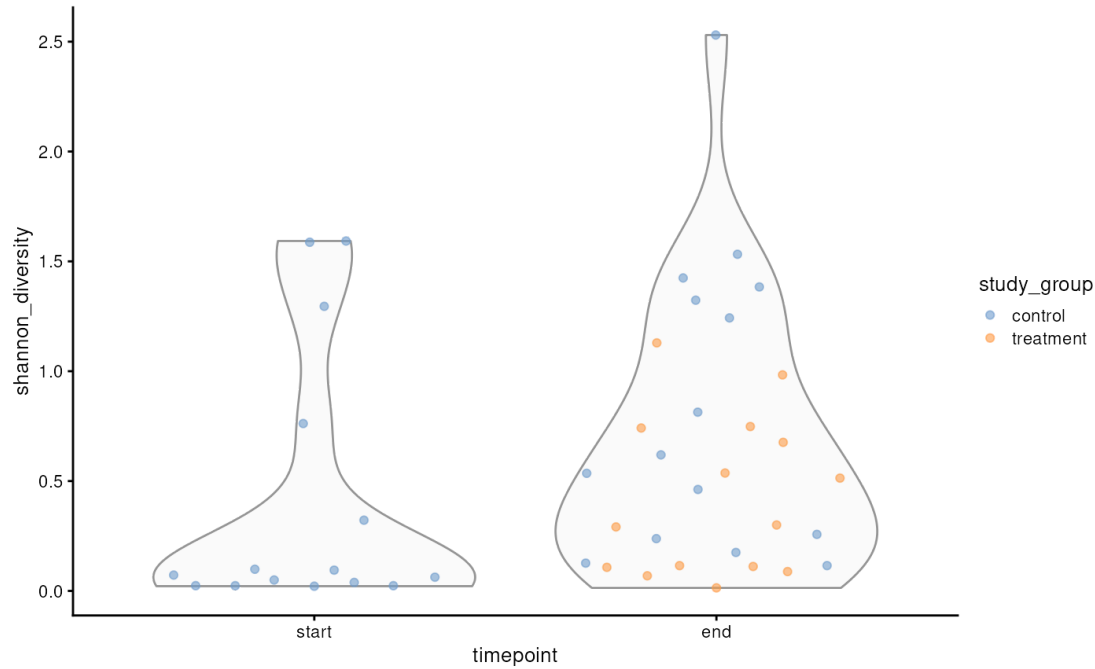
# Now to the actual results

- We did some pre-processing and transformation. You can read more about it in the case study
- We did not find any effect of the treatment on the fatty acid concentrations
- But we did find time effect



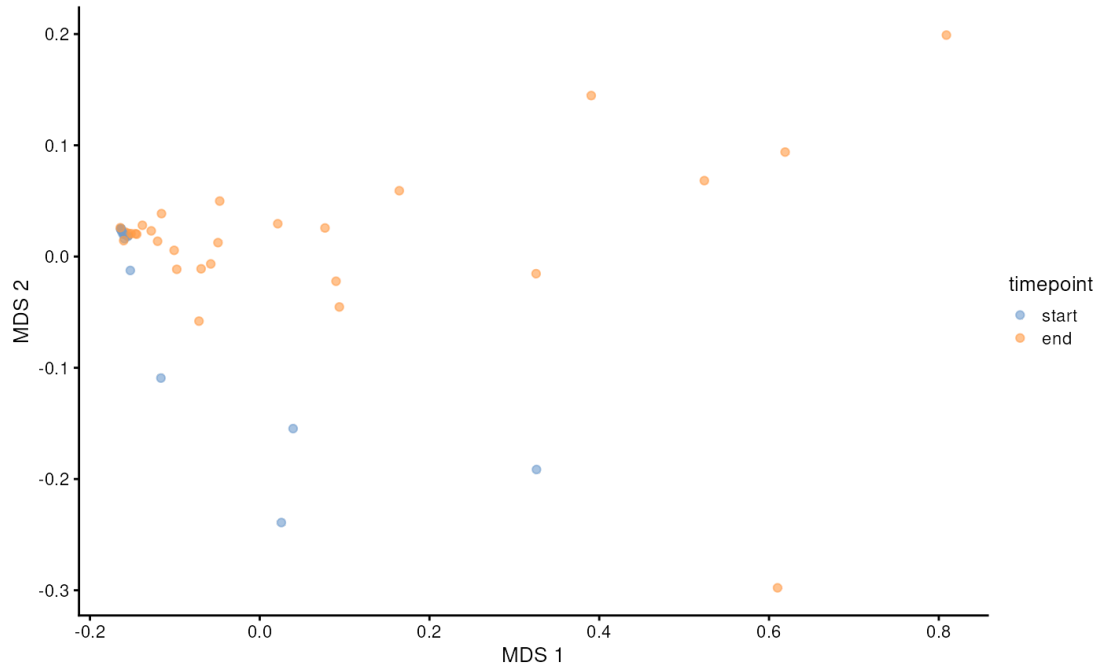
# Shannon alpha-diversity

- Alpha-diversity increased with time ( $p < 0.01$ )



# Beta-diversity

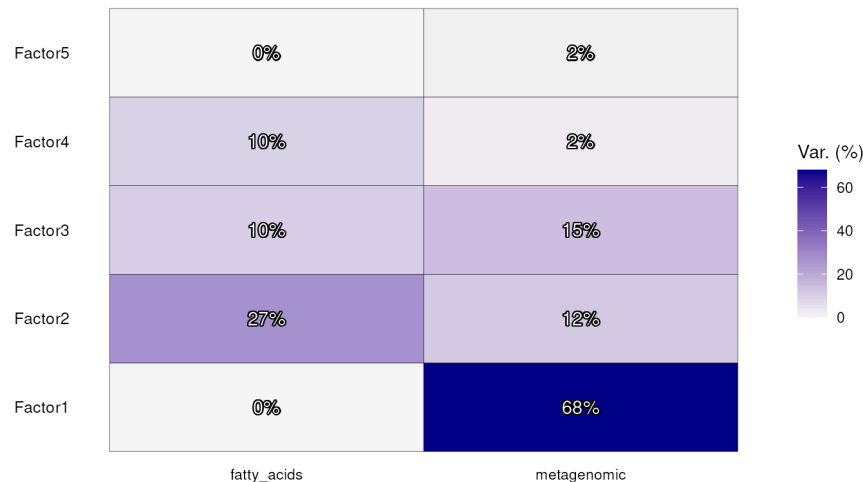
- PCoA (Bray-Curtis) of microbial data
- Samples cluster by timepoint confirming the effect observed in alpha-diversity



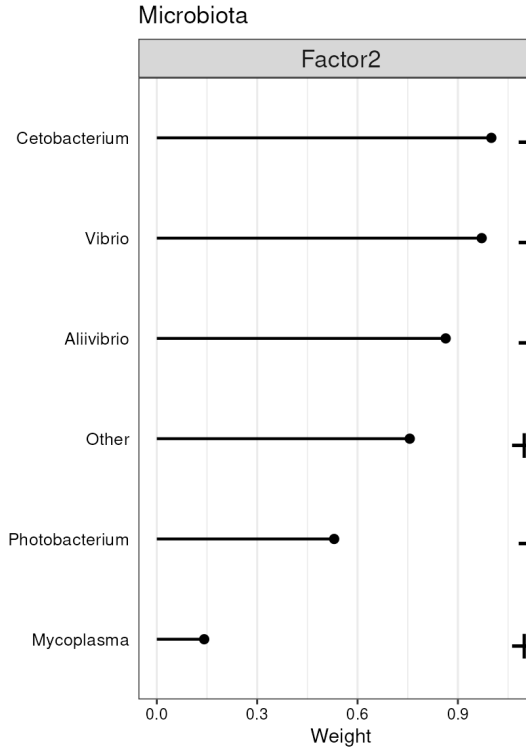
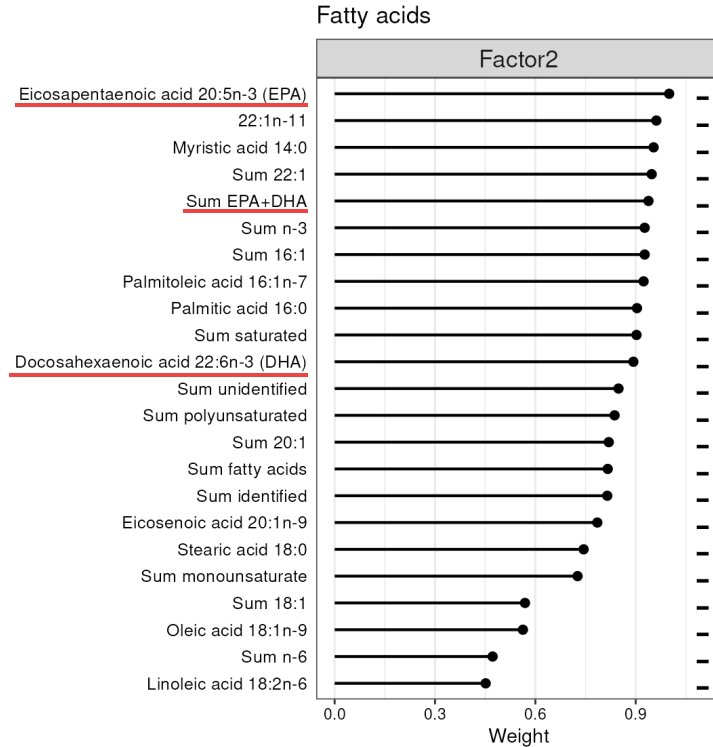
# Multi-omics integration

- Multi-omic factor analysis (MOFA)
- Discover latent factors that underlie the biological differences across multiple omic layers
- Is any fatty acid connected to any taxon?

Explained variance by factor



# Factor 2



# Discussion and conclusions

- Holo-omic analysis relies on curated data
- We bridge the gap between data retrieval and downstream analysis by using standard data containers
- HoloFoodR can facilitate teaching → learn-by-doing for advanced learners
- Raw spectral metabolite data require external tools (e.g. notame)



# Authors



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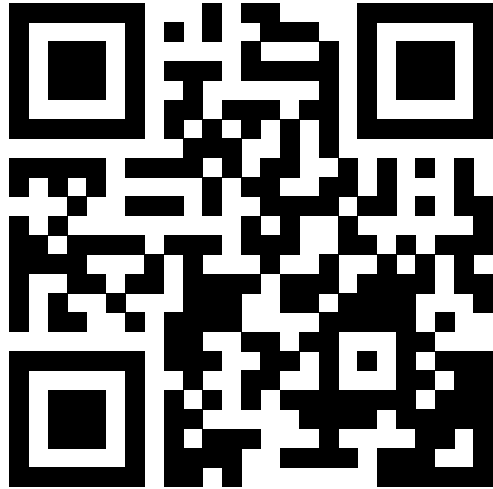
- HoloFood consortium for providing curated data and API
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# Further references

- Tuomas Borman, Artur Sannikov, Robert D Finn, Morten Tønberg Limborg, Alexander B Rogers, Varsha Kale, Kati Hanhineva, Leo Lahti, HoloFoodR: a statistical programming framework for holo-omics data integration workflows, Bioinformatics, Volume 41, Issue 11, November 2025, btaf605, <https://doi.org/10.1093/bioinformatics/btaf605>
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- [HoloFood data portal documentation](#)
- Borman, Tuomas et al. (2025) Orchestrating Microbiome Analysis with Bioconductor. doi: [10.1101/2025.10.29.685036](https://doi.org/10.1101/2025.10.29.685036).
- [HoloFood consortium publications](#)

# Thank you and kiitos! Any questions?

Contact me



Paper

