Hologenomics

Applied to host-microbiota interactions in marine organisms

Antton Alberdi
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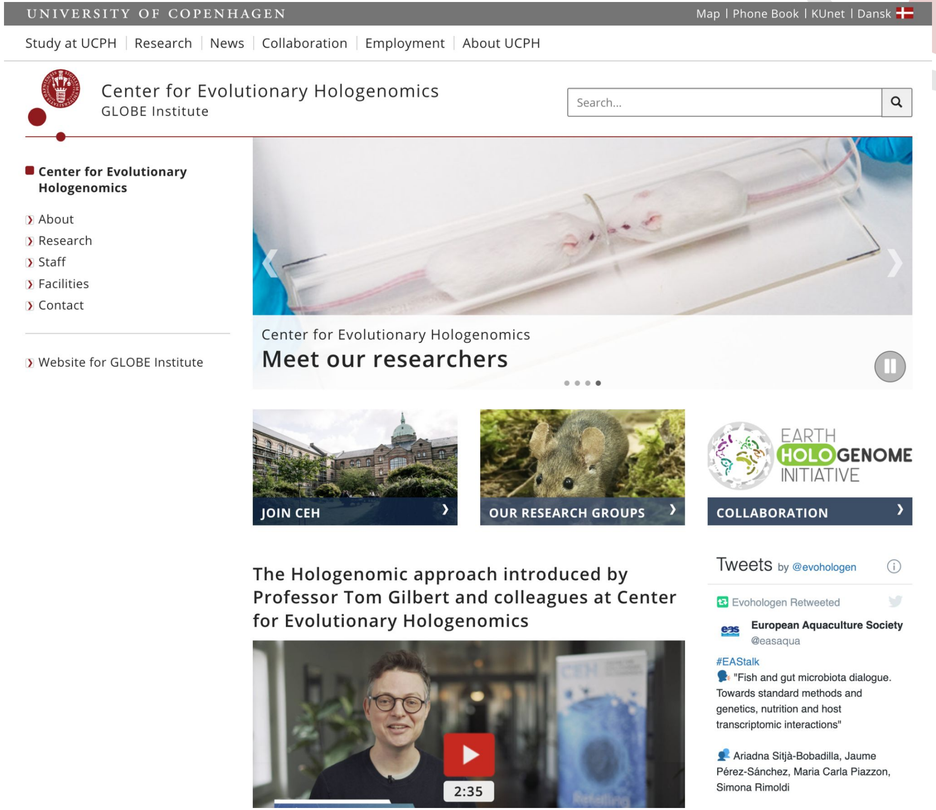
Hologenomics

CENTER FOR EVOLUTIONARY HOLOGENOMICS

UNIVERSITY OF COPENHAGEN



Hologenomics

alberdilab.dk

Hologenomics

55’ **09.30 - 10.25**	**Session 1** Introduction to hologenomics
50’ **10.30 - 11.25**	**Session 2** Experimental design for hologenomics
75’ **11.30 - 12.25**	**Session 3** Bioinformatics methods for hologenomics
30’ **12.30 - 13.30**	**Session 4** Statistics methods for hologenomics

Assignment

Hologenomic grant proposal

Length: 10,000-15,000 characters (3-4 pages)
Submission: May 9th, 2025

Hologenomics

- **Background:** ca. 3000 chr.
- **Hypothesis and objectives:** ca. 1000 chr.
- **Methodology:** ca. 2000 chr.
- **Work plan:** ca. 2000 chr.
- **Impact:** ca. 1000 chr.
- **References**: ca. 15-20

Background

- Start from the big picture and narrow down to the study questions
- Provide enough information to contextualise the hypotheses and objectives
- Avoid cluttering information that does not contribute to the application

Hypotheses and objectives

- Ensure the background information to understand the hypotheses are provided in the background
- Ensure hypotheses are addressable with the proposed methodology and study design

Methodology

- Study system
- Experimental / field work to produce samples
- Laboratory
- Bioinformatics
- Statistics

Work plan

- How is the project going to be structured?
- How long will it take for each task or work package to be accomplished?
- Who is going to conduct each task?

Impact

- What is the scientific impact of your research?
  - How will it contribute to the community?
  - How will it change your field?

- What is the societal impact of your expected results?
  - Environment, sustainability, biodiversity…

References

- Use databases
- Proritise peer-reviewed articles
- Use a reference manager like Mendeley

Assignment

Hologenomic grant proposal

Length: 10,000-15,000 characters (3-4 pages)
Submission: May 9th, 2025, through this form:

https://airtable.com/appi3wfndMqVyksv3/pag6S4jLcyzVV79BP/form

Session 1
Introduction to HOLOGENOMICS

Do not edit

How to change the design

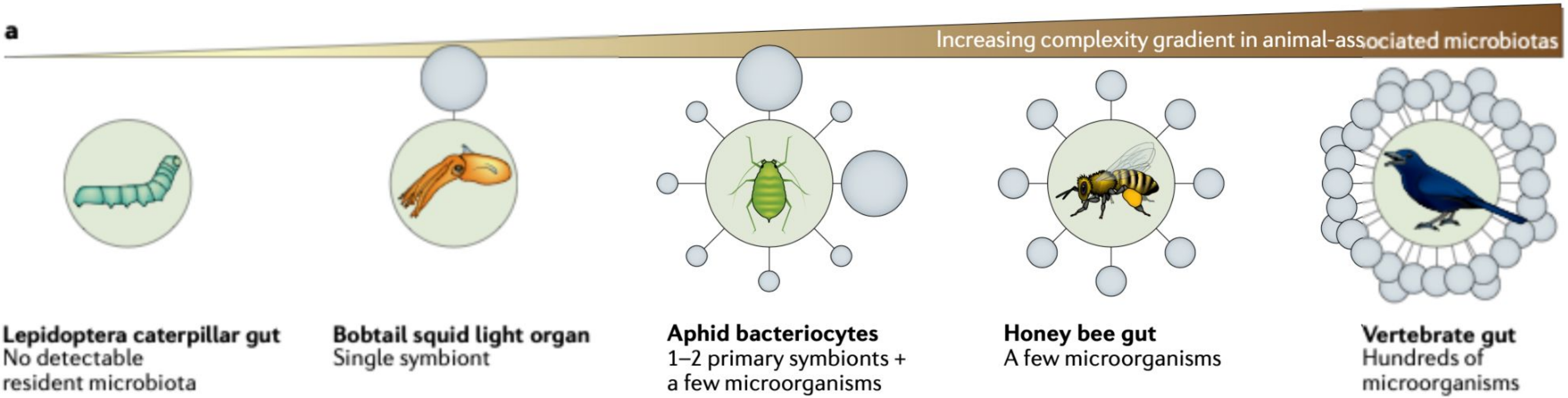
Do all animals have an associated microbiome?

Presenting with animations, GIFs or speaker notes? Enable our Chrome extension

slido

Are animals able to detect and react against all microbes?

Hologenomics



Alberdi et al. 2022

Nature Reviews Genetics

Hologenomics

Corals and dinoflagellates Carbon provision in nutrient-poor waters

Termites and wood decay Lignocellulose degradation

Crop plants and root microbiome Nutrient provision

Cows and rumen microbiota Nutrient metabolism

Laboratory mice and gut microbiota Disease modelling

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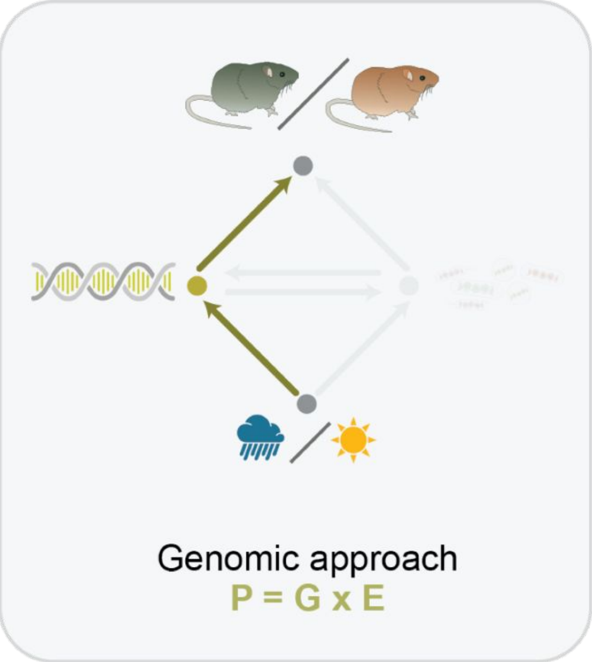
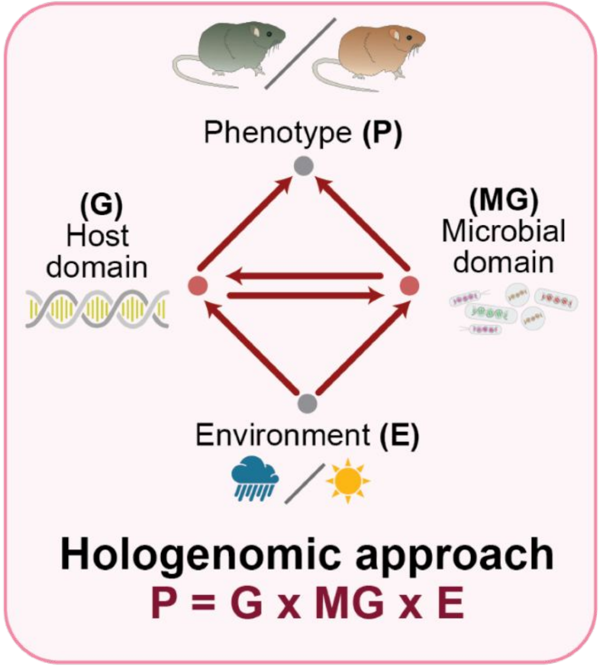
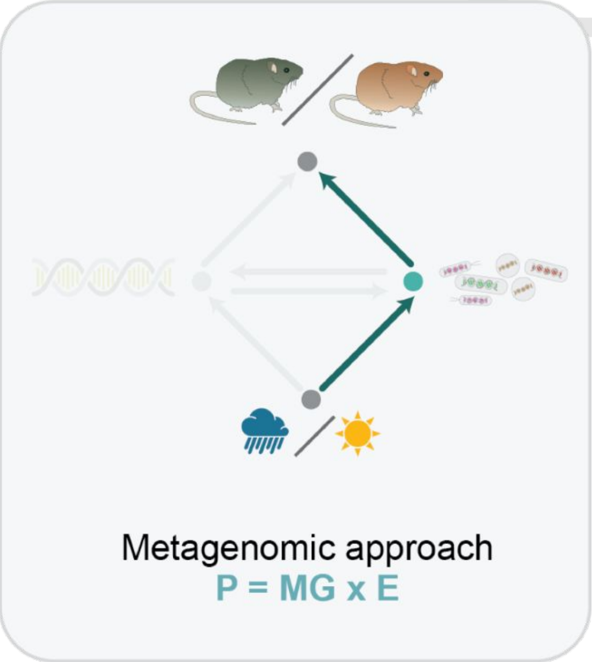
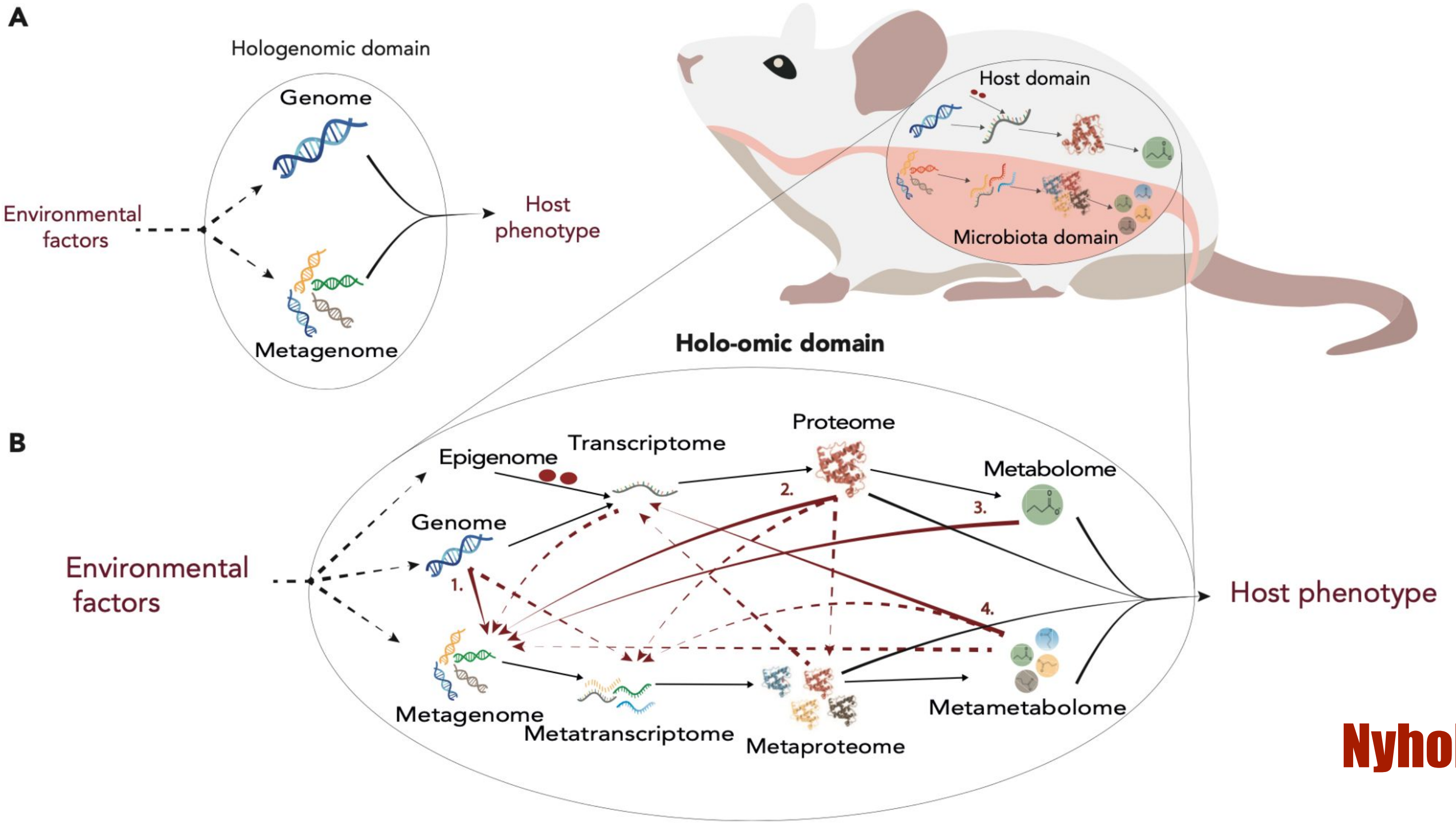
Hologenomics







Hologenomics



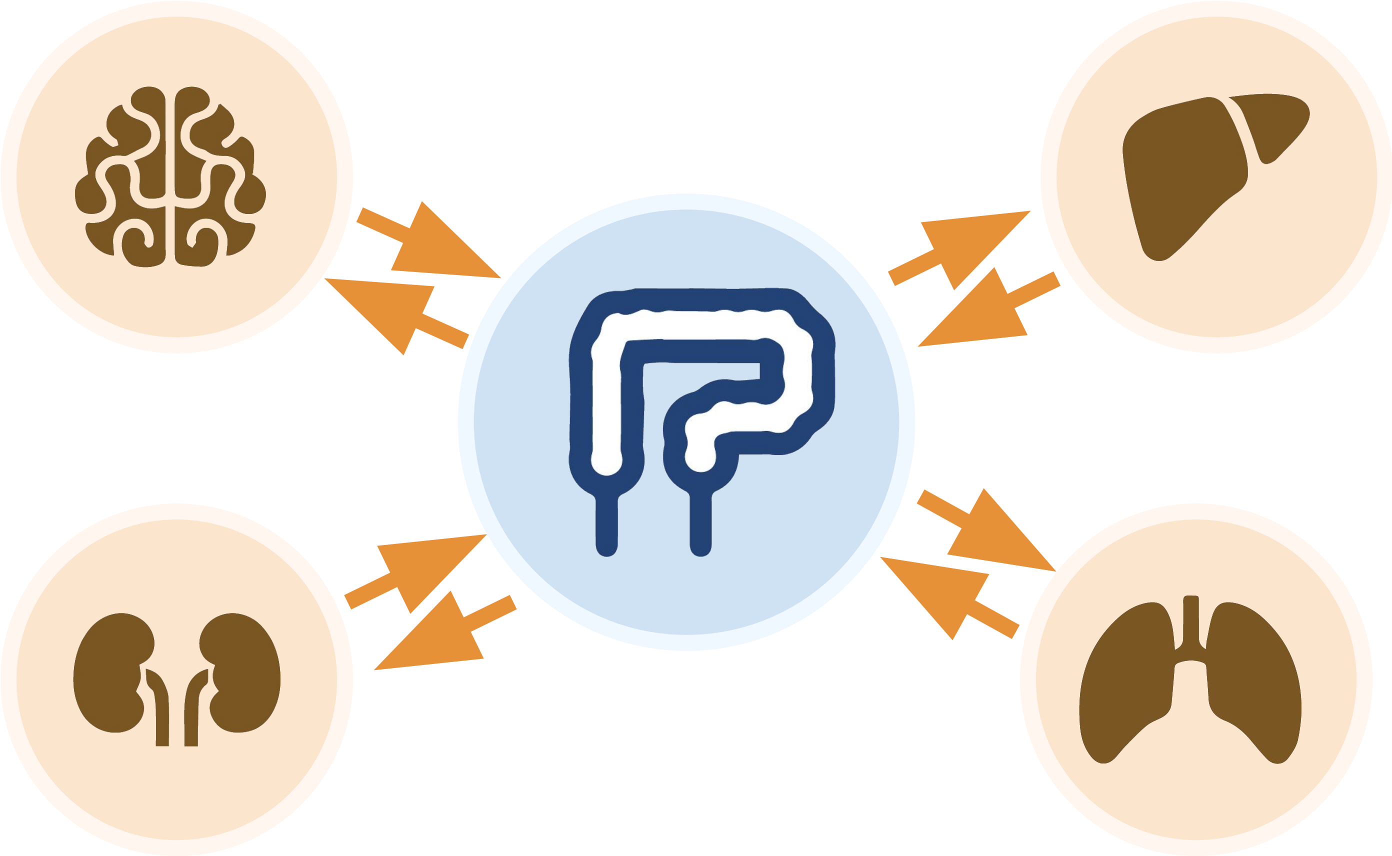
Nyholm et al. 2020
iScience

Host-microbiota interactions

Hologenomics

Gut-brain axis

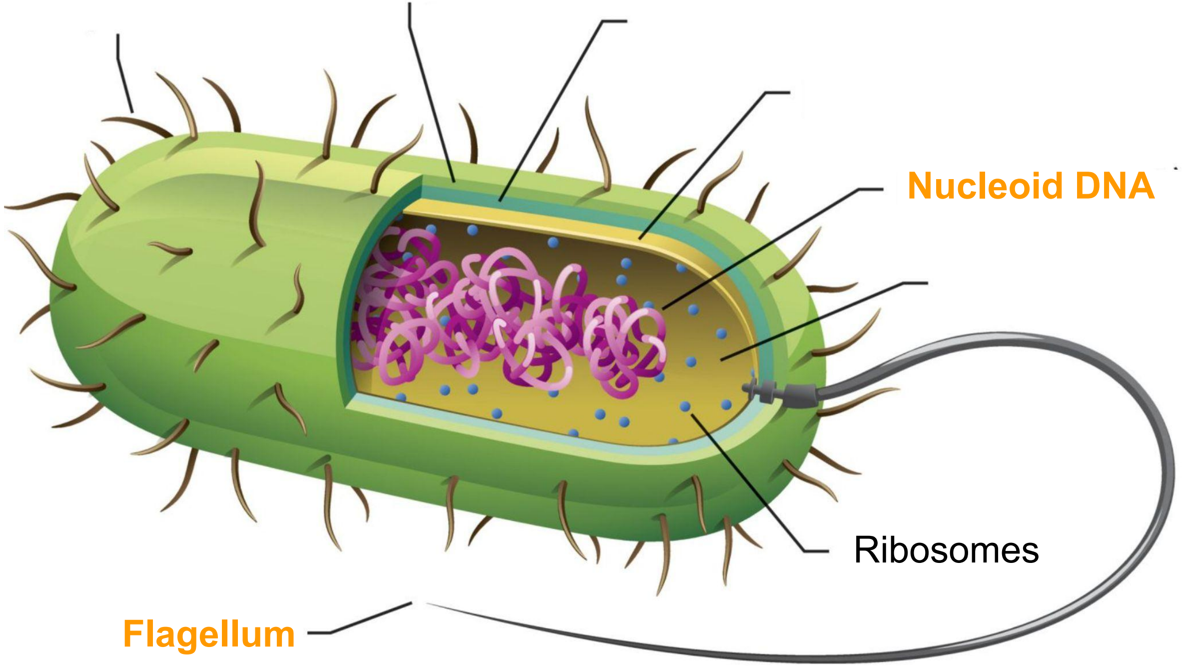
Gut-liver axis



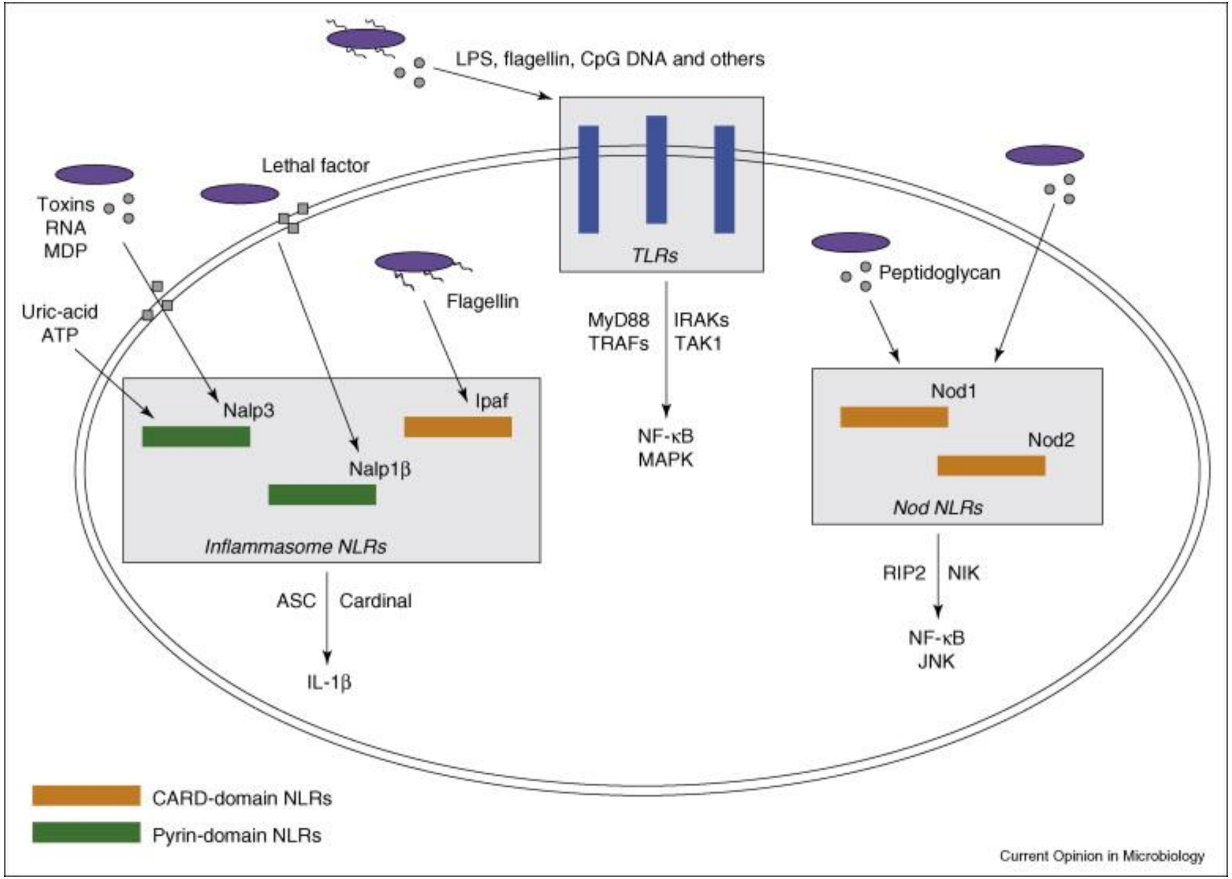
Gut-kidney axis

Gut-lung axis

Hologenomics



Hologenomics

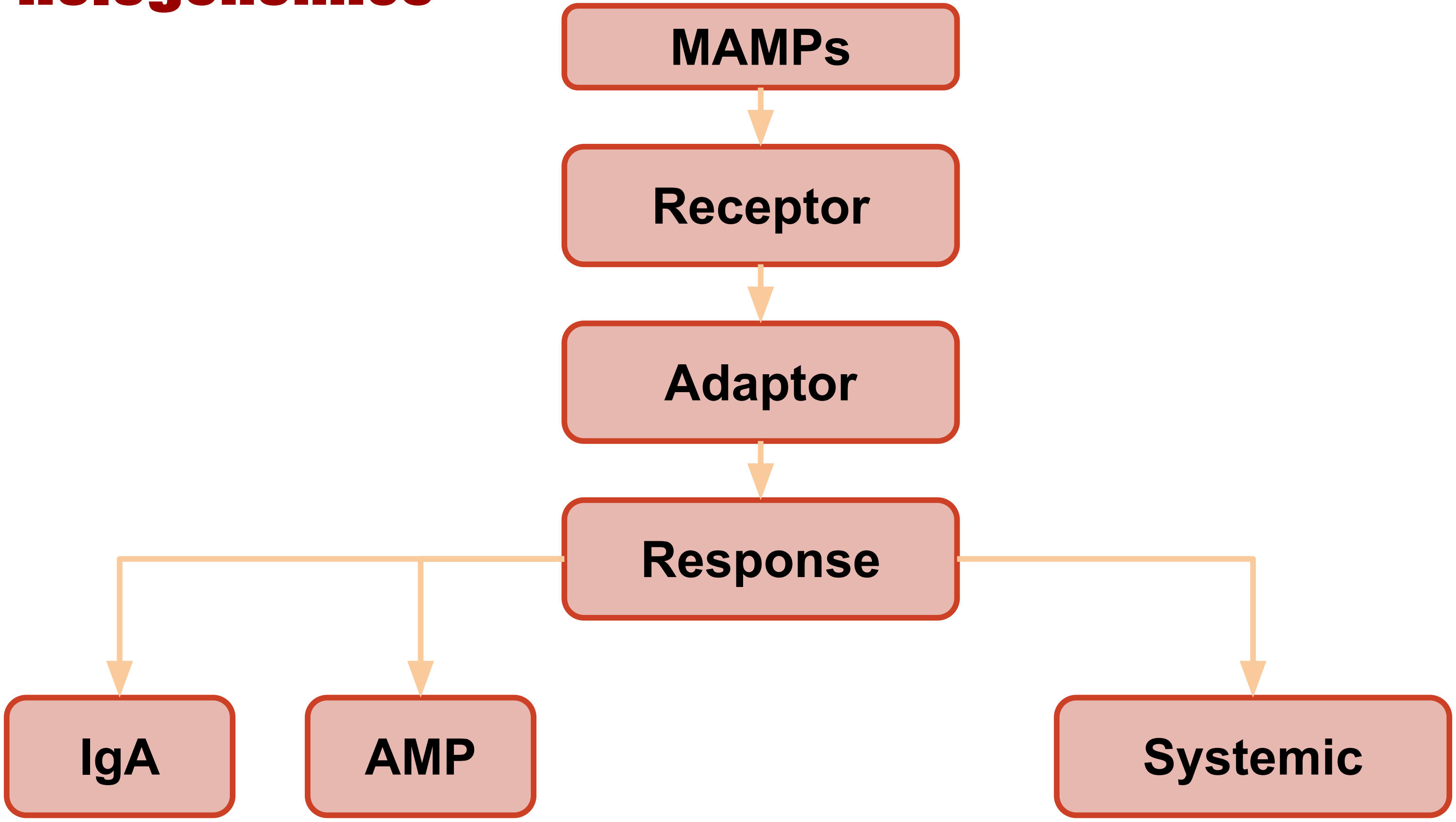


Toll-like receptors (TLR)

Nod-like Receptors (NLR)

Kufer et al. 2007
Current Opinion in Microbiology

Hologenomics



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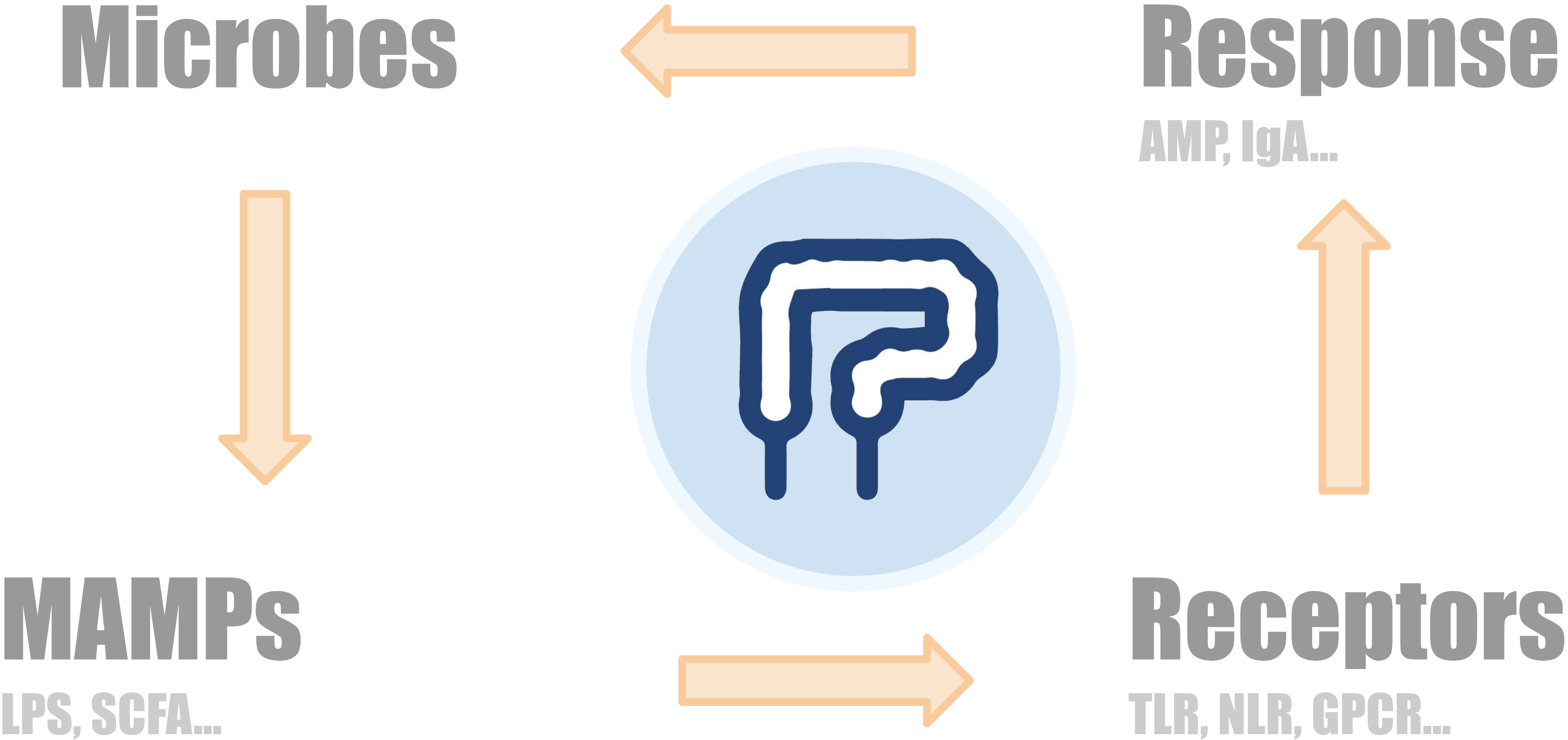


How much of the explanations of "Introduction to Hologenomics" did you understand?

Session 2

Experimental designs for HOLOGENOMICS

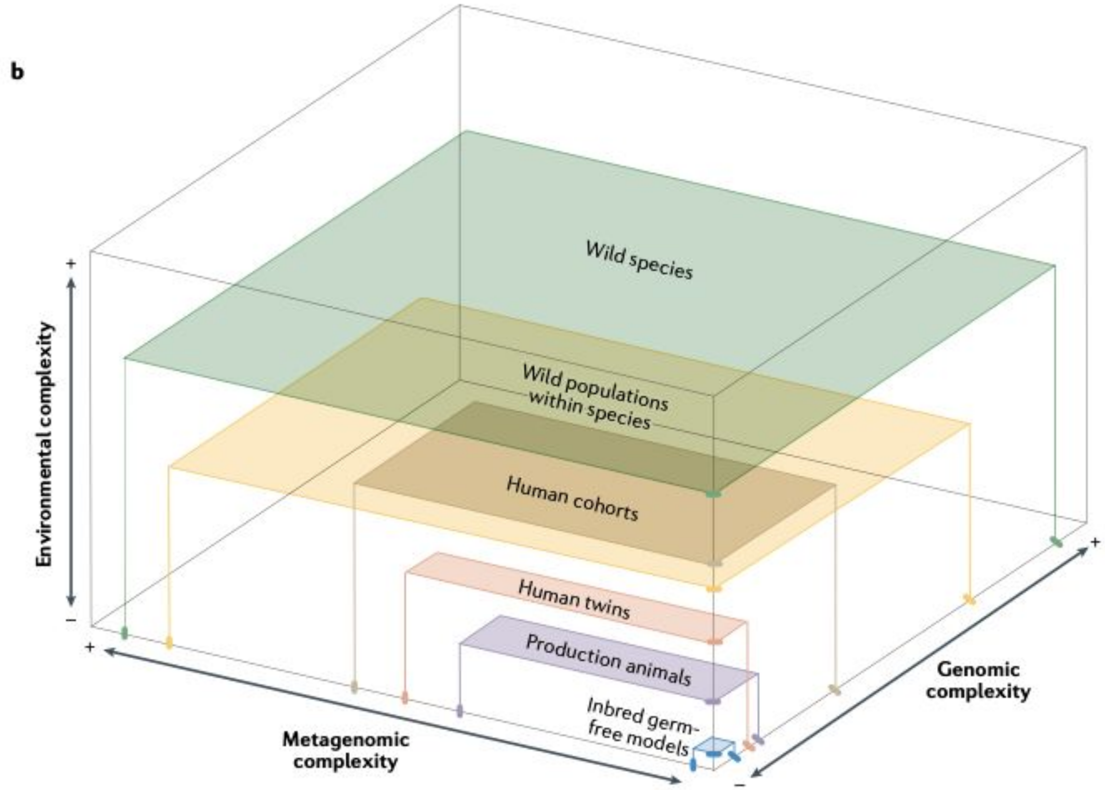
Hologenomics

P = G x MG x E

P = G x MG x E

Interactions

Hologenomics



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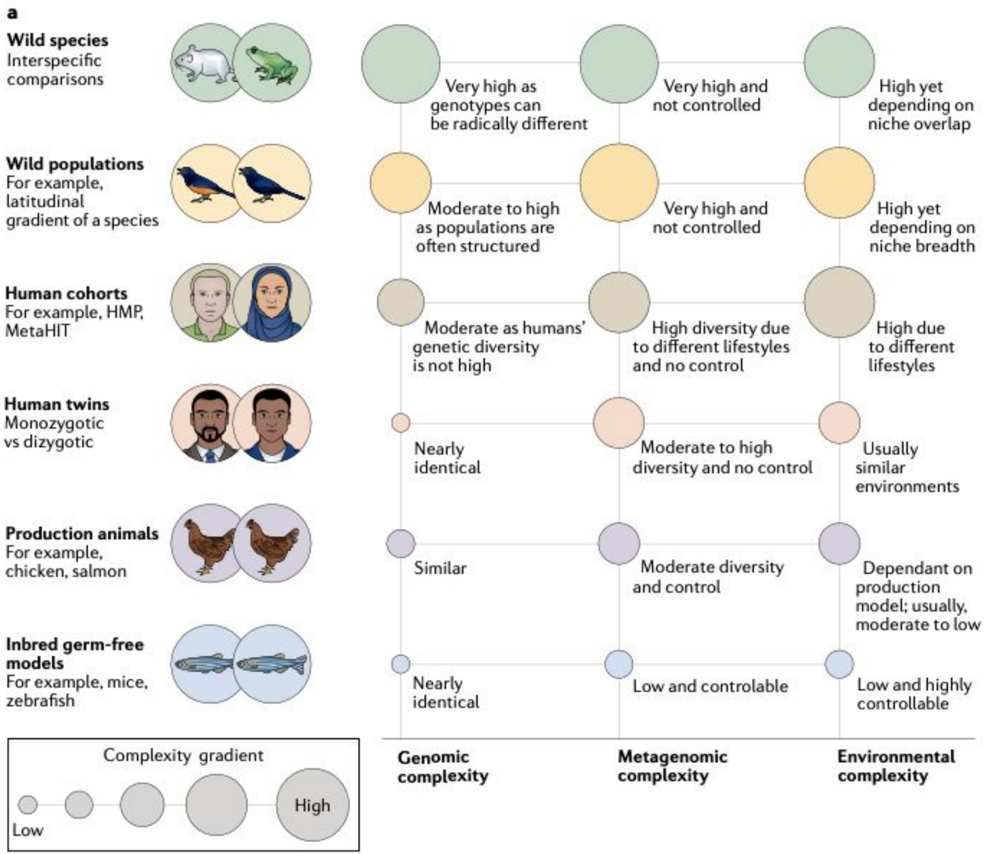
Nature Reviews Genetics

Hologenomics



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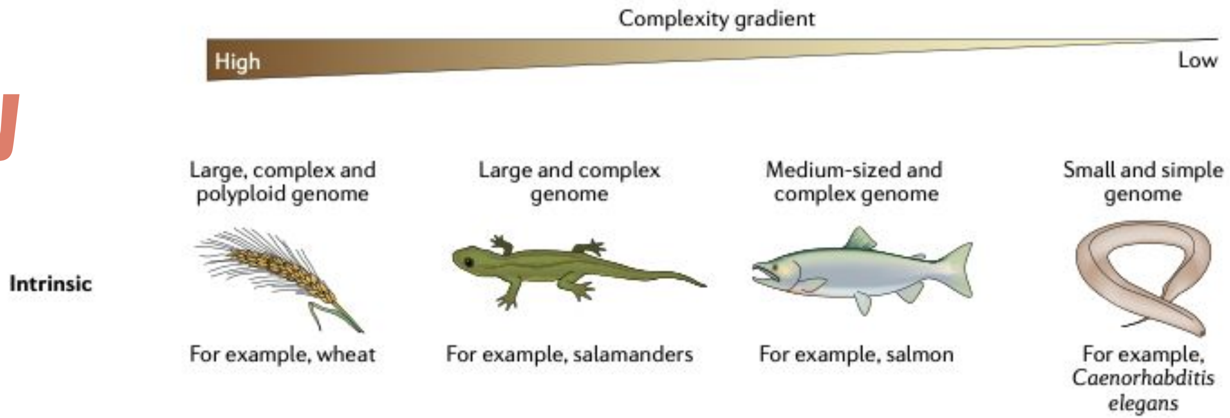
Hologenomics

Genomic complexity



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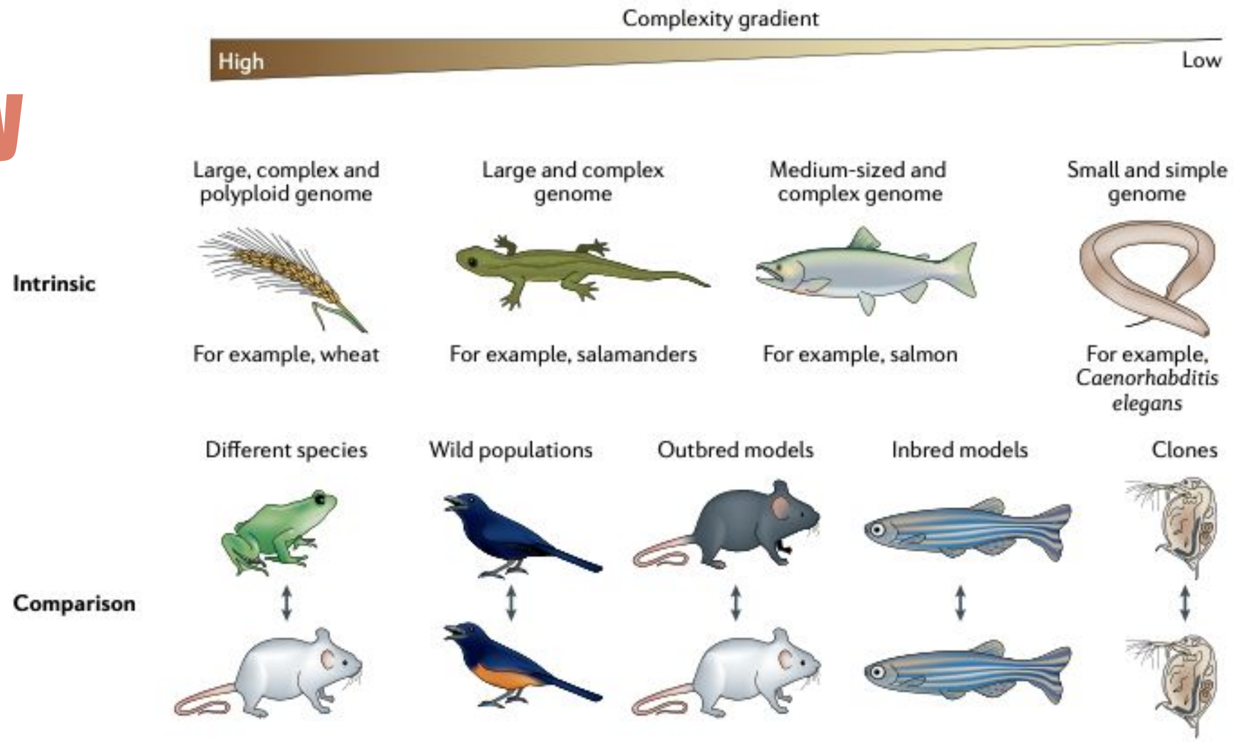
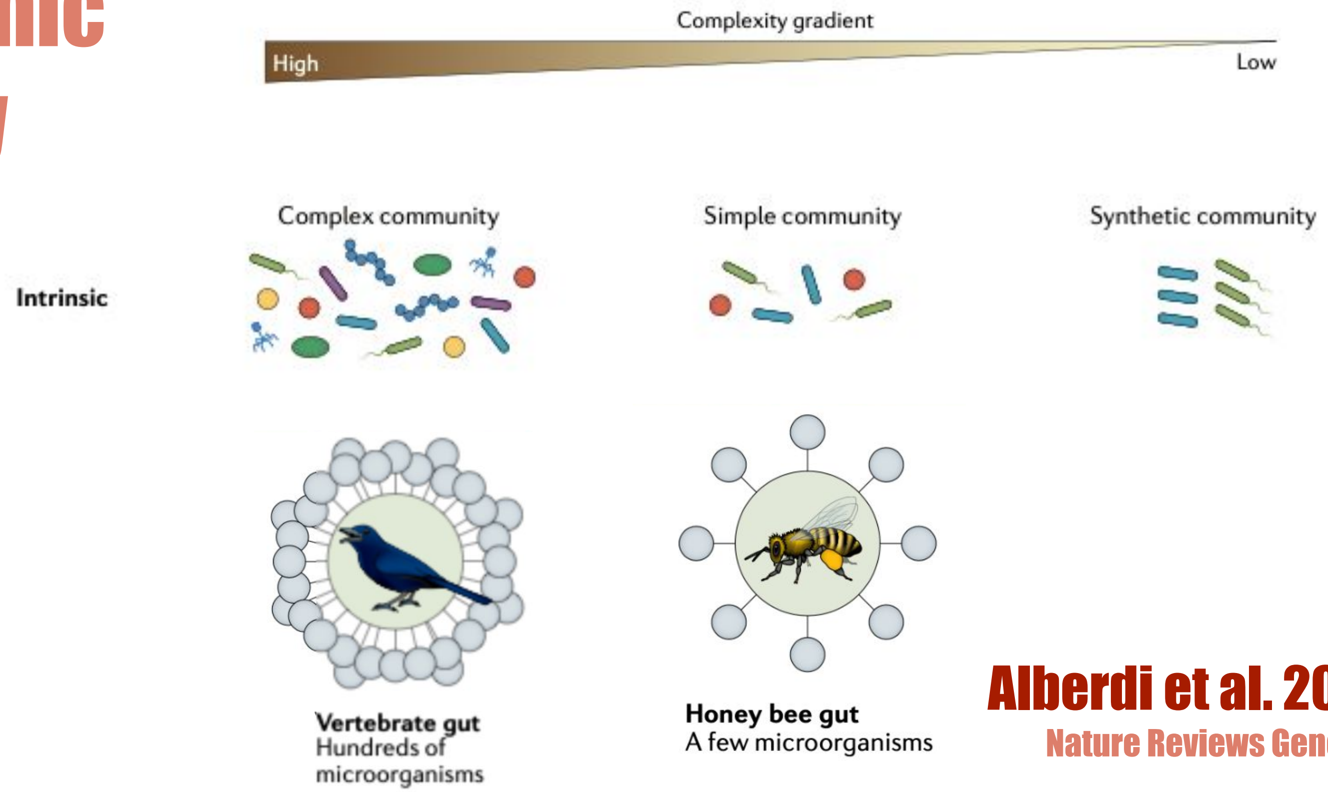
Hologenomics

Genomic complexity



Metagenomic complexity



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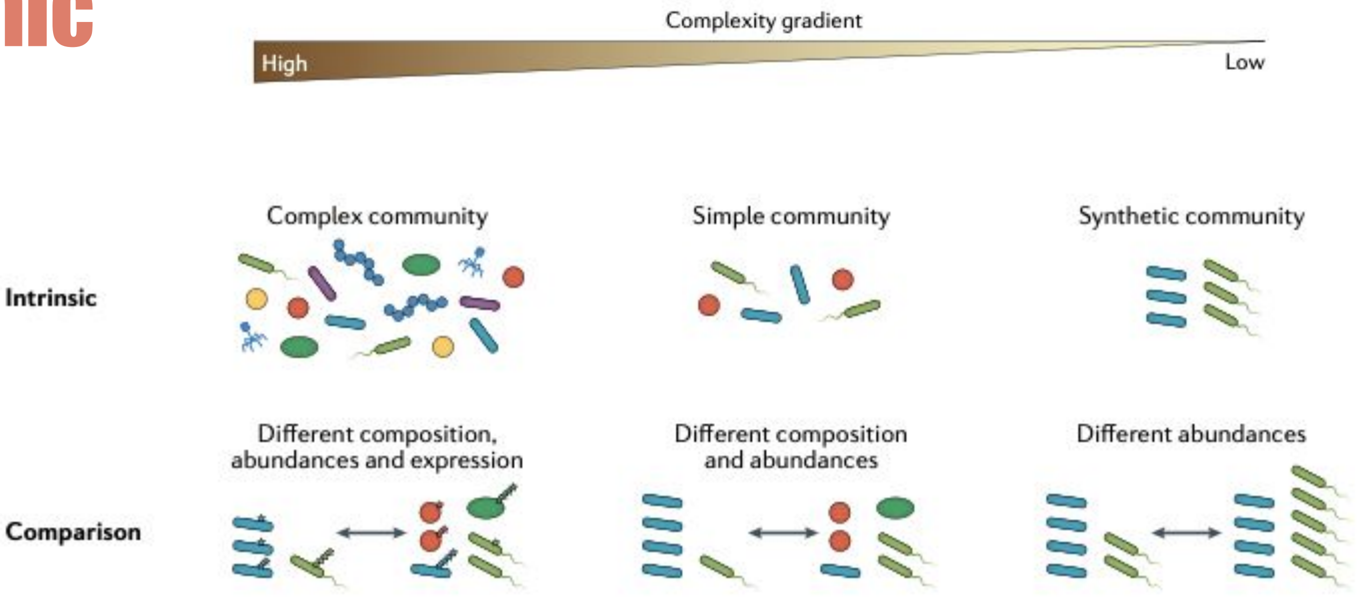
Nature Reviews Genetics

Metagenomic complexity



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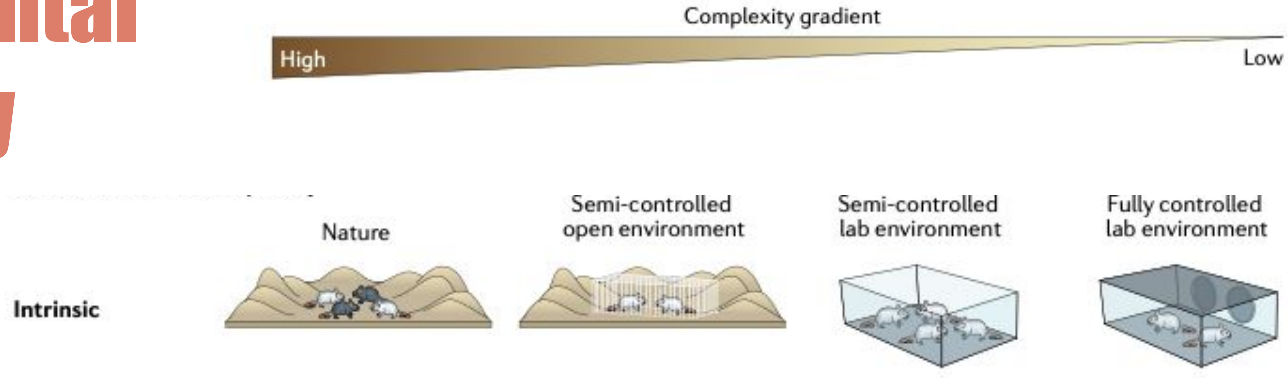
Nature Reviews Genetics

Environmental complexity



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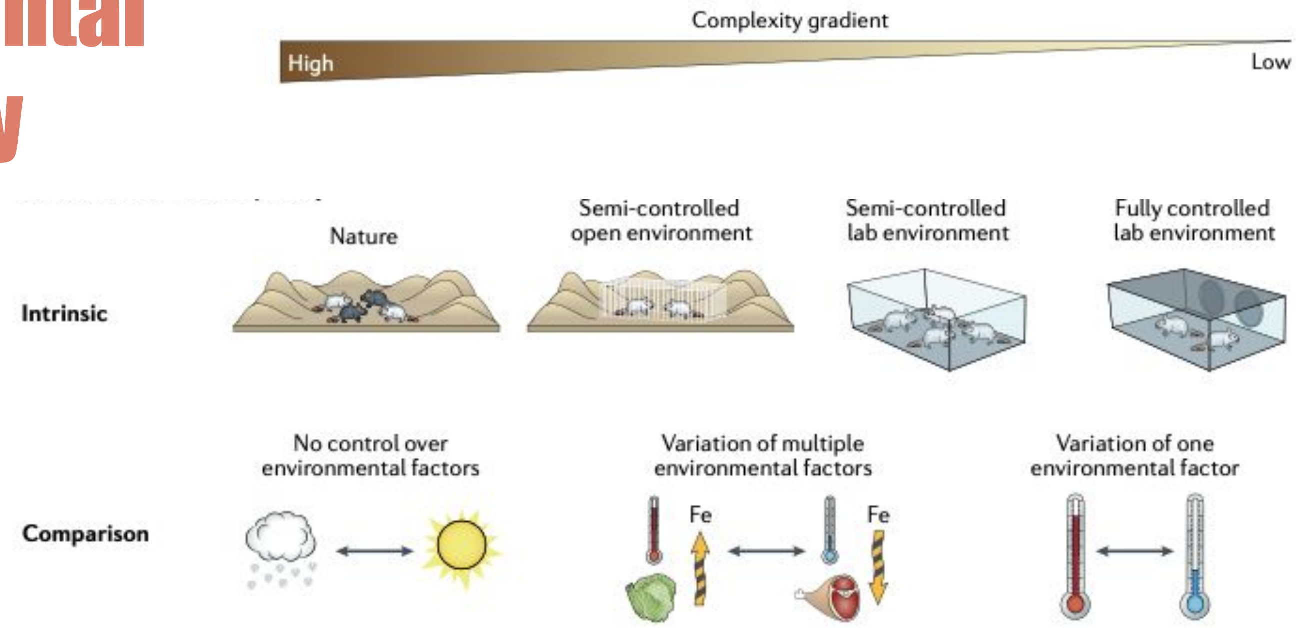
Nature Reviews Genetics

Hologenomics

Environmental complexity



Alberdi et al. 2022

Nature Reviews Genetics

Rank these systems from maximum to minimum according to genomic complexity

Rank these systems from maximum to minimum according to metagenomic complexity

Rank these systems from maximum to minimum according to environmental complexity

Scientific approaches

Hologenomics

Field observation

Received: 25 July 2024 | Accepted: 29 October 2024
DOI: 10.1111/2041-210X.14456

Methods in Ecology and Evolution

RESEARCH ARTICLE

Hologenomic data generation and analysis in wild vertebrates

Carlotta Pietroni[1] | Nanna Gaun[1] | Aoife Leonard[1,2] | Jonas Lauritsen[1] | Garazi Martin-Bideguren[1] | Iñaki Odriozola[1] | Ostaizka Aizpurua[1] | Antton Alberdi[1] | Raphael Eisenhofer[1]

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Handling Editor: Pablo Duchen

Abstract

1. Hologenomics, the joint analysis of host genomes and microbial metagenomes, has the potential to address fundamental biological questions from a systemic host-microbiota perspective. However, multiple fieldwork, laboratory and bioinformatic steps challenge quality, representativeness and comparability of hologenomic data.
2. Leveraging the first 2025 samples sourced from 151 wild vertebrate species analysed in the Earth Hologenome Initiative, we scrutinise hologenomic data generation steps, including laboratory and bioinformatic procedures. Comparisons across taxa and sample types provide novel insights into the relationships between laboratory quality metrics and derived data, the variation of host, prokaryotic and non-prokaryotic fractions of shotgun data, and the relationship between data quality and quantity with genome and metagenome reconstruction.
3. Our results show that faecal samples are significantly better than anal and cloacal swabs to study intestinal microbiomes using genome-resolved metagenomics. We also report that birds and bats both have substantially lower microbial DNA fractions and a higher degree of sample-to-sample variability compared to amphibians, reptiles and non-flying mammals.
4. Based on these data, we provide suggestions to the field for robustly and efficiently generating hologenomic data from wild vertebrates.

KEYWORDS
bioinformatics, ecological genetics, laboratory methods, microbial ecology, molecular biology, molecular methods, population genetics

1 | INTRODUCTION

Mounting evidence points towards the relevance of host-microbiota interactions in ecological and evolutionary processes of both animals and their associated microorganisms (Comizzoli et al., 2021; Davidson et al., 2020; Moeller & Sanders, 2020). Microorganisms play key roles in many eco-evolutionary features of their hosts, including dietary shifts (Kohl et al., 2014), pathogen resistance (Knutie et al., 2017), and defence mechanisms (Vaelli et al., 2020). Meanwhile, spatial–temporal features and functions of animal-associated microbial communities are strongly influenced by the phylogenetic, behavioural, environmental

EARTH HOLOGENOME INITIATIVE

www.earthhologenome.org

Hologenomics

Sampling event metadata (A)

Fieldwork metadata sheet A

Sampling ID	201006_LIMU
Country	France
Region	Limousin
Date	2020/09/23
Latitude	46.552398
Longitude	1.323186
Biome	0196
Env Feature	Dense Pinus radiata plantation
Weather	D
Temperature	17 ºC

All these sample data are related to this animal specimen code

Animal Specimen metadata (B1)

Specimen ID	MMY12
Sampling event ID	201006_LIMU
Species	Myotis myotis
Trapping method	Mistnetting
Trapped time	01:20
Length	5.34 cm
Weight	32.5 grams
Sex	Male
Dev & Repro	Adult

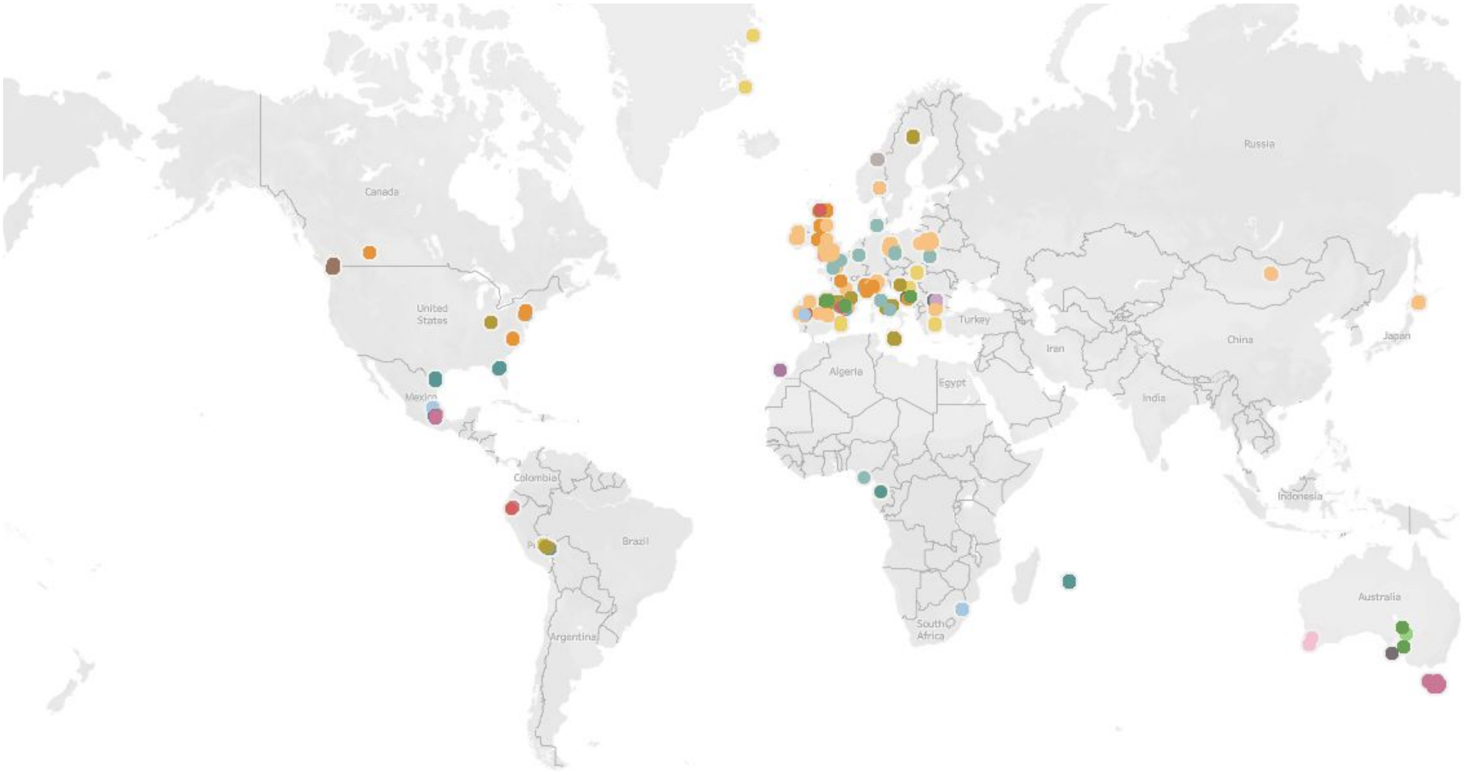
Sample metadata (B2)

Fieldwork metadata sheet B

Tube code	Type	Sample origin	Freshness	Time to freezing
AAB34	Faeces	H	10 minutes	24h
AAB35	Oral swab	D	Immediately	24h
AAB36	Tissue	D	Immediately	24h

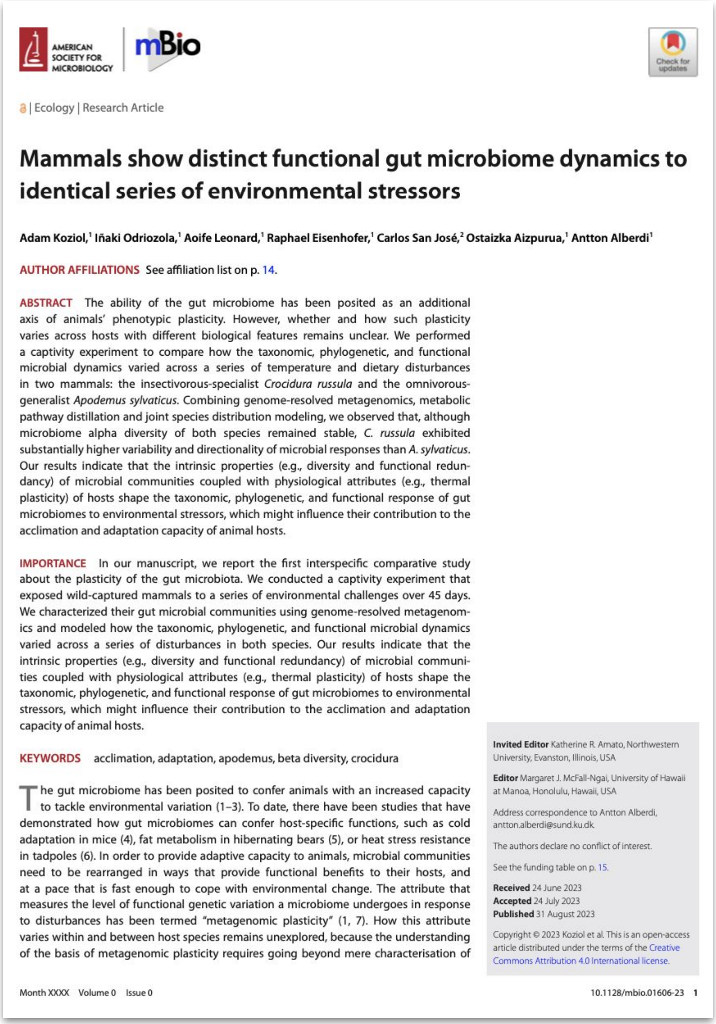
Notes: Full of scars in the wings. Probably quite old.

Hologenomics



Hologenomics

Experimental manipulation



AMERICAN SOCIETY FOR MICROBIOLOGY | mBio

Check for updates

| Ecology | Research Article

Mammals show distinct functional gut microbiome dynamics to identical series of environmental stressors

Adam Koziol,[1] Iñaki Odriozola,[1] Aoife Leonard,[1] Raphael Eisenhofer,[1] Carlos San José,[2] Ostaizka Aizpurua,[1] Antton Alberdi[1]

AUTHOR AFFILIATIONS See affiliation list on p. 14.

ABSTRACT The ability of the gut microbiome has been posited as an additional axis of animals' phenotypic plasticity. However, whether and how such plasticity varies across hosts with different biological features remains unclear. We performed a captivity experiment to compare how the taxonomic, phylogenetic, and functional microbial dynamics varied across a series of temperature and dietary disturbances in two mammals: the insectivorous-specialist *Crocidura russula* and the omnivorous-generalist *Apodemus sylvaticus*. Combining genome-resolved metagenomics, metabolic pathway distillation and joint species distribution modeling, we observed that, although microbiome alpha diversity of both species remained stable, *C. russula* exhibited substantially higher variability and directionality of microbial responses than *A. sylvaticus*. Our results indicate that the intrinsic properties (e.g., diversity and functional redundancy) of microbial communities coupled with physiological attributes (e.g., thermal plasticity) of hosts shape the taxonomic, phylogenetic, and functional response of gut microbiomes to environmental stressors, which might influence their contribution to the acclimation and adaptation capacity of animal hosts.

IMPORTANCE In our manuscript, we report the first interspecific comparative study about the plasticity of the gut microbiota. We conducted a captivity experiment that exposed wild-captured mammals to a series of environmental challenges over 45 days. We characterized their gut microbial communities using genome-resolved metagenomics and modeled how the taxonomic, phylogenetic, and functional microbial dynamics varied across a series of disturbances in both species. Our results indicate that the intrinsic properties (e.g., diversity and functional redundancy) of microbial communities coupled with physiological attributes (e.g., thermal plasticity) of hosts shape the taxonomic, phylogenetic, and functional response of gut microbiomes to environmental stressors, which might influence their contribution to the acclimation and adaptation capacity of animal hosts.

KEYWORDS acclimation, adaptation, apodemus, beta diversity, crocidura

The gut microbiome has been posited to confer animals with an increased capacity to tackle environmental variation (1–3). To date, there have been studies that have demonstrated how gut microbiomes can confer host-specific functions, such as cold adaptation in mice (4), fat metabolism in hibernating bears (5), or heat stress resistance in tadpoles (6). In order to provide adaptive capacity to animals, microbial communities need to be rearranged in ways that provide functional benefits to their hosts, and at a pace that is fast enough to cope with environmental change. The attribute that measures the level of functional genetic variation a microbiome undergoes in response to disturbances has been termed "metagenomic plasticity" (1, 7). How this attribute varies within and between host species remains unexplored, because the understanding of the basis of metagenomic plasticity requires going beyond mere characterisation of

Invited Editor Katherine R. Amato, Northwestern University, Evanston, Illinois, USA

Editor Margaret J. McFall-Ngai, University of Hawaii at Manoa, Honolulu, Hawaii, USA

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The authors declare no conflict of interest.

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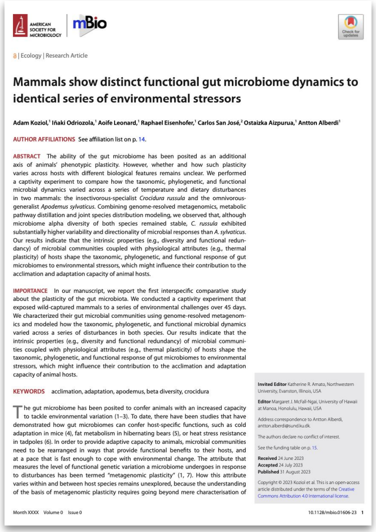
Hologenomics

Experimental manipulation



a | Ecology | Research Article

Mammals show distinct functional gut microbiome dynamics to identical series of environmental stressors

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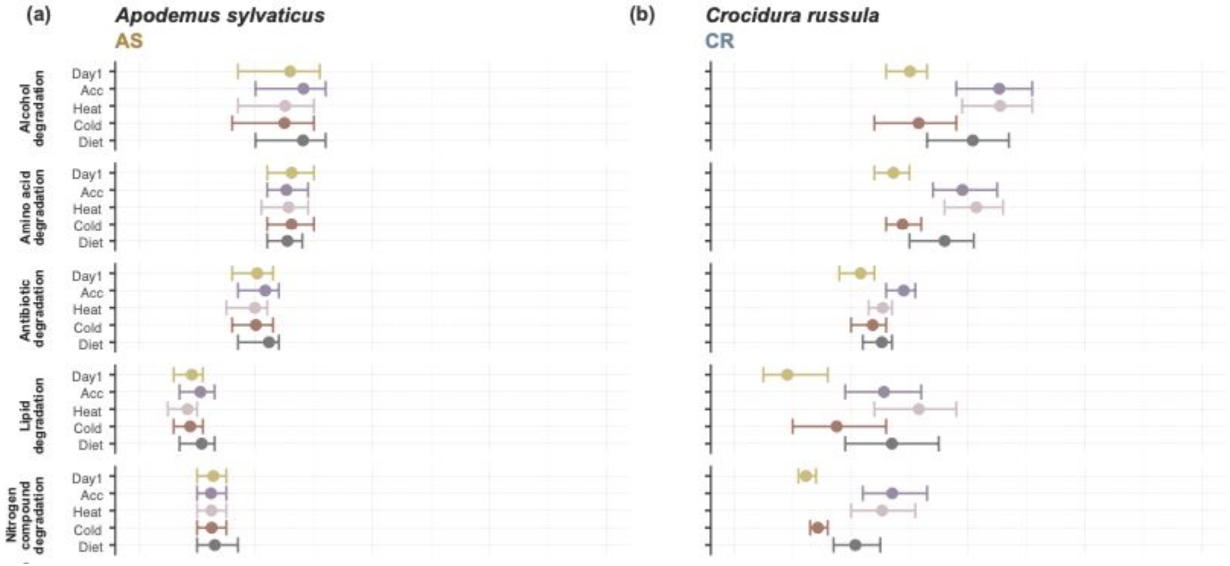
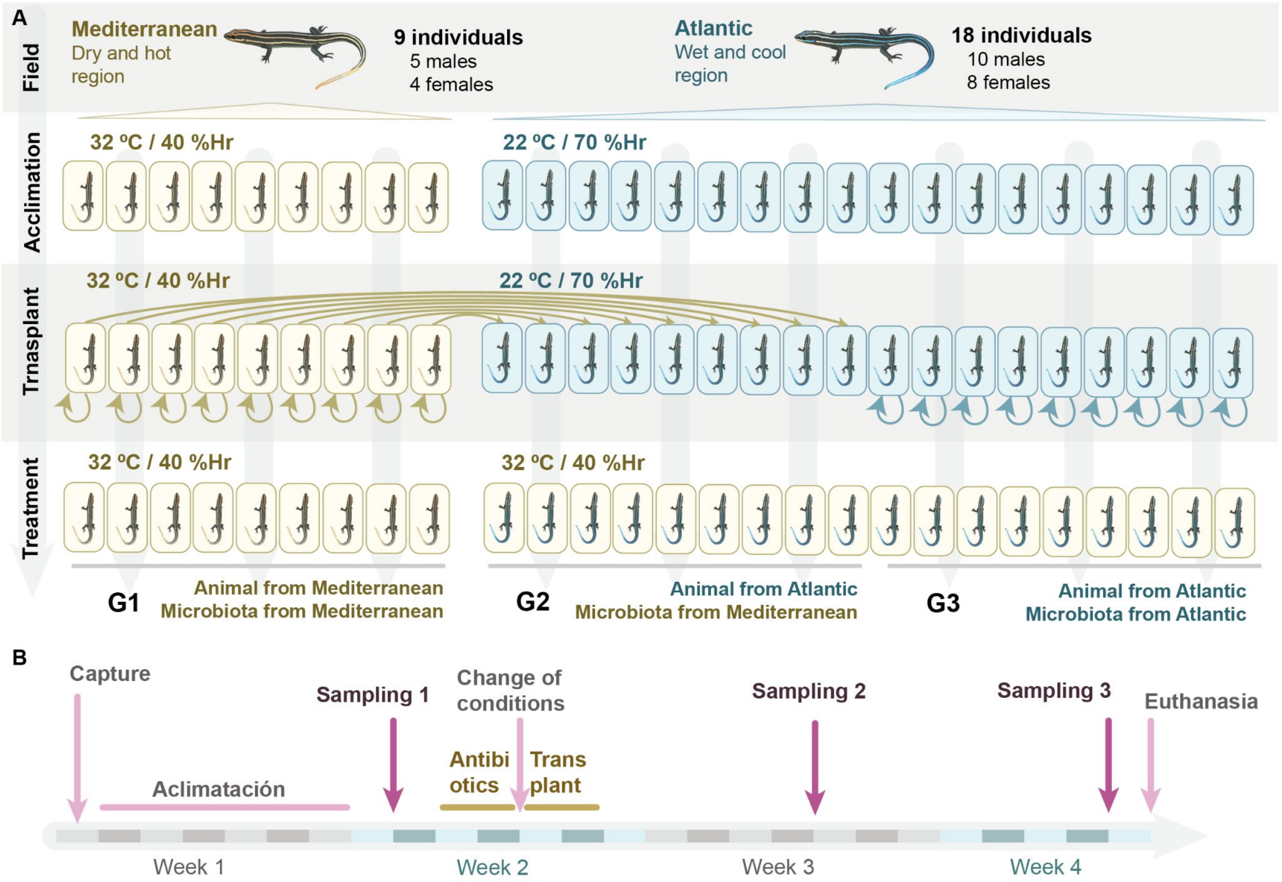


Hologenomics



Hologenomics

In vitro experimentation

Trends in Microbiology

CellPress

Opinion

Unravelling animal–microbiota evolution on a chip

Ostaizka Aizpurua [1,*], Kees Blijleven, [1] Urvish Trivedi [2], M. Thomas P. Gilbert [1,3] and Antton Alberdi [1]

Whether and how microorganisms have shaped the evolution of their animal hosts is a major question in biology. Although many animal evolutionary processes appear to correlate with changes in their associated microbial communities, the mechanistic processes leading to these patterns and their causal relationships are still far from being resolved. Gut-on-a-chip models provide an innovative approach that expands beyond the potential of conventional microbiome profiling to study how different animals sense and react to microbes by comparing responses of animal intestinal tissue models to different microbial stimuli. This complementary knowledge can contribute to our understanding of how host genetic features facilitate or prevent different microbiomes from being assembled, and in doing so elucidate the role of host–microbiota interactions in animal evolution.

Highlights

Host–microbiota interactions can influence biological functions in animals, but direct evidence of their impact on animal evolution is limited.

Gut-on-a-chip systems emulate biological properties of the natural intestine, including establishment of simplified microbial communities in the epithelial barrier.

Development of chips derived from multiple animal hosts can enable evolutionary aspects of animal–microbiota interactions to be studied with unparalleled resolution.

Introduction

Many microorganisms that are associated with animals partake in, influence, or even drive their hosts' biological functions [1]. This realisation has led to an intuitive notion that host–microbiota interactions might have shaped the evolutionary trajectories of animals. Large-scale studies spanning dozens of host species and hundreds of microorganisms have revealed patterns (e.g., diet-driven convergence [2], cophylogeny [3], phylosymbiosis [4]) that suggest some relevance of microorganisms for animal evolution. However, due to the observational and correlative nature of the research conducted so far, direct evidence that supports such claims is still limited [5,6].

In theory, microbial communities, and in particular those that reside in the animal gut, can impact the evolutionary trajectories of animals through different mechanisms, such as modifying dietary niches, modulating ontogenic development, or conferring increased adaptive capacity [5]. To understand under which circumstances microbes can affect animal evolution, animal-associated microorganisms should not be treated as external organs that only serve their hosts, but as diverse and dynamic communities of microscopic organisms that continuously interact both with each other and with their hosts [7]. In fact, animal hosts react to the presence of microbes by not only modifying their physiological parameters, but also altering the environment in which microbes live [8], thus exerting some level of control over their associated microbial community [9,10]. Therefore, any evolutionary process that involves adaptive changes in the microbiota would be expected to exert selective pressure on how animals react towards microbial stimuli.

However, our knowledge about how such animal–microbiota interactions vary across the tree of life is practically non-existent. The study of molecular host–microbiota interactions, such as how epithelial transporters respond to specific microbial metabolites [11], requires a reductionist

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Technical considerations

Hologenomics

Taylor & Francis

Critical Reviews in Biotechnology

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Field and laboratory guidelines for reliable bioinformatic and statistical analysis of bacterial shotgun metagenomic data

Ostaizka Aizpurua, Robert R. Dunn, Lars H. Hansen, M. T. P. Gilbert & Antton Alberdi

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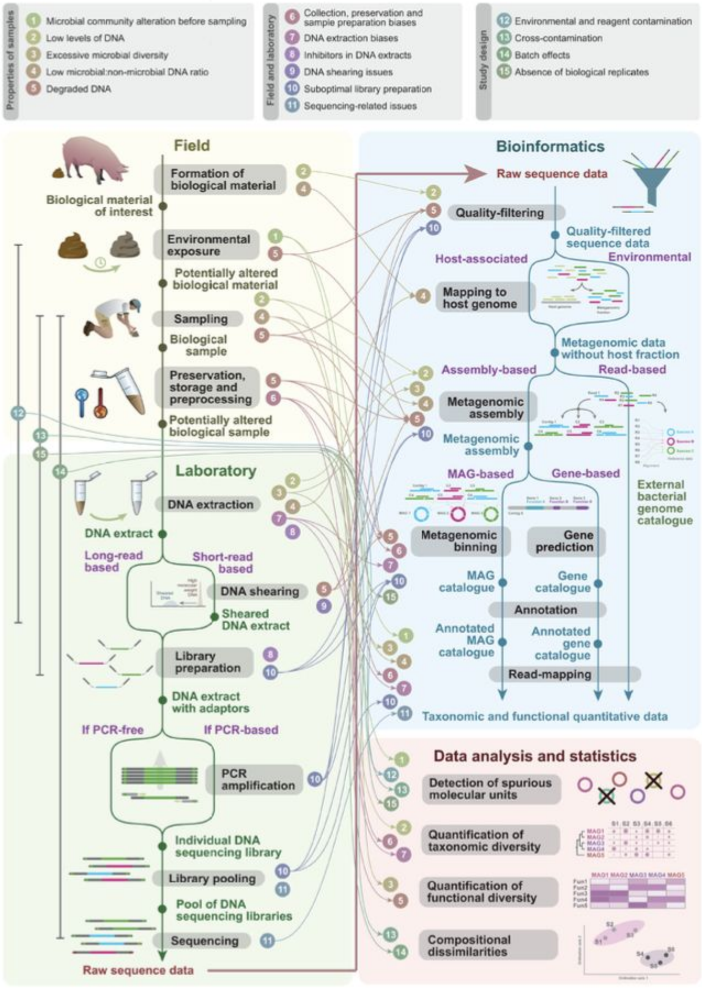

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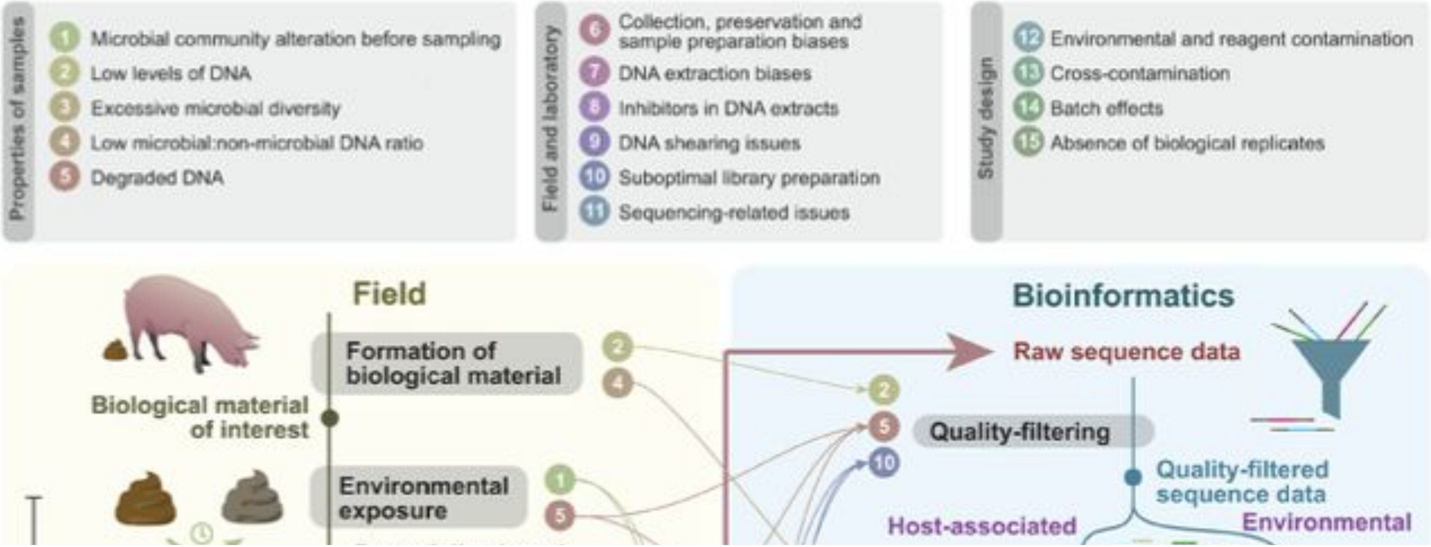

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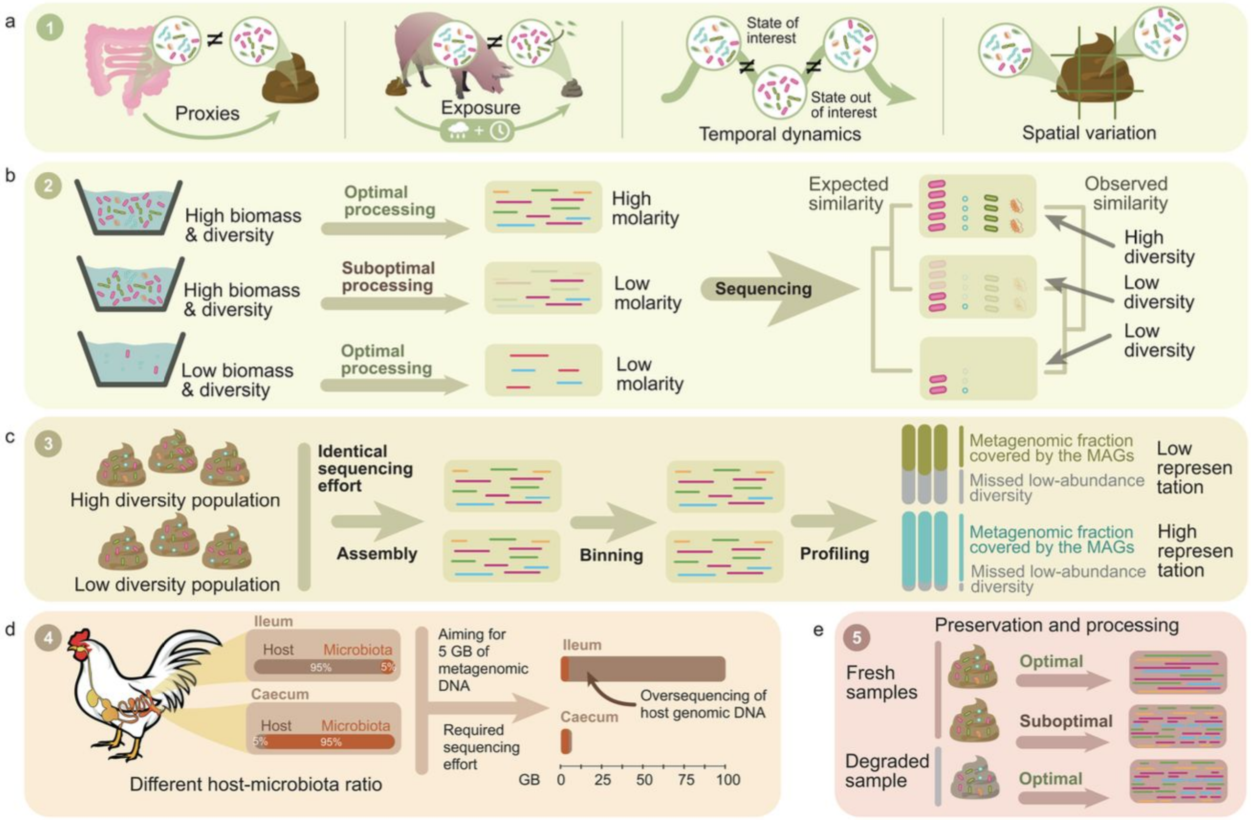

Intrinsic sample properties

Aizpurua et al. 2023

Critical Reviews in Biotechnology

Microbial community alteration before sampling

Intrinsic sample properties

Aizpurua et al. 2023
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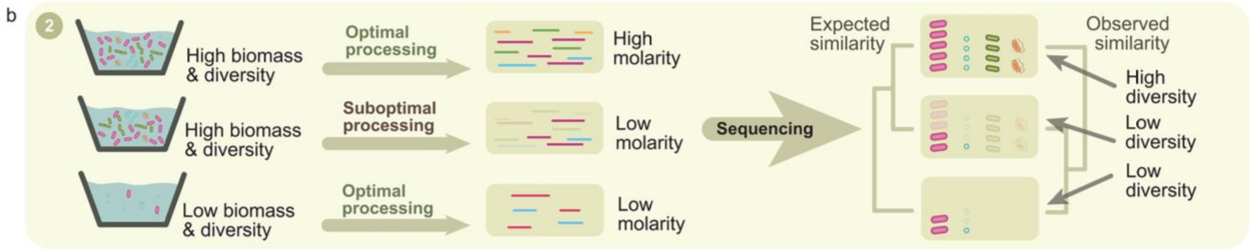
Low levels of DNA



Intrinsic sample properties

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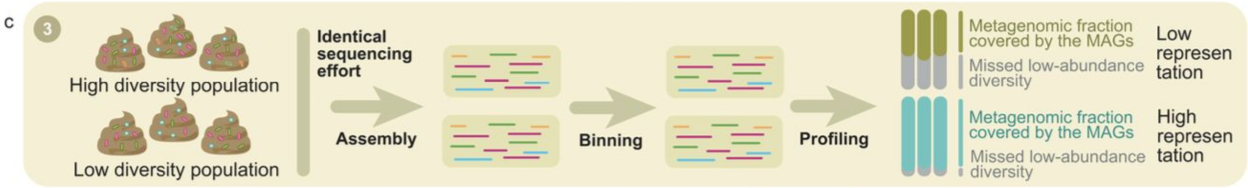
High microbial diversity



Intrinsic sample properties

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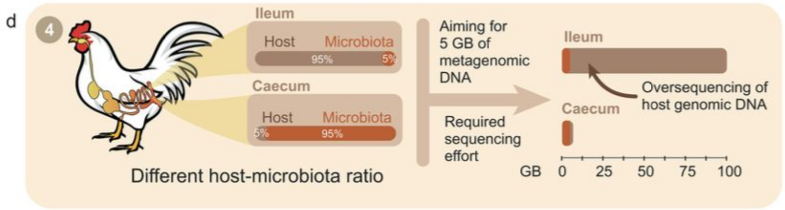
Low ratio of microbial:non-microbial DNA



Intrinsic sample properties

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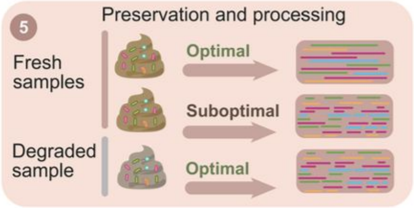
Degraded DNA



Intrinsic sample properties

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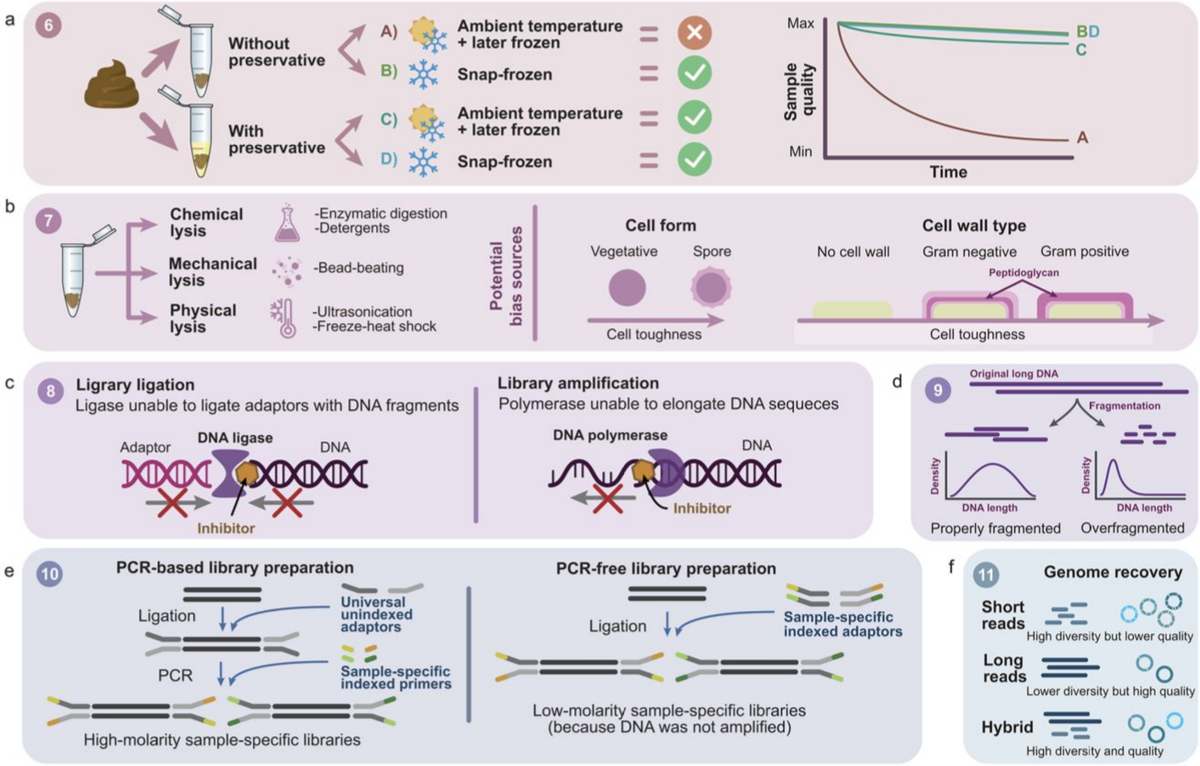
Hologenomics



Laboratory steps

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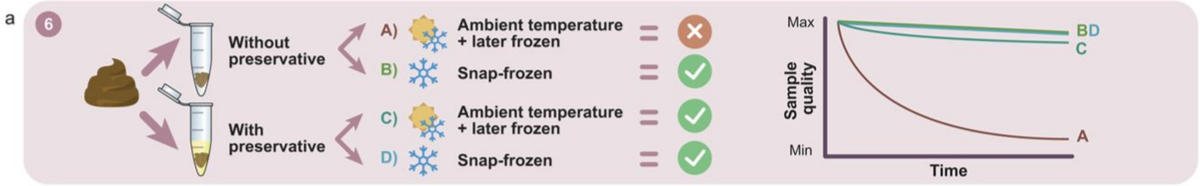
Collection, preservation, and sample preparation biases

Intrinsic sample properties



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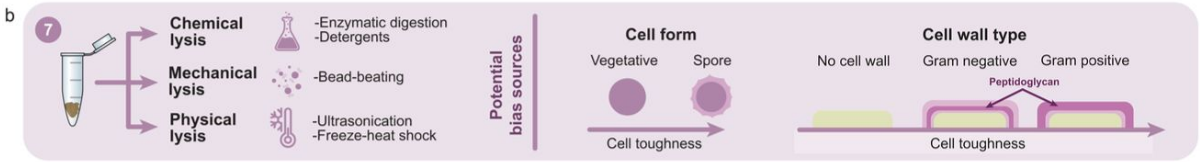
DNA extraction biases



Intrinsic sample properties

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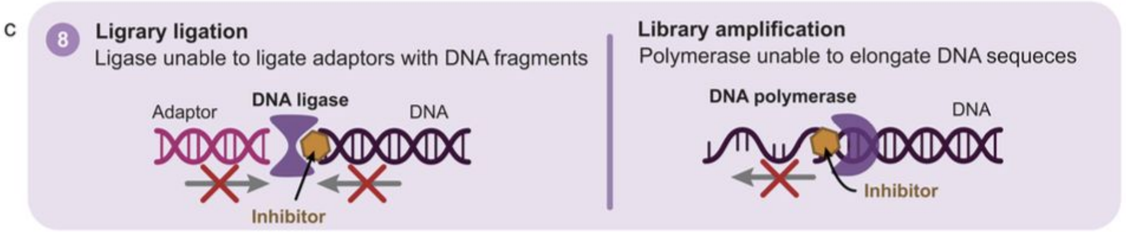
Inhibitors in DNA extracts



Intrinsic sample properties

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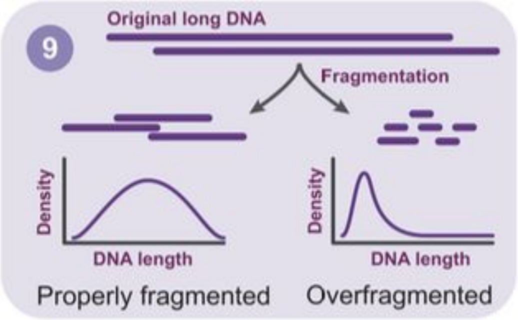
DNA shearing issues

d



Intrinsic sample properties

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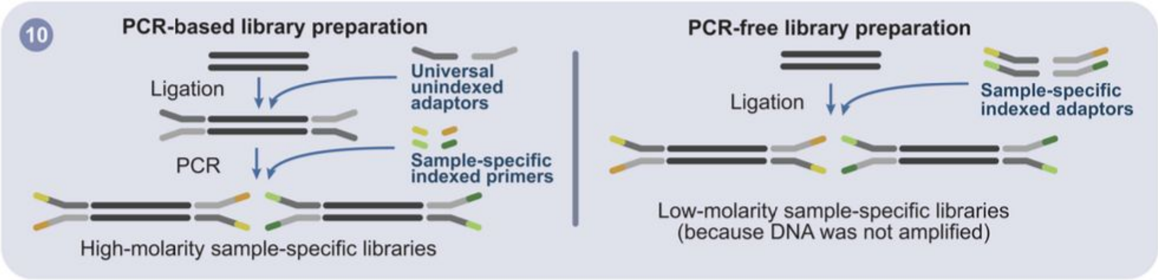
Suboptimal library preparation

Intrinsic sample properties

e



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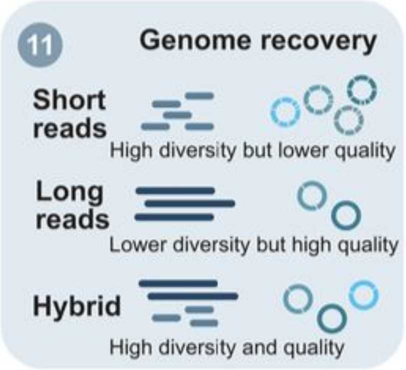
Sequencing-related issues

f



Intrinsic sample properties

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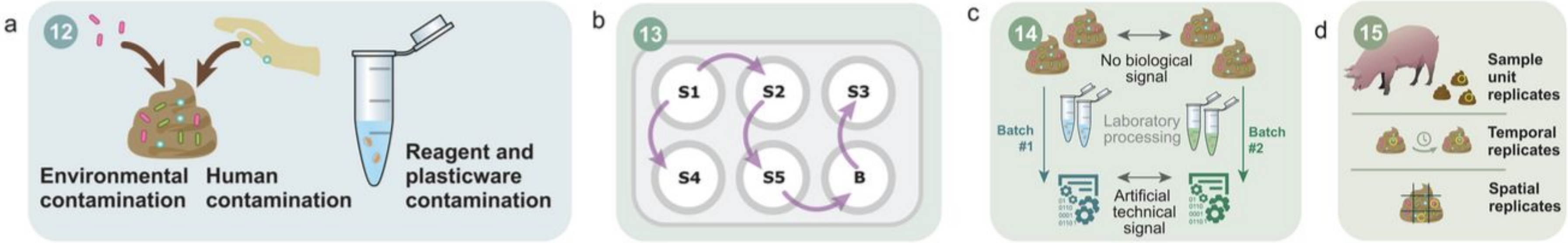
Hologenomics

Study design



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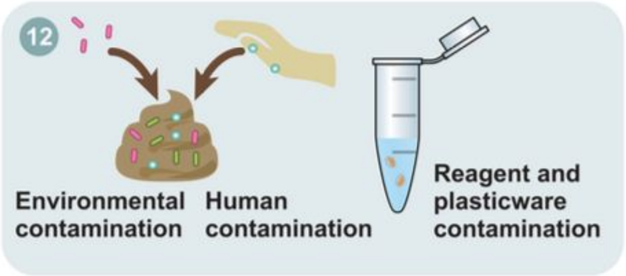
Environmental and reagent contamination

Study design

a



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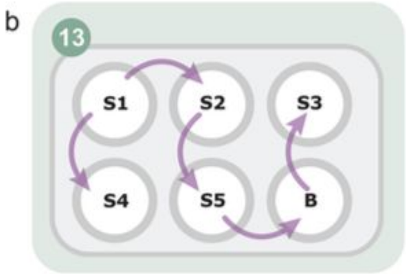
Cross-contamination

Study design



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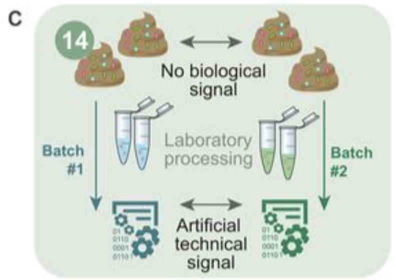
Hologenomics

Batch effects

Study design



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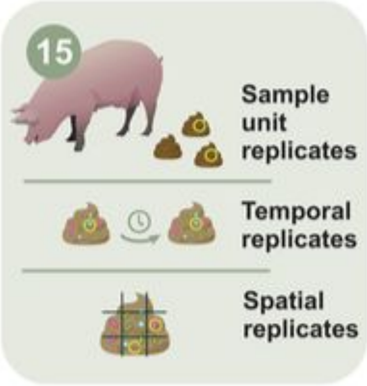
Absence of biological replicates

Study design

d



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Which of these problems could you anticipate with your samples?

How much of the explanations of "Experimental designs for Hologenomics" did you understand?

Session 3
Bioinformatics methods
HOLOGENOMICS

Hologenomics

Cell Reports Methods

CellPress
OPEN ACCESS

Review

A practical introduction to holo-omics

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[2]University Museum, NTNU, Trondheim, Norway
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SUMMARY

Holo-omics refers to the joint study of non-targeted molecular data layers from host-microbiota systems or holobionts, which is increasingly employed to disentangle the complex interactions between the elements that compose them. We navigate through the generation, analysis, and integration of omics data, focusing on the commonalities and main differences to generate and analyze the various types of omics, with a special focus on optimizing data generation and integration. We advocate for careful generation and distillation of data, followed by independent exploration and analyses of the single omic layers to obtain a better understanding of the study system, before the integration of multiple omic layers in a final model is attempted. We highlight critical decision points to achieve this aim and flag the main challenges to address complex biological questions regarding the integrative study of host-microbiota relationships.

INTRODUCTION

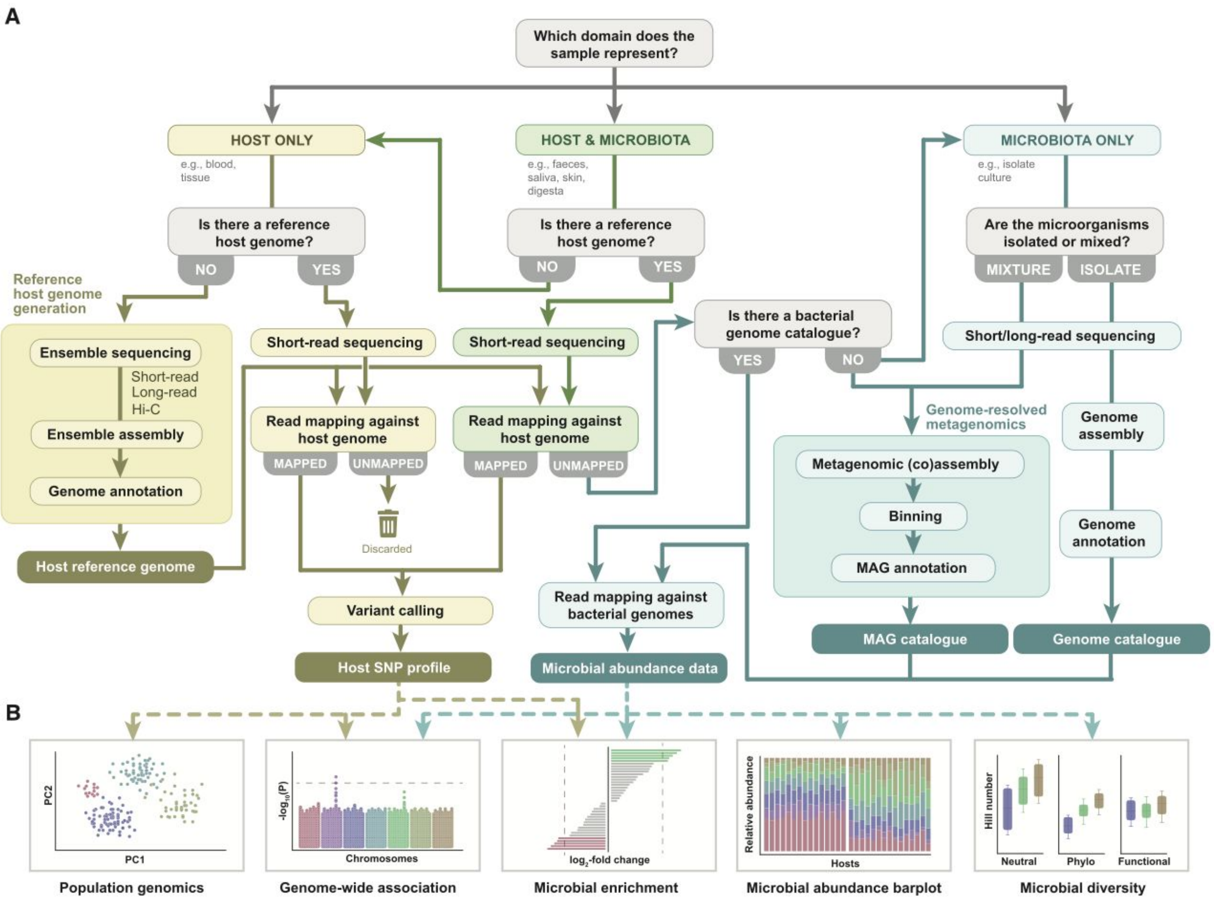
The realization of the importance of microorganisms for animal and plant biology,[1] along with the increased capacity to generate and process molecular data,[2] has given rise to a new holistic way to study biological systems.[3] Holo-omics refers to the technical approach to jointly (hence the prefix holo-) analyze multiple non-targeted molecular data layers (known as multi-omics) from both hosts and their associated microorganisms,[4,5] aimed at unraveling their intricate relationships.[3] The generation, analysis, and integration of holo-omic datasets requires deep knowledge of the myriad of conceptual and technical steps involved in the process.[4] Here, we provide an overview of the main steps researchers must undergo while highlighting the challenges that should be overcome to obtain meaningful results that enable them to address complex biological questions.

While acknowledging the relevance and value of other methods for studying host-microbiota interactions (e.g., 16S rRNA amplicon sequencing, spatial transcriptomics), in this review we primarily consider seven omic layers characterized by a non-targeted data generation approach without spatial resolution. These methods require specific data generation and analysis strategies before integrating them into multi-omic statistical models (Figure 1). Four of them are based on nucleic acid sequencing, namely host genomics (HG), host transcriptomics (HT), microbial metagenomics (MG), and microbial metatranscriptomics (MT). The three remaining layers are based on molecular spectroscopy, namely host proteomics (HP), microbial metaproteomics (MP), and (meta)metabolomics (ME), which is not split between hosts and microorganisms for the difficulties in assigning an origin to a given metabolite. Each omic layer contains fundamentally different information, at different levels of biological organization. A host contains a single genome (HG) that encodes thousands of genes (HT) which are expressed to produce an even larger number of proteins (HP). A host might have multiple (often hundreds or thousands) associated bacterial species (n), each with a distinct genome (MG_n) containing a few thousand genes that can be expressed (MT_n), thus potentially encoding microbial proteins (MP_n). The biological activity enabled by those proteins builds the metabolomic (ME) landscape that not only shapes host phenotype but also conditions the environment in which host-associated microbes live (e.g., the gut).

HG—which in this manuscript is solely discussed in terms of nucleotide sequences without considering other levels such as epigenetic and DNA folding that may also shape the hologenome[3,6,7]—can inform about population structure and the genetic features of individuals but is invariable to treatments or environmental disturbances. In contrast, MG contains the genetic information of microbial communities that are likely to change over very short timescales and reflects the immediate responses of hosts to treatments or disturbances. Although HG and MG inform about the potential of hosts and microorganisms to perform biological functions, HT and MT provide snapshots of the actual functional activity of the system, which can be validated using HP, MP, and ME that result from the activity of the expressed genes. Acknowledging the distinct biological characteristics of the omic layers is therefore essential to design experiments and analytical pipelines for better solving the complex puzzle of host-microbiota relationships.

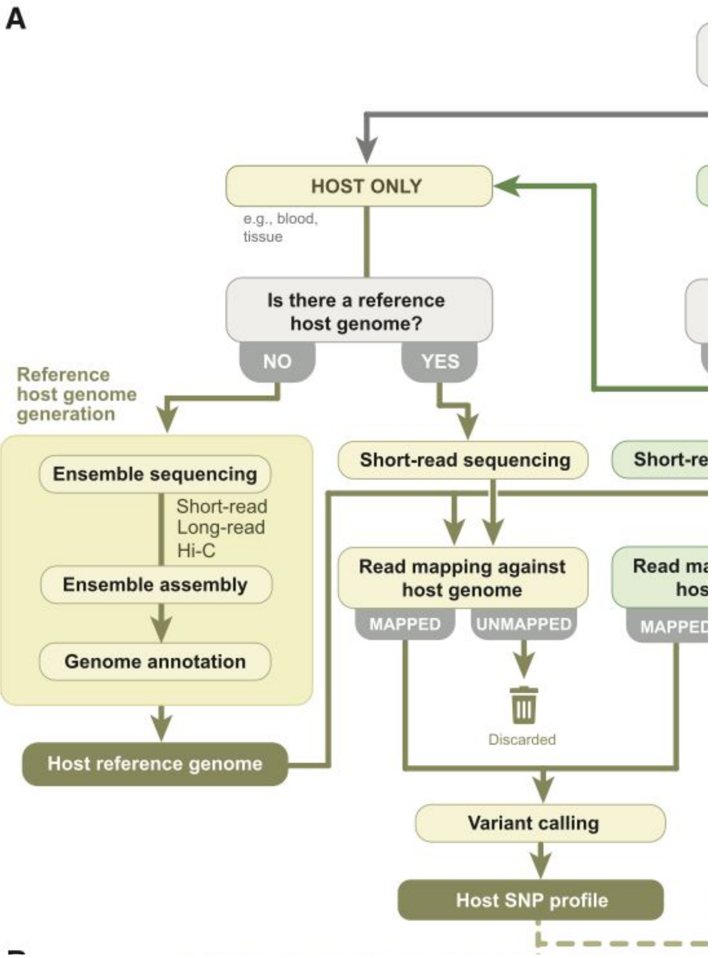
In light of this, we navigate from sample acquisition to data interpretation through six sections: (1) sample collection and preservation, (2) laboratory sample processing, (3) bioinformatic analysis of raw data, (4) data filtering, imputation, and distillation, (5) initial quantitative exploration of omic layers, and (6) multi-omic data integration. Each of these sections deals with key methodological aspects, focusing on the commonalities and

Hologenomics



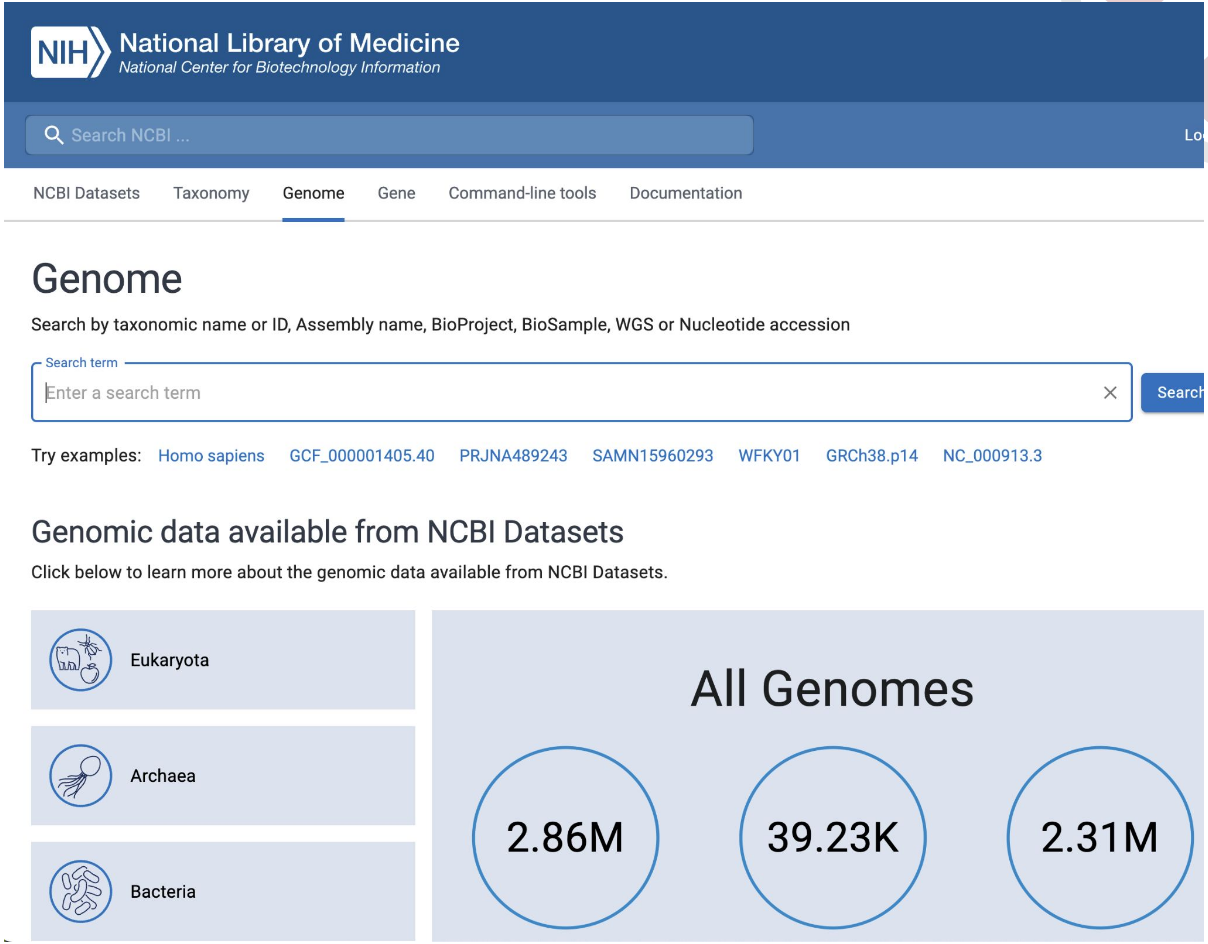
Hologenomics

Host genomes



Hologenomics

Host genomes



Host genomes

- Contig
- Scaffold
- Chromosome
- Complete

Reference

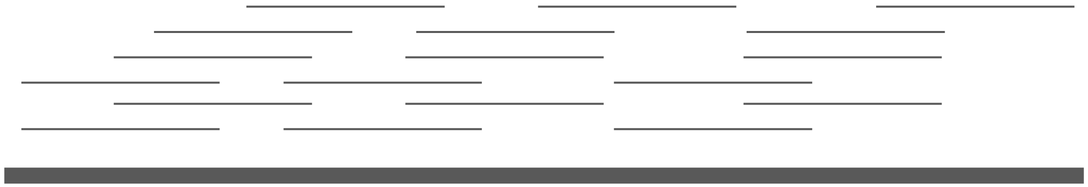
Does your study species have a reference genome available? If yes, which quality is it? Mention species and quality.

Host genomes

Resequencing

Host genomes

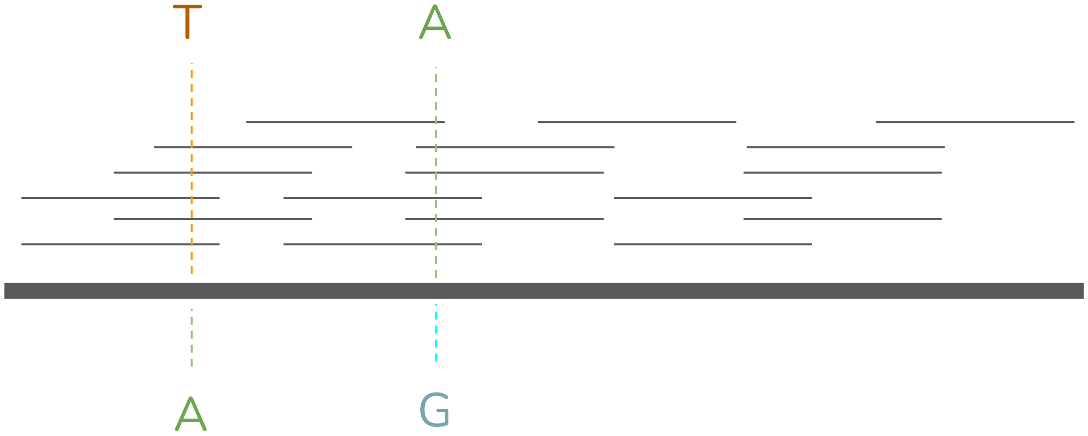
Resequencing



Hologenomics

Host genomes

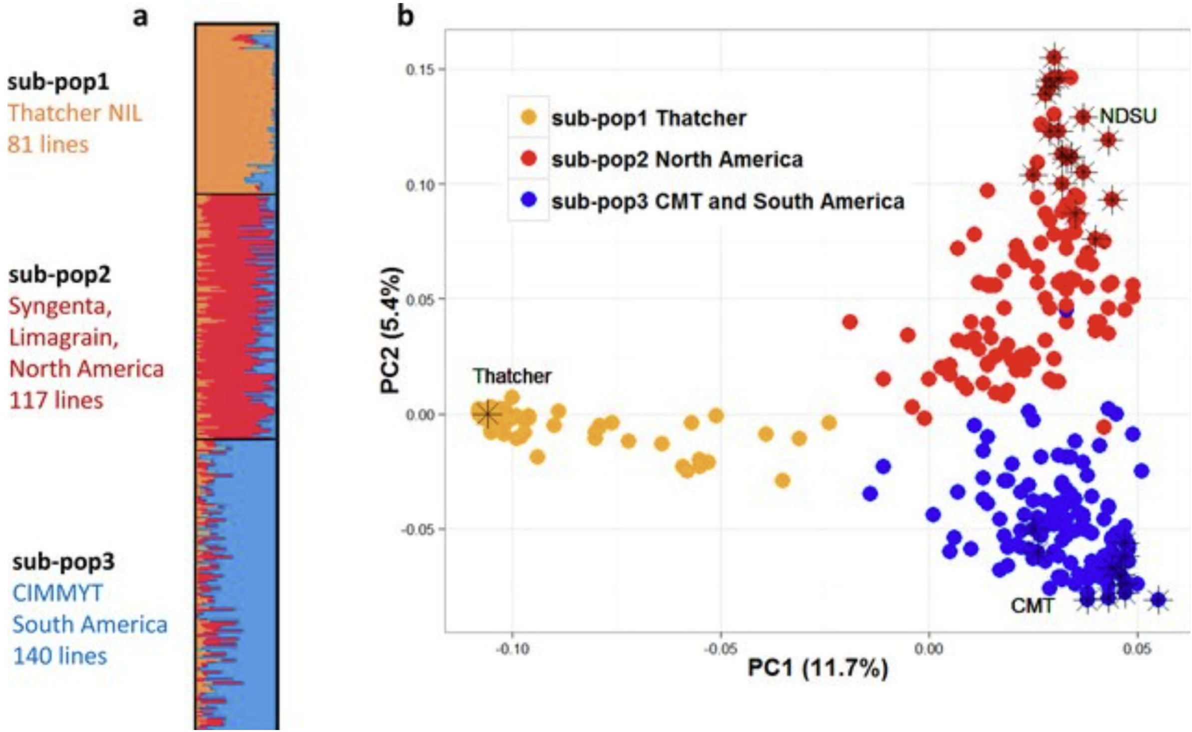
Variant calling



Hologenomics

Host genomes

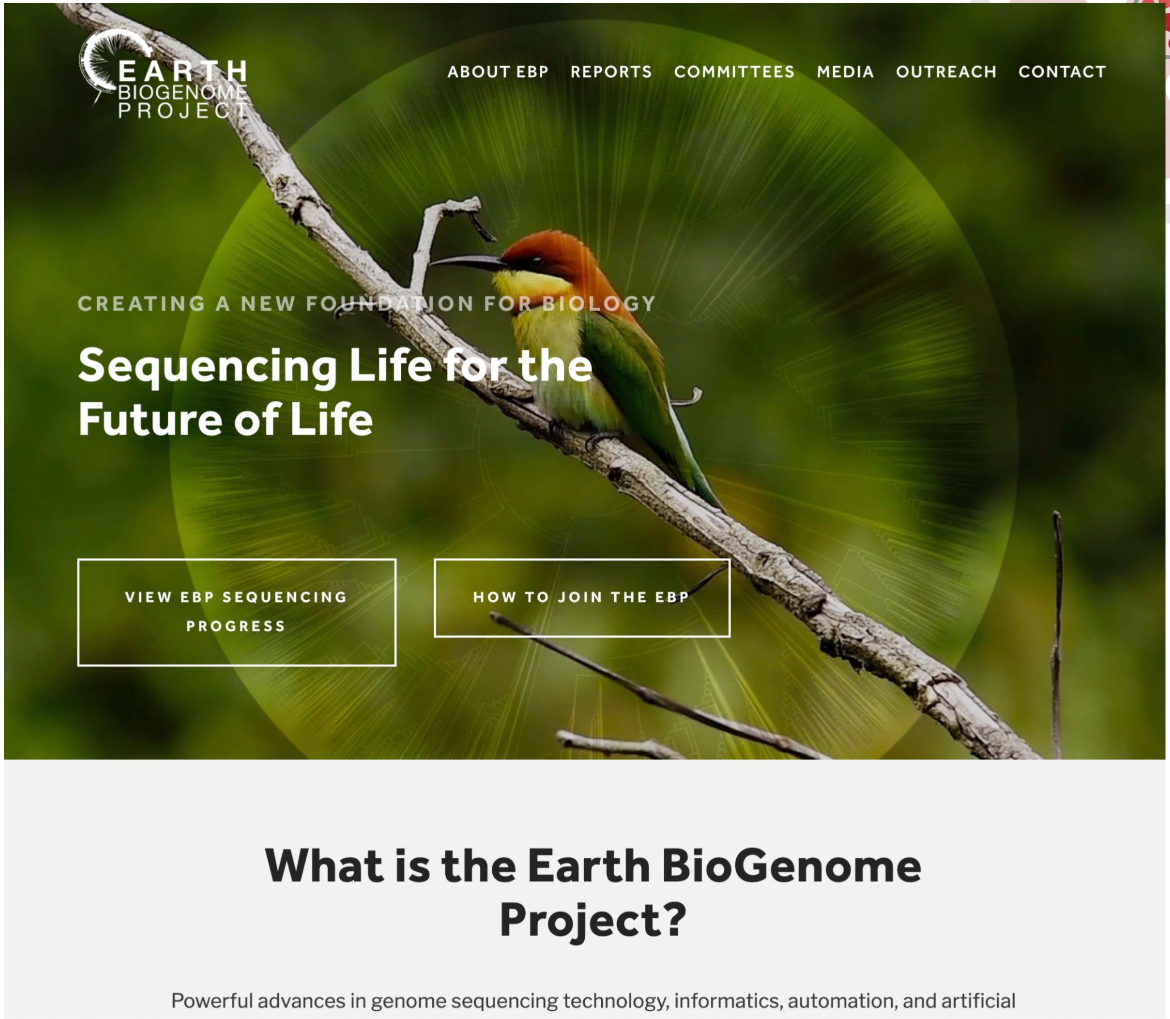
Population structure



Hologenomics

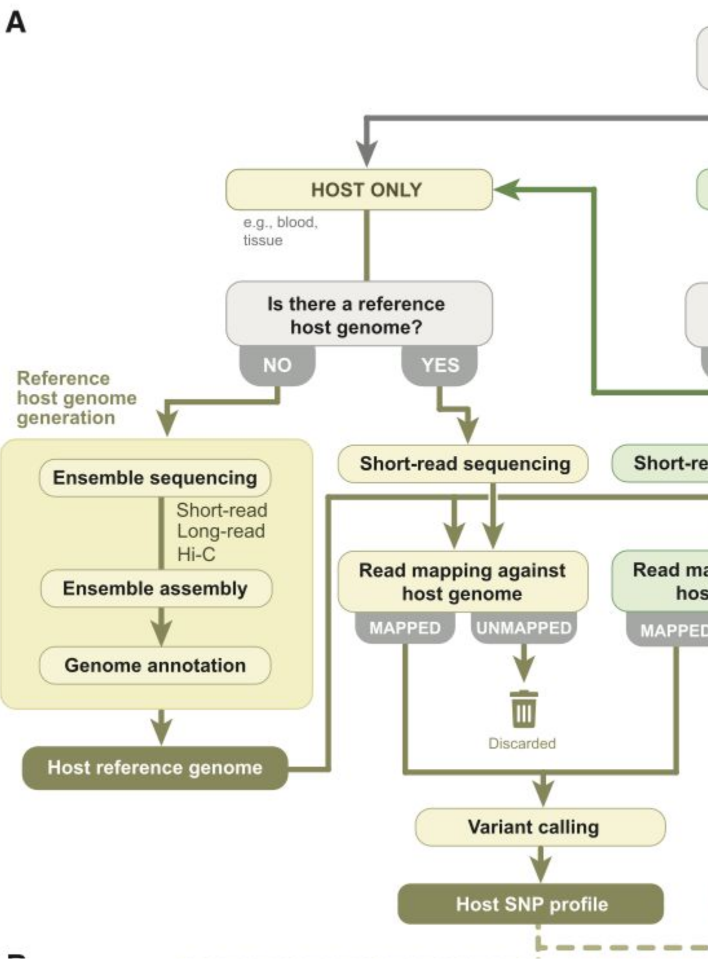
Host genomes

Reference genome generation

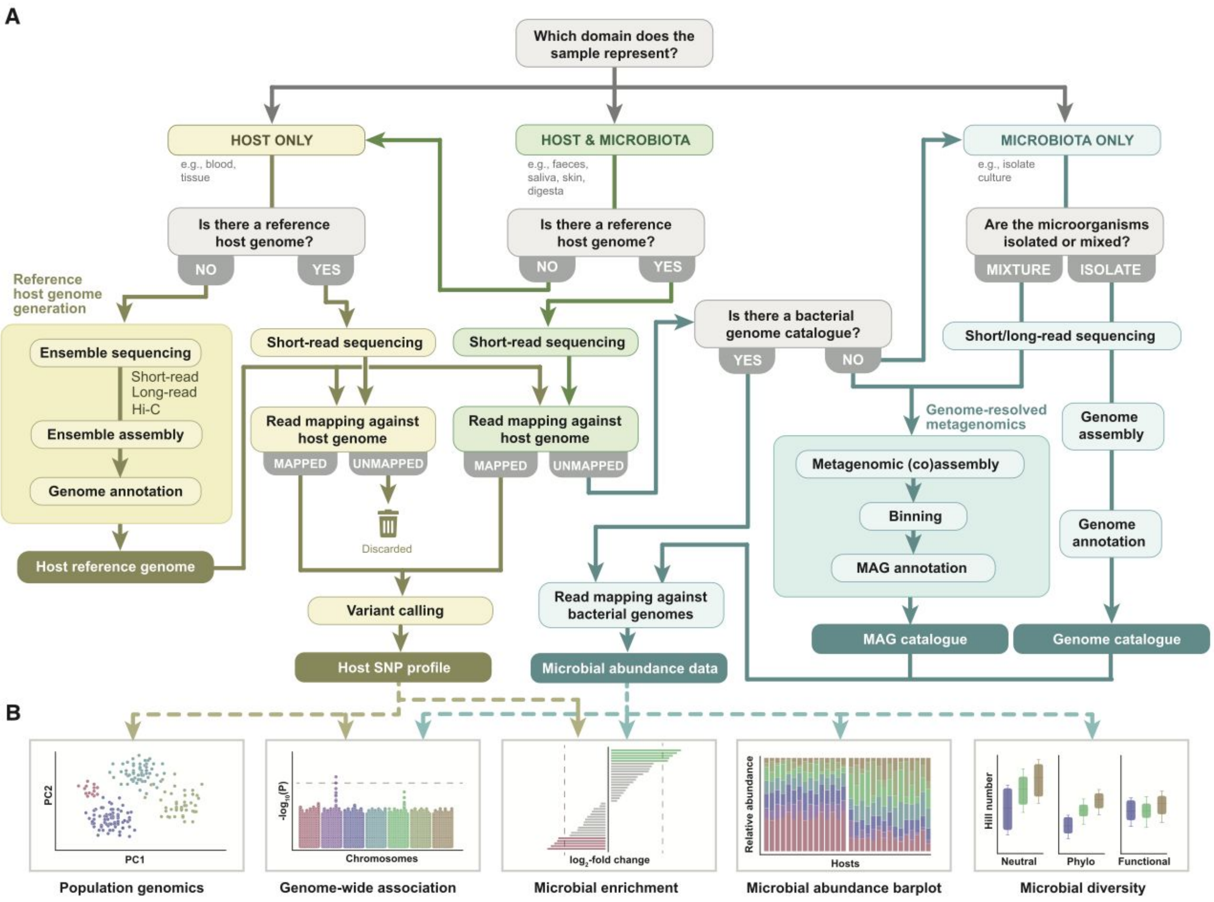


Hologenomics

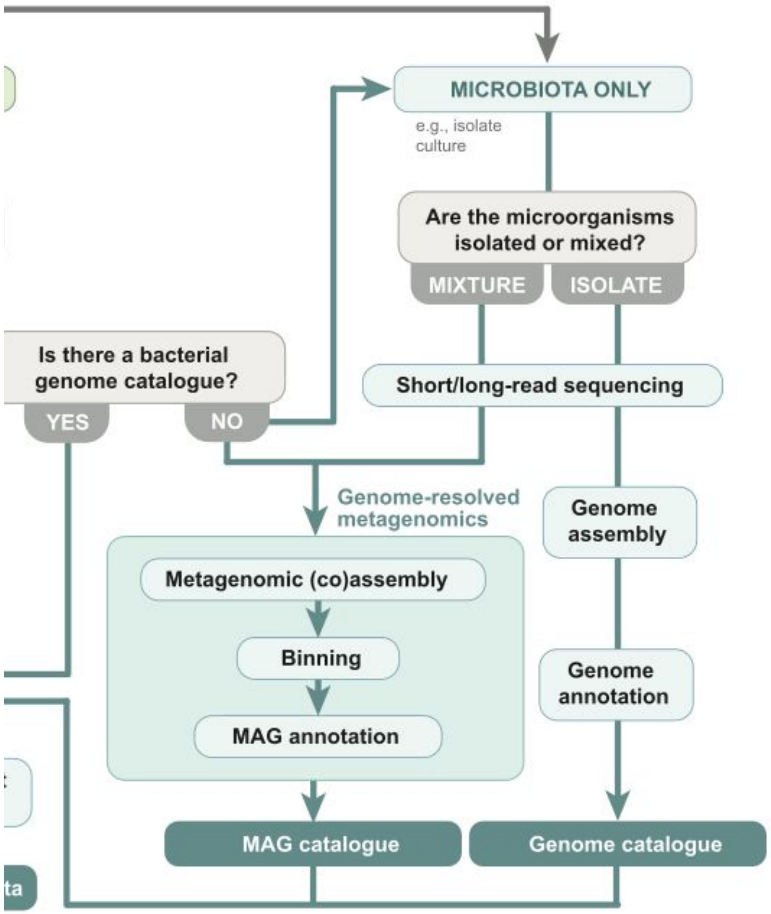
Host genomes



Hologenomics



Microbial metagenomes



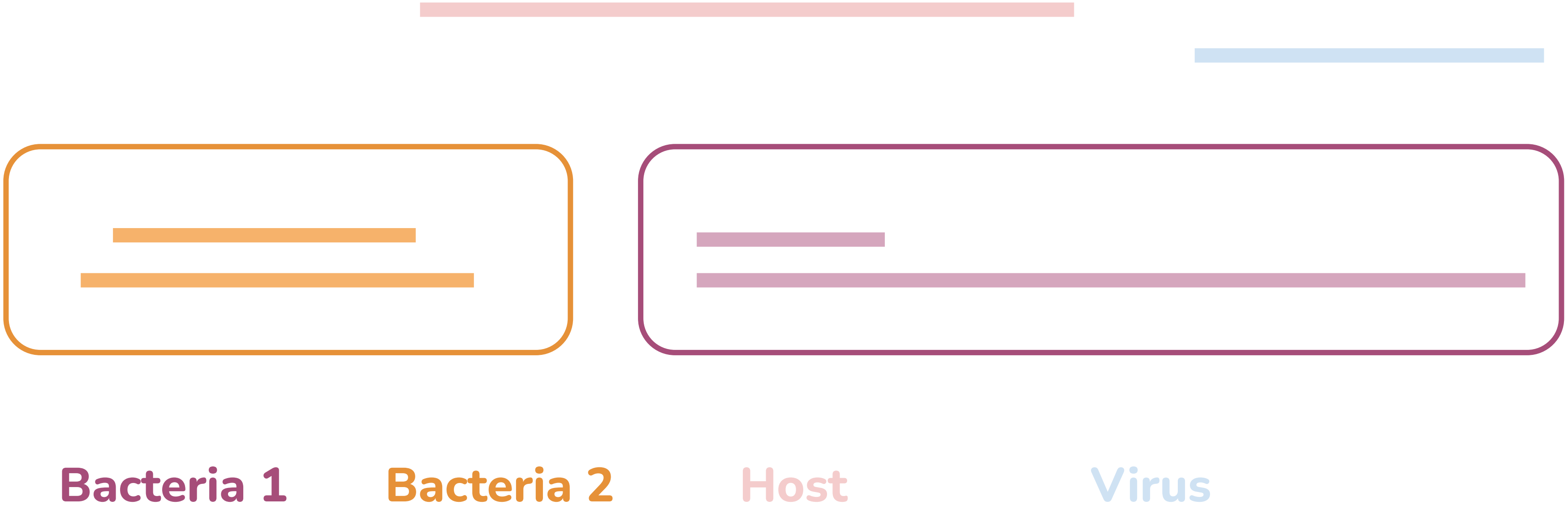
Genome resolved metagenomics

Genome resolved metagenomics

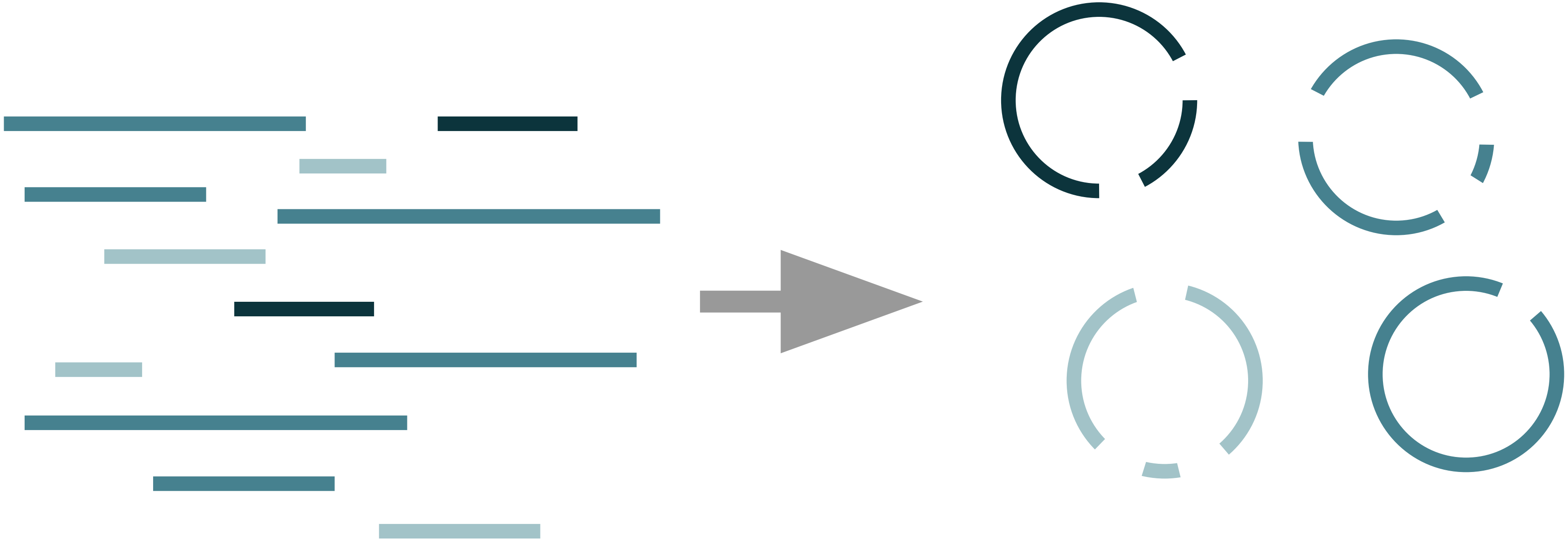
Genome resolved metagenomics

Hologenomics

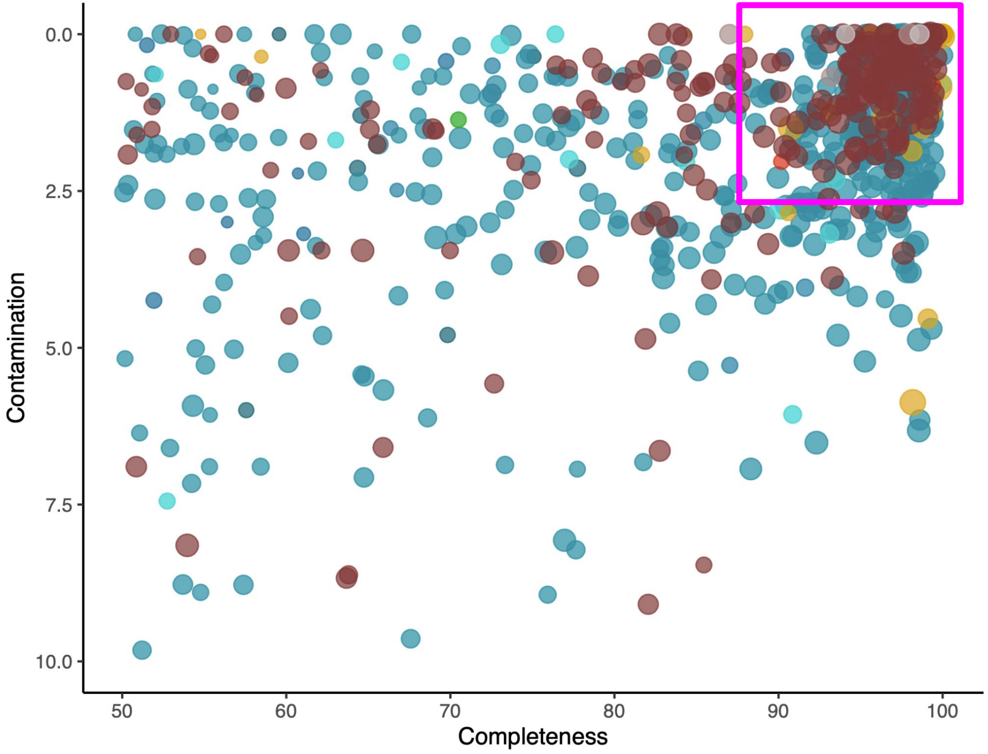
Genome resolved metagenomics



Genome resolved metagenomics



Genome resolved metagenomics



Completeness

Percentage of single-copy core genes present

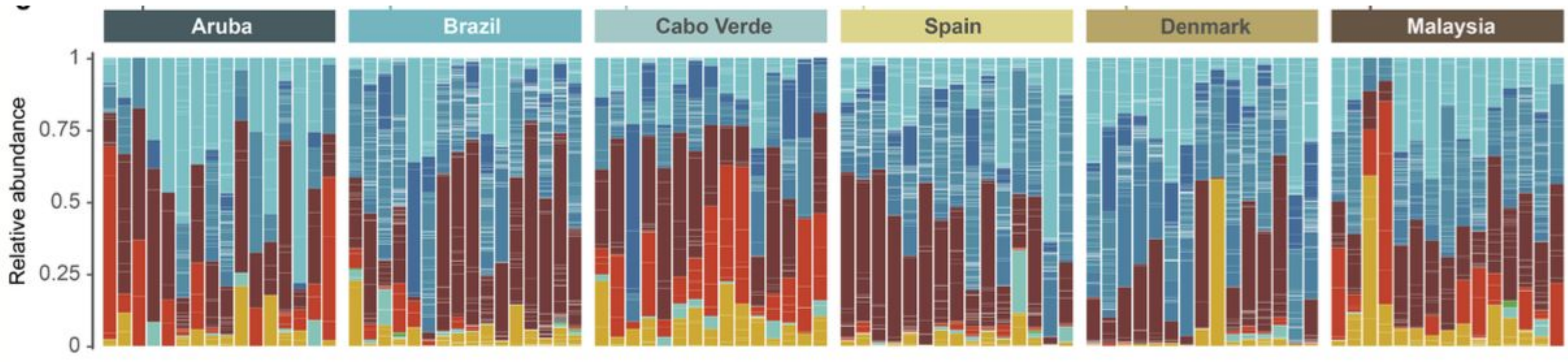
Contamination/ redundance

Excess of single-copy core genes present

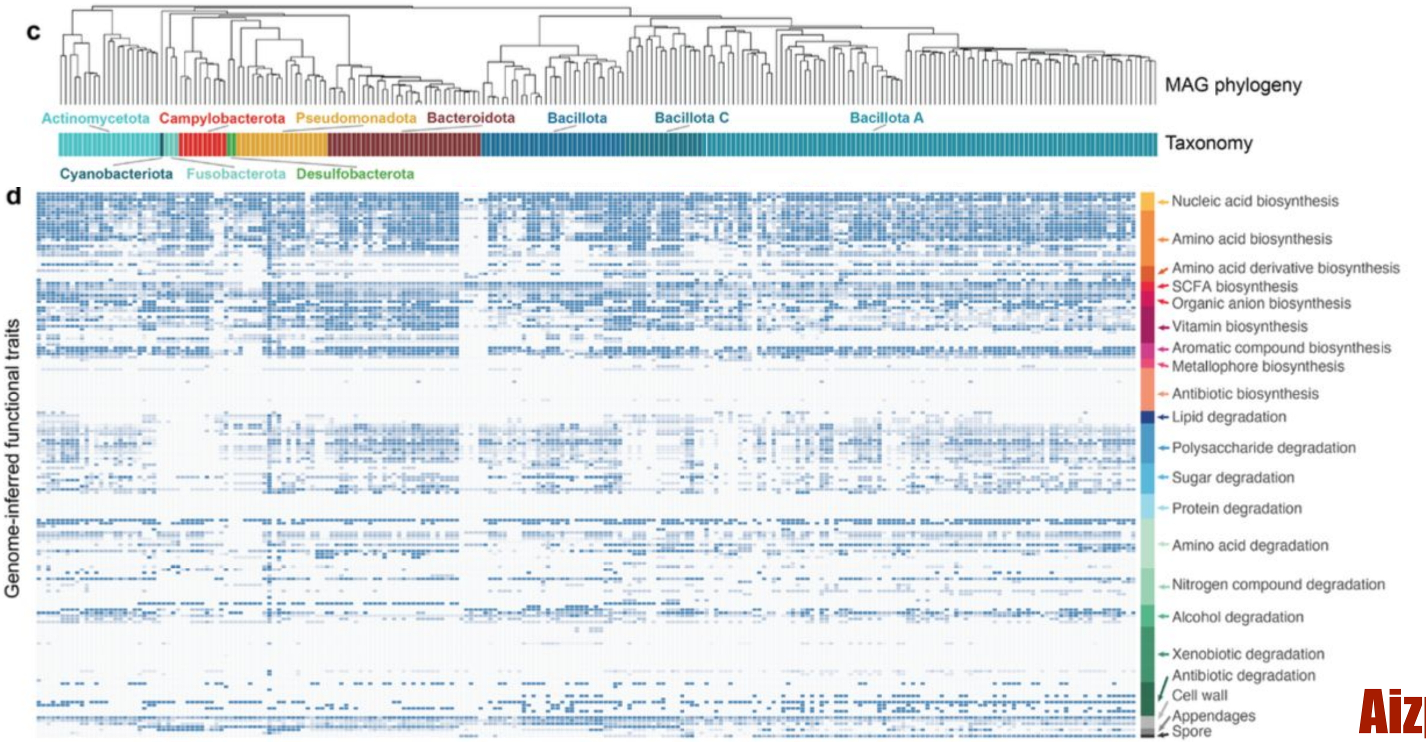
Hologenomics

Genome resolved metagenomics

Genome resolved metagenomics



Hologenomics



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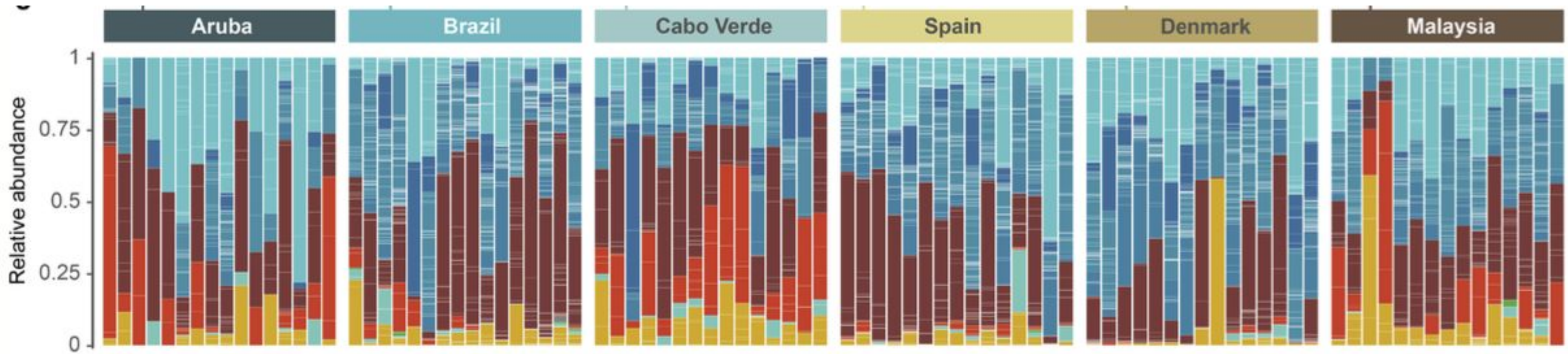
Molecular Ecology

Genome resolved metagenomics



Genome resolved metagenomics

- Which bacteria are there?
- At which proportions are they?
- Which functional capacities do they carry?

How much of the explanations of "Bioinformatics methods for Hologenomics" did you understand?

Session 4
Statistics methods for HOLOGENOMICS

Univariate vs multivariate modelling

value = var1 + var2

matrix = var1 + var2

Univariate vs multivariate modelling

value = var1

matrix = var1

univariable

value = var1 + var2

matrix = var1 + var2

multivariable

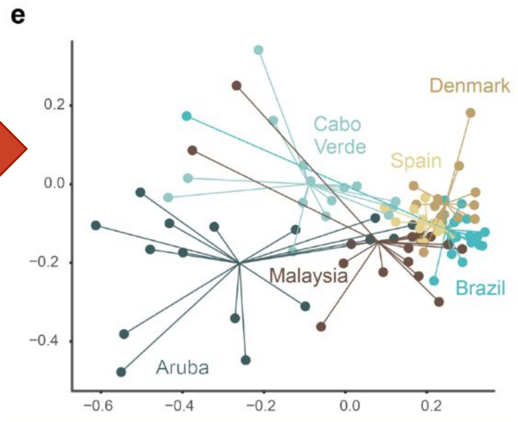
Univariate vs multivariate modelling

alpha diversity = var1 + var2

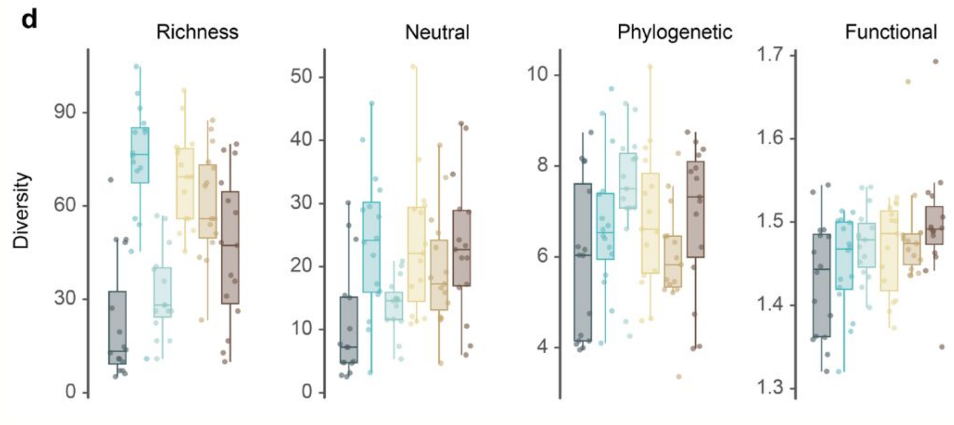
beta diversity = var1 + var2

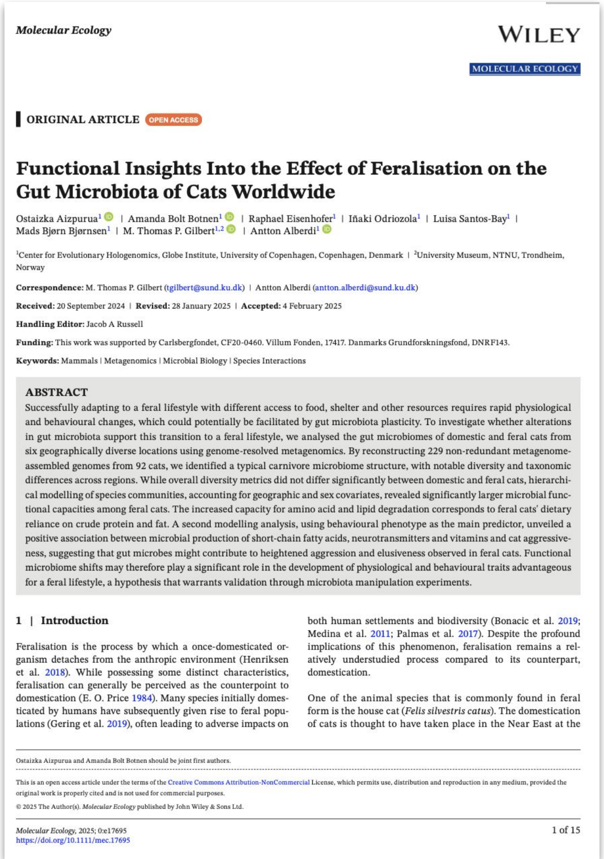
Hologenomics

Multivariate



Univariate





Molecular Ecology

WILEY

MOLECULAR ECOLOGY

ORIGINAL ARTICLE OPEN ACCESS

Functional Insights Into the Effect of Feralisation on the Gut Microbiota of Cats Worldwide

Ostaizka Aizpurua[1] | Amanda Bolt Botnen[1] | Raphael Eisenhofer[1] | Iñaki Odriozola[1] | Luisa Santos-Bay[1] | Mads Bjørn Bjørnsen[1] | M. Thomas P. Gilbert[1,2] | Antton Alberdi[1]

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Keywords: Mammals | Metagenomics | Microbial Biology | Species Interactions

ABSTRACT

Successfully adapting to a feral lifestyle with different access to food, shelter and other resources requires rapid physiological and behavioural changes, which could potentially be facilitated by gut microbiota plasticity. To investigate whether alterations in gut microbiota support this transition to a feral lifestyle, we analysed the gut microbiomes of domestic and feral cats from six geographically diverse locations using genome-resolved metagenomics. By reconstructing 229 non-redundant metagenome-assembled genomes from 92 cats, we identified a typical carnivore microbiome structure, with notable diversity and taxonomic differences across regions. While overall diversity metrics did not differ significantly between domestic and feral cats, hierarchical modelling of species communities, accounting for geographic and sex covariates, revealed significantly larger microbial functional capacities among feral cats. The increased capacity for amino acid and lipid degradation corresponds to feral cats' dietary reliance on crude protein and fat. A second modelling analysis, using behavioural phenotype as the main predictor, unveiled a positive association between microbial production of short-chain fatty acids, neurotransmitters and vitamins and cat aggressiveness, suggesting that gut microbes might contribute to heightened aggression and elusiveness observed in feral cats. Functional microbiome shifts may therefore play a significant role in the development of physiological and behavioural traits advantageous for a feral lifestyle, a hypothesis that warrants validation through microbiota manipulation experiments.

1 | Introduction

Feralisation is the process by which a once-domesticated organism detaches from the anthropic environment (Henriksen et al. 2018). While possessing some distinct characteristics, feralisation can generally be perceived as the counterpoint to domestication (E. O. Price 1984). Many species initially domesticated by humans have subsequently given rise to feral populations (Gering et al. 2019), often leading to adverse impacts on both human settlements and biodiversity (Bonacic et al. 2019; Medina et al. 2011; Palmas et al. 2017). Despite the profound implications of this phenomenon, feralisation remains a relatively understudied process compared to its counterpart, domestication.

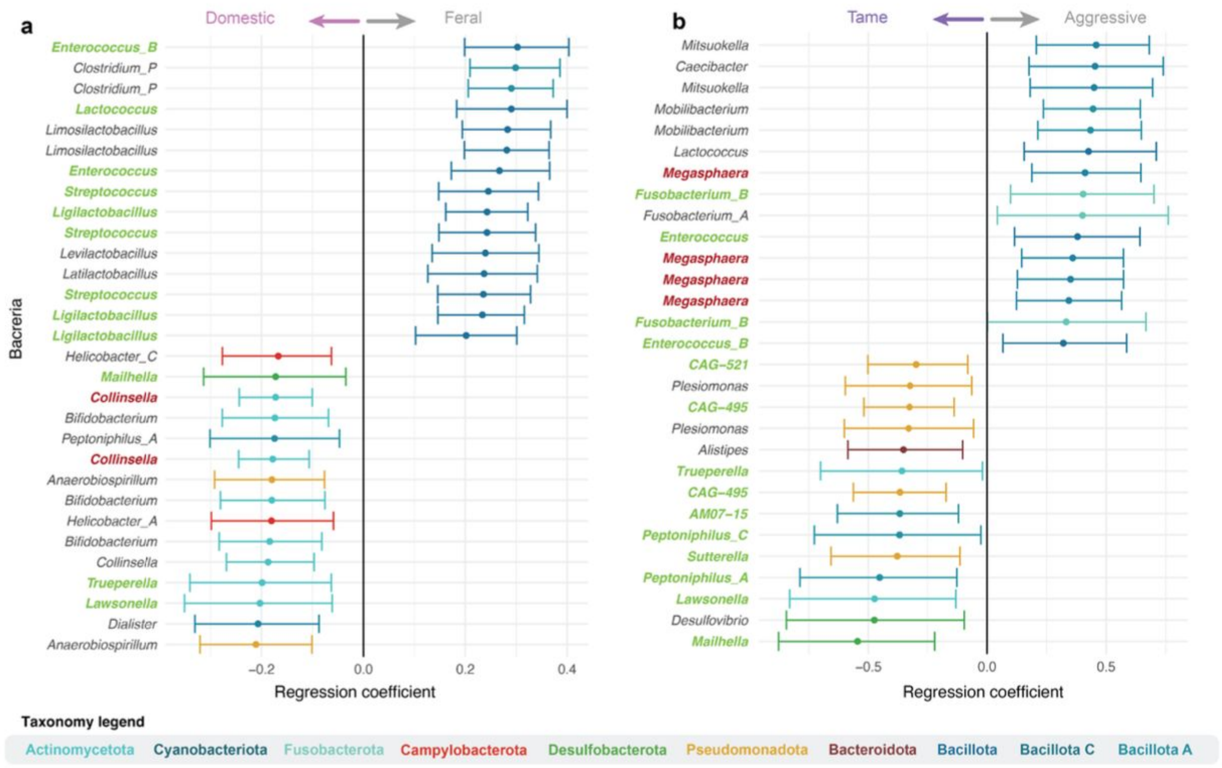
One of the animal species that is commonly found in feral form is the house cat (*Felis silvestris catus*). The domestication of cats is thought to have taken place in the Near East at the

Ostaizka Aizpurua and Amanda Bolt Botnen should be joint first authors.

Univariate vs multivariate modelling

Multiple samples
> Multiple bacteria
>> Multiple functions

Hologenomics



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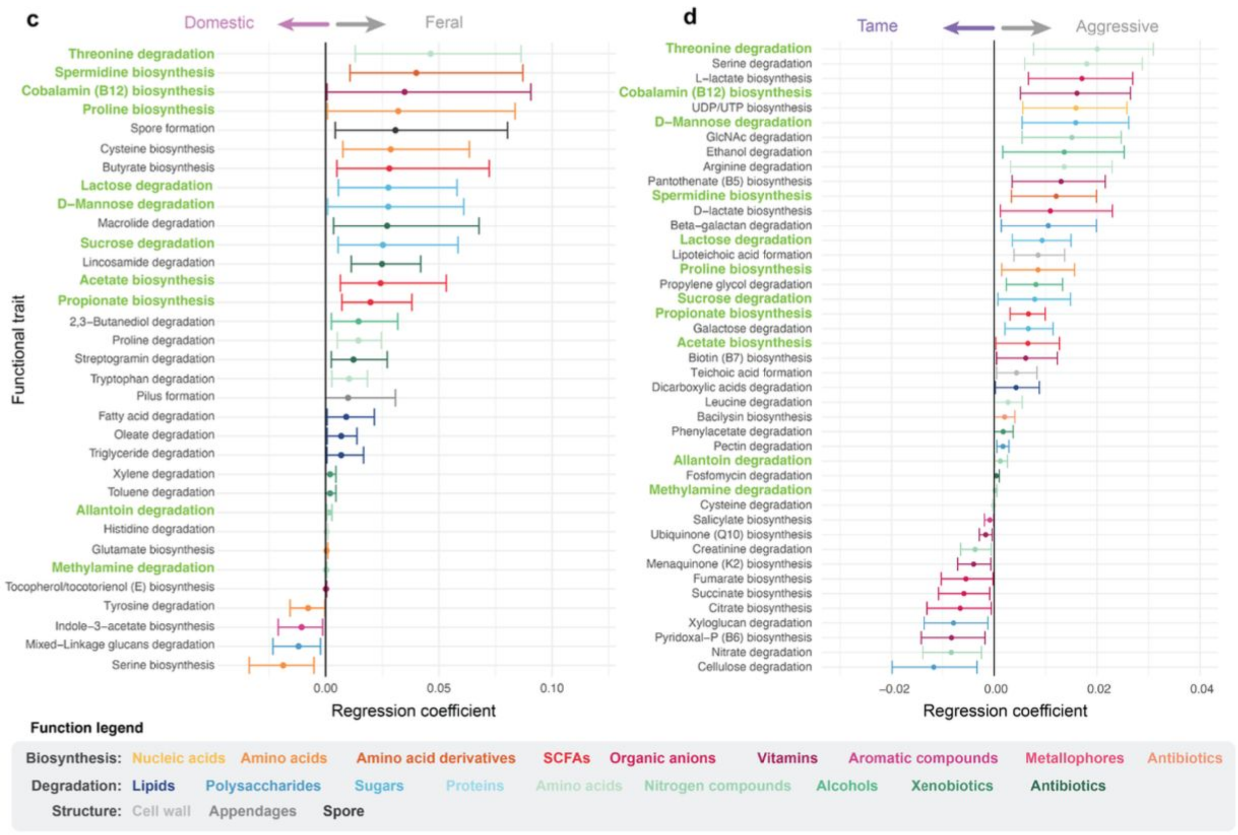
Molecular Ecology

Hologenomics



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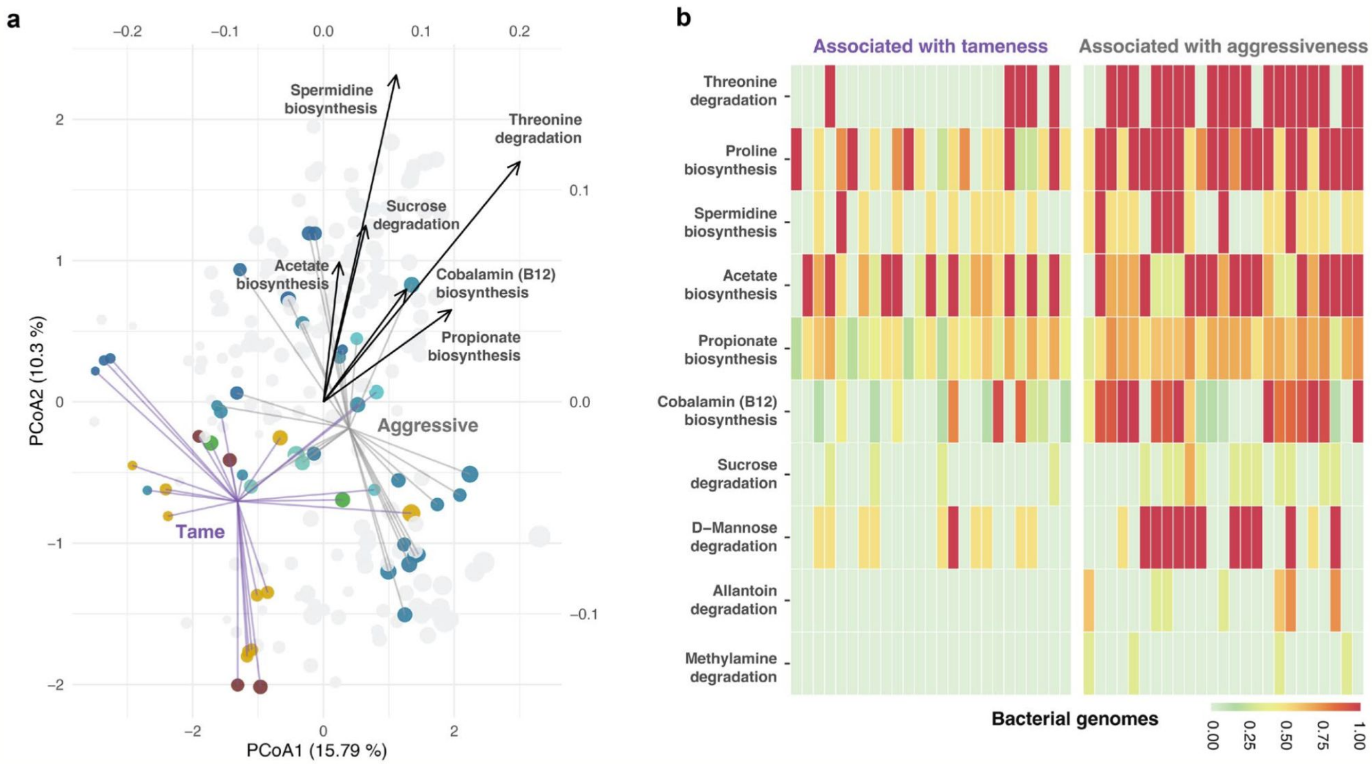
Molecular Ecology

Hologenomics



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Molecular Ecology

How much of the explanations of "Statistics methods for Hologenomics" did you understand?

Hologenomics

Assignment

Hologenomic grant proposal

Length: 10,000-15,000 characters (3-4 pages)
Submission: May 9th, 2025

Hologenomics

- **Background:** ca. 3000 chr.
- **Hypothesis and objectives:** ca. 1000 chr.
- **Methodology:** ca. 2000 chr.
- **Work plan:** ca. 2000 chr.
- **Impact:** ca. 1000 chr.
- **References**: ca. 15-20

Assignment

Hologenomic grant proposal

Length: 10,000-15,000 characters (3-4 pages)
Submission: May 9th, 2025, through this form:

https://airtable.com/appi3wfndMqVyksv3/pag6S4jLcyzVV79BP/form

Assessment