ETH zürich

Food Systems Biotechnology

MISHMASH: Microbiome Sequence and Metadata Availability Standards

Lina Kim

January 2026

NCCR Winter School


RURAL
URBAN
SUBURBAN


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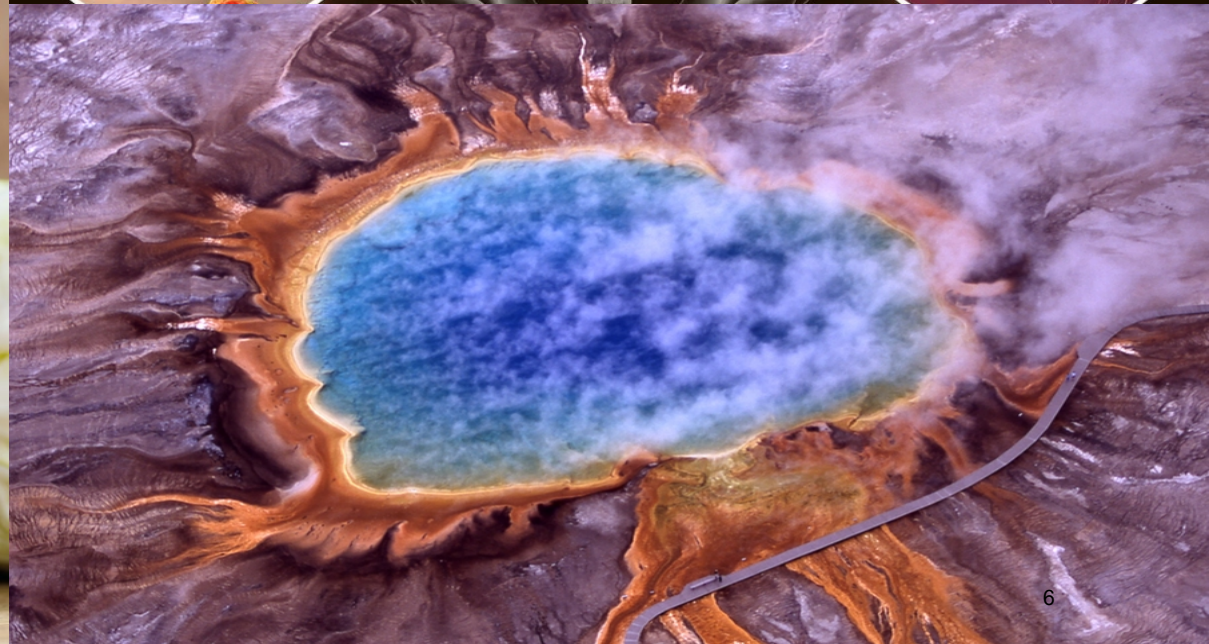
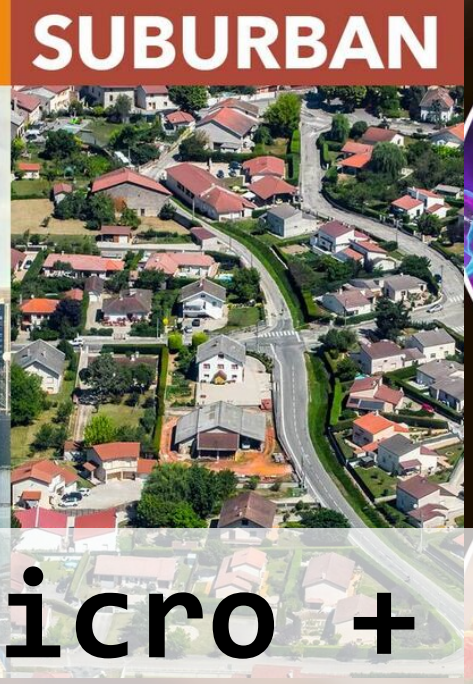
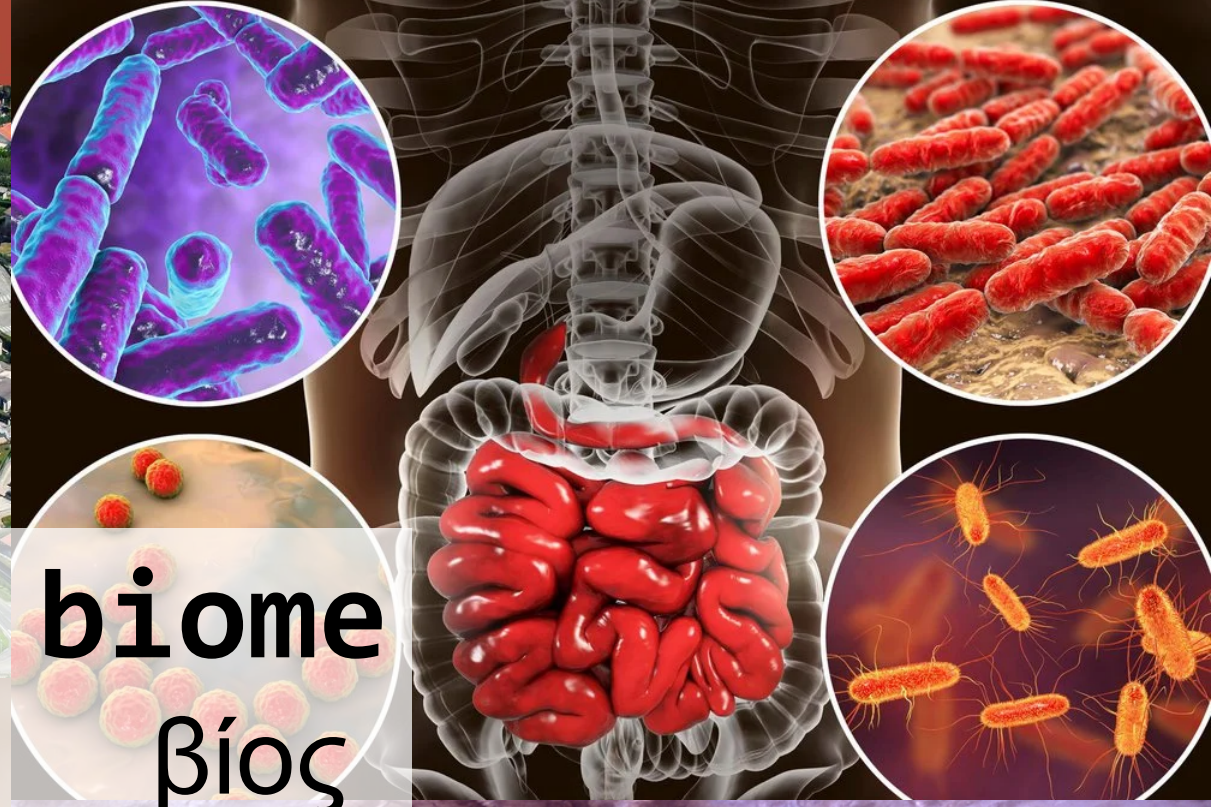


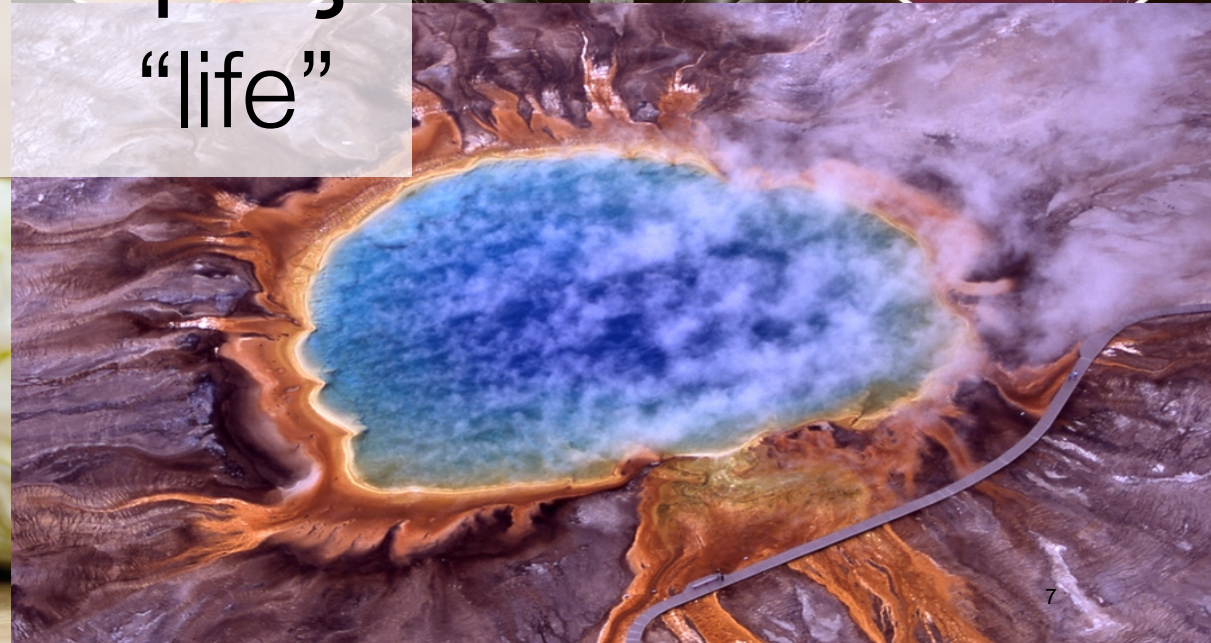




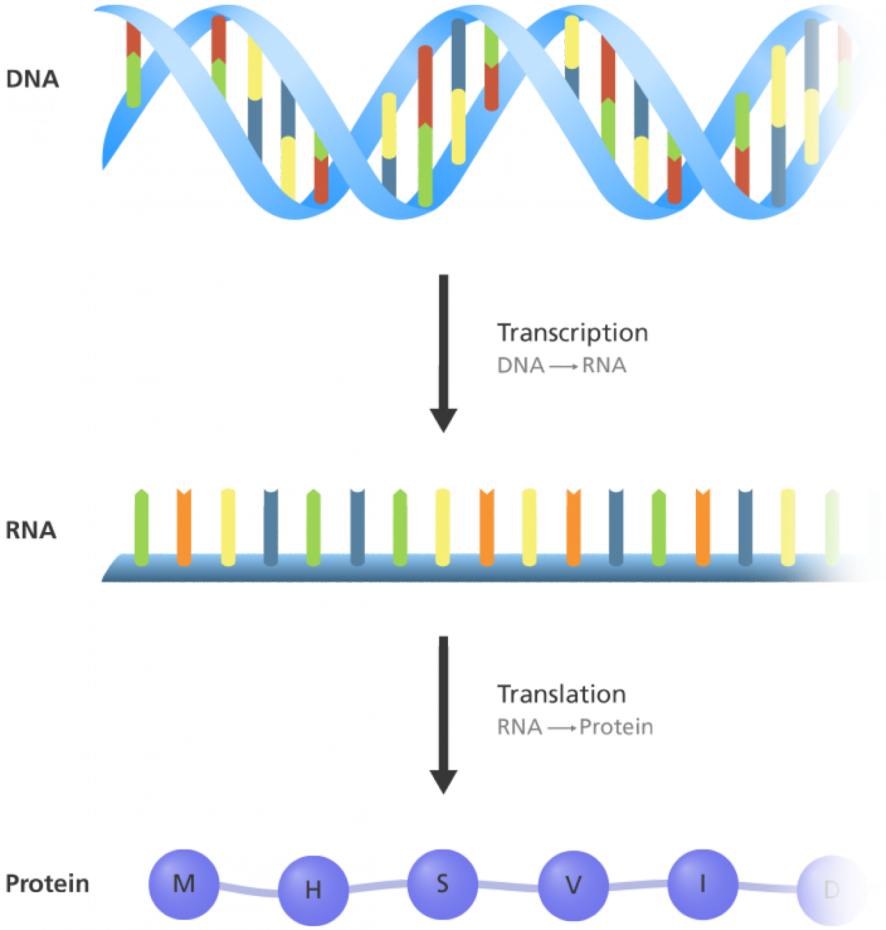
micro + **biome**

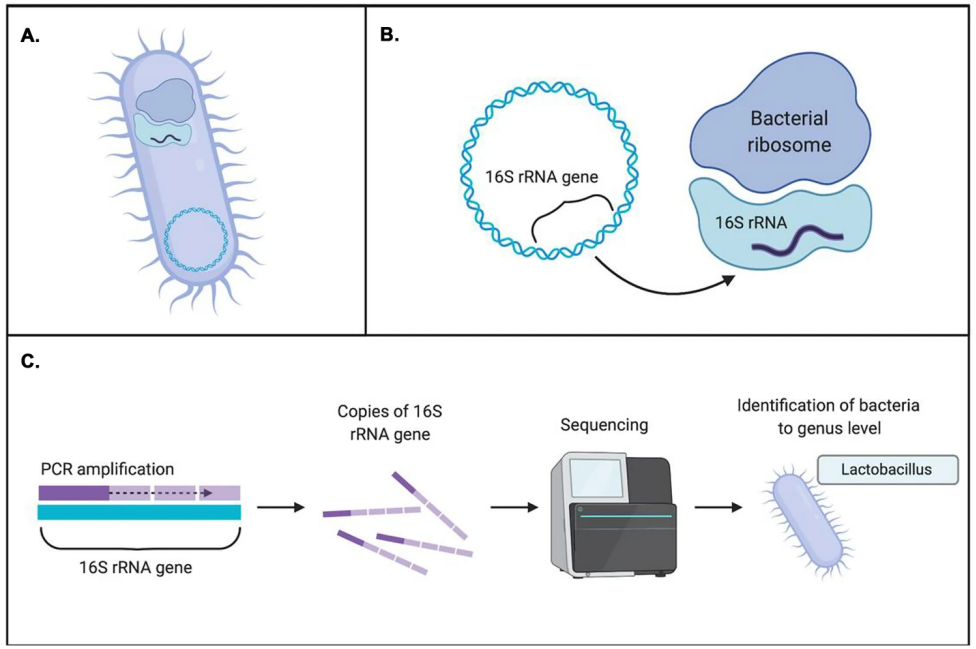
μικρός
“small”

βίος
“life”



Sequencing reveals bacterial composition and function

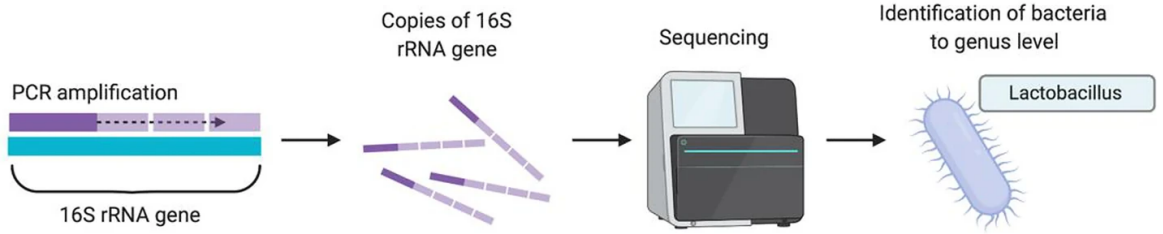




Patel et al. (2022), Current Urology Reports

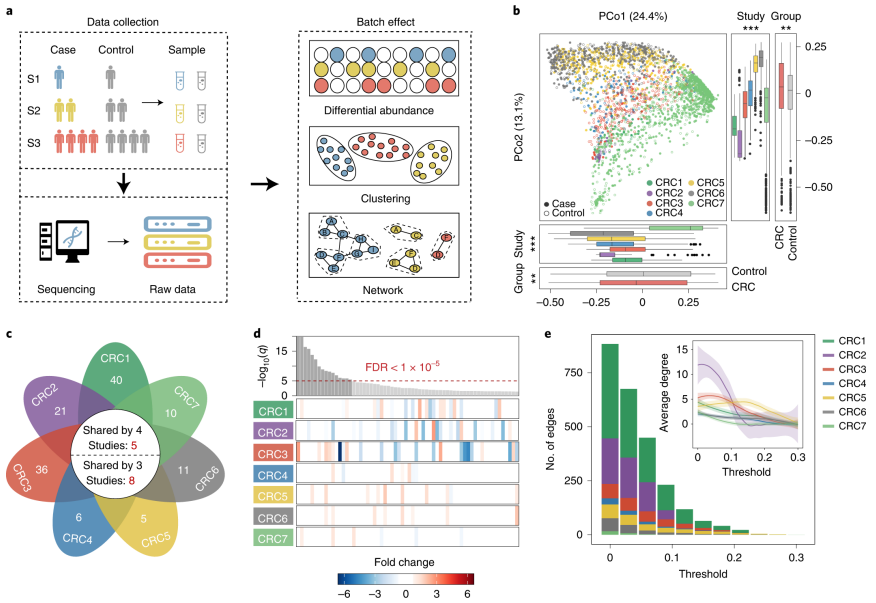
Sequencing data come in various forms

Data available for upload



Patel et al. (2022), Current Urology Reports

Hypotheses and clinical relevance



Xiao et al. (2022), Nature Computational Science

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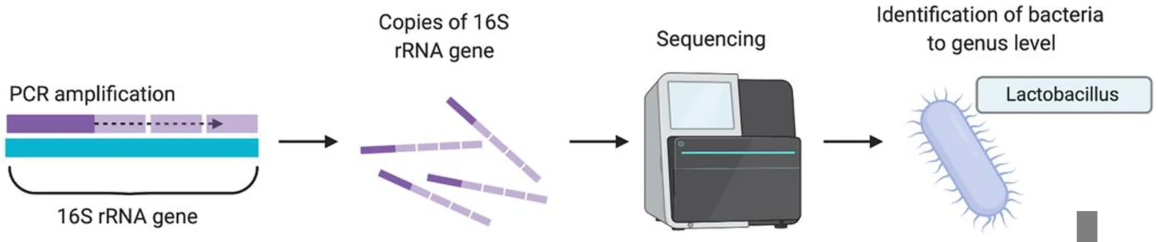

Patel et al. (2022), Current Urology Reports

Data available for upload

Raw sequence data: FASTQ file

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GTGGCGAAGGCGGCTTTCTGGACGATGACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGAT
+
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GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGFGGGG*8CCGGGCFFGGGGGGGGGGFF7
```

Bacterial identification and quantification: Feature table

Bacterial species (columns) / *Sample* (rows)

	1986030e3c5cd5df6d...	c5adecb440a6bac20...	5e151aa3f416a2fa6f0...
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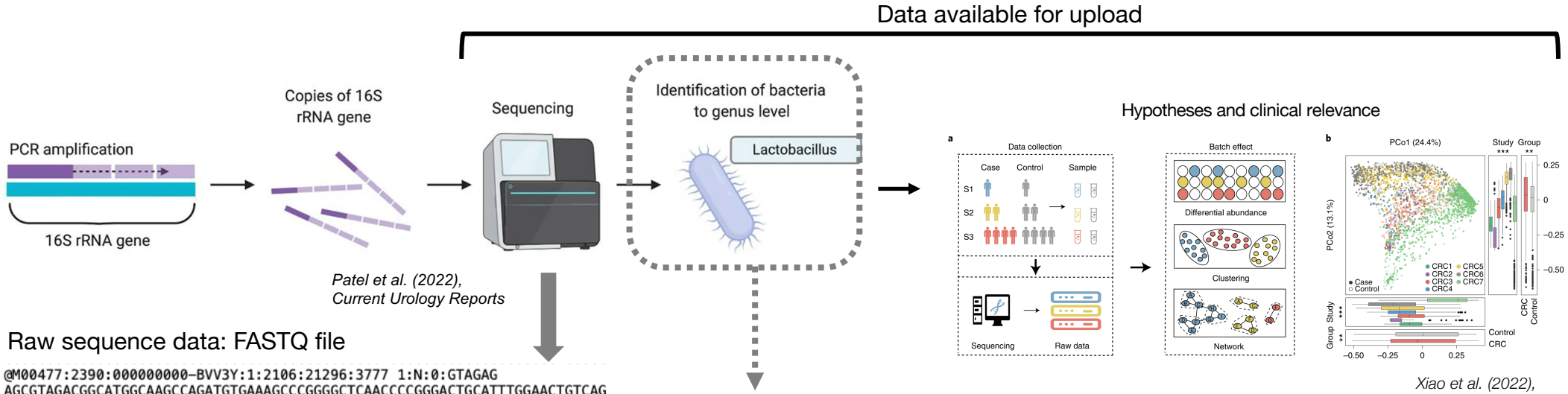

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TTGCGAAGGCGGCTCTCTGGACTGTAACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGGATTAGATA
+
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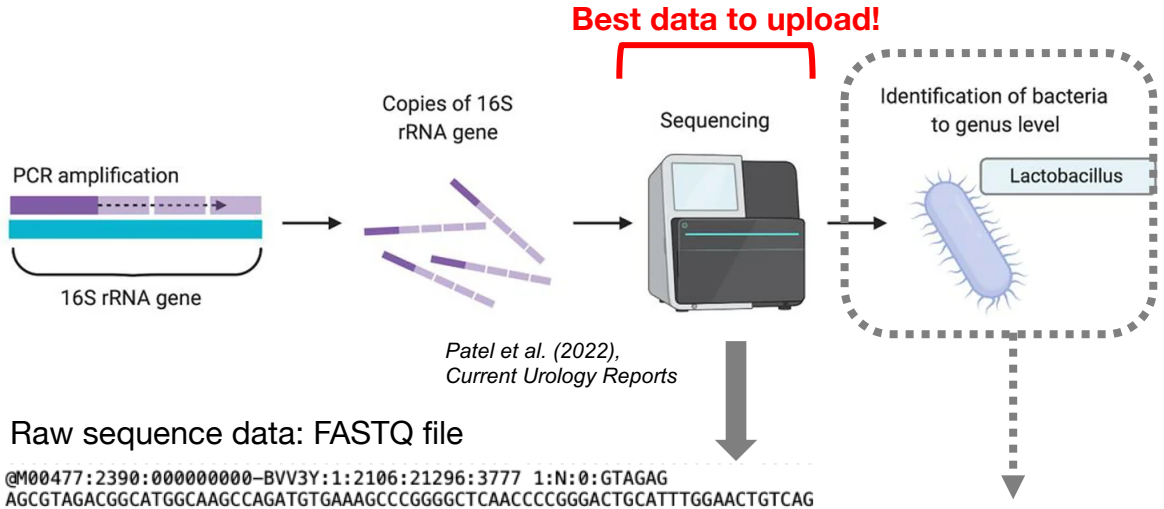
This process has many diverse steps, with many different options for tools and parameters!

Sequencing data come in various forms



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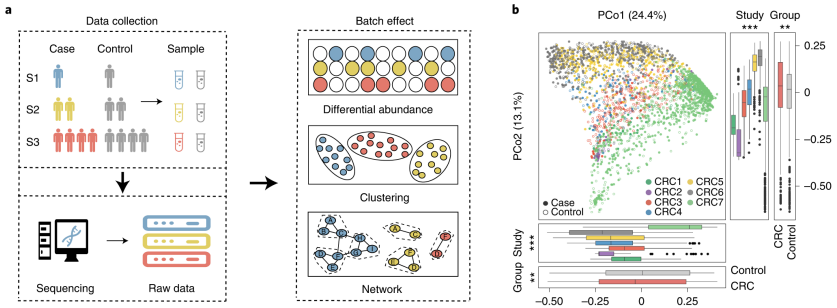
Hypotheses and clinical relevance



Xiao et al. (2022), Nature Computational Science

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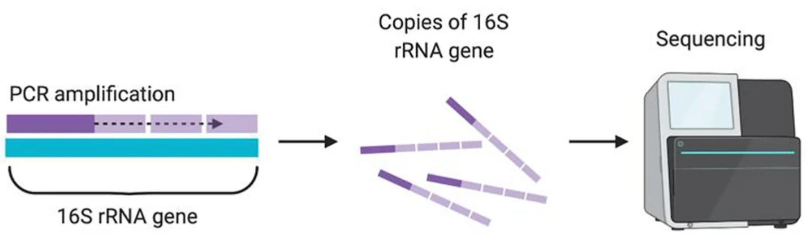
Sequencing data come in various forms

Best data to upload!



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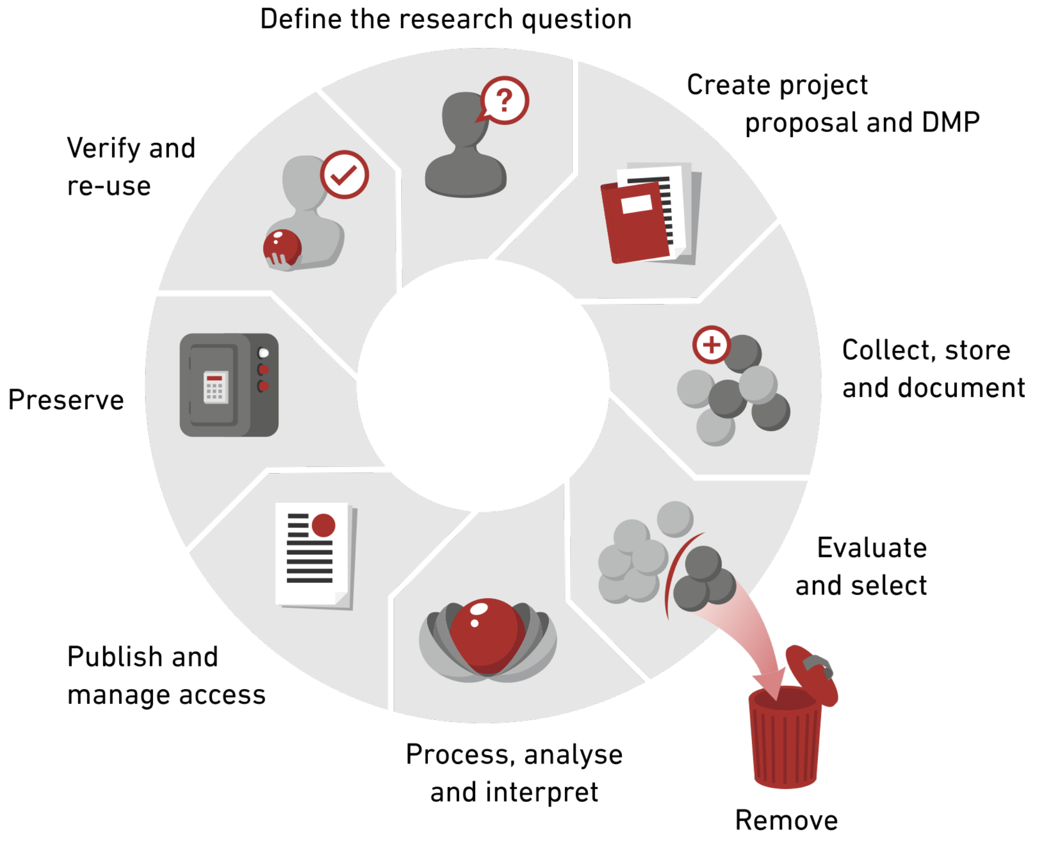

ETH Library: Research Data Life Cycle

Evaluating published microbiome data

- Data Availability Statements (DAS) required by journals
  - “Data available upon reasonable request”

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> The datasets generated for this study are available on request to the corresponding author at <REDACTED>; procedures to also have sequencing data available in a centralized repository (ENA and/or NCBI SRA archives) are ongoing at the time of publication.

original article by the developers [33]. Data from this study have been stored in the NCBI Sequence Read Archive (http://www.ncbi.nlm.nih.gov/sra).

Evaluating published microbiome data

- Data Availability Statements (DAS) required by journals
  - “Data available upon reasonable request”
  - **7%** of 1,800 publications provided usable data (Gabelica 2022)

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- Project MiShMASh: **Mi**crobiome **S**equence and **M**etadata **A**vailability **S**tandards

ETH BOARD

1. Develop a tier-based FAIR ORD standard for the field
2. Build software to assess adherence to standards

Aim 1: Tier availability for microbiome sequence analysis

For each paper, assign a badge (bronze, silver, gold) based on sequencing data availability:

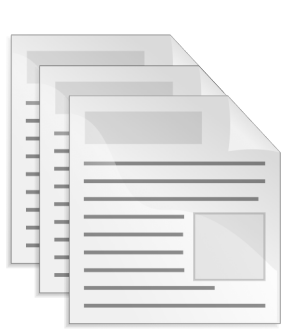
Requirement Type	Bronze	Silver	Gold
Data accessibility	Sequence data are downloadable and not paywalled	Sequence data are downloadable and not paywalled	Sequence data are downloadable and not paywalled
Data accessibility	Accession numbers provided	Accession numbers provided	Accession numbers provided
Data accessibility	Raw sequences given as BCL or FASTQ	Raw sequences given as BCL or FASTQ	Raw sequences given as BCL or FASTQ
Sample processing metadata		Sequencing method provided: 16S or metagenomics	Sequencing method provided: 16S or metagenomics
Sample processing metadata		PCR primer sequences	PCR primer sequences
Data accessibility			If data are not public, DAS clarifies access requirements
Data accessibility			Database is publicly accessible, with no login and/or institutional affiliation e.g. SRA or Figshare
Data processing metadata			Code provided

Each badge mandates all requirements from the previous tier!

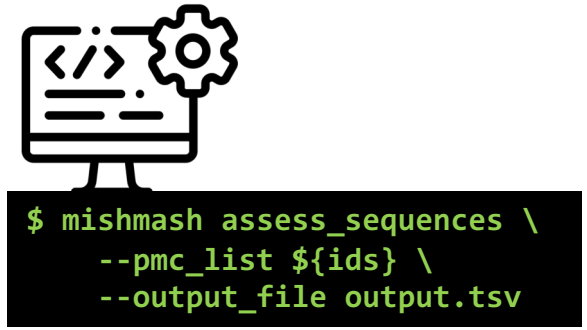
Note that “No badge” is also an assessment option.

Aim 2: Automated evaluation of standard adherence

Software easily validates data accessibility statements to ensure compliance



Scientific literature



Programmatic evaluation

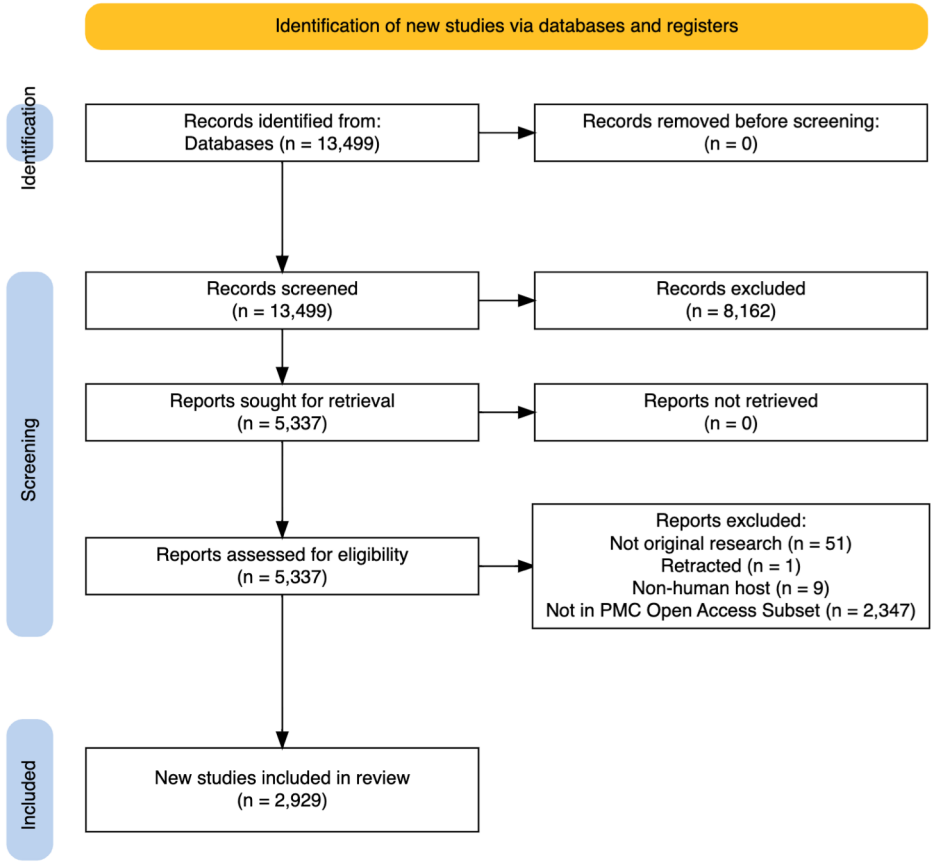
Sequence or metadata tier badging

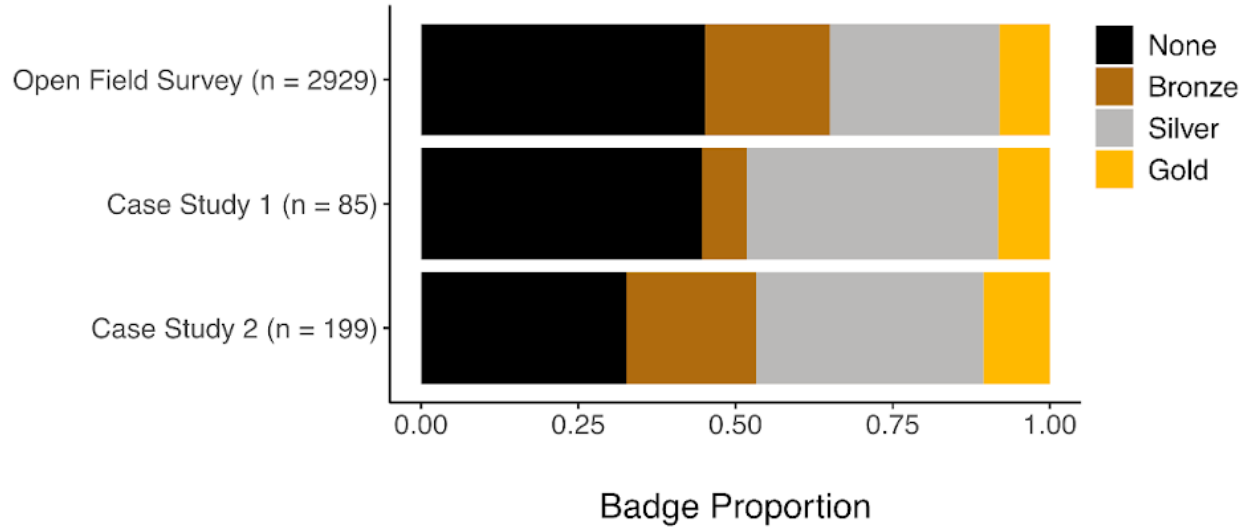
Programmatic tool encourages:

- Researchers to self-assess data availability in own publications
- Users to evaluate meta-analysis data prior to engagement
- Journal editors or grant agencies to verify data FAIRness in stakeholder publications

Aim 2: Automated evaluation of standard adherence

Open field survey of 2,929 human gut microbiome papers over 20 years reveals shockingly high proportion of papers with no accessible sequence data!





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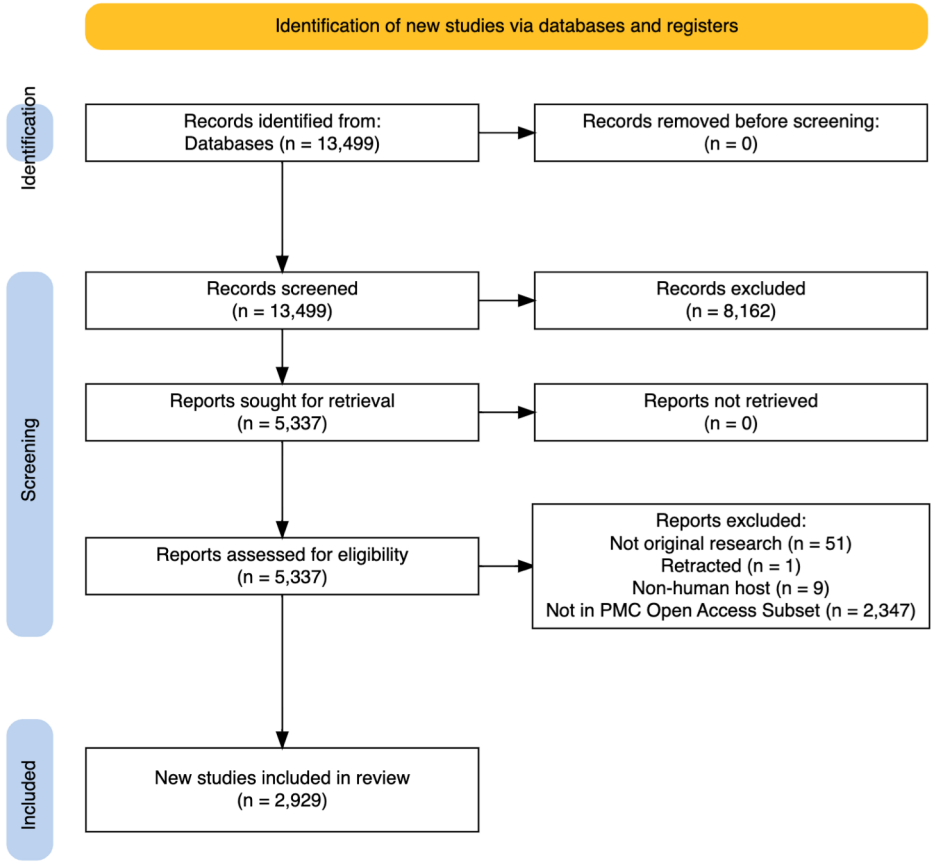
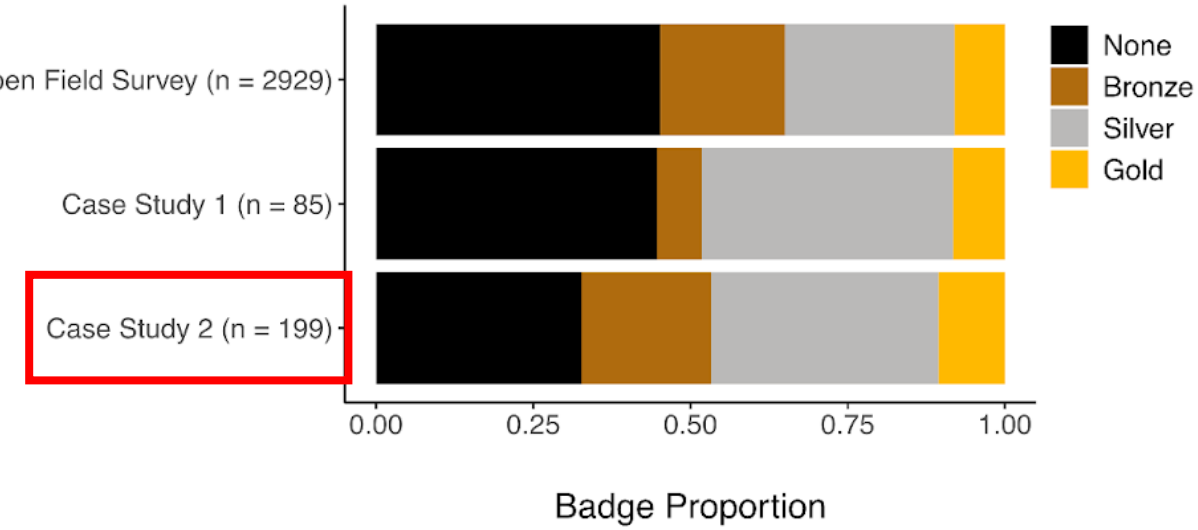
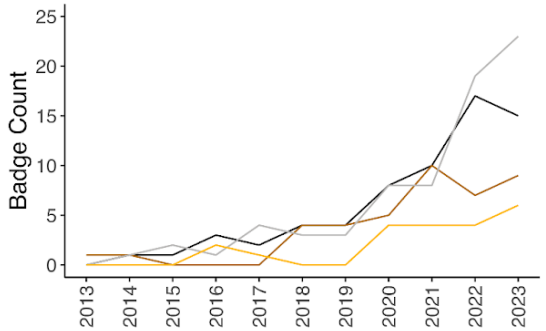


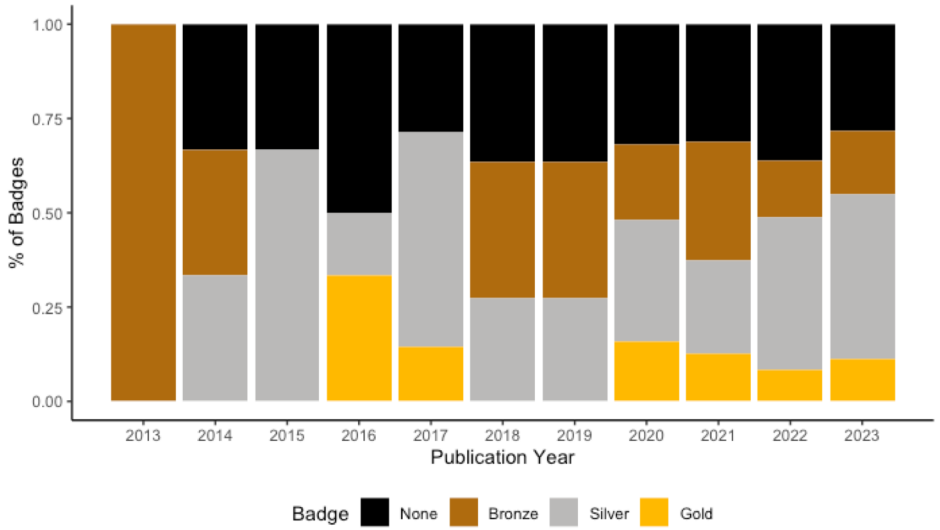


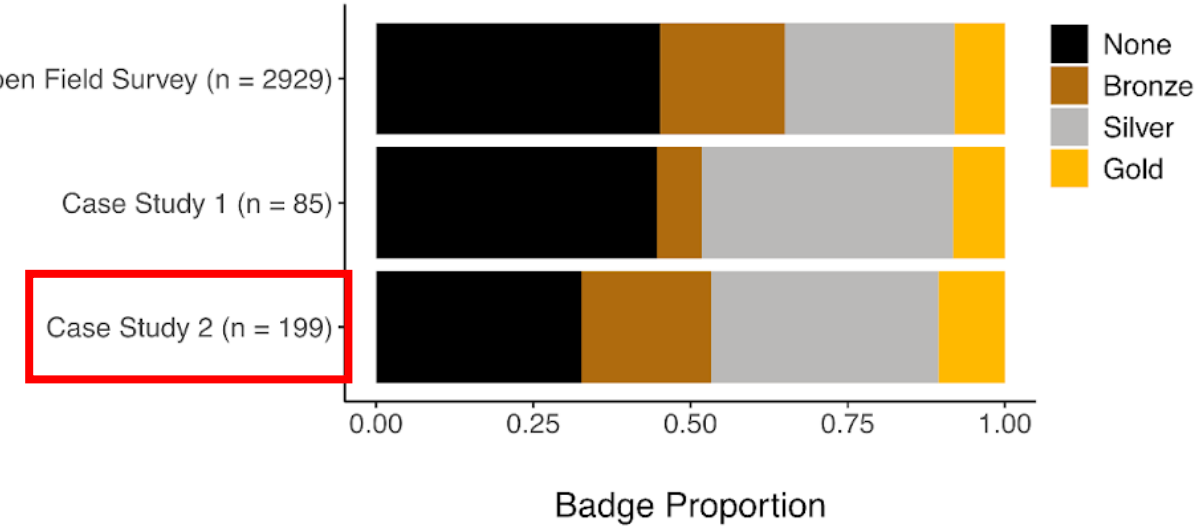
Aim 2: Automated evaluation of standard adherence

We see interesting temporal trends in data accessibility. Data from Case Study 2: A comprehensive assessment of gut mycobiome literature over past decade.



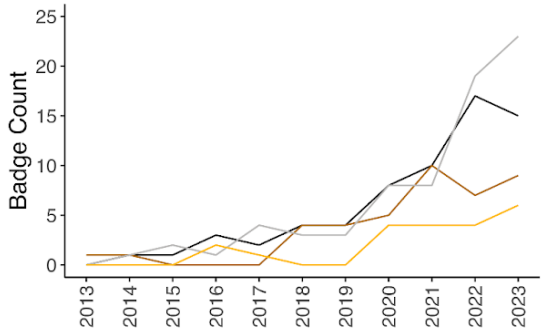
Human mycobiome publications have exploded in absolute number over time!





Aim 2: Automated evaluation of standard adherence

We see interesting temporal trends in data accessibility. Data from Case Study 2: A comprehensive assessment of gut mycobiome literature over past decade.



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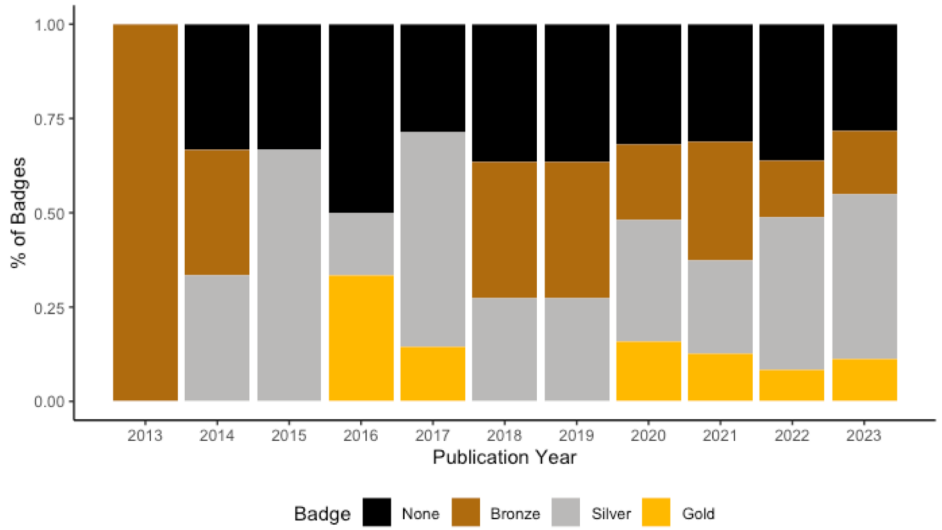
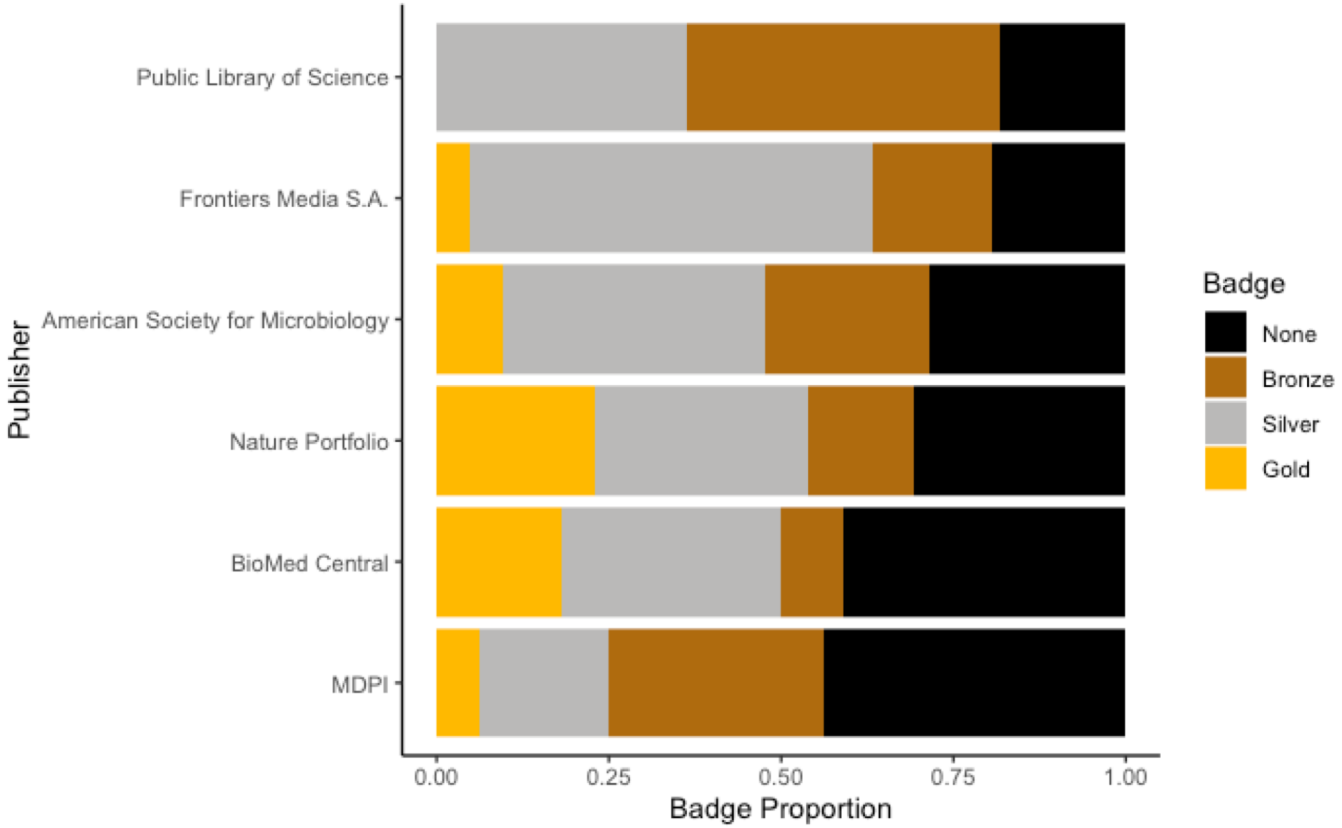




Aim 1: Tier availability for microbiome metadata analysis

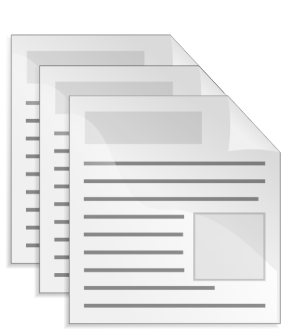
These tiers are prototype standards for human gut microbiome data, based on existing MIxS (Minimal Information about any [x] Sequence) standards.

MIxS v.6.0 Source	Bronze	Silver	Gold	MIxS requirement
MIxS core	Sample name	Sample name	Sample name	Mandatory [1]
MIxS core	Project name	Project name	Project name	Mandatory
MIxS core	Taxonomy ID of DNA sample	Taxonomy ID of DNA sample	Taxonomy ID of DNA sample	Mandatory [1]
MIxS core	Collection date	Collection date	Collection date	Mandatory [1,2]
MIxS core	Geographic location (latitude/longitude)	Geographic location (latitude/longitude)	Geographic location (latitude/longitude)	Mandatory [1,2]
MIxS core	Geographic location (country/region)	Geographic location (country/region)	Geographic location (country/region)	Mandatory [1]
MIxS core	Broad-scale environmental context	Broad-scale environmental context	Broad-scale environmental context	Mandatory
MIxS core	Local-scale environmental context	Local-scale environmental context	Local-scale environmental context	Mandatory
MIxS core	Environmental medium	Environmental medium	Environmental medium	Mandatory
MIxS core		Sequencing method	Sequencing method	Mandatory
MIxS core		Negative control type	Negative control type	Optional

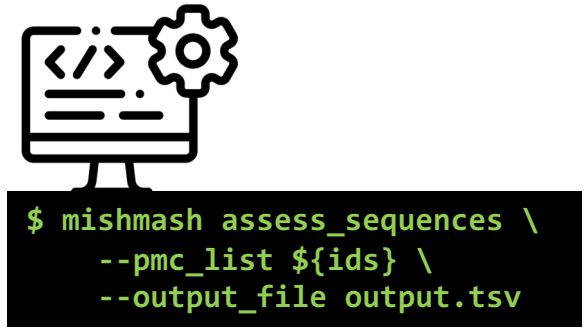
MIxS core / MIMARKS checklist		Target gene	Target gene	Mandatory
MIxS core / MIMARKS checklist		PCR primers	PCR primers	Optional
MIxS human-gut package		Host subject ID	Host subject ID	Optional
MIxS human-gut package		Host disease status	Host disease status	Optional
MIxS human-gut package		Host total mass	Host total mass	Optional
MIxS human-gut package		Host sex	Host sex	Optional
MIxS core			Sample material processing	Optional
MIxS core			Nucleic acid extraction	Optional
MIxS human-gut package			Host height	Optional
MIxS human-gut package			Host diet	Optional
MIxS human-gut package			Host occupation	Optional

Aim 2: Automated evaluation of standard adherence

Software easily validates data accessibility statements to ensure compliance



Scientific literature



Programmatic evaluation

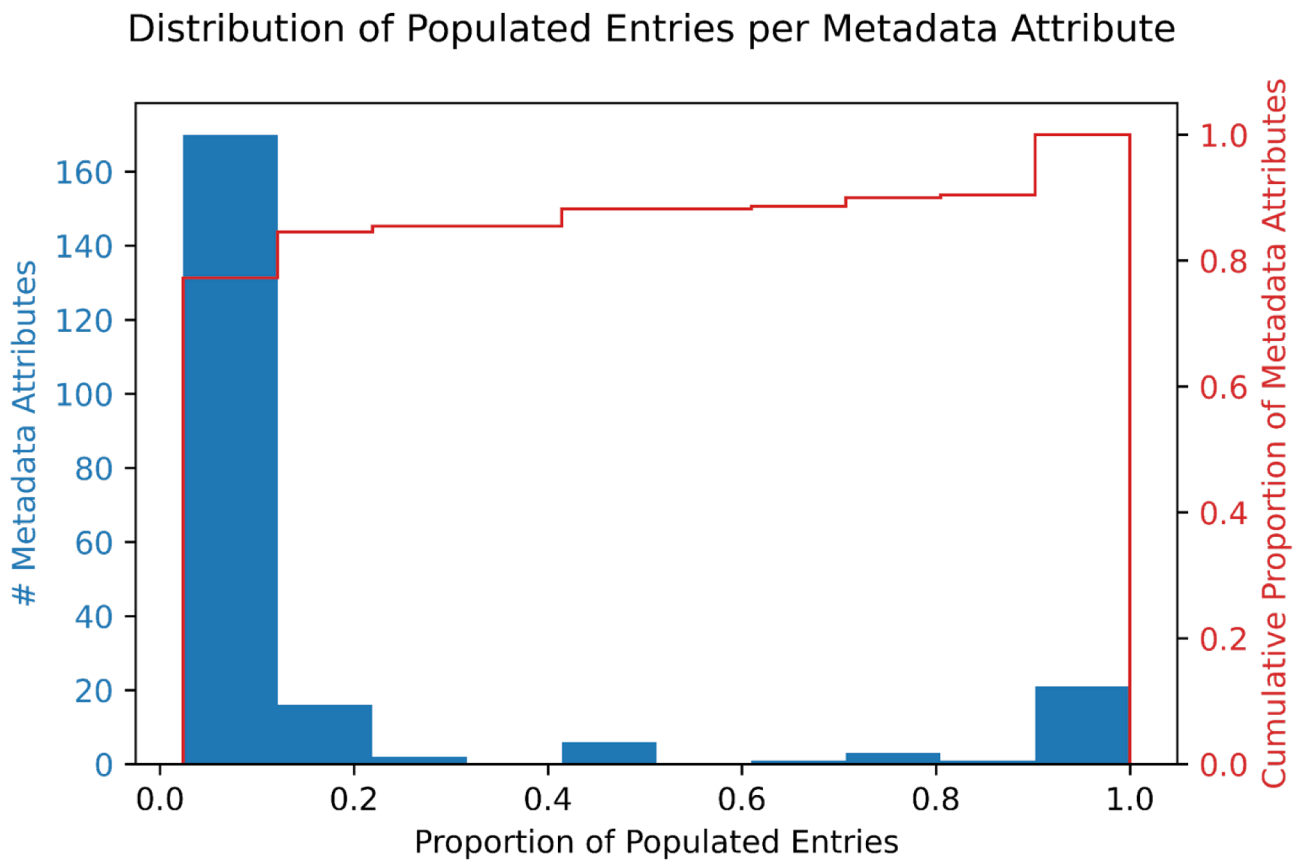
Sequence or metadata tier badging

Programmatic tool encourages:

- Researchers to self-assess data availability in own publications
- Users to evaluate meta-analysis data prior to engagement
- Journal editors or grant agencies to verify data FAIRness in stakeholder publications

Aim 2: Automated evaluation of standard adherence

Metadata are not easily interoperable across studies!



Sample ID
Sample-ID
sample_id
Sample.num
sam_number
Sample accession
Sample_accession_ID

Microbiome data must meet FAIR standards

- Project MISHMASH: Microbiome Sequence and Metadata Availability Standards
- Aims:
  1. Develop a tier-based FAIR ORD standard for the field, for microbiome sequence data and metadata
  2. Build software to assess adherence to standards

Impact:
1. Self-assess data availability in own publications
2. Evaluate meta-analysis data prior to engagement
3. Promote dialogue and efforts in microbiome ORD

Bronze: Available data meet the minimum standard for data re-use.

Silver: Facilitated reproducibility; this is a balance between comprehensiveness and feasibility for most.

Gold: These data provide valuable information to address research questions beyond the original scope.

Food Systems Biotechnology

Thank you!

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Dr. Alan Pacheco
Chumei Tang
Prof. Dr. Shana Sturla

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  - Yellowstone: https://news.mit.edu/2018/mit-eaps-research-shows-how-life-survives-extreme-environments-1214
  - Gut: https://www.smithsonianmag.com/science-nature/scientists-find-possible-link-between-gut-bacteria-and-depression-180971411/
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  - Central dogma: https://www.yourgenome.org/wp-content/uploads/2022/04/dna_central_dogma_yourgenome.png

TARA OCEANS

HMP

earth microbiome project

Microbiomes impact our health and our environment!

MISHMASH impact requires partnership

1 Release

2 Community adoption

3 Infrastructure integration

4 Publisher and funding body utilization

qiime2

Search

SLSP
Swiss Library Service Platform

Springer

NON SOLUS

ELSEVIER

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