

ONE HEALTH Codeathon

February 26-28, 2020 | USF Library Grace Allen Room

Host-microbiome interactions in global health

Collaborative coding integrating data sciences, public health, & humanities research



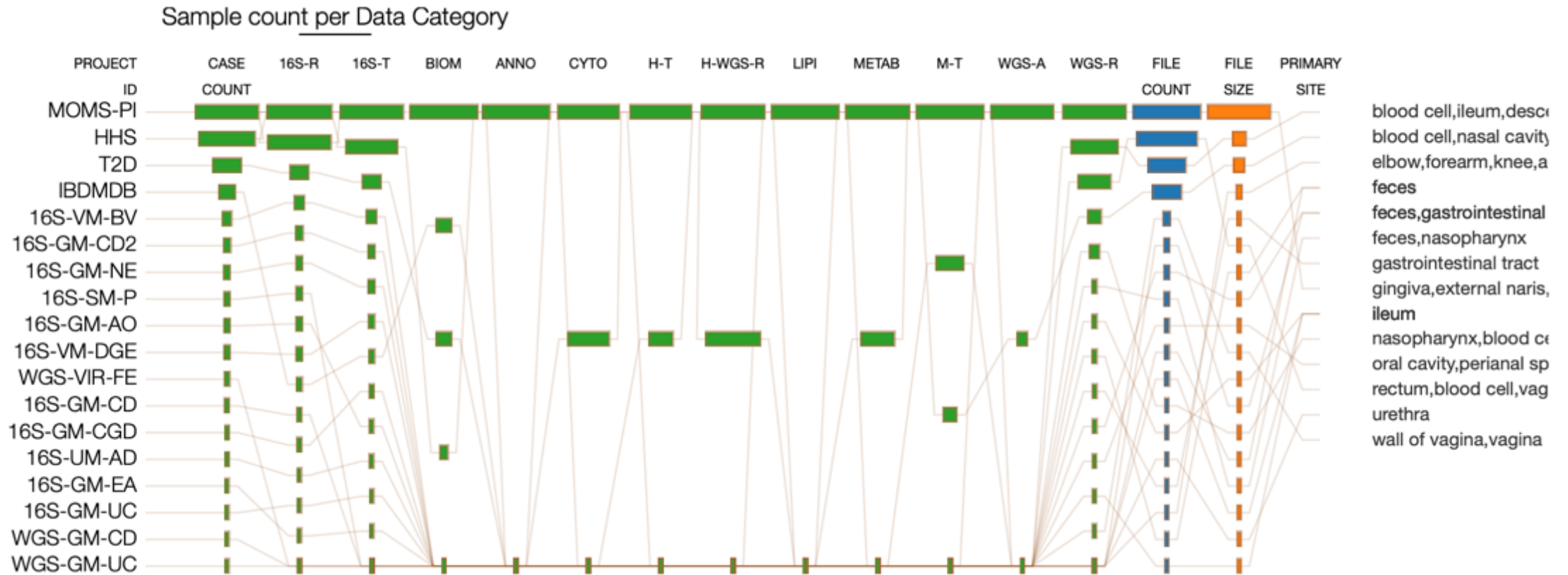
POTENTIAL TEAM QUESTIONS

- Can we track human migratory history with the patterns of microbiome evolution? (e.g. GIS mapping of temporal omics data)
- Are human geographical differences reflected in microbiota differentiations and adaptations? (e.g. mining patterns such as human nutrition and evolution)
- Is there a diaspora microbiota unifying human social and culture entities? (e.g. uncovering the many “human dimensions” of human health (e.g., public policy, culture, race, history, migration))

Resources for Codeathon:

- HMPDACC - Human Microbiome Project - Data Analysis and Coordination Portal.
- Mgnify (EBI): Metagenome database with assemblies
- MDB: A microbiome database hosted by China National GeneBank(CNGB)
- QIITA: Precomputed 16S datasets and analysis tool for microbiome
- CORE Database:
- PATRIC: Antibiotic resistance data
- Earth Microbiome Project: 16S data on lots and lots of samples (animal, human, soil, freshwater, ocean etc.)
 - Qiita portal for the Earth Microbiome Project (EMP)
- TARA Oceans project: 16S tables etc. from lots of sites in the ocean.
- curatedMetagenomicData : Curated and processed metagenomic data through ExperimentHub
- CARD: antibiotic resistance gene database
- dbCAN: carbohydrate degradation enzyme database and search engine
- MicrobiomeDB: A EupathDB resource for analyzing and mining microbiome datasets
- IMG/M: integrated genome and metagenome comparative data analysis system
- More....

Human Microbiome Project Data Analysis and Coordination Portal



Mgnify (EBI): Metagenome database with assemblies

<https://www.ebi.ac.uk/metagenomics>



Human
(97725)



Digestive
system
(65625)



Aquatic
(41710)



Marine
(30841)



Plants
(22217)



Digestive
system
(19016)



Soil
(17232)



Skin
(7780)



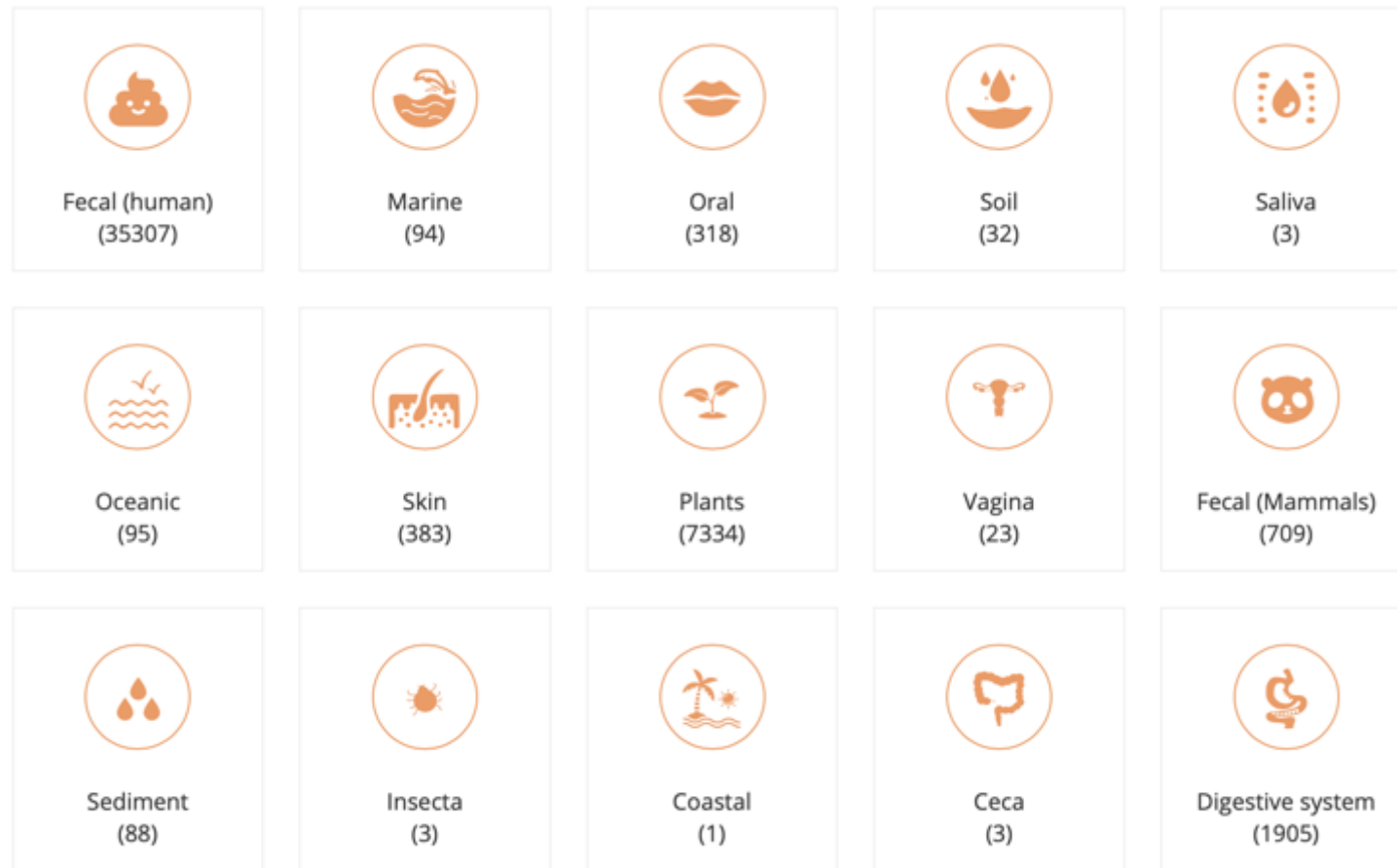
Wastewater
(3477)



Food
production
(1801)

MDB: A microbiome database hosted by China National GeneBank(CNGB)

<https://db.cngb.org/microbiome>



QIITA: rapid, web-enabled microbiome meta-analysis

<https://qiita.ucsd.edu>

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Studies

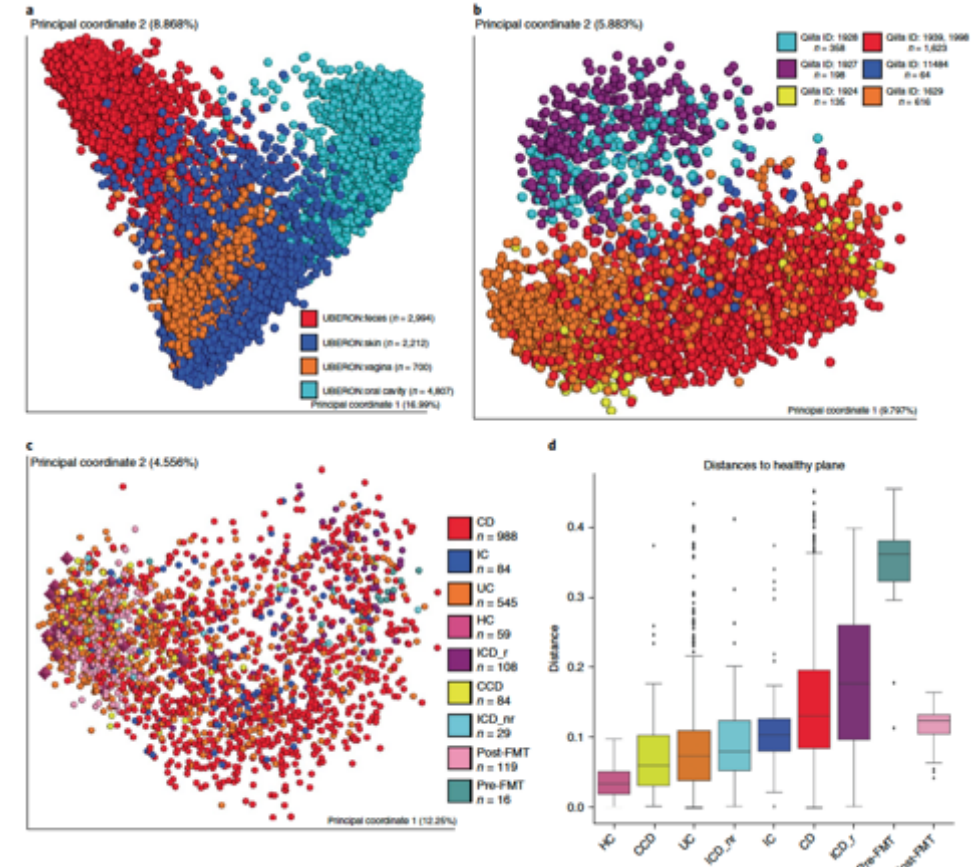
public: 521
private: 245
sandbox: 1,241
submitted to EBI: 346

Samples

public: 235,726
private: 133,675
sandbox: 305,419
submitted to EBI: 149,948
submitted to EBI (prep): 167,264

Samples per data type

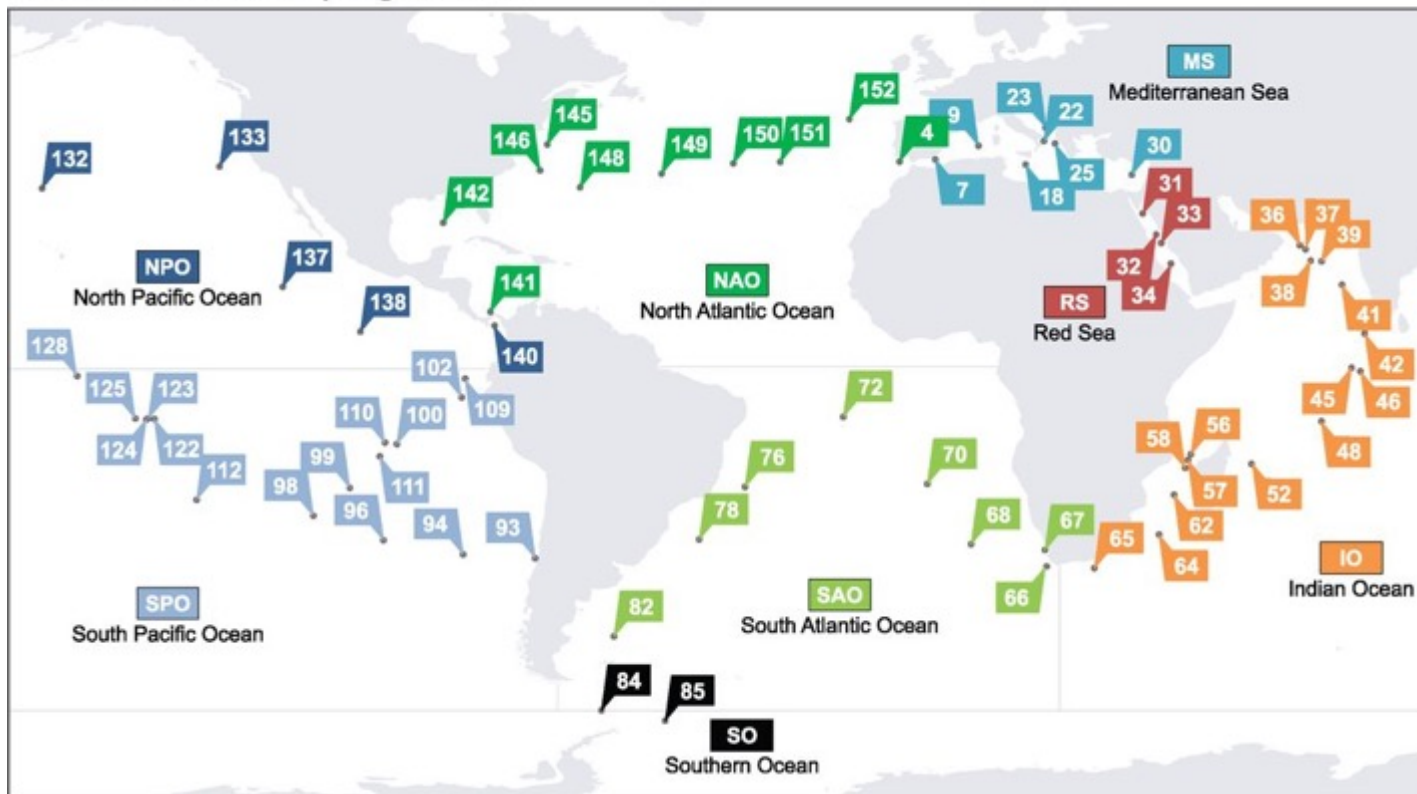
16S: 236,801
18S: 7,425
ITS: 9,569
Metagenomic: 7,555
Metabolomic: 407



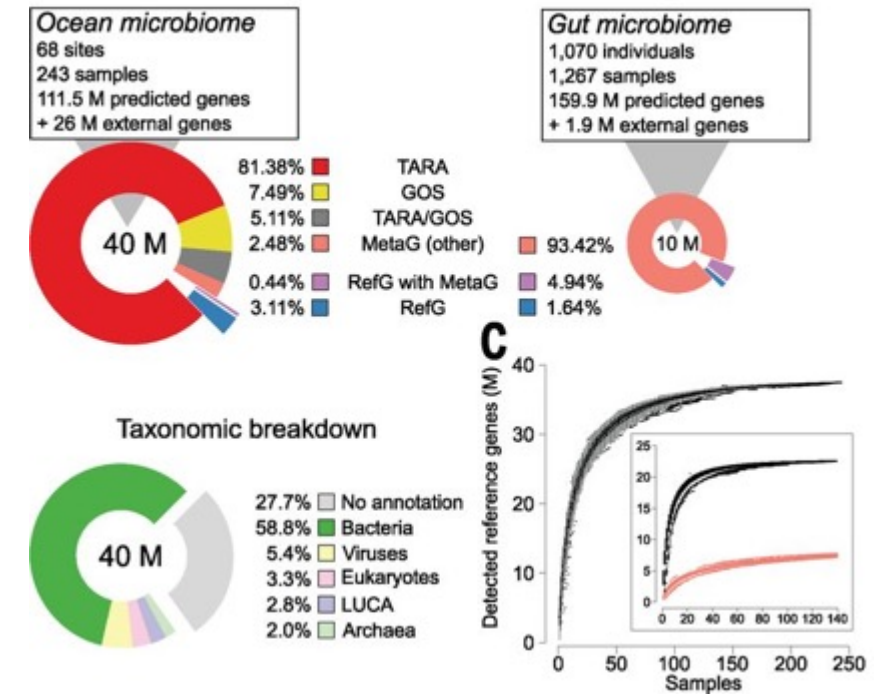
Gonzalez, A., Navas-Molina, J. A., Kosciulek, T., McDonald, D., Vázquez-Baeza, Y., Ackermann, G., ... & Sanders, J. G. (2018). Qiita: rapid, web-enabled microbiome meta-analysis. *Nature methods*, 15(10), 796-798.

TARA Oceans project: 16S tables, metagenomics, metatranscriptomics etc. from lots of sites in the ocean.

A Tara Oceans sampling stations



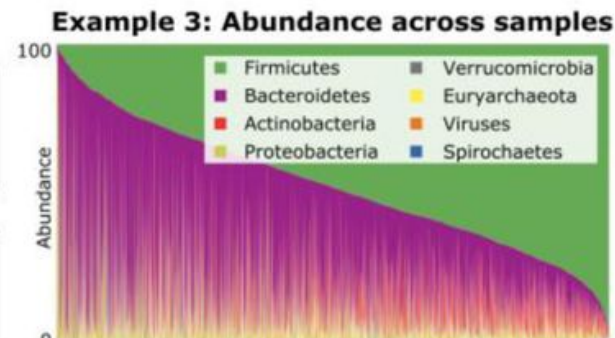
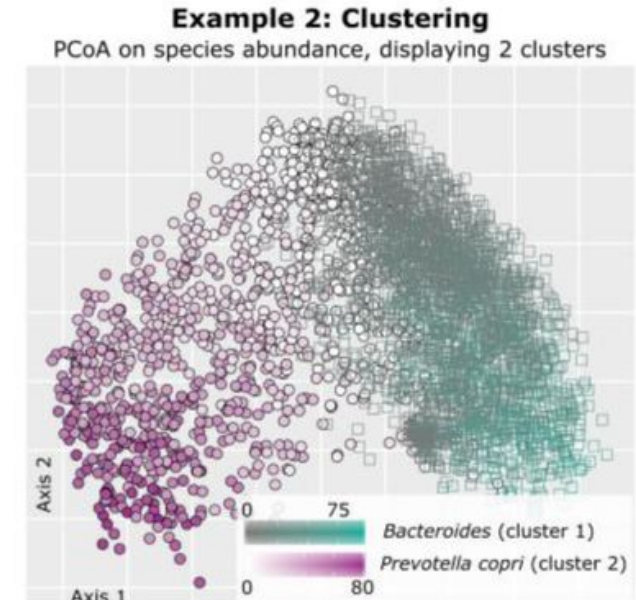
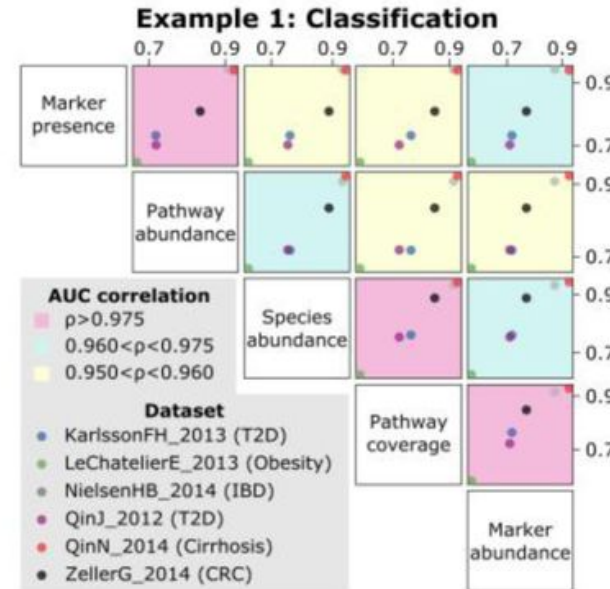
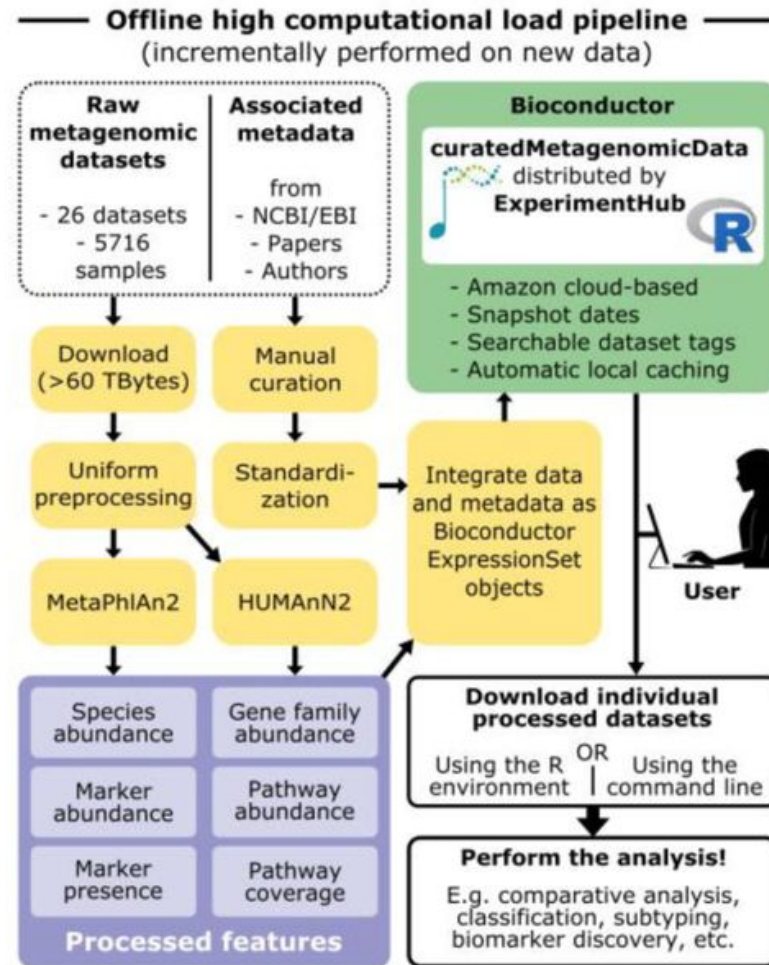
B Ocean Microbial Reference Gene Catalog



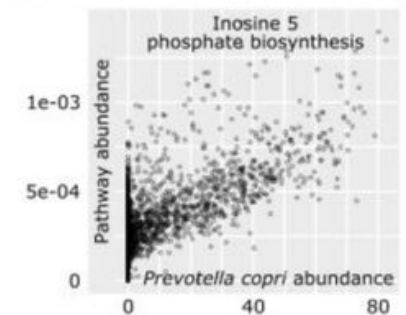
Salazar, G., Paoli, L., Alberti, A., Huerta-Cepas, J., Ruscheweyh, H. J., Cuenca, M., ... & Gregory, A. C. (2019). Gene expression changes and community turnover differentially shape the global ocean metatranscriptome. *Cell*, 179(5), 1068-1083.

Sunagawa, S., Coelho, L. P., Chaffron, S., Kultima, J. R., Labadie, K., Salazar, G., ... & Cornejo-Castillo, F. M. (2015). Structure and function of the global ocean microbiome. *Science*, 348(6237), 1261359.

curatedMetagenomicData : Curated and processed metagenomic data through ExperimentHub



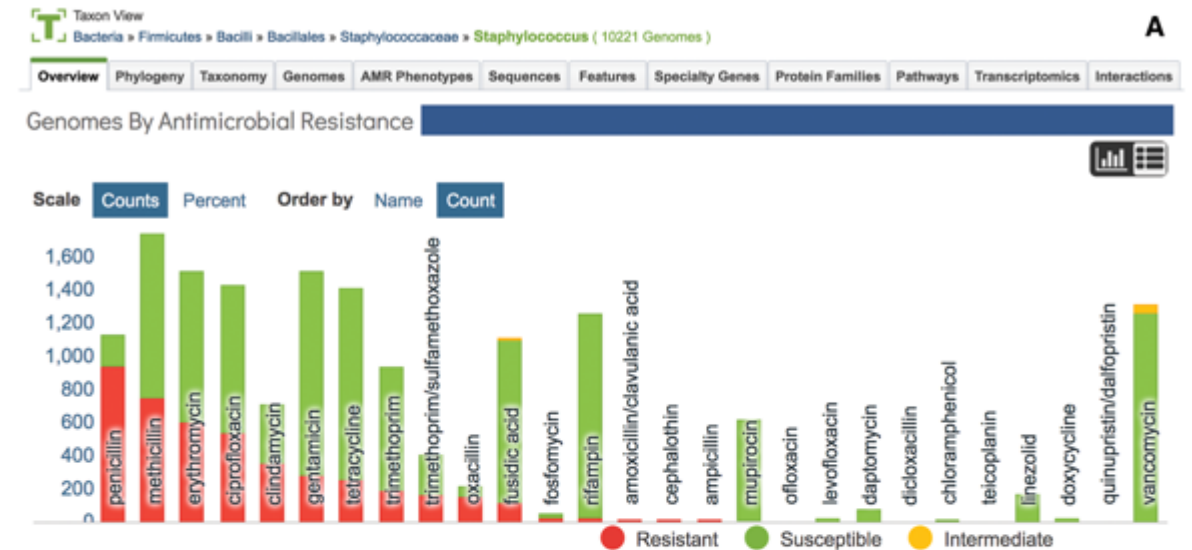
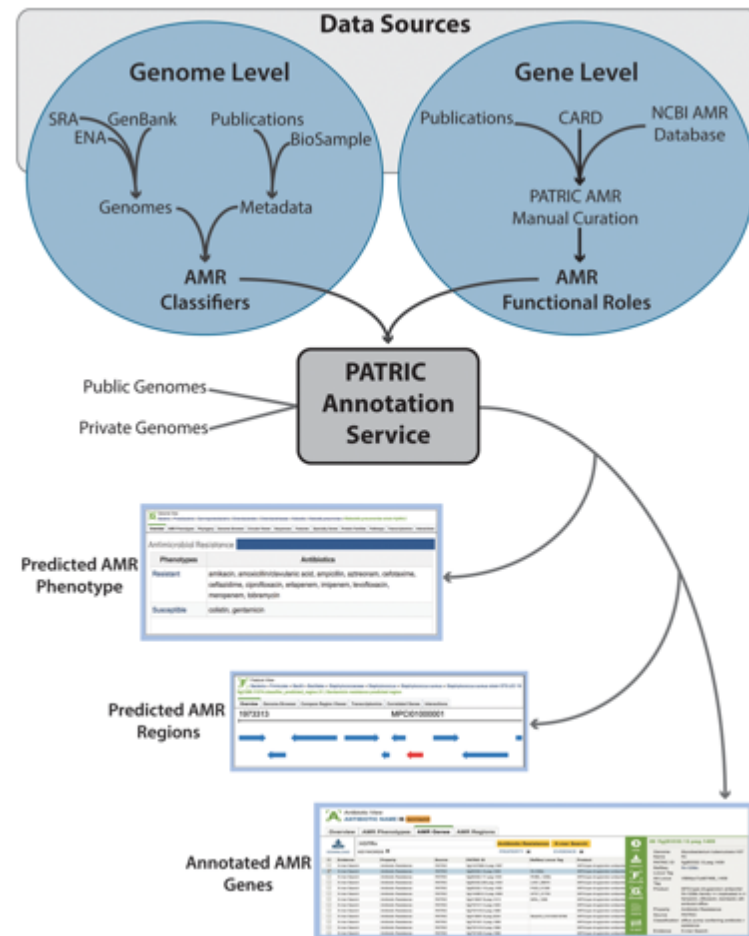
Example 4: Species-pathway correlation



Low barrier to user-centric analyses

PATRIC: Antibiotic resistance data

<https://patricbrc.org>



Antibiotic

Antibiotic	Resistant Phenotype	Laboratory Typing Method	Laboratory Typing Platform	Testing Standard
methicillin (1761)	Susceptible (10953)	MIC (1718)	E-test (1549)	CLSI (1690)
erythromycin (1507)	Resistant (4295)	disk diffusion (1234)	AdaBoost Classifier (667)	EUCAST (1245)
gentamicin (1507)	Intermediate (92)	Computational Prediction (667)	broth microdilution (70)	
ciprofloxacin (1430)			population analysis (70)	
vancomycin (1416)				

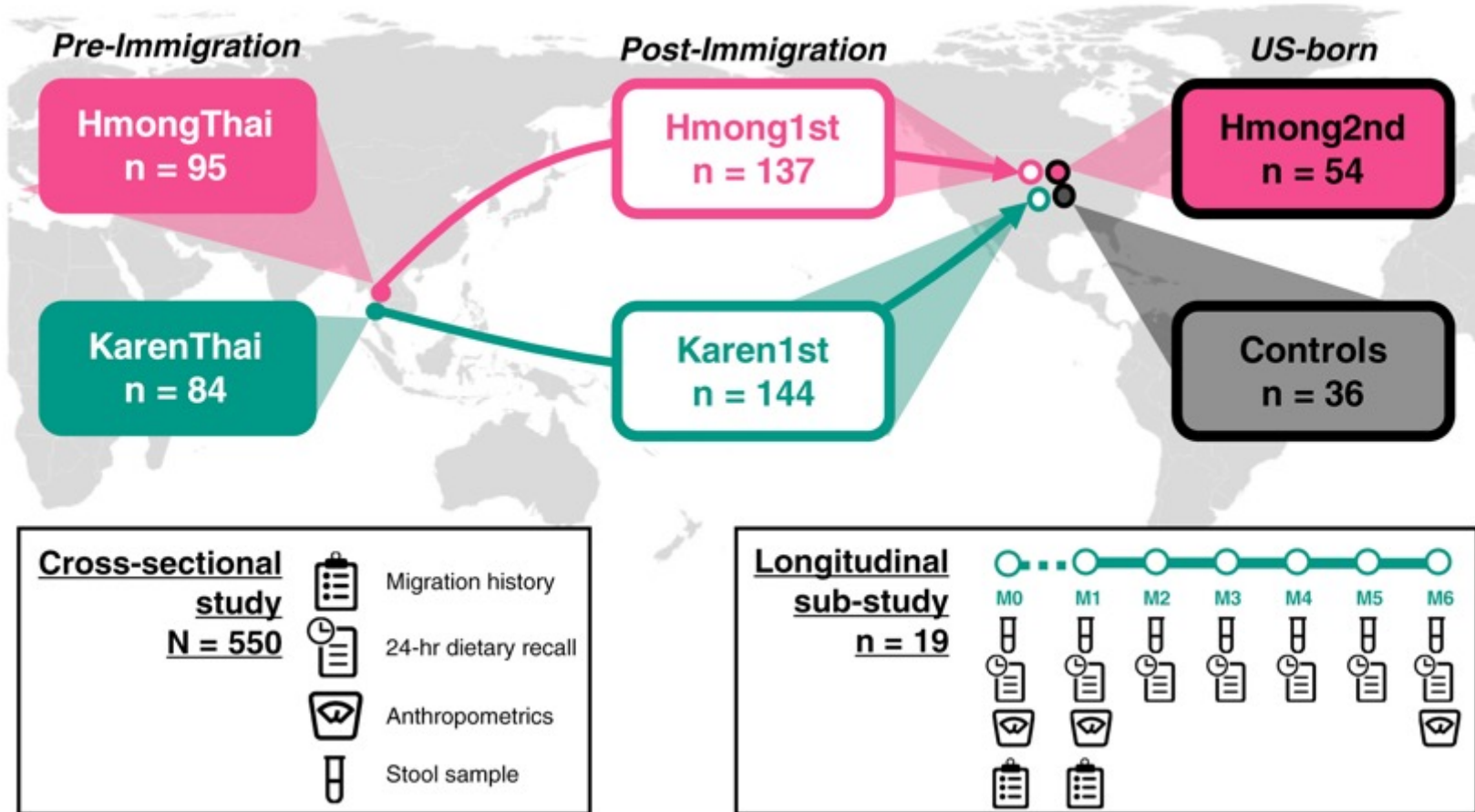
Genome Name

Genome Name	Antibiotic	Resistant Phenotype	Measurement Sign	Measurement Value	Measurement Units	Lab typing Method	Lab typing Platform	Lab typing Vendor	Lab typing Version	Testing standard
Staphylococcus aureus AB117	deptomycin	Resistant		2	mg/L	MIC				
Staphylococcus aureus 107	vancomycin	Intermediate		4	mg/L	MIC	broth microdilution			CLSI
Staphylococcus aureus 107	vancomycin	Intermediate		1.52	mg/L	MIC	population analysis			CLSI
Staphylococcus aureus 109	vancomycin	Intermediate		4	mg/L	MIC	broth microdilution			CLSI
Staphylococcus aureus 109	vancomycin	Intermediate		1.8	mg/L	MIC	population analysis			CLSI

National Database of Antibiotic Resistant Organisms (NDARO)

Antonopoulos, D. A., Assaf, R., Aziz, R. K., Brettin, T., Bun, C., Conrad, N., ... & Kenyon, R. W. (2019). PATRIC as a unique resource for studying antimicrobial resistance. *Briefings in bioinformatics*, 20(4), 1094-1102.

Vangay, P., Johnson, A. J., Ward, T. L., Al-Ghalith, G. A., Shields-Cutler, R. R., Hillmann, B. M., ... & Batres, R. (2018). US immigration westernizes the human gut microbiome. *Cell*, 175(4), 962-972.



- Groussin, M., Poyet, M., Sistiaga, A., Kearney, S. M., Moniz, K., Noel, M., . . . Alm, E. J. (2020). Industrialization is associated with elevated rates of horizontal gene transfer in the human microbiome. *bioRxiv*, 2020.
- Poyet, M., Groussin, M., Gibbons, S. M., Avila-Pacheco, J., Jiang, X., Kearney, S. M., . . . Alm, E. J. (2019). A library of human gut bacterial isolates paired with longitudinal multiomics data enables mechanistic microbiome research. *Nature Medicine*, 25(9), 1442-1452.
- Dill-McFarland, K. A., Tang, Z. Z., Kemis, J. H., Kerby, R. L., Chen, G., Palloni, A., ... & Herd, P. (2019). Close social relationships correlate with human gut microbiota composition. *Scientific reports*, 9(1), 1-10.
- Jensen, T. Z. T., Niemann, J., Iversen, K. H., Fotakis, A. K., Gopalakrishnan, S., Vågene, Å. J., . . . Schroeder, H. (2019). A 5700 year-old human genome and oral microbiome from chewed birch pitch. *Nature Communications*, 10(1), 5520.