

Microbiome and Metagenomics, Clinical, Terrestrial, and in Space



**Weill Cornell
Medicine**



@mason_lab

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at Weill Cornell Medicine,

Fellow of the Information Society Project, Yale Law School

March 30th, 2021

Conflicts

Onegevity



illumina®



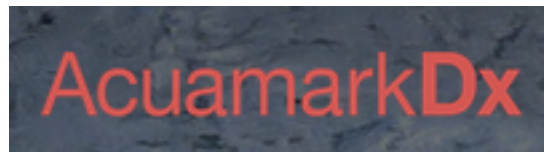
WHOLE BIOME



abbvie

Renno**va**Health

KARIUS™





Jacobs Institute Runway Program at Cornell Tech

- First of its kind – academic/business hybrid program accepts new PhDs to commercialize cutting-edge research.
- Provides 1-3 years of support.
- Niamh is in 3rd cohort – now accepting applications for 5th cohort.
- Mini MBA – take business classes along with Cornell Tech master's students and have access to widespread business mentorship and investor network.



Hospital-acquired infection prevention powered by AI.



Biotia Provides Microbial Surveillance for Hospitals

On average, one in 25 people who check into a hospital get an infection— and one in nine die of that infection. These numbers are staggering and costing hospitals billions. Our team is taking advantage of the current genomics revolution to provide a service to hospitals to swab and sequence their high risk environments. We have a proprietary software and databases which we use to analyze these data and generate reports for hospitals to 1) monitor hygiene, 2) identify pathogens, and 3) track antibiotic resistance.

FDA EUA for NGS-capture assay

Home / The Scientist /

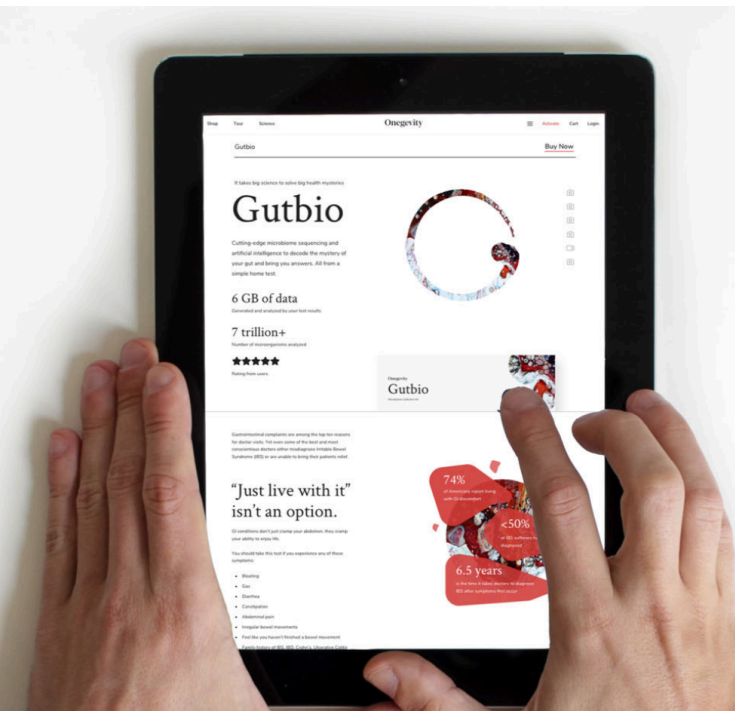
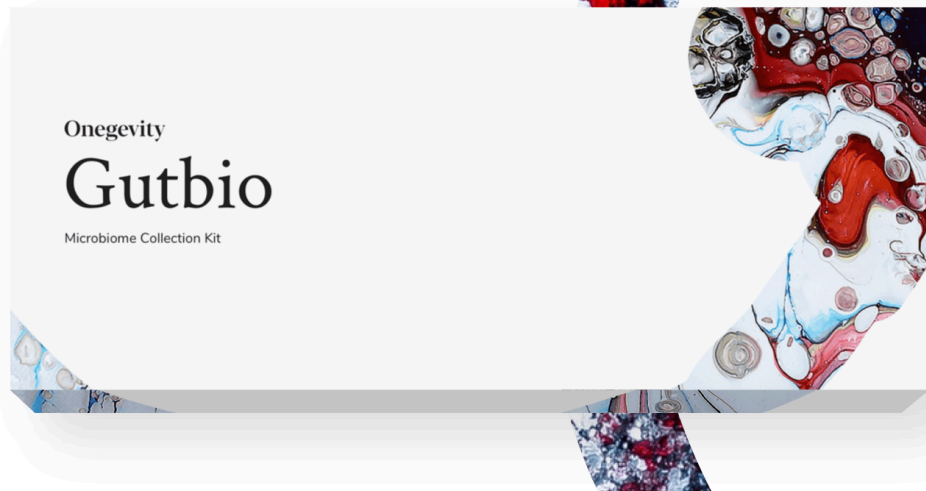
Twist Bioscience And Biotia Receive U.S. FDA Emergency Use Authorization For First Hybridization Capture-Based Next-Generation Sequencing SARS-CoV-2 Assay

Twist Bioscience and Biotia Receive U.S. FDA Emergency Use Authorization for First Hybridization Capture-Based Next-Generation Sequencing SARS-CoV-2 Assay

Twist Bioscience Corporation (NASDAQ: TWST), a company enabling customers to succeed through its offering of high-quality synthetic DNA using its silicon platform, and Biotia, Inc., a company that uses proprietary analytical software for infectious disease diagnostics, today received Emergency Use Authorization (EUA) from the U.S. Food and Drug Administration (FDA) for the SARS-CoV-2 Next-Generation Sequencing (NGS) Assay.

Test Your Gut's Microbiome

Gutbio™ is an at-home test designed to help individuals manage their gut health. The test examines the body's unique gut microbiome and offers AI driven personalized interventions for diet, exercise, and supplementation.



Micronutrients

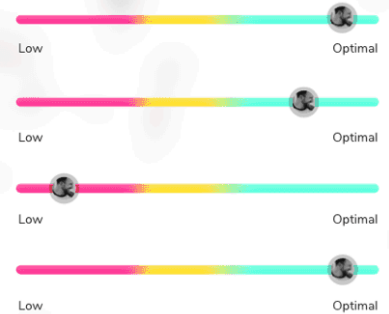
Our analysis of your gut bacteria reveals the types of food you currently digest best.

Never is it more true that "you are what you eat" than in your gut microbiome. Your diet is a primary driver of diversity in your gut microbiome. Different gut microbiota specialize in the digestion of different foods, so what you eat on a regular basis largely determines which microbiota live in your gut.

If you eat a diet rich in plant fiber, for instance, you're likely to have high levels of Prevotella and other microbial species that thrive on fiber. If you consume a ketogenic diet, which tends to be low in plant fiber, those types of bacteria will be less common. It's generally best to consume a diet that encourages microbial diversity. Doing so will enable you to efficiently digest many different types of food while lowering your risk of diseases related to a nondiverse gut microbiome.

Study, Clinical. Study Name: Here's an example of the headline of the study. Lab Med 2018;49(2):123-129.

Micronutrients



Improve your score

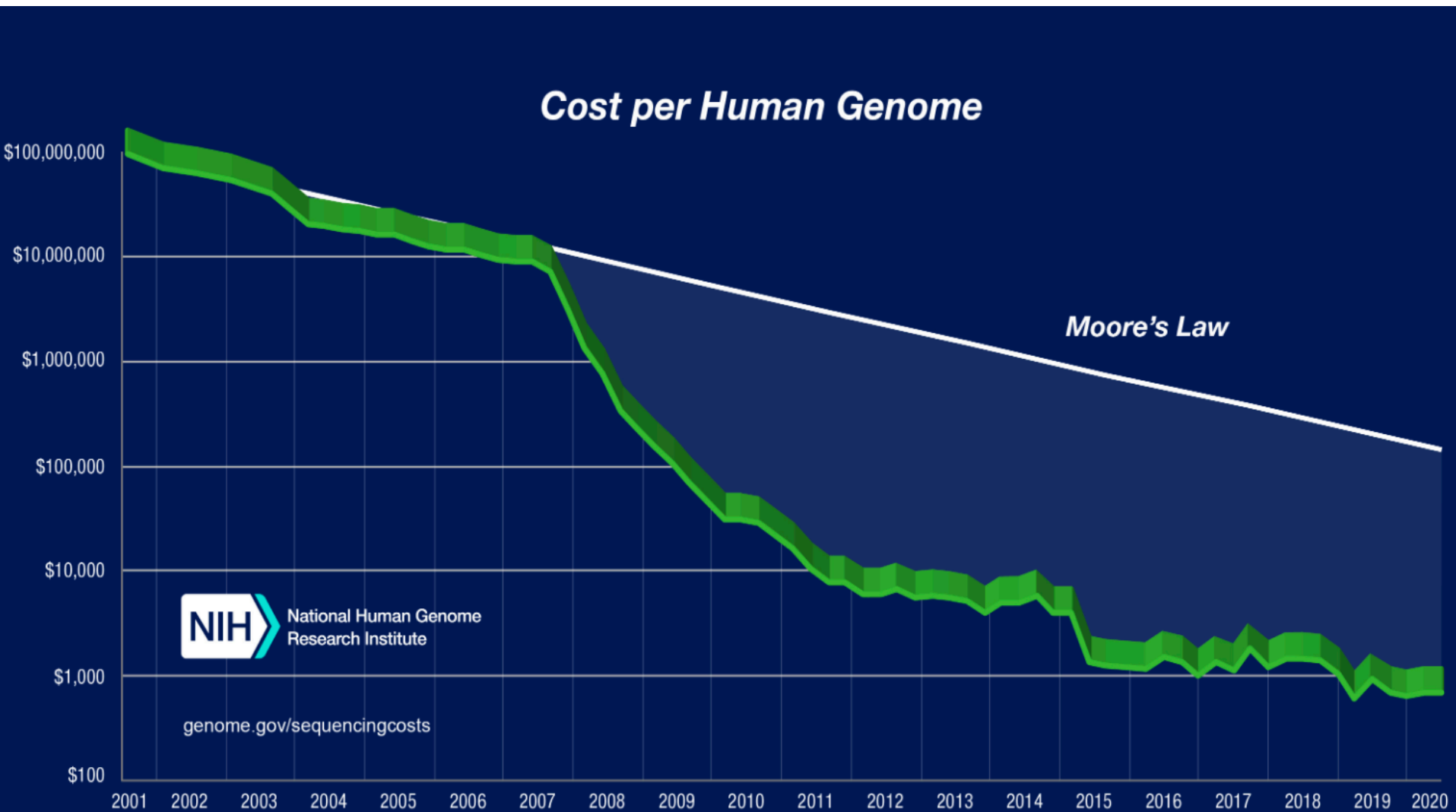


[Review the 3 interventions](#) recommended to improve your irritation score.

(0)

Background

The fastest-ever technological pace



Every Day

is the

Best Day

But!

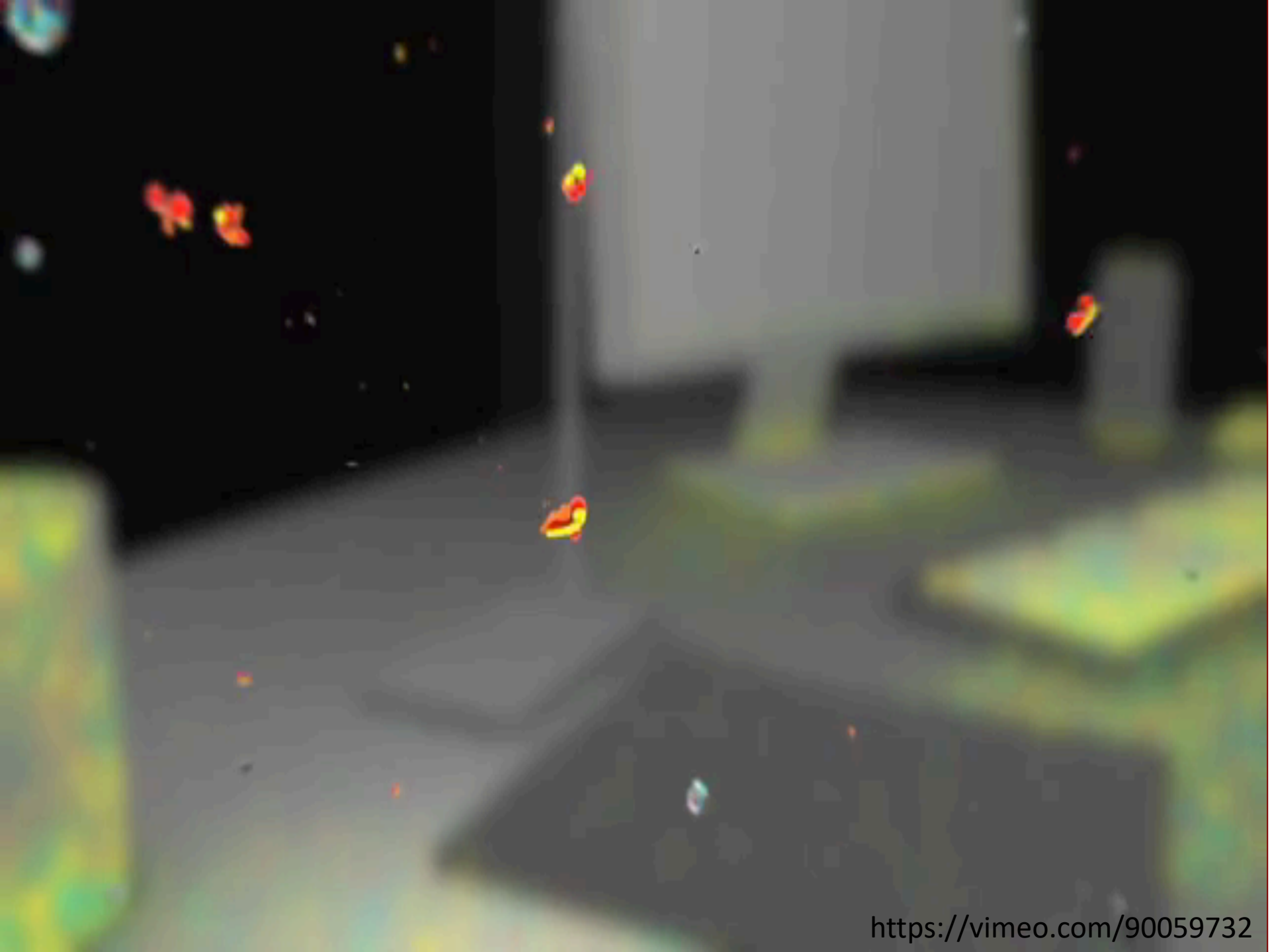
**There is more
than one genome:**

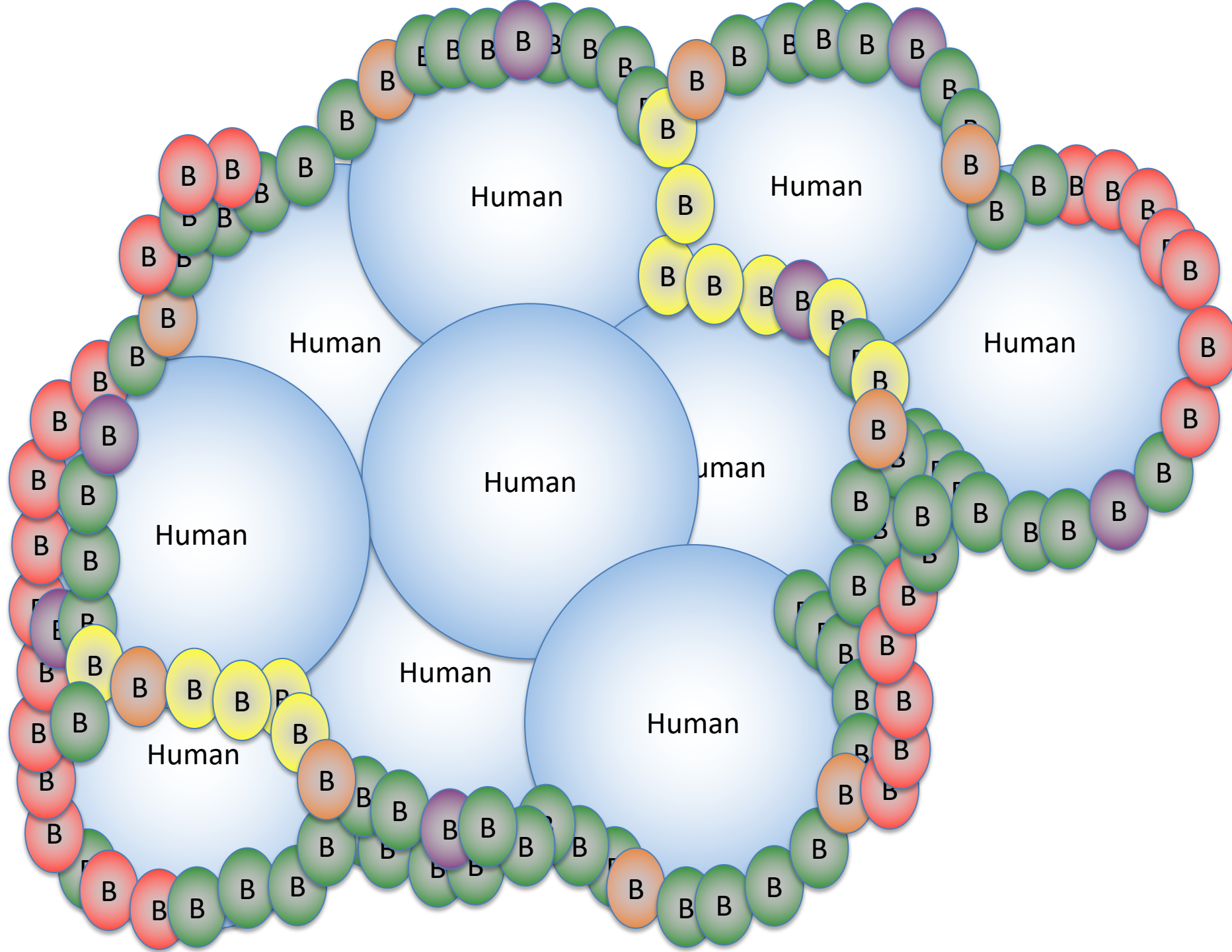


**In your body's cellular democracy,
YOU are a minority party:**

>50%-90% of your cells are bacterial cells

(Zhu et al., 2010, Sender et al, 2016)





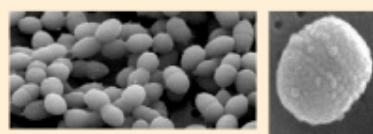


200 pounds

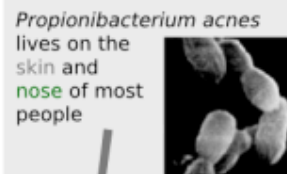
3-5 pounds bacteria

195-97 pounds **human**

A map of diversity in the human microbiome



Streptococcus dominates the oral cavity with *S. mitis* > 75% in the **cheek**

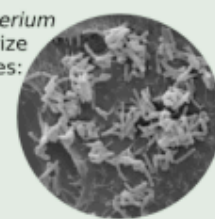


Propionibacterium acnes lives on the skin and **nose** of most people



Many *Corynebacterium* species characterize different body sites:

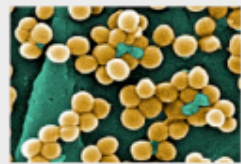
C. matruchoti the **plaque**
C. accolens the **nose**
C. croppenstedtii the **skin**



Lactobacillus species (*L. gasseri*, *L. jensenii*, *L. crispatus*, *L. iners*) are predominant but mutually exclusive in the **vagina**



Staphylococcus epidermidis colonizes external body sites



○ Commensal microbes
☆ Potential pathogens

The four most abundant phyla

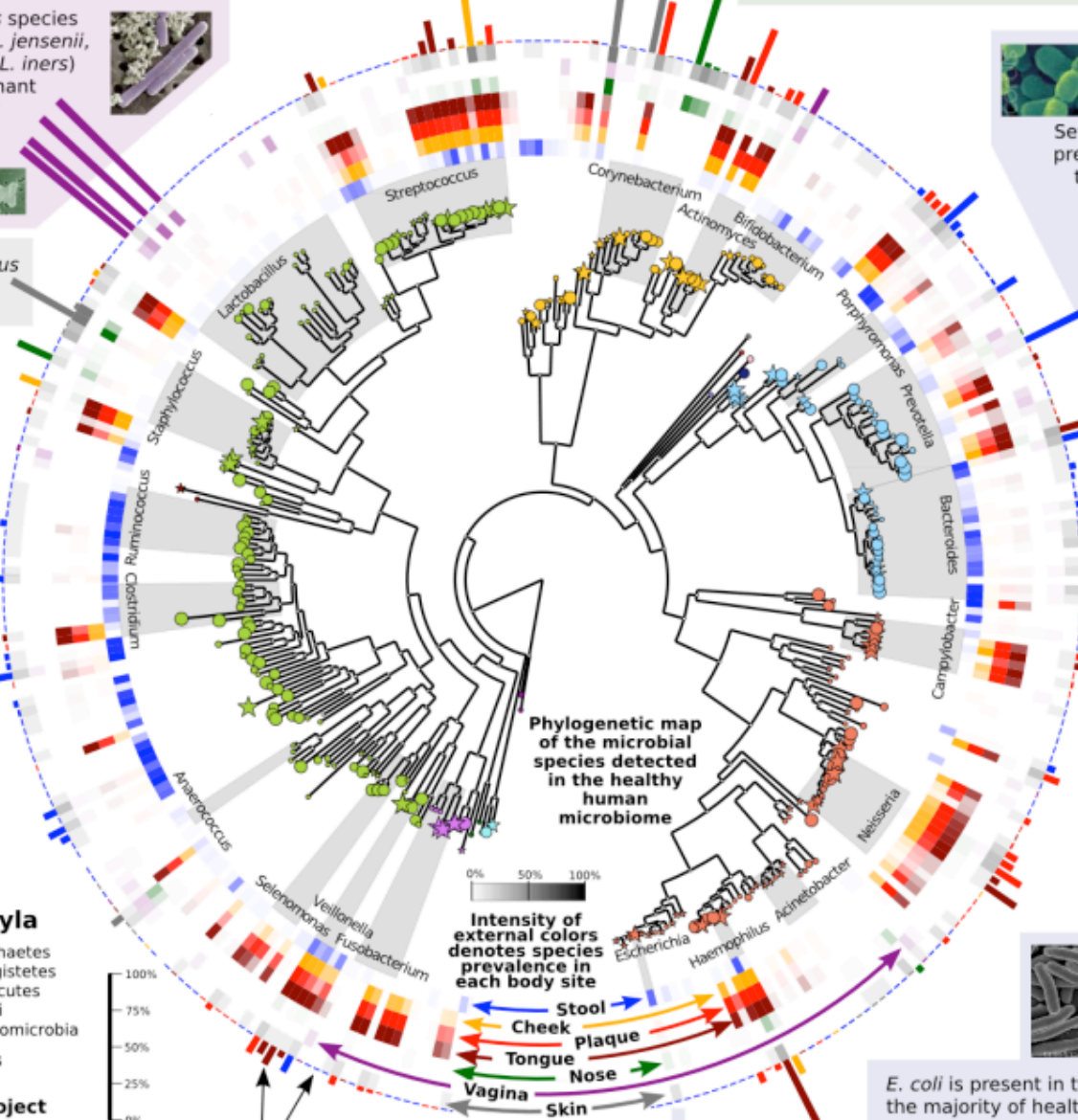
- Actinobacteria
- Bacteroidetes
- Firmicutes
- Proteobacteria

Low abundance phyla

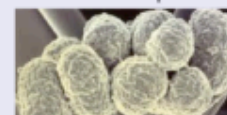
- Chloroflexi
- Cyanobacteria
- Euryarchaeota
- Fusobacteria
- Lentisphaerae
- Spirochaetes
- Synergistetes
- Tenericutes
- Thermi
- Verrucomicrobia

National Institutes of Health
Human Microbiome Project

R. Segata & C. Huttenhower
<http://huttenhower.sph.harvard.edu>
(generated using Cytoscape and rCytoscape from Microbiome analysis)



Several *Prevotella* species are present in the gastrointestinal tract. *P. copri* is present in 19% of the subjects and dominates the **intestinal** flora when present

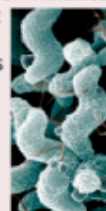


Microscopy from <http://bacmap.wishartlab.com>

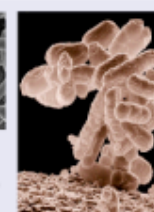
Bacteroides is the most abundant genus in the **gut** of almost all healthy subjects



Campylobacter includes opportunistic pathogens, but members live in the oral cavities of most healthy people in the cohort



E. coli is present in the **gut** of the majority of healthy subjects but at very low abundance



Bar lengths indicate microbial abundance (colored by body site of greatest prevalence)

[Home](#) > [Science Magazine](#) > [8 June 2012](#) > Hood, 336 (6086): 1209

Article Views

► [Summary](#)

► [Full Text](#)

► [Full Text \(PDF\)](#)

VERSION HISTORY

► [336/6086/1209](#)

Published Online June 6 2012

Science 8 June 2012:

Vol. 336 no. 6086 p. 1209

DOI: 10.1126/science.1225475

EDITORIAL

Tackling the Microbiome

Leroy Hood

36%

of the small molecules
in your blood
transit the microbiome



Altmetric: 1254

24% of the drugs with human targets, including members of all therapeutic classes, inhibited the growth of at least one strain *in vitro*

Article

Extensive impact of non-antibiotic drugs on human gut bacteria

Lisa Maier, Mihaela Pruteanu, Michael Kuhn, Georg Zeller[✉], Anja Telzerow, Exene Erin Anderson, Ana Rita Brochado, Keith Conrad Fernandez, Hitomi Dose, Hirotada Mori, Kiran Raosaheb Patil[✉], Peer Bork[✉] & Athanasios Typas[✉]

Nature **555**, 623–628 (29 March 2018)

doi:10.1038/nature25979

[Download Citation](#)

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Published: 19 March 2018

Many organisms work on your behalf!

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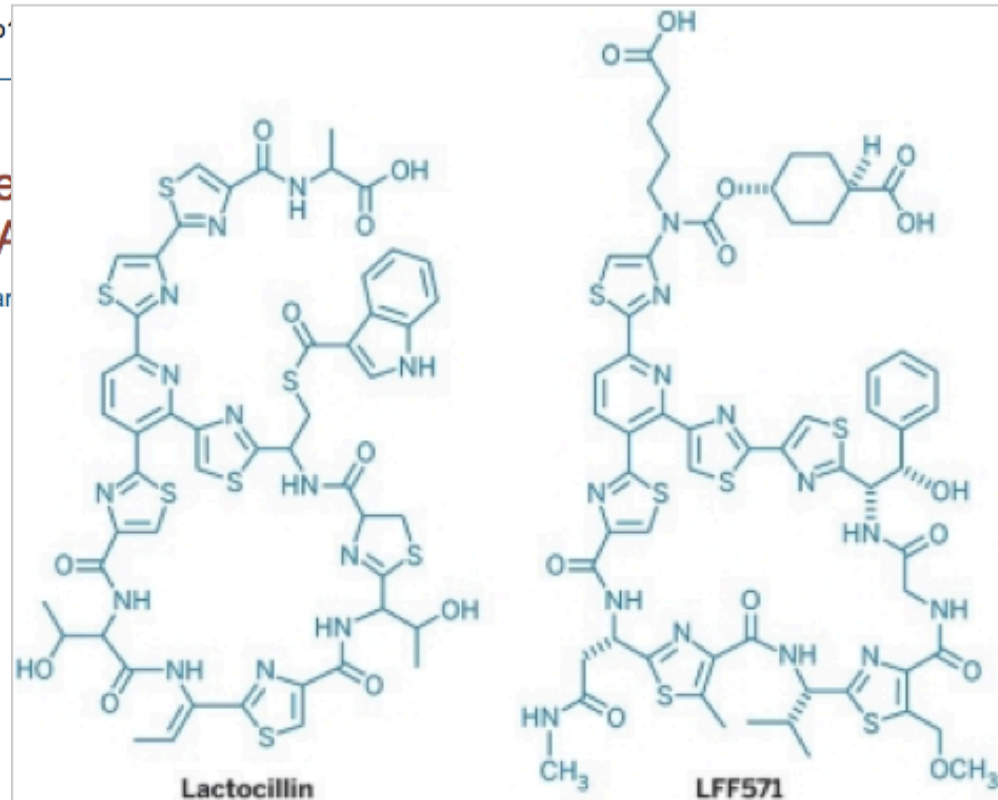
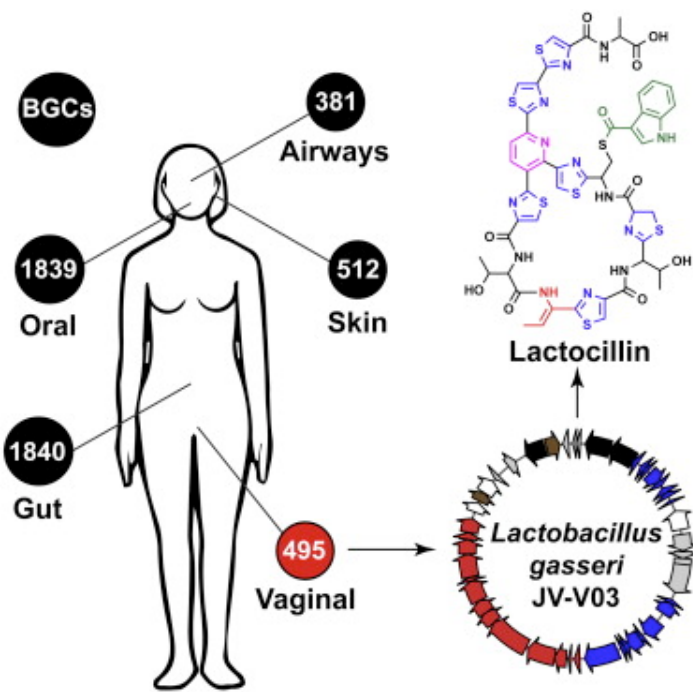
< Previous Article

Volume 158, Issue 6, p

Article

A Systematic Analysis of Biosynthetic Gene Microbiome Reveals a Common Family of A

Mohamed S. Donia, Peter Cimermancic, Christopher J. Schulze, Laura C. Wieland, Jon Clardy, Roger G. Linington, Michael A. Fischbach



SELF-MEDICATING

A peptide (left) made by a human microbe bears a resemblance in form and function to a semisynthetic drug candidate (right).

<http://cen.acs.org/articles/92/i39/Mining-Microbiome-Therapeutics.html>

Fecal Microbiota Transplants (FMT)

GASTROENTEROLOGY & HEPATOLOGY
The Independent Peer-Reviewed Journal

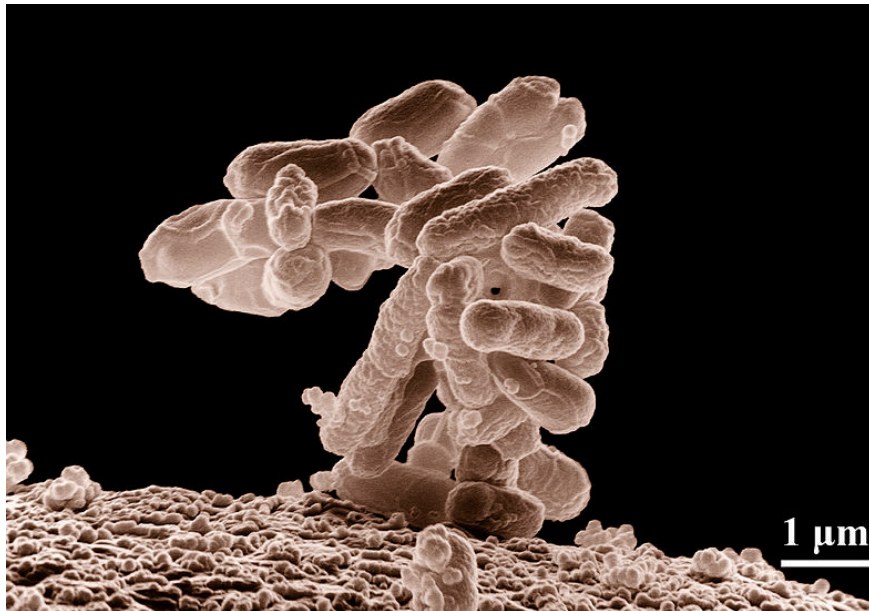
Gastroenterol Hepatol (N Y). 2012 March; 8(3): 191–194.

PMCID: PMC3365524

Fecal Transplantation for the Treatment of *Clostridium difficile* Infection

[Lawrence J. Brandt](#), MD, MACG, AGAF, FASGE*

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FDA Comes to Grips with Fecal Transplants

Efforts are under way to standardize fecal transplants, which helps re-establish healthy microbe populations in the guts of patients

By [Beth Mole](#) and [Nature magazine](#)

The POWER of POOP

promoting safe, accessible fecal microbiota transplant
for all who need it

<http://thepowerofpoop.com/>

The POWER of POOP

WELCOME TO POP ▾

SUCCESS STORIES ▾

E-PATIENTS ▾

RESOURCES ▾

FECAL TRANSPLANT FAQs



Success Stories



Leah's Success Using FMT for Arthritis

T. A. Buhr - June 4, 2016

Where do you live? Connecticut How old are you? 29
What percentage better are you? 90- 95% What was
your diagnosis and what treatments did you try...



Family Helps Kate Fight Ulcerative Colitis with FMT

February 17, 2016



Tracy Mac's Story of FMT for Brain & Digestive Disorders

September 1, 2015



Tracy S's Story of FMT for C. diff

August 15, 2015



Yasmin's story

July 15, 2015

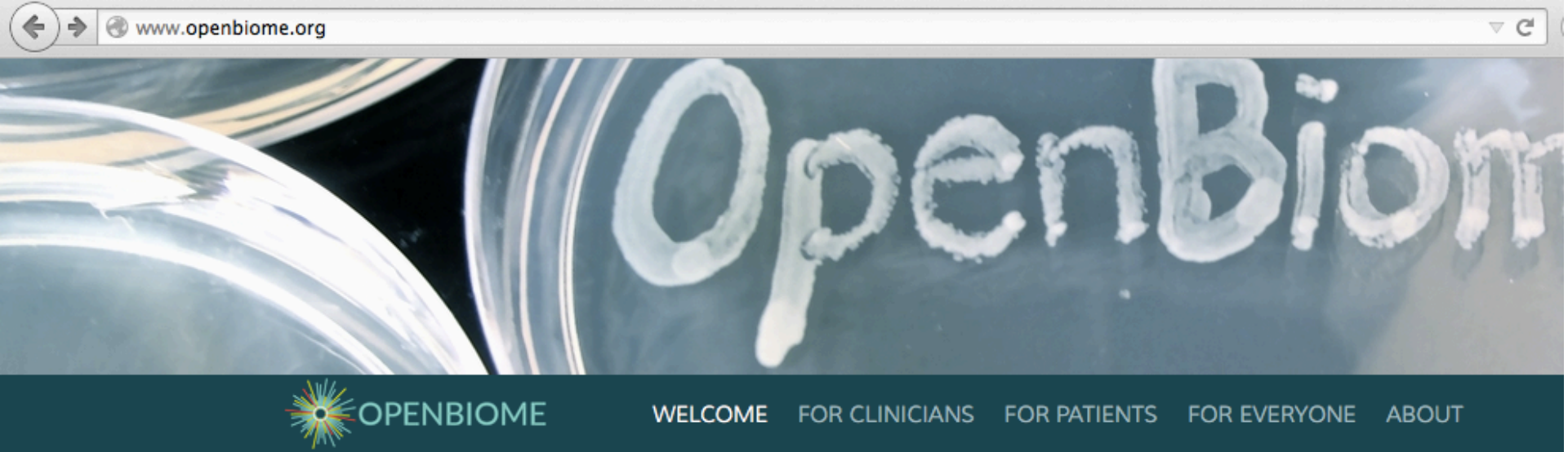
Check Out
our "Best of" list
of books & supplies



As funny as it may sound, Fecal Transplants are now a part of medicine. Our goal is to help answer your questions and get you started on your journey.

95% success rate for C. diff
70-80% success rate for ulcerative colitus
- David Shepard, MD

<http://thepowerofpoop.com/>



Welcome to OpenBiome.

What we do

We work with clinicians to make FMT easier, cheaper, safer and more widely available. We do so by providing hospitals with screened, filtered, and frozen material ready for clinical use. This service eliminates the time, staff, protocols, and facilities needed to screen and prepare material from new donors for each treatment. With OpenBiome, all that's needed to deliver FMT is a doctor and an endoscope.

Why we're here

We founded OpenBiome, a nonprofit 501(c)(3) organization, after watching a friend and family member suffer through 18 months of [C. difficile](#) and 7 rounds of vancomycin before finally receiving a successful, life-changing [Fecal Microbiota Transplantation](#) (FMT). The remarkable efficacy of this treatment and the great lengths required to receive it convinced us that we needed to help expand access. After many discussions with local clinicians and the FDA, we launched OpenBiome in 2012 to make FMT faster and easier for patients and doctors alike.



OpenBiome's Give a Sh!t Campaign

Medford, Massachusetts, United States | Health



THE MOST IMPORTANT THING
YOU'LL DO ALL DAY!



Sharing

=

Caring

Whatever your lifestyle, discover
banking solutions built around it.

Visit the Citi Benefits Hub

citi

Ad

Speaking of Science

You can earn \$13,000 a year selling your poop



A



87



size of poop	# of people treated
50g	1
100g	2
150g	3
200g	4
250g	5
300g	6
350g	7
400g	8
450g	9

THE MOST IMPORTANT THING
YOU'LL DO ALL DAY!

Policy: How to regulate faecal transplants

Mark B. Smith, Colleen Kelly & Eric J. Alm

19 February 2014

For medical use, human stool should be considered a tissue, not a drug, argue Mark B. Smith, Colleen Kelly and Eric J. Alm.



PDF



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Subject terms: [Policy](#) • [Therapeutics](#) • [Infection](#) • [Microbiology](#)



Top Story



WHO says 21-century could be "post-antibiotic era"

Emergence of resistant bacteria means common infections and minor injuries can kill.

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1. [Accusations pile up amid Japan's stem-cell controversy](#)

Current Issue > vol. 109 no. 2 > Sharon Greenblum, 594–599, doi: 10.1073/pnas



Performing your original search "microbiome disease links science" in *PNAS* retrieves 80

Metagenomic systems biology of the human g reveals topological shifts associated with obes inflammatory bowel disease

Sharon Greenblum^a, Peter J. Turnbaugh^b, and Elhanan Borenstein^{a,c,d,1}

Author Affiliations

nature

International weekly journal of science

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NATURE | LETTER



Diet rapidly and reproducibly alters the human gut microbiome

Lawrence A. David, Corinne F. Maurice, Rachel N. Carmody, David B. Gootenberg, Julie E. Button, Benjamin E. Wolfe, Alisha V. Ling, A. Sloan Devlin, Yug Varma, Michael A. Fischbach, Sudha B. Biddinger, Rachel J. Dutton & Peter J. Turnbaugh

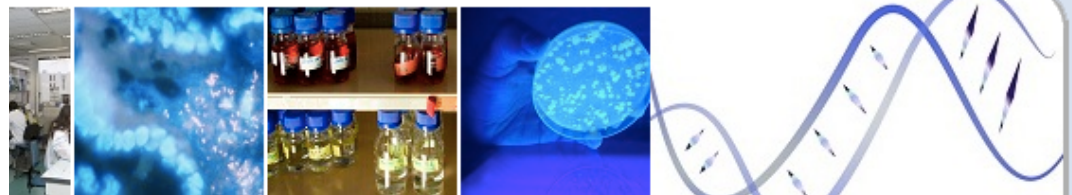
Affiliations | Contributions | Corresponding author

Nature (2013) | doi:10.1038/nature12820

Received 18 April 2013 | Accepted 29 October 2013 | Published online 11 December 2013

- Acne
- Antibiotic-associated diarrhea
- Asthma/allergies
- Autism
- Autoimmune diseases
- Cancer
- Dental cavities
- Depression and anxiety
- Diabetes
- Eczema
- Gastric ulcers
- Hardening of the arteries
- Inflammatory bowel diseases
- Malnutrition
- Obesity

learn.genetics.utah.edu/content/microbiome/disease/



Human Microbiome Consortium

 OPEN ACCESS  PEER-REVIEWED

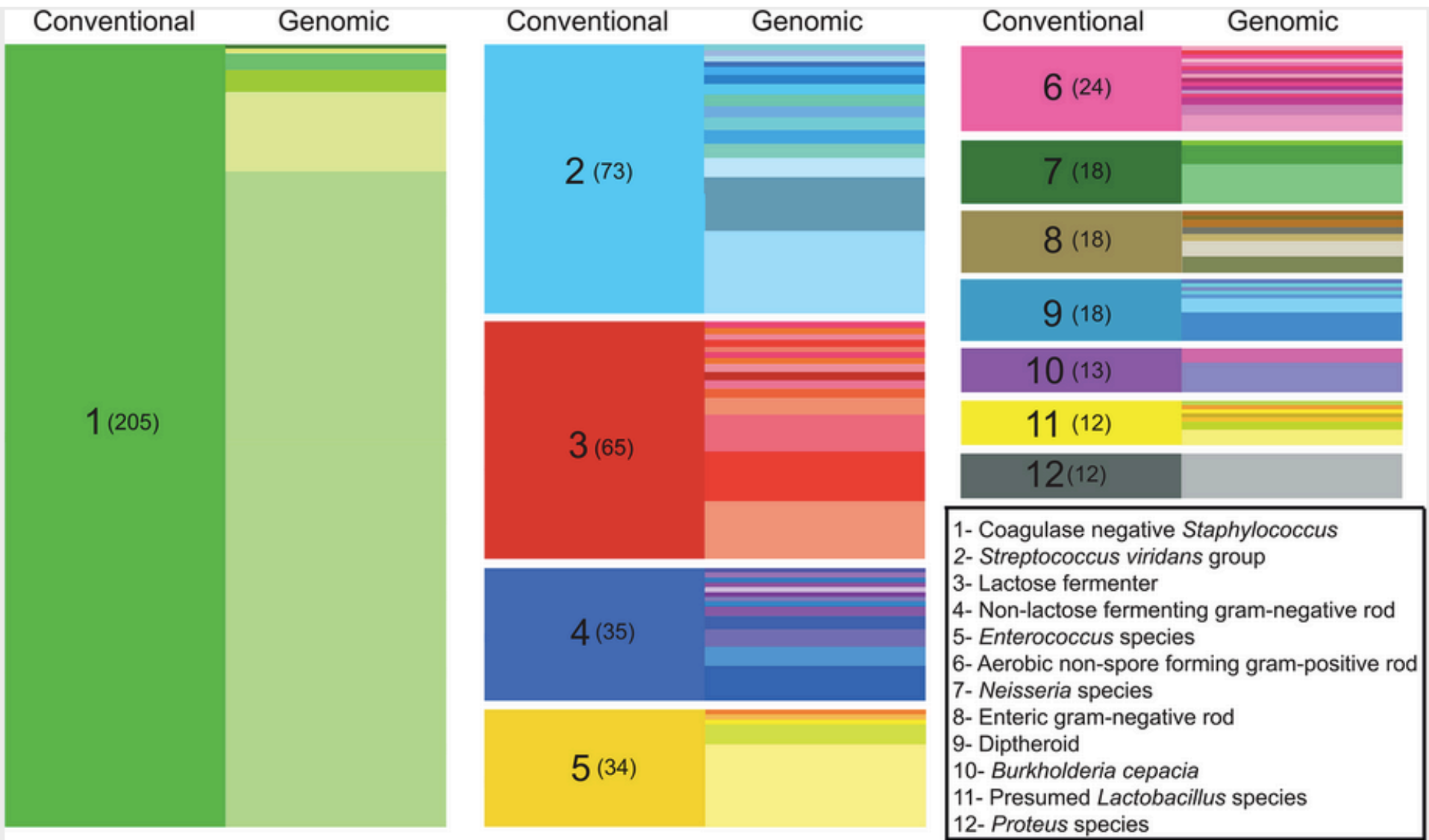
RESEARCH ARTICLE

A Year of Infection in the Intensive Care Unit: Prospective Whole Genome Sequencing of Bacterial Clinical Isolates Reveals Cryptic Transmissions and Novel Microbiota

David J. Roach, Joshua N. Burton, Choli Lee, Bethany Stackhouse, Susan M. Butler-Wu, Brad T. Cookson, Jay Shendure  ,
Stephen J. Salipante  

Published: July 31, 2015 • DOI: 10.1371/journal.pgen.1005413

Genomic Classification gives more granularity of species present



But!

Are we any good at measuring?

Can we reach precision metagenomics?

(1)

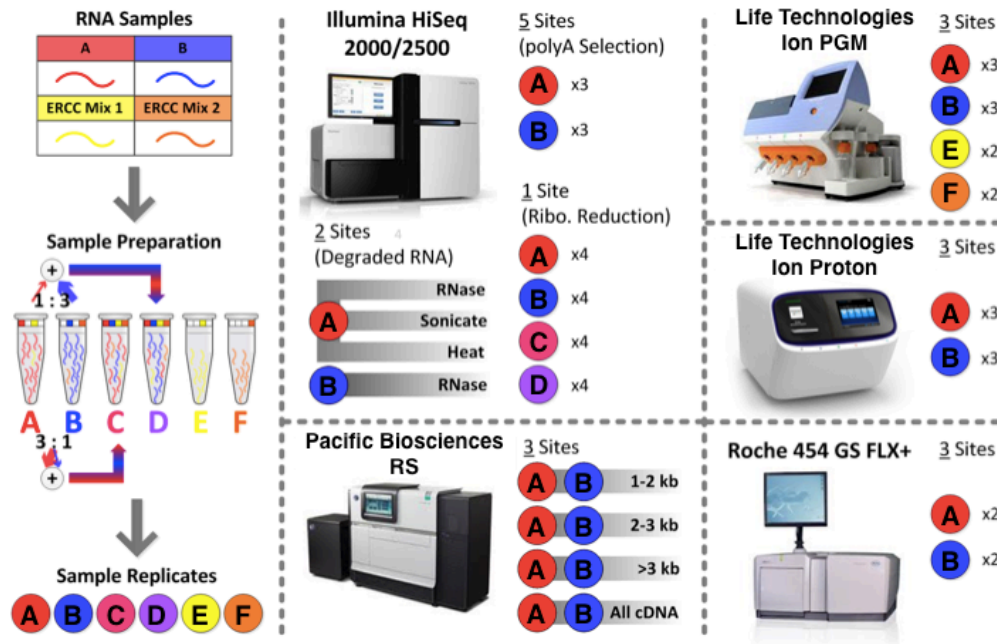
Measurements
are lenses

FDA's Mission and Personalized Medicine

- **MicroArray Quality Control (MAQC) Project**
 - **MAQC-I:** Differentially expressed genes (2006)
 - **MAQC-II:** Predictive models, GWA, CNV (2010)
 - **MAQC-III (SEQC: Sequencing Quality Control),** (2014)
 - **SEQC-II/MAQC-IV:** FDA's Precision and Personalized Medicine: 2014-2019

SEQC2: Metagenomics and epigenomics

Many methods for sequencing a sample

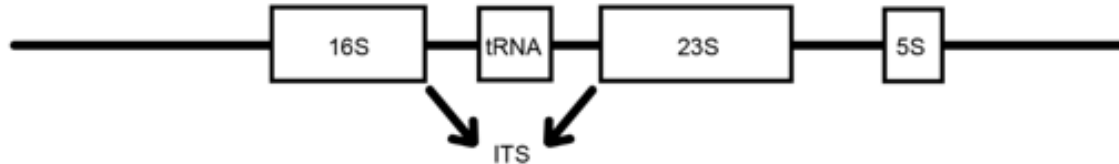


2014. 2018

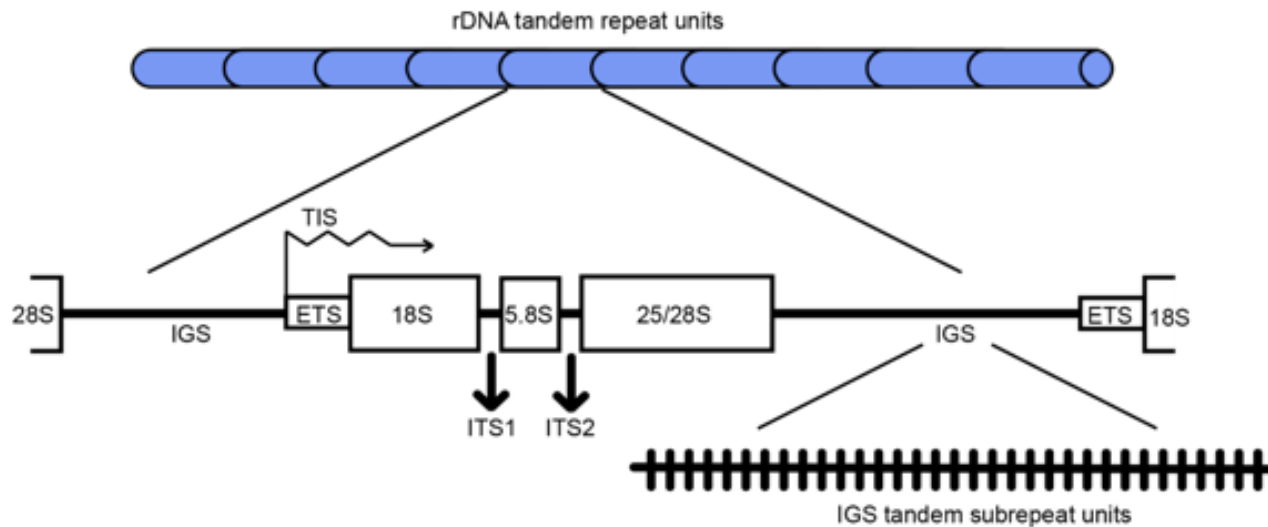
<http://www.nature.com/nbt/focus/seqc/index.html>

16S rRNA / 18S rRNA / ITS

Prokaryotes



Eukaryotes

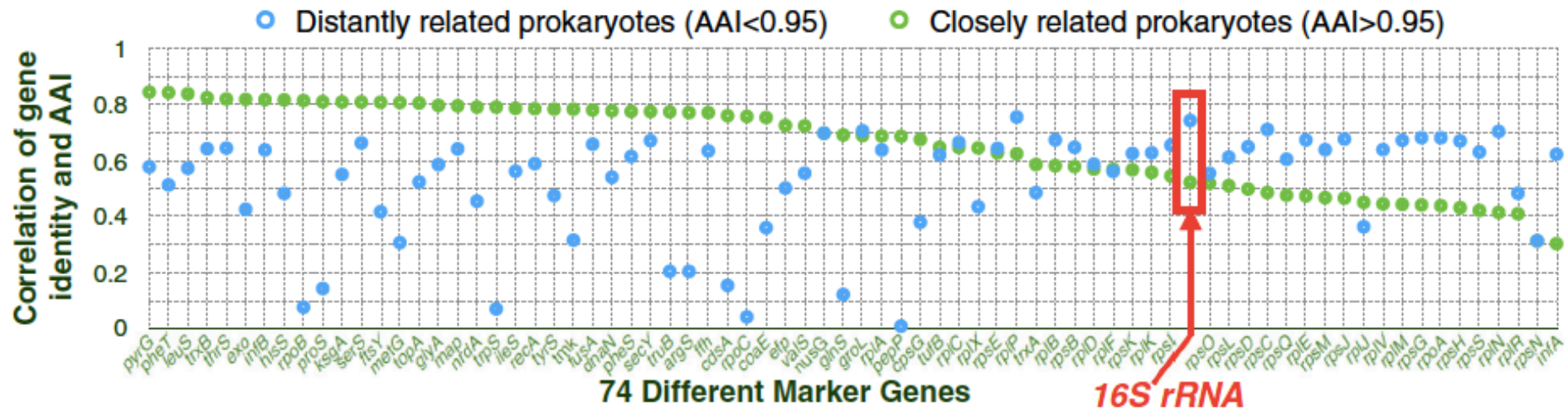


Internal transcribed spacer (ITS)

Intergenic spacers (IGS)

16S rRNA is limited

“16s rRNA predicts genome-wide levels of similarity very well for distantly related prokaryotes, but not for closely related ones.”



Lan Y, Rosen G, Hershberg R. “Marker genes that are less conserved in their sequences are useful for predicting genome-wide similarity levels between closely related prokaryotic strains.” *Microbiome*. 2016.



Article | **OPEN** | Published: 31 July 2017

Large-scale differences in microbial biodiversity discovery between 16S amplicon and shotgun sequencing

Michael Tessler , Johannes S. Neumann, Ebrahim Afshinnkoo, Michael Pineda, Rebecca Hersch, Luiz Felipe M. Velho, Bianca T. Segovia, Fabio A. Lansac-Toha, Michael Lemke, Rob DeSalle, Christopher E. Mason  & Mercer R. Brugler 

Metagenomics can expand the microbiome to query across kingdoms

Data Type	16S	18S	ITS	Shotgun
Taxonomic Classification	Yes	Yes	Yes	Yes
Prokaryotes	Yes	No	No	Yes
Archaea	Yes	No	No	Yes
Eukaryotes	No	Yes	Yes	Yes
Parasites	No	Yes	No	Yes
Plasmids	No	No	No	Yes
Phages	No	No	No	Yes
Human Ancestry	No	No	No	Yes
Biosynthetic Gene Clusters	No	No	No	Yes
Antimicrobial Resistance (AMR) Markers	No	No	No	Yes
Kingdom Specificity	Yes	Yes	Yes	No
Approximate Raw Cost / Sample	\$100	\$100	\$125	\$300


From <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5359768/>

Many methods to analyze a metagenomic sample



INTERNATIONAL METAGENOMICS AND MICROBIOME STANDARDS ALLIANCE

Bioinformatic Resources

 > Bioinformatic Resources

IMMSA (2018):

At least 71 tools available for profiling microbial communities using WGS

microbialstandards.org/index.php/bioinformatic-resources

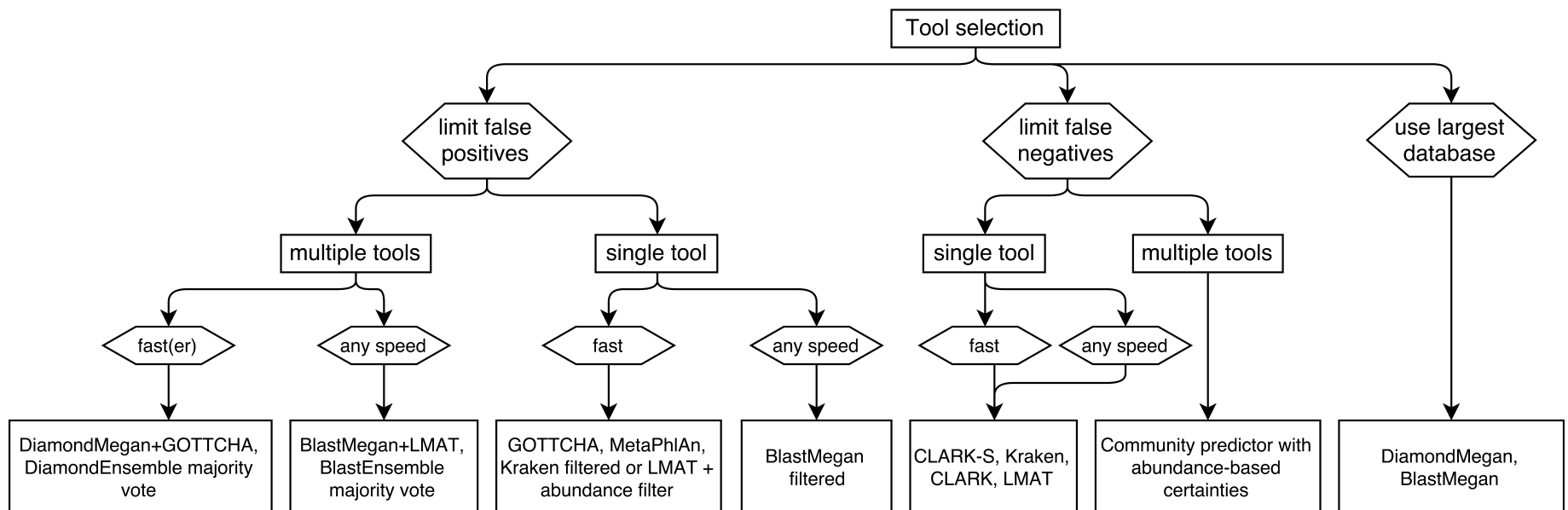
RESEARCH

Open Access

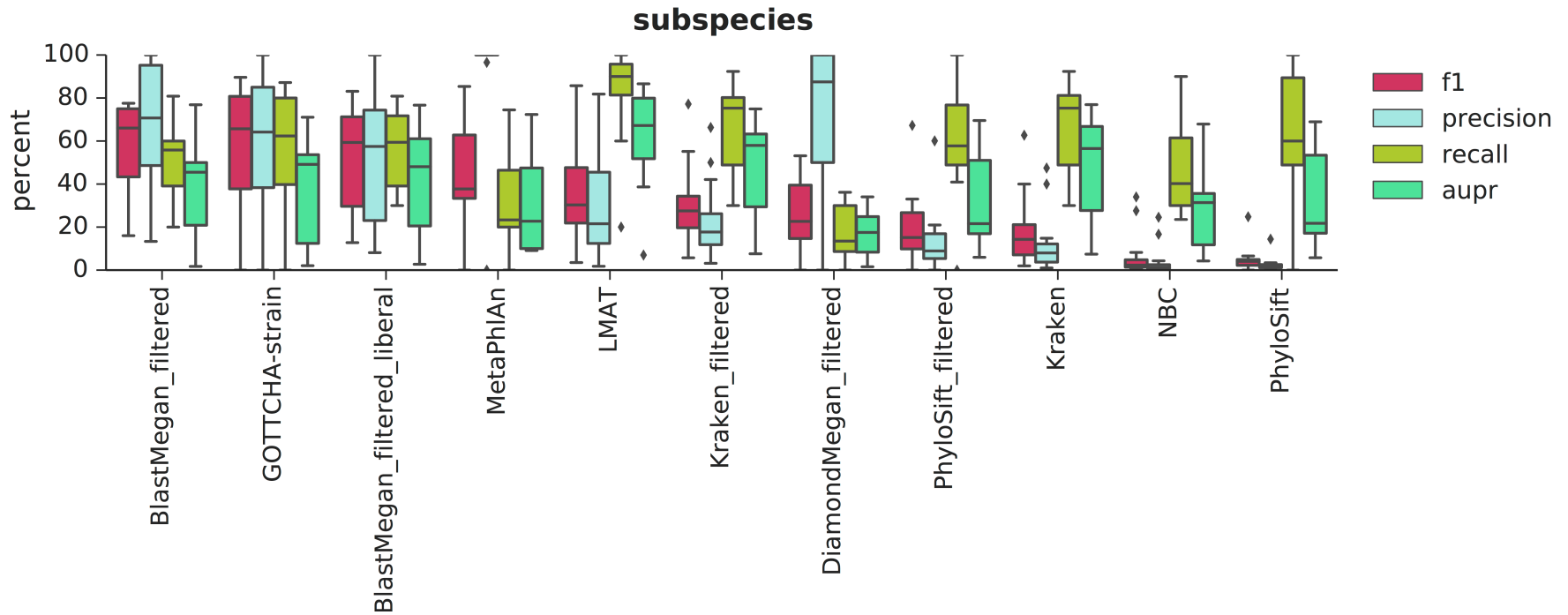


Comprehensive benchmarking and ensemble approaches for metagenomic classifiers

Alexa B. R. McIntyre^{1,2,3}, Rachid Ounit⁴, Ebrahim Afshinnkoo^{2,3,5}, Robert J. Prill⁶, Elizabeth Hénaff^{2,3}, Noah Alexander^{2,3}, Samuel S. Minot⁷, David Danko^{1,2,3}, Jonathan Foox^{2,3}, Sofia Ahsanuddin^{2,3}, Scott Tighe⁸, Nur A. Hasan^{9,10}, Poorani Subramanian⁹, Kelly Moffat⁹, Shawn Levy¹¹, Stefano Lonardi⁴, Nick Greenfield⁷, Rita R. Colwell^{9,12}, Gail L. Rosen^{13*} and Christopher E. Mason^{2,3,14*}



Performance profiles across 35 datasets



Precision = false positive rate = $TP/(TP+FP)$


Recall = sensitivity = $TP/(TP+FN)$

F1 score = $2(\text{precision} * \text{recall}) / (\text{precision} + \text{recall})$

AUPR = area under the precision recall curve

With FDA/NIST International Standards Being Tested



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[Material Measurement Laboratory](#)

BIOSYSTEMS AND BIOMATERIALS DIVISION

About BBD



Core Capabilities



Primary Focus Areas



Resources



IMMSA Mission Statement

The International Metagenomics and Microbiome Standards Alliance (IMMSA) is a non-hierarchical association of microbiome-focused researchers from industry, academia, and government. IMMSA was formed for the mutual benefit of the entire microbiome and metagenomics community and will focus specifically on coordinating cross-cutting efforts that address microbiome and metagenomic measurement challenges. IMMSA members are representative experts for all major microbiological ecosystems (e.g. human/animal, built, and environmental ecosystems) and are representative experts from various scientific disciplines; including, but not limited to, microbiology, genomics, epidemiology, bioinformatics and statistics.

While remaining non-hierarchical, IMMSA will consist of a governing board that oversees the activities of the alliance as well as defines and implements the major directives of the alliance. The founding governing board consists of a single representative from the four founding institutes:

1. Baylor College of Medicine: Russell Carmical
2. Weill Cornell Medicine: Christopher Mason
3. National Institute of Standards and Technology: Scott Jackson
4. University of Vermont (ABRF): Scott Tighe

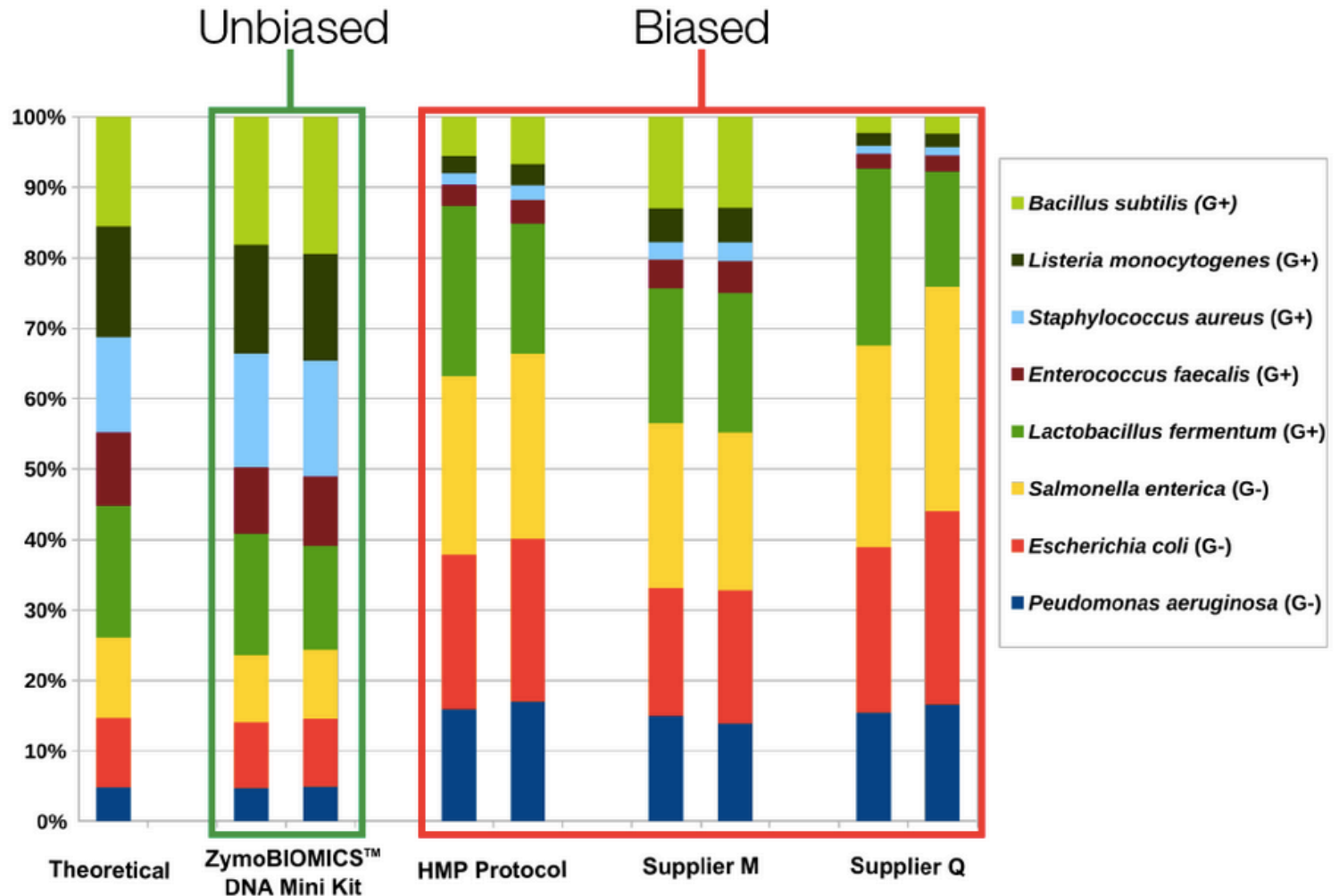
<https://www.nist.gov/mml/bbd/immsa-mission-statement>

Zymo Research: ZymoBIOMICS Microbial Community Standard

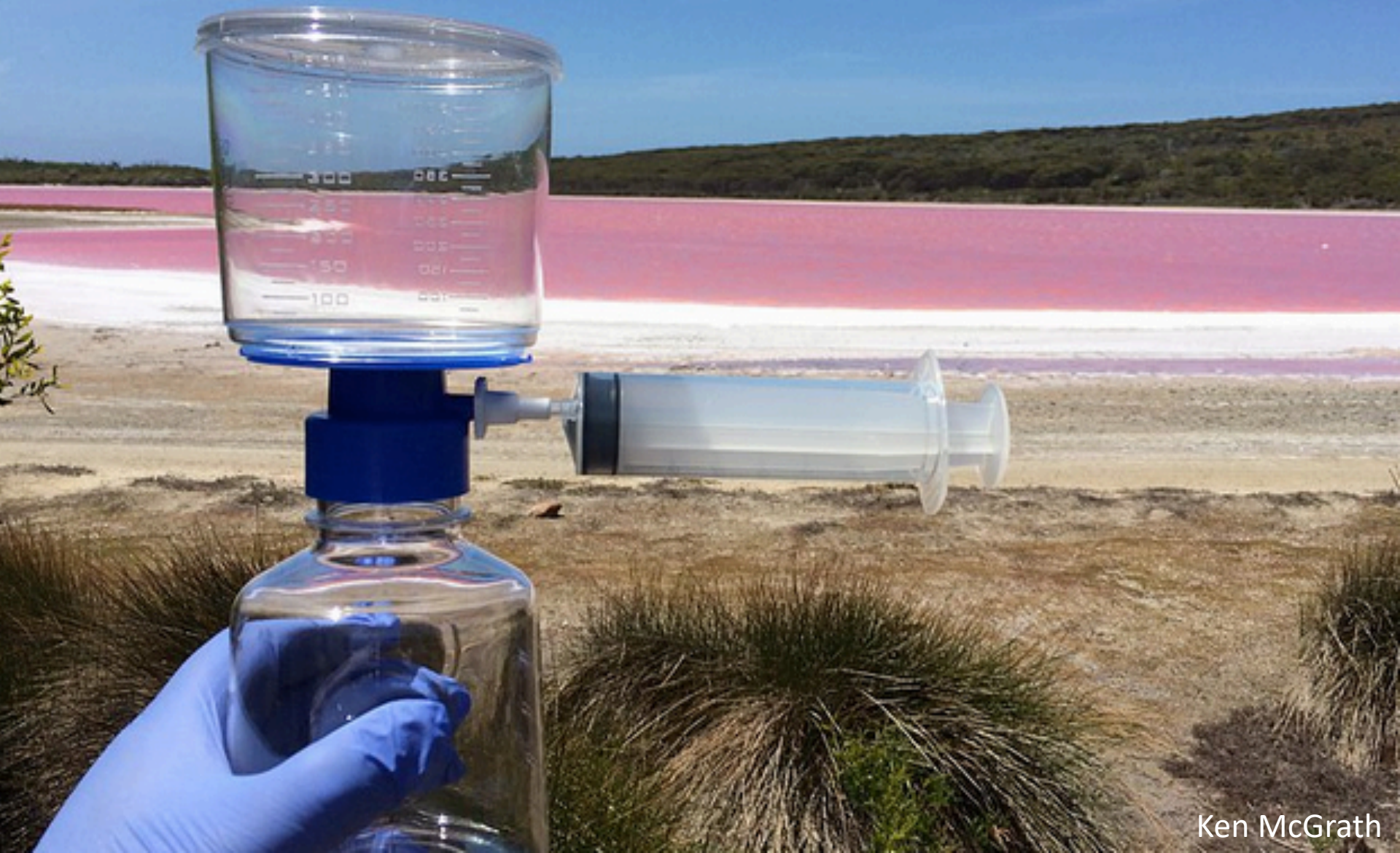


Species	GC %	Gram Stain	gDNA Abun. (%)
<i>Pseudomonas aeruginosa</i>	66.2	-	12
<i>Escherichia coli</i>	56.8	-	12
<i>Salmonella enterica</i>	52.2	-	12
<i>Lactobacillus fermentum</i>	52.8	+	12
<i>Enterococcus faecalis</i>	37.5	+	12
<i>Staphylococcus aureus</i>	32.7	+	12
<i>Listeria monocytogenes</i>	38.0	+	12
<i>Bacillus subtilis</i>	43.8	+	12
<i>Saccharomyces cerevisiae</i>	38.4	Yeast	2
<i>Cryptococcus neoformans</i>	48.2	Yeast	2

Zymo BioOMICs testing



No standards yet for THIS!





Or THIS!

Gowanus Canal EPA SuperFund site
Brooklyn, NY

Or THIS!





Metropolome

Researchers take advantage of rapid and cheap DNA sequencing technologies to map the bacterial microbiome of New York City.


By Jef Akst | December 1, 2013


 [Comment](#) 

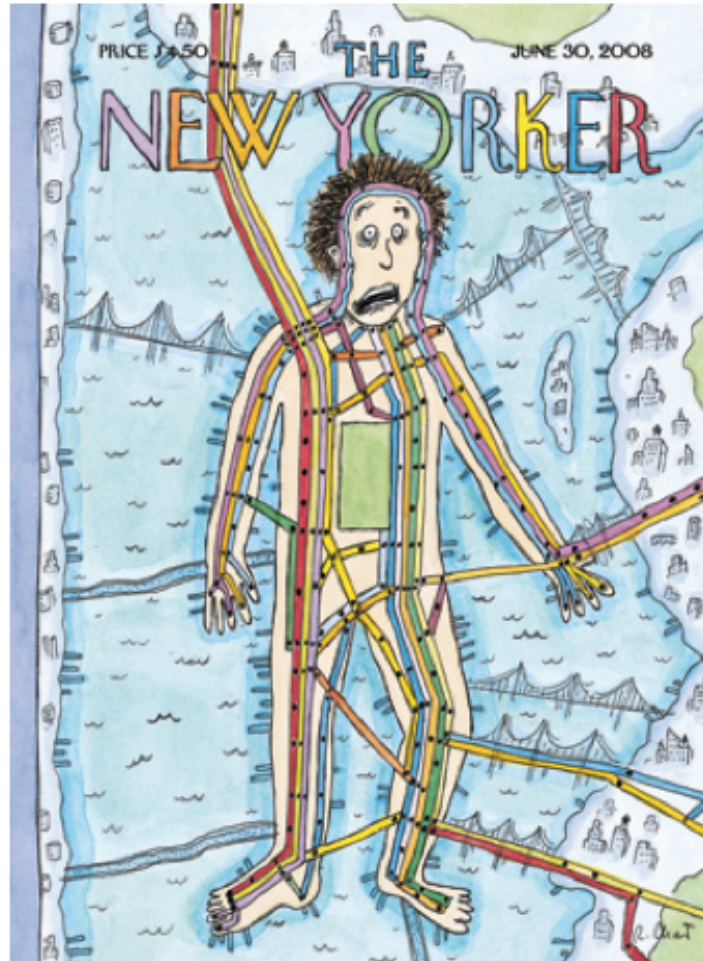
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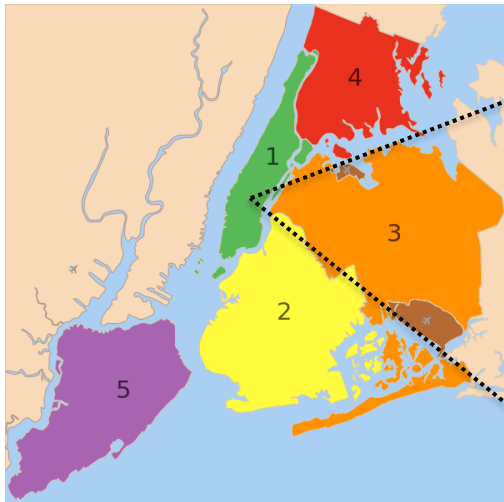
When Weill Cornell Medical College genomicist Chris Mason would drop his 6-month-old daughter off at day care in 2011, he'd encounter more than a room filled with active toddlers. He'd step into a microbial nightmare. "Seeing how they all shared toys and put them in their mouths, I wanted to swab everything before and after," he recalls.

Mason learned that there was an ongoing day-care microbiome project, led by researchers at Drexel University and Brooklyn College. But he didn't necessarily want to study just the day care's microbiome. Rather, the experience sparked a bigger idea: Mason wondered if he could explore the bacterial microbiome of New York City.

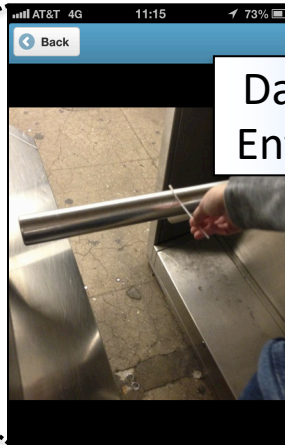
Last summer, Mason led a team of five NYC undergraduate students in the collection of more than 1,400 samples: three from each of the city's 468 subway stations. "We did swabs of the kiosks, the turnstiles, and then trains at each one of the stations," Mason says. "They pretty much just went and swabbed every day all day for about a month and a half." For each sample collected, the students took a photo of the spot, and their smart phones noted the GPS location.

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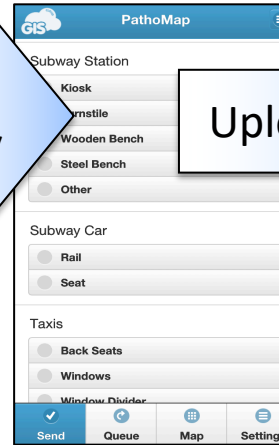


1. Swab (3 min)



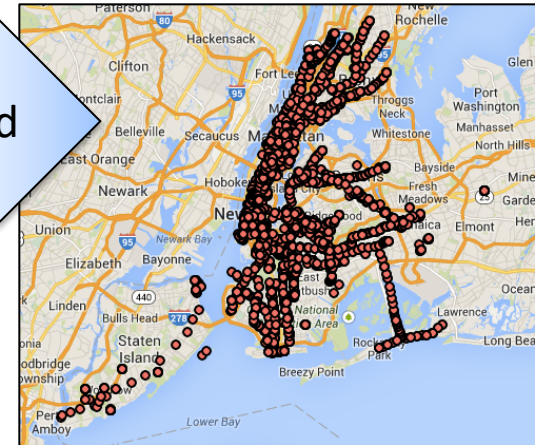
Data
Entry

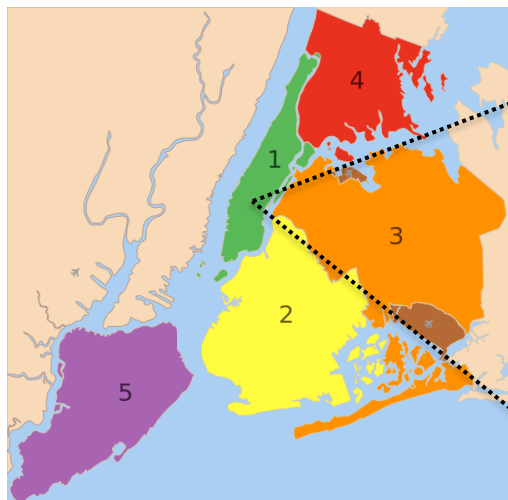
2. Annotate



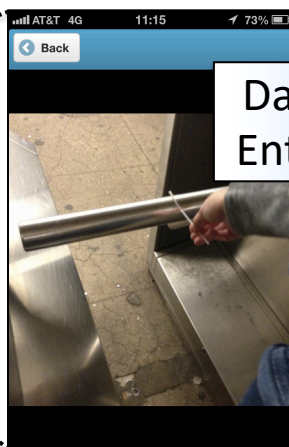
Upload

3. GPS-tag/timestamp

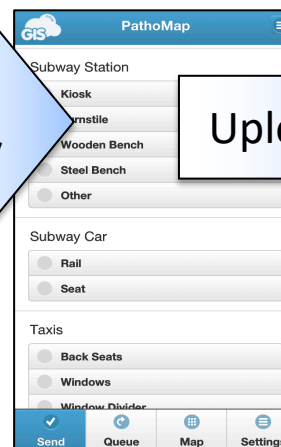




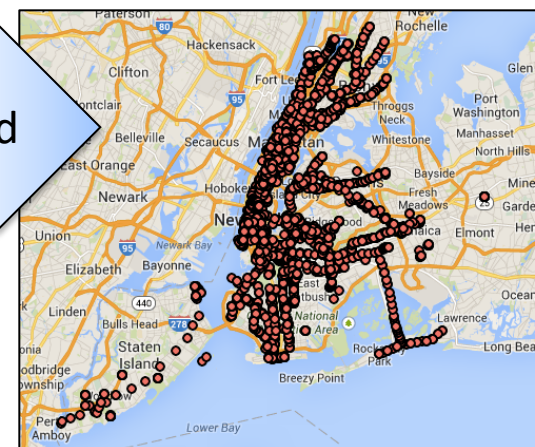
1. Swab (3 min)



2. Annotate



3. GPS-tag/timestamp



Data
Entry

Upload

Extract DNA (n=1,457 samples)

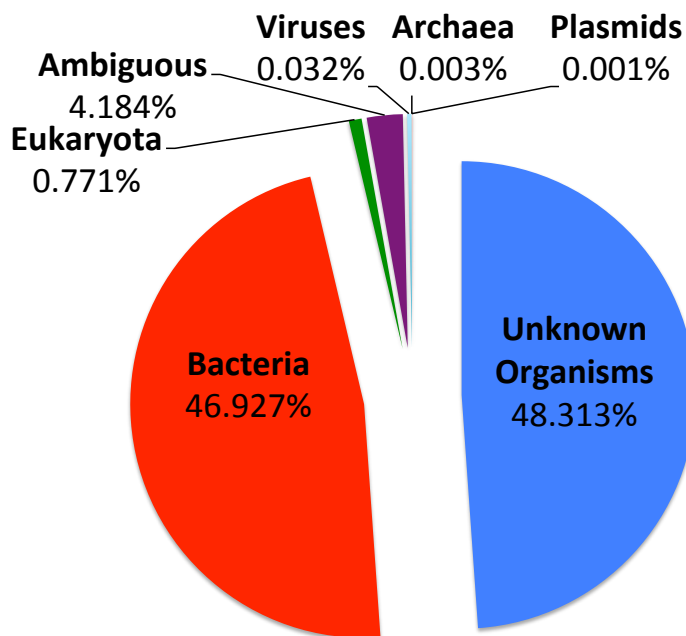
96-plex TruSeq/Qiagen Libraries

10.2 billion 125x125 DNA Seqs.

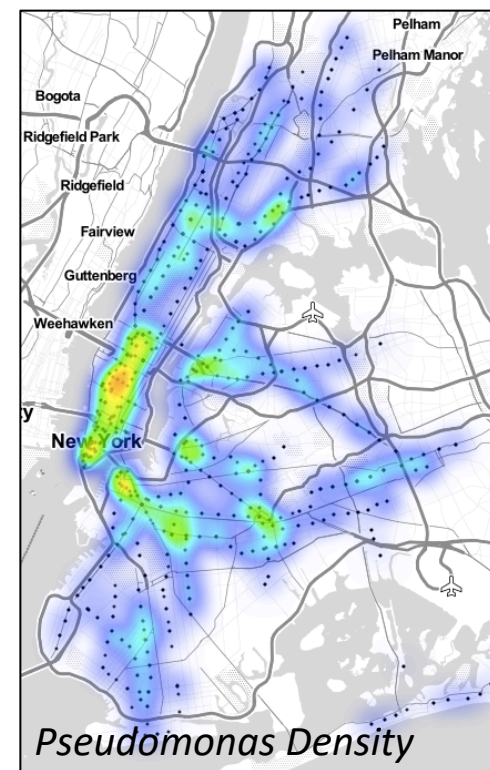
Quality Trim (Q20)

MegaBLAST-LCA alignment

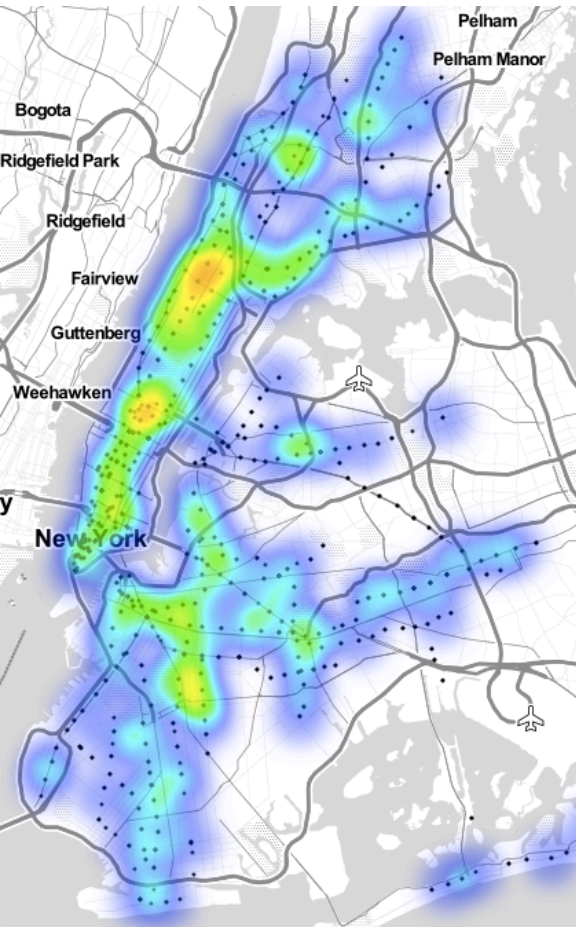
Confirm with MetaPhlan



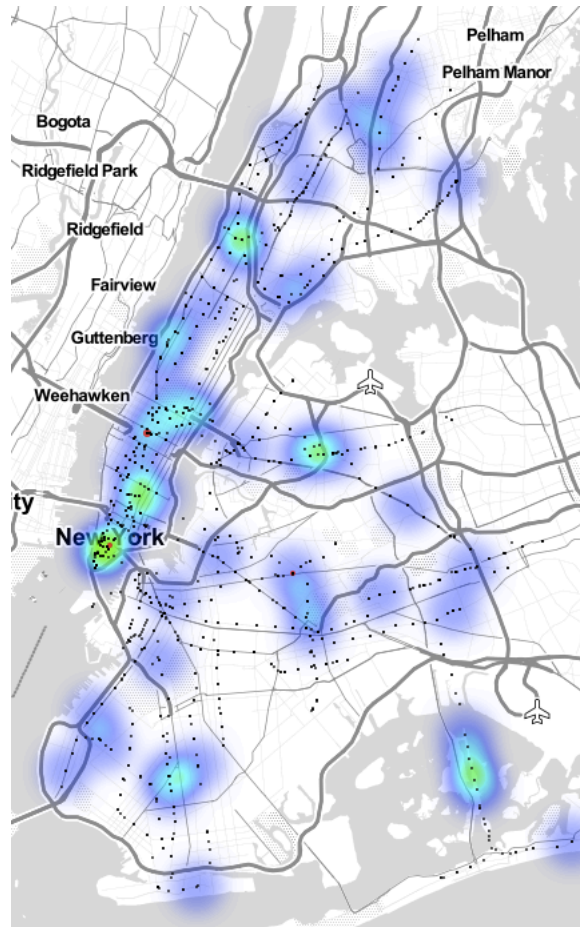
Half of the world
under our fingertips is unknown



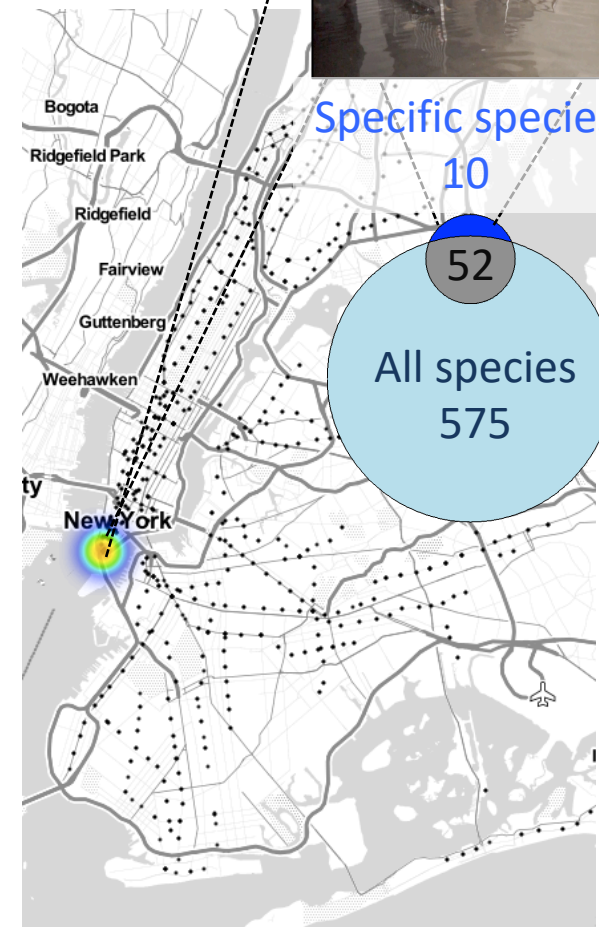
Species diversity varies by area of the city



Enterococcus faecium

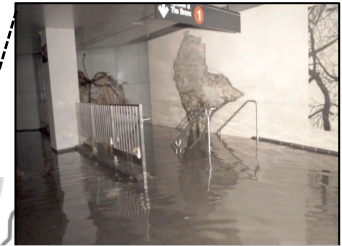


Staphylococcus aureus



Pseudoalteromonas haloplanktis

Hurricane-Flooded



Specific species

10

52

All species
575

Hurricane Sandy



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Web Site Offline

29 October 2012

Our web site is currently offline due to emergency facilities issues related to severe weather from Hurricane Sandy. Please check back later.

Our apologies for any inconvenience, and we are working to get services restored as soon as possible!

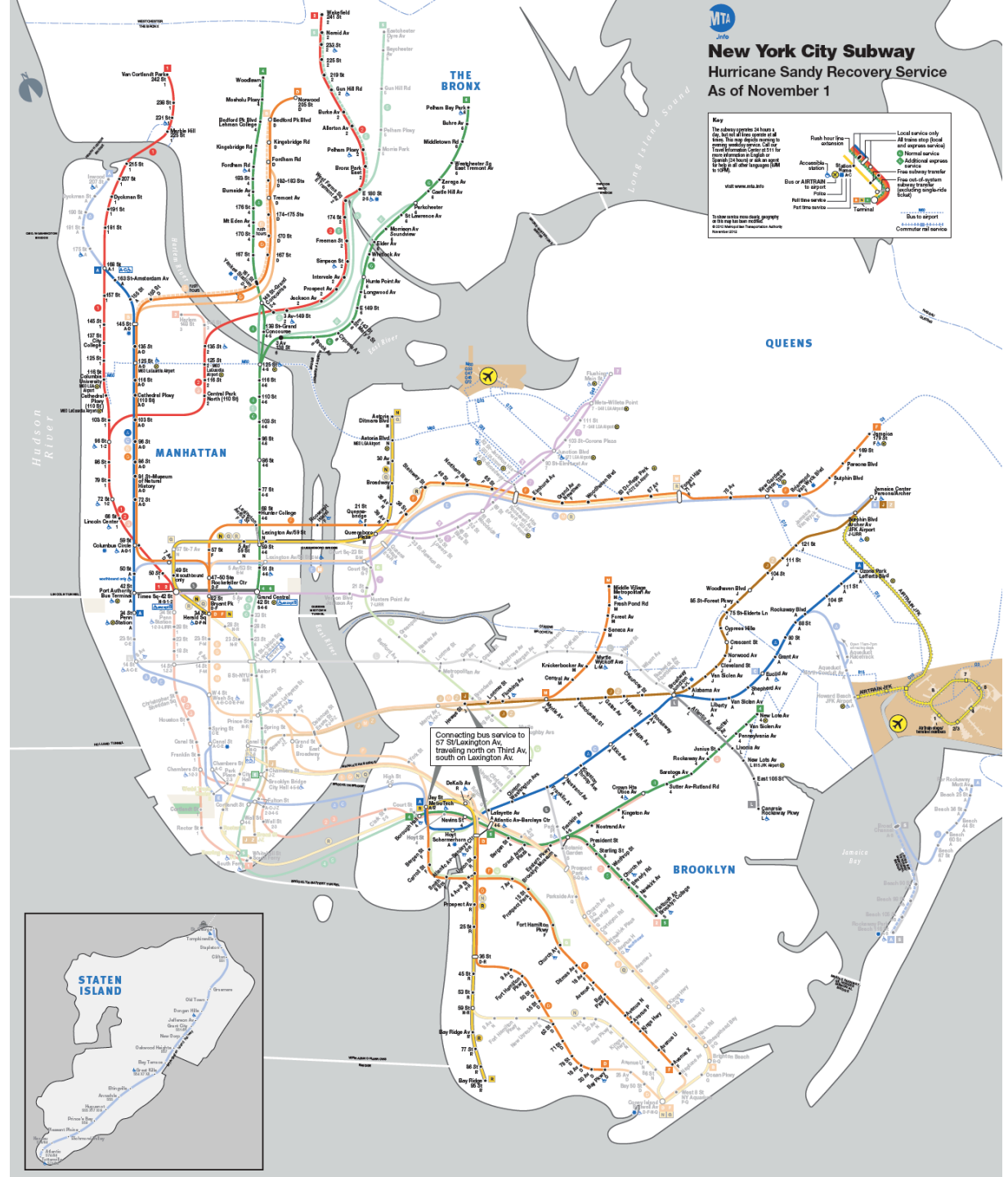
Hurricane Sandy






The Day After Tomorrow (2004)

A tale of two cities



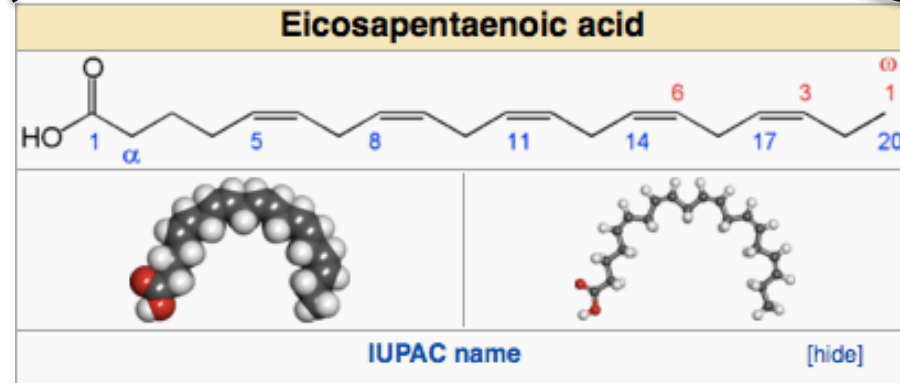
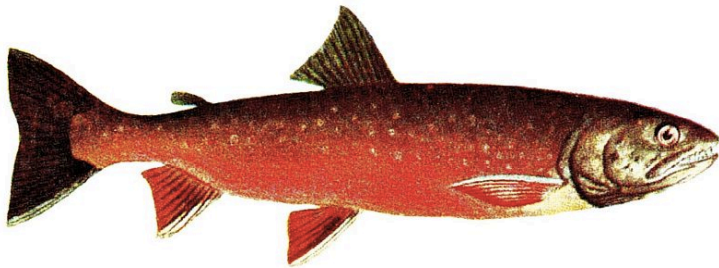
A photograph of a flooded subway station. The floor is covered in dark, still water that reflects the surrounding environment. In the background, a large map of New York City is mounted on a light-colored wall. To the left, a metal railing runs along the edge of the platform. Above the railing, a black sign with a white downward-pointing arrow and the text 'Down to The Bronx' is visible, with a red circle containing the number '1' next to it. On the right side of the wall, there is a large mural of bare tree branches. The overall atmosphere is cold and somber.

A persistent “molecular echo” of the
cold, ocean water

Shewanella frigidimarina

An Antarctic species with the ability to produce eicosapentaenoic acid. It grows anaerobically by dissimilatory Fe (III) reduction.[1] Its cells are motile and rod shaped

EPA is obtained in the human diet by eating oily fish or fish oil, e.g. cod liver, herring, mackerel, and salmon.



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A Journal of Psychiatric Neuroscience and Therapeutics

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Biological Psychiatry
[Volume 56, Issue 7](#), Pages 490–496, October 1, 2004

Suicide attempt and n-3 fatty acid levels in red blood cells: A case control study in china

Frolova, G. M.; Gumerova, P. A.; Romanenko, L. A.; Mikhailov, V. V. (2011). "Characterization of the lipids of psychrophilic bacteria *Shewanella frigidimarina* isolated from sea ice of the Sea of Japan". *Microbiology* 80 (1): 30–36

Licking Subway Poles "Probably Fine," Says Expert



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Randomized Trial of Peanut Consumption in Infants at Risk for Peanut Allergy

George Du Toit, M.B., B.Ch., Graham Roberts, D.M., Peter H. Sayre, M.D., Ph.D., Henry T. Bahnson, M.P.H., Suzana Radulovic, M.D., Alexandra F. Santos, M.D., Helen A. Brough, M.B., B.S., Deborah Phippard, Ph.D., Monica Basting, M.A., Mary Feeney, M.Sc., R.D., Victor Turcanu, M.D., Ph.D., Michelle L. Sever, M.S.P.H., Ph.D., Margarita Gomez Lorenzo, M.D., Marshall Plaut, M.D., and Gideon Lack, M.B., B.Ch. for the LEAP Study Team

N Engl J Med 2015; 372:803-813 | [February 26, 2015](#) | DOI: 10.1056/NEJMoa1414850

Replicated!



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ORIGINAL ARTICLE

Effect of Avoidance on Peanut Allergy after Early Peanut Consumption

George Du Toit, M.B., B.Ch., Peter H. Sayre, M.D., Ph.D., Graham Roberts, D.M., Michelle L. Sever, M.S.P.H., Ph.D., Kaitie Lawson, M.S., Henry T. Bahnson, M.P.H., Helen A. Brough, M.B., B.S., Ph.D., Alexandra F. Santos, M.D., Ph.D., Kristina M. Harris, Ph.D., Suzana Radulovic, M.D., Monica Basting, M.A., Victor Turcanu, M.D., Ph.D., Marshall Plaut, M.D., and Gideon Lack, M.B., B.Ch., for the Immune Tolerance Network LEAP-On Study Team*

March 4, 2016 | DOI: 10.1056/NEJMoa1514209

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Abstract

Article

References

Citing Articles (1)

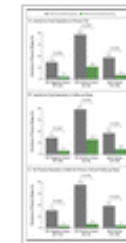
Metrics

BACKGROUND

In a randomized trial, the early introduction of peanuts in infants at high risk for allergy was shown to prevent peanut allergy. In this follow-up study, we investigated whether the rate of peanut allergy remained low after 12 months of peanut avoidance among participants who had consumed peanuts during the primary trial (peanut-consumption group), as compared with those who had avoided peanuts (peanut-avoidance group).

MEDIA IN THIS ARTICLE

FIGURE 1

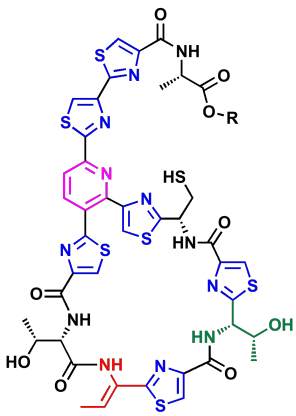
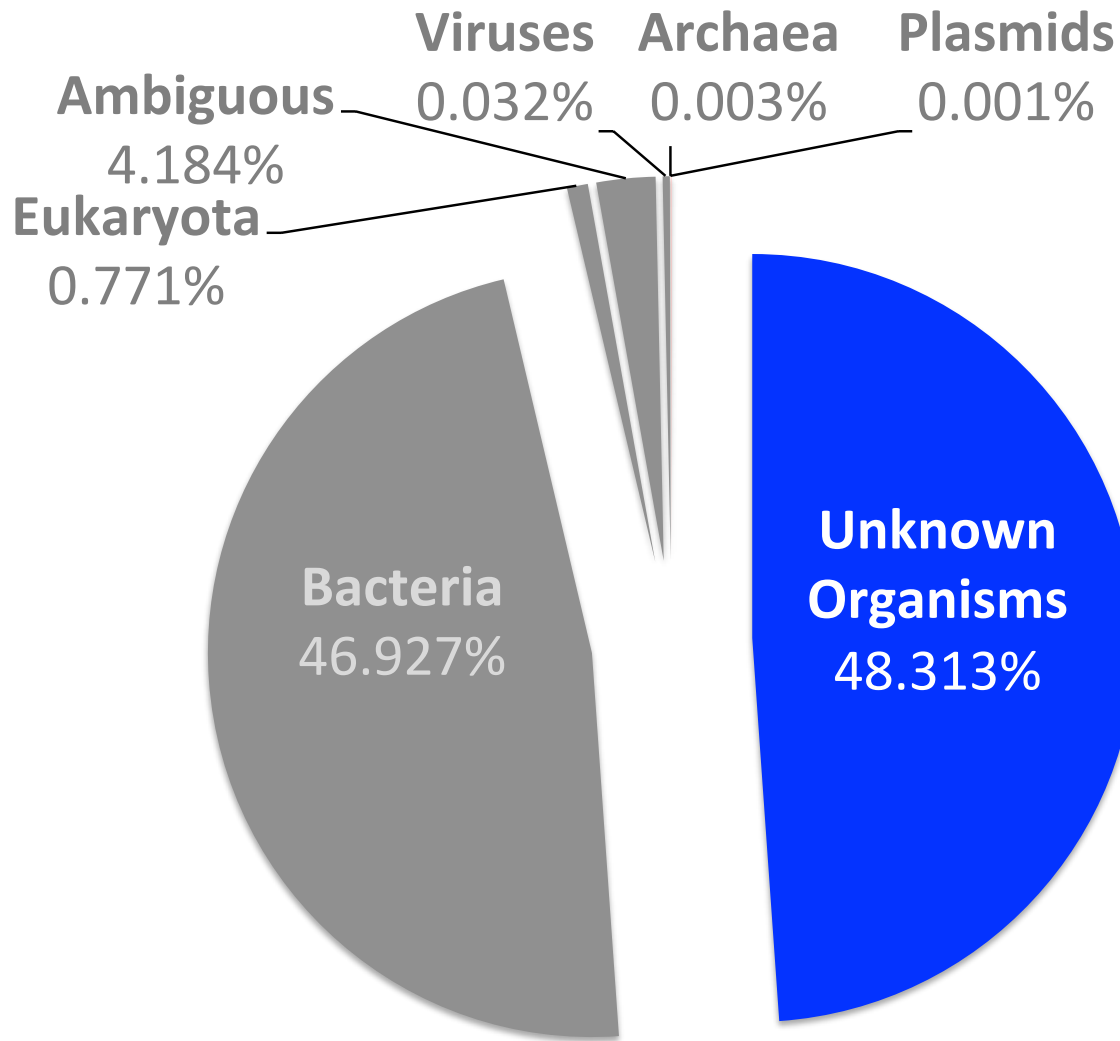


Primary Outcome.

Note:

Does not apply during pandemics.

Who is there, and what are they making?



(2)

What have we
been missing?

Global Distribution and Epigenetic Stratification of Antimicrobial Resistance

GRAND CHALLENGES EXPLORATIONS | DRUG RESISTANCE BURDEN | 1 MAY 2016

Christopher Mason of Weill Medical College of Cornell University in the U.S. will generate a global map of antimicrobial resistance by using biochemical and computational methods on available samples taken monthly over one year from 24 developed and developing cities across six continents. Each city will be sampled from both high-density (e.g. train stations) and low-density (e.g. parks) areas. They will sequence DNA isolated from two samples per area from each city to identify the bacterial species present and determine whether they carry any antimicrobial resistance genes or markers, or chemically modified DNA bases (epigenetic modifications) that may influence microbial function. The results will then be geographically mapped, and analyzed for associations with population density and proximity to health centers.

SHARE THIS AWARDED GRANT

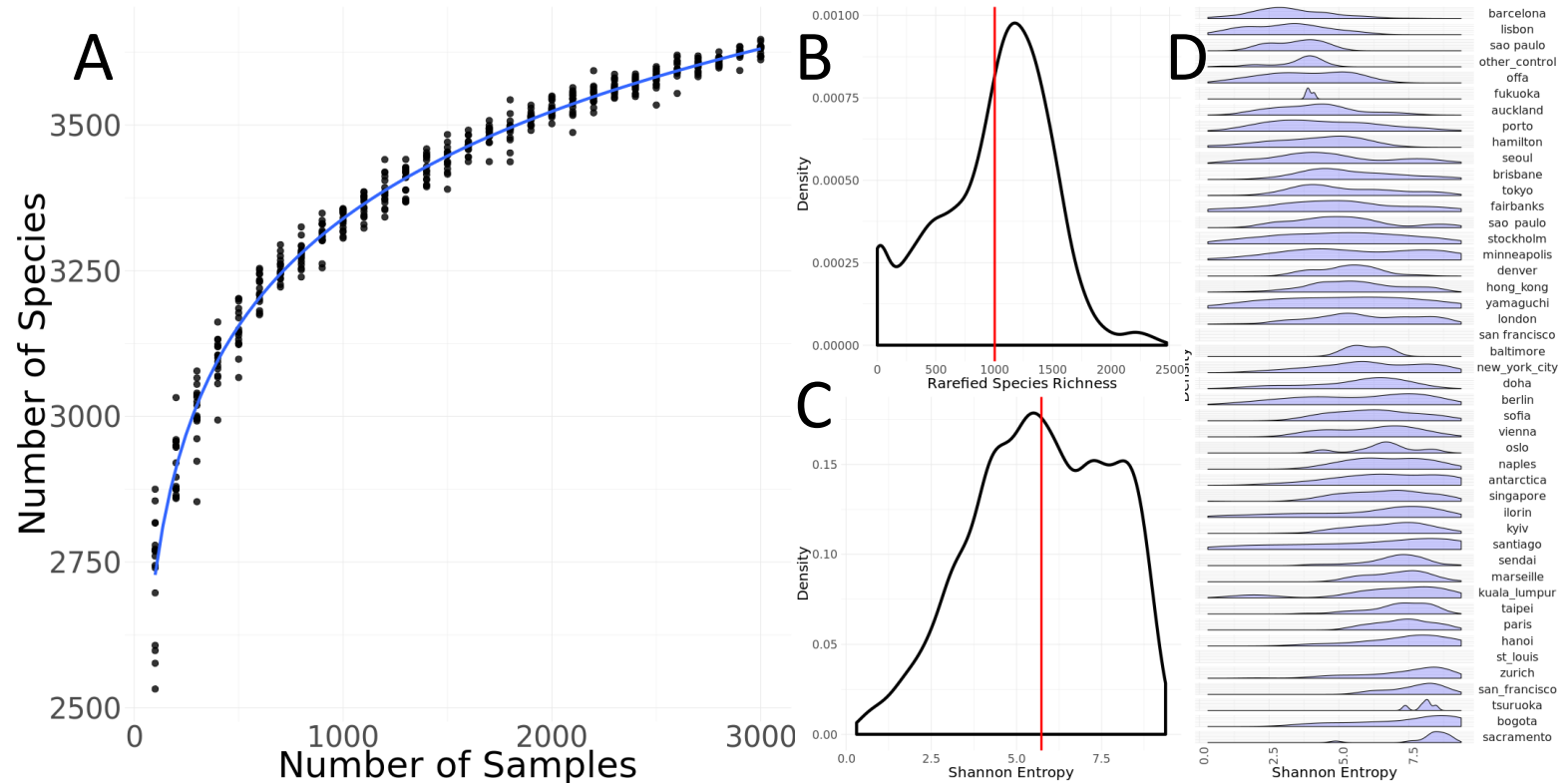


PRINCIPAL INVESTIGATOR

Christopher Mason

<http://gcgh.grandchallenges.org/grant/global-distribution-and-epigenetic-stratification-antimicrobial-resistance>

Significant Diversity, More to be Discovered



MetaSUB

Metagenomics & Metadesign of Subways & Urban Biomes

3 Goals:

1. Geospatial Metagenomic and Forensic Maps
2. Anti-microbial resistance (AMR) marker tracking by genetics and epigenetics
3. New Biosynthetic Gene Clusters (BGCs); new drugs

www.metasub.org

NGS on sewage in Florida, Wisconsin, and New York

DEVELOPMENT AND PROOF-OF-CONCEPT IMPLEMENTATION OF THE SOUTH FLORIDA MIAMI RADX-RAD SARS-COV-2 WASTEWATER-BASED SURVEILLANCE INFRASTRUCTURE

Award Number: U01DA053941

ORGANIZATION: NATIONAL INSTITUTE ON DRUG ABUSE

OPDIV: NIH

AWARD CLASS: COOPERATIVE AGREEMENT

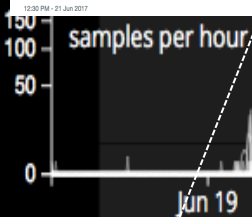
AWARD ACTIVITY TYPE: SCIENTIFIC/HEALTH RESEARCH (INCLUDES SURVEYS)

Group Awards By Issue Date FY or Funding FY: ☒ Issue Date FY ☐ Funding FY

HIDE AWARD ABSTRACT

PROJECT SUMMARY The University of Miami (UM), with three primary campuses in Miami, Florida, is geographically spread within one of the worst current COVID-19 hotbeds. UM has deployed an elaborate human surveillance testing, tracking and tracing (3T) system to monitor the student body, faculty, and staff. This 3T system includes a major hospital that is part of UM and that treats COVID-19 patients. To augment this COVID-19 monitoring system, UM has deployed a pilot wastewater surveillance program for detecting SARS-CoV-2 from clusters of buildings on campus. Weill Cornell Medicine (WCM) is located in New York City, NY, an area that until recently had one of the worst outbreaks of COVID-19. WCM has established an international consortium for SARS-CoV-2 environmental surveillance, including in NYC and globally with the [MetaSUB Consortium](#), which is creating metagenomic and metatranscriptomic maps of the world's sewage. Based on this work at both UM and WCM, this proposal aims to develop, implement, and demonstrate effective and predictive wastewater surveillance by optimizing sampling, concentration, and detection strategies. Working closely with the RADx-rad Data Coordination Center (DCC), this application (SF-RAD) will

https://taggs.hhs.gov/Detail/AwardDetail?arg_AwardNum=U01DA053941&arg_ProgOfficeCode=114



Worldwide MetaSUB collection
 2016 = 6,058 samples
 2017 = 7,309 samples
 2018 = 6,104 samples
 2019 = 9,320 samples
 2020 = >5,000 samples



etaSUB
arseille

3X increase in size of the tree of life, including 10,928 new viruses (vs. JGI/NCVBI)



Altmetric: 499

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Article | [OPEN](#)

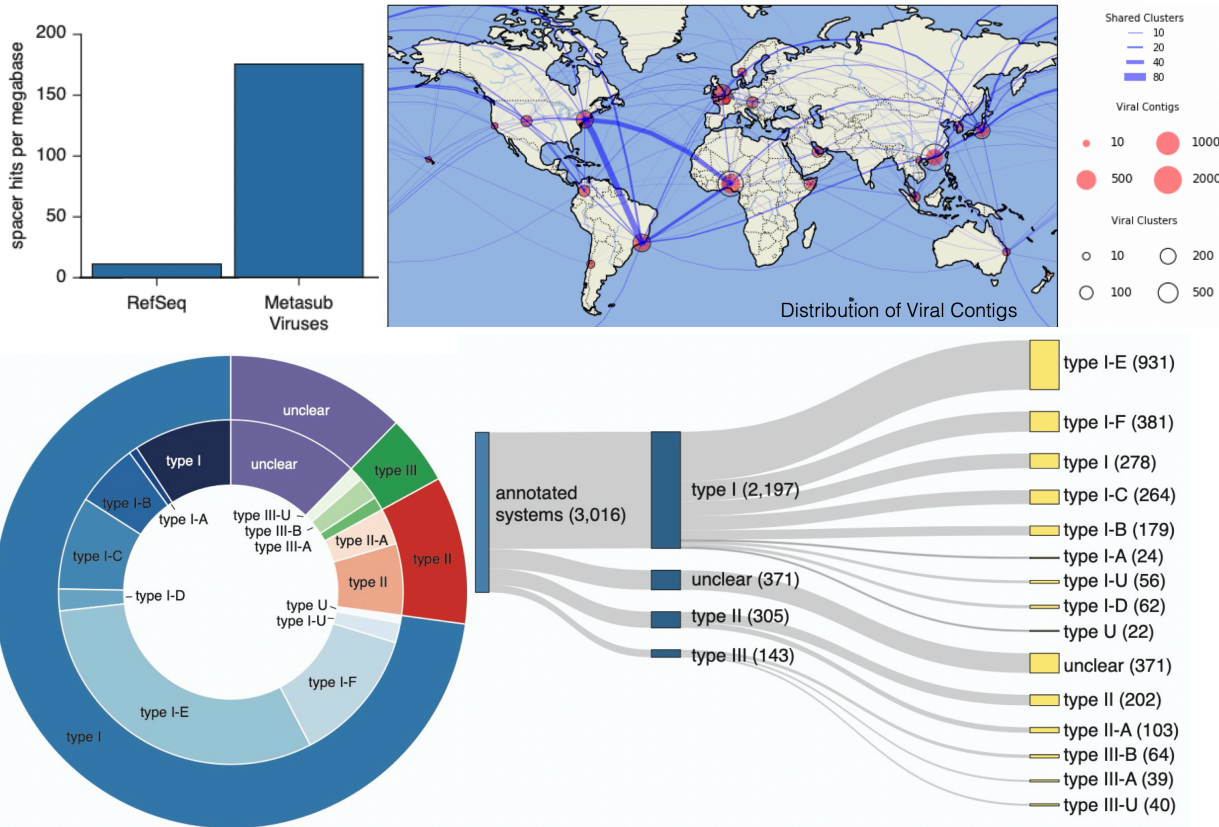
Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life

Global Genetic Cartography of Urban Metagenomes and Anti-Microbial Resistance

David Danko^{1,2,*}, Daniela Bezdán^{1,2,*}, Ebrahim Afshinnekoo^{1,2,*}, Sofia Ahsanuddin^{3,*}, Chandrima Bhattacharya^{1,2,*}, Daniel J Butler^{1,2,*}, Kern Rei Chng^{4,*}, Francesca De Filippis^{5,*}, Jochen Hecht^{6,*}, Andre Kahles^{7,*}, Mikhail Karasikov^{7,*}, Nikos C Kyrpides^{8,*}, Marcus H Y Leung^{9,*}, Dmitry Meleshko^{1,2,*}, Harun Mustafa^{7,*}, Beth Mutai^{10,6,*}, Russell Y Neches^{8,*}, Amanda Ng^{4,*}, Marina Nieto-Caballero^{11,*}, Olga Nikolayeva^{12,*}, Tatyana Nikolayeva^{12,*}, Eileen Png^{4,*}, Jorge L Sanchez^{13,*}, Heba Shaaban^{1,2,*}, Maria A Sierra^{1,2,*}, Xinzha Tong^{9,*}, Ben Young^{1,2,*}, Josue Alicea^{1,2,*}, Malay Bhattacharyya^{14,*}, Ran Blekhman^{15,*}, Eduardo Castro-Nallar^{16,*}, Ana M Cañas^{13,*}, Aspasia D Chatziefthimiou^{17,*}, Robert W Crawford^{18,*}, Youping Deng^{19,*}, Christelle Desnues^{20,*}, Emmanuel Dias-Neto^{21,*}, Daisy Donnellan^{13,*}, Marius Dybwad^{22,*}, Eran Elhaik^{23,*}, Danilo Ercolini^{5,*}, Alina Frolova^{24,*}, Alexandra B Graf^{25,*}, David C Green^{26,*}, Iman Hajirasouliha^{1,2,*}, Mark Hernandez^{11,*}, Gregorio Iraola^{27,*}, Soojin Jang^{28,*}, Frank J Kelly^{26,*}, Kaymisha Knights^{13,*}, Pawel P Labaj^{29,*}, Patrick K H Lee^{9,*}, Per Ljungdahl^{30,*}, Abigail Lyons^{13,*}, Gabriella Mason-Buck^{31,*}, Ken McGrath^{32,*}, Emmanuel F Mongodin^{33,*}, Milton Ozorio Moraes^{34,*}, Niranjan Nagarajan^{4,*}, Houtan Noushmehr^{35,*}, Manuela Oliveira^{36,*}, Stephan Ossowski^{37,*}, Olayinka O Osuolale^{38,*}, Orhan Özcan^{39,*}, David Paez-Espino^{8,*}, Nicolas Rascovan^{40,*}, Hugues Richard^{41,*},

<https://www.nature.com/articles/s41564-017-0012-7>
<https://www.biorxiv.org/content/10.1101/724526v1>

And >800K new CRISPR arrays



>4.3M putative novel peptides

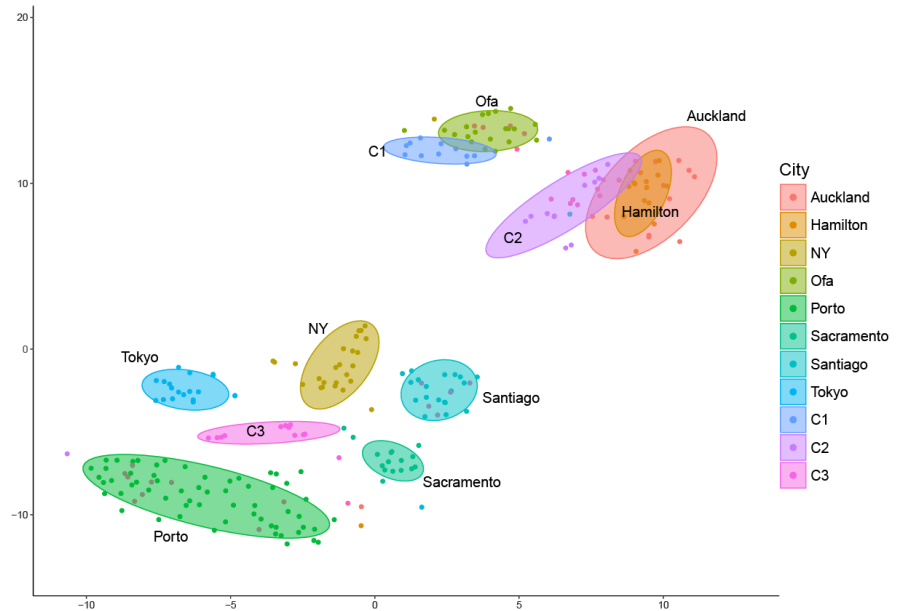
metasub city	sum_contig_size	protein_cnt	metasub c95 ratio	metasub c80 ratio
new_york_city	23,237,773,149	10,424,821	44.3%	8.4%
london	11,698,381,507	5,453,860	47.2%	11.0%
ilorin	12,083,747,553	5,173,133	47.6%	11.5%
(blank)	4,877,902,237	2,450,185	46.8%	12.8%
rio_de_janeiro	2,594,610,094	1,199,482	41.6%	16.8%
hong_kong	1,900,750,111	1,169,336	53.9%	9.8%
tokyo	1,862,832,603	959,027	73.5%	54.9%
bogota	1,518,739,125	778,938	56.9%	26.4%
hamilton	1,690,325,223	708,354	37.5%	7.4%
fairbanks	1,486,245,088	680,871	51.8%	19.6%
berlin	1,145,162,542	583,137	58.4%	33.5%
porto	839,222,657	443,986	66.5%	37.2%
auckland	811,476,604	352,826	47.1%	10.5%
ofa	802,189,444	345,587	41.4%	9.7%
santiago	446,643,762	252,230	63.0%	35.6%
oslo	187,649,603	96,419	49.7%	10.2%
sacramento	75,398,186	37,901	66.3%	17.1%
Grand Total	67,259,049,488	31,110,093	47.9%	14.0%

>1.5kb compared to JGI/NCBI, with Arbor Biotechnology, and Jonathan Gootenberg / Omar Abudayyeh

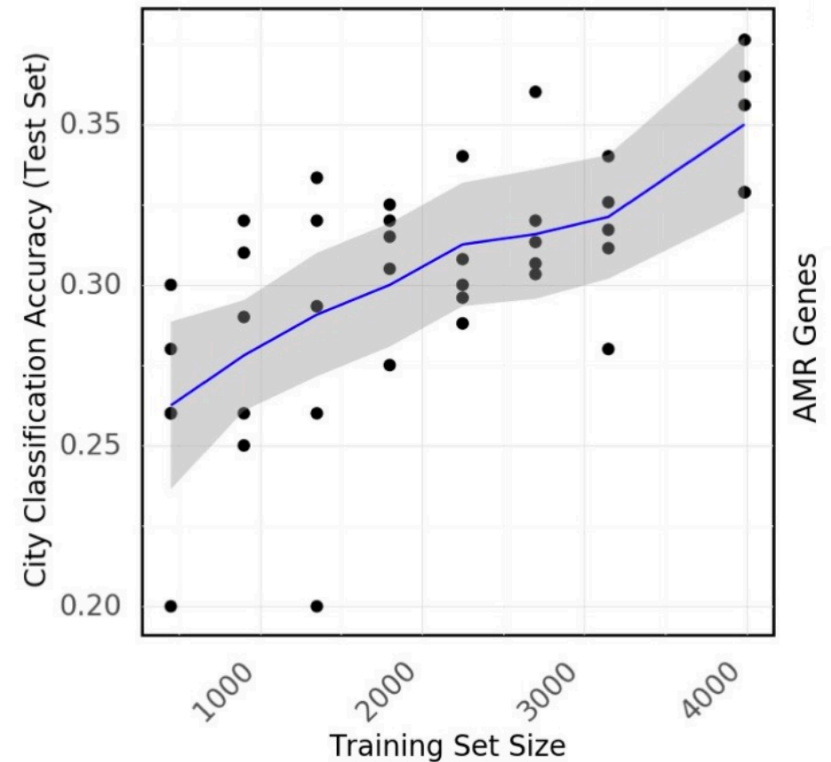
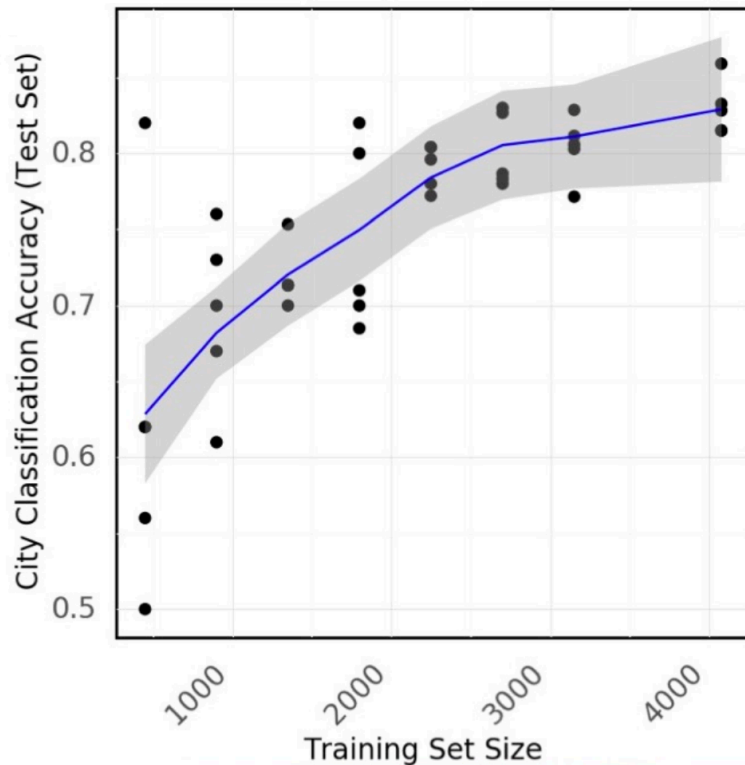
Can we predict where you are from?

Yes.

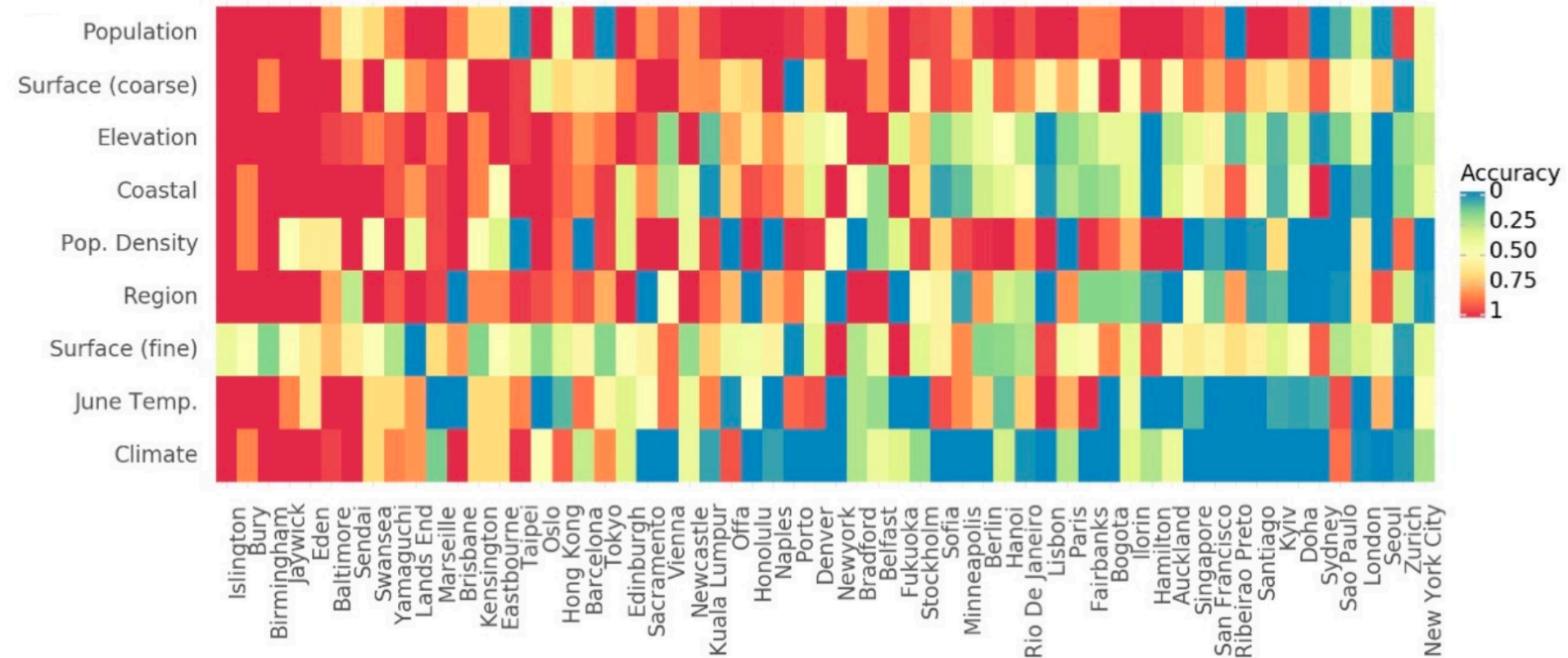
- R implementation of t-Distributed Stochastic Neighbor Embedding (t-SNE)
- Perplexity 50
- $K = 2$
- Only features from Kaiju with relative abundance of at least 0.5% in at least 1 sample



More data helps, but species are the better markers

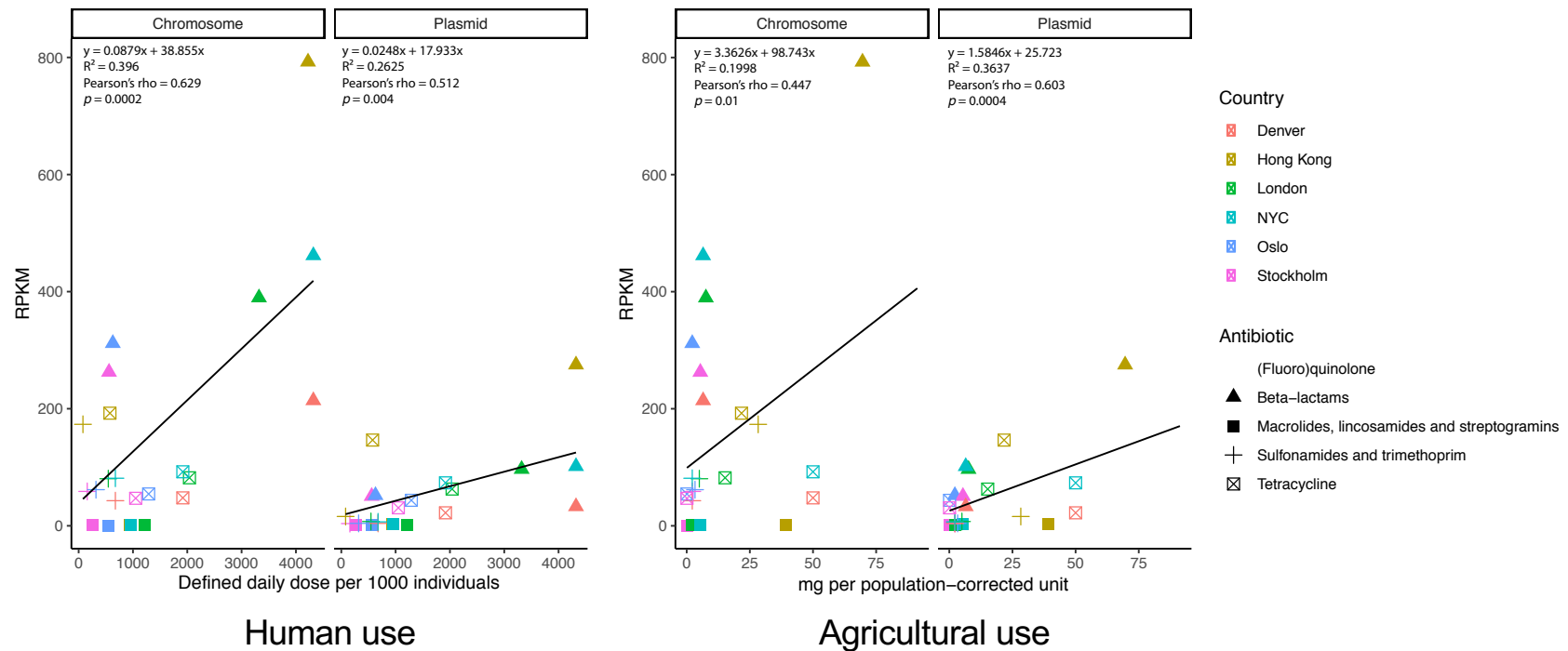


Environment, city, and population drive these features

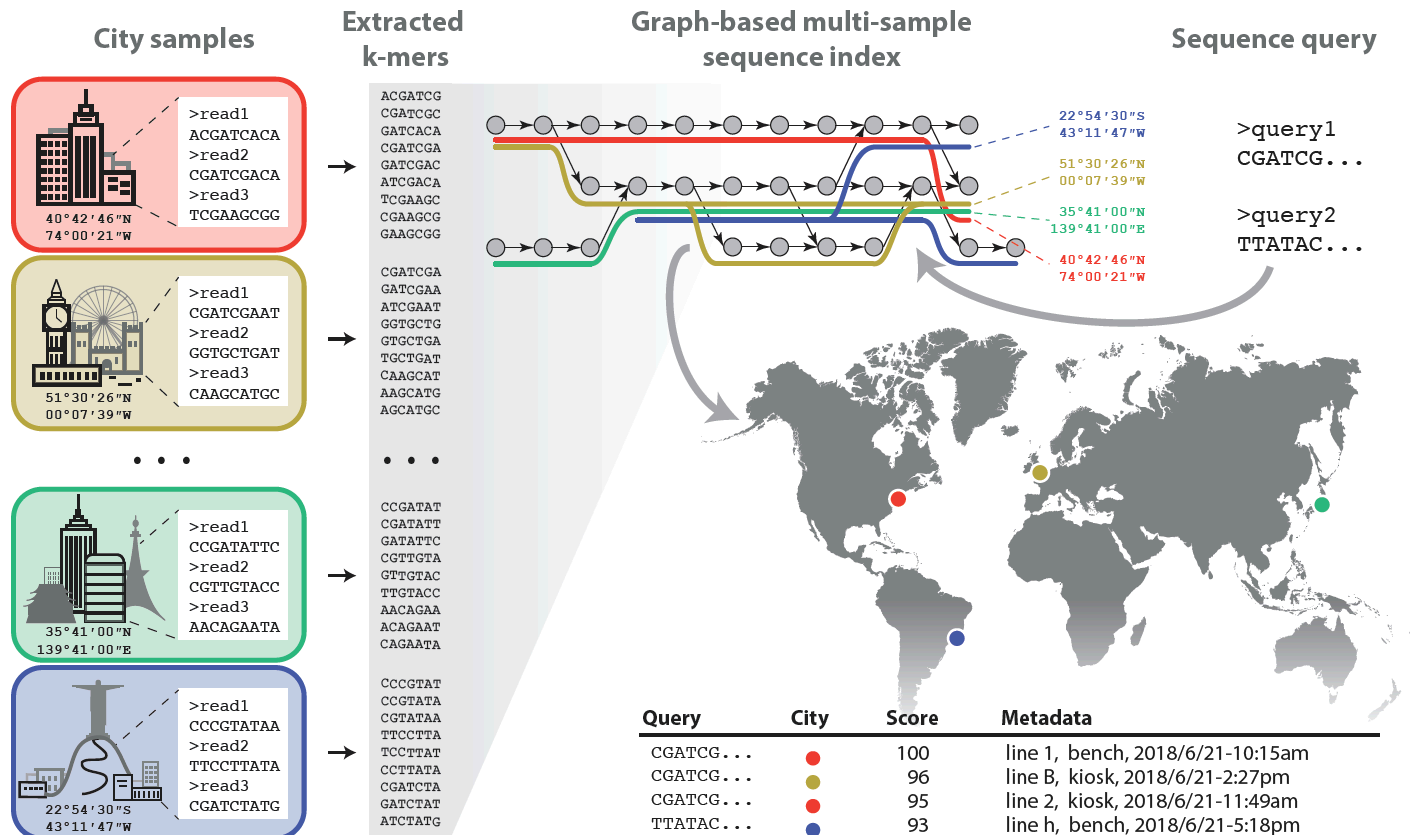


City-specific antibiotic use & ARG profiles

Pearson's correlation is significant



Global K-mer index



<https://metagraph.ethz.ch/graphs>

Planetary Genomics

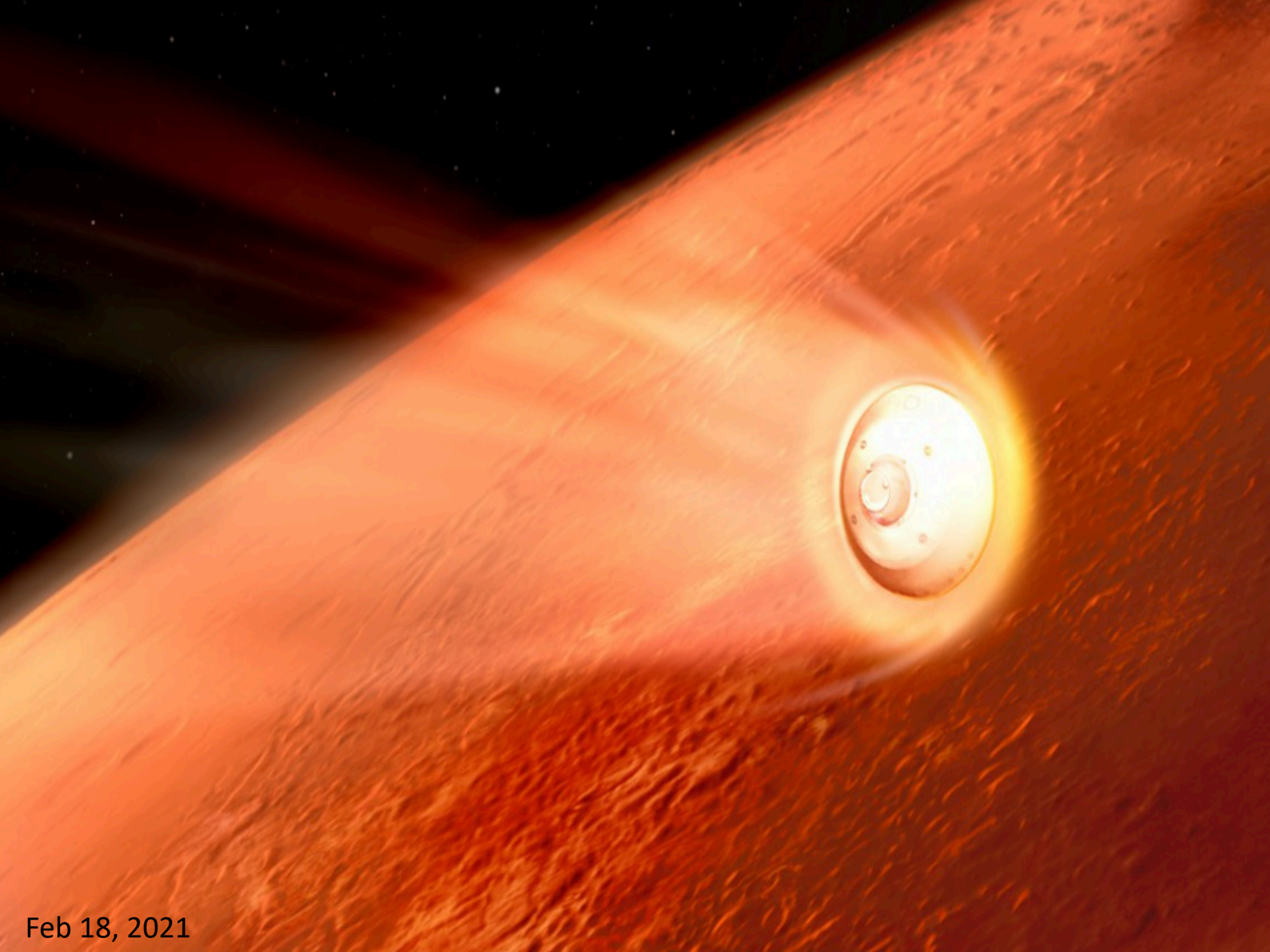






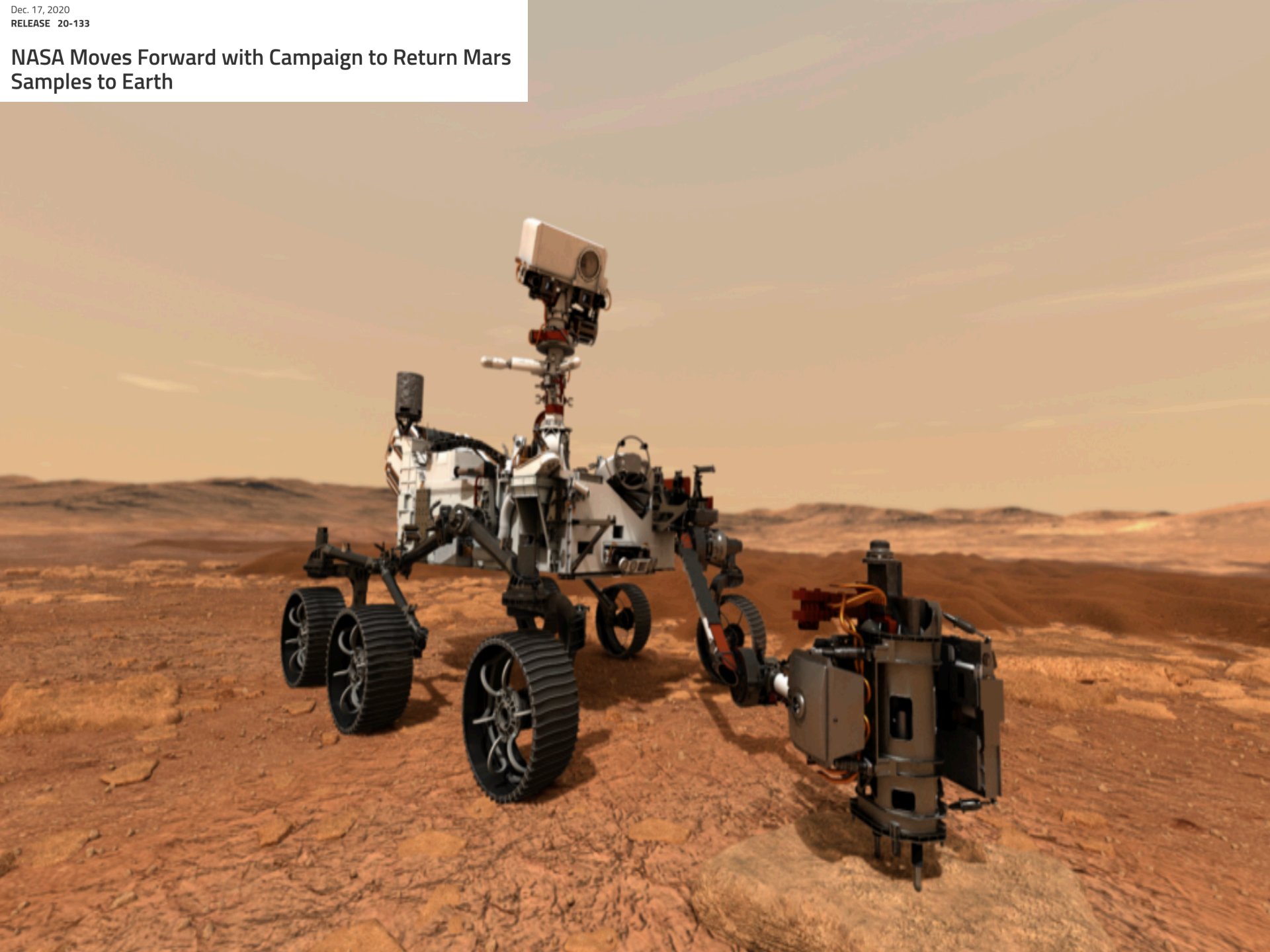


NASA/JPL



Feb 18, 2021

NASA Moves Forward with Campaign to Return Mars Samples to Earth





Jet Propulsion Laboratory
California Institute of Technology

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Mars Sample Return

MSR

Mars Sample Return is a proposed mission to return samples from the surface of Mars to Earth.

ETA: 2032

<https://www.jpl.nasa.gov/missions/mars-sample-return-msr/>



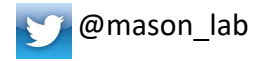


A New View

↖ Earth

View from Curiosity rover, evening of January 31, 2014 (Mars year 32, late spring)
Earth-Mars distance: 180 million km (112 million mi)
JPL

These People are Awesome



Thanks to Funding from:

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Deep Gratitude to Many People:



@mason_lab

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Questions?