


Bacterial diversity and molecular echoes measured across subways and cities using metagenomics

 @mason_lab

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Department of Physiology and Biophysics &

The Institute for Computational Biomedicine at the

Weill Cornell Medical College and the

Tri-Institutional Program on Computational Biology and Medicine

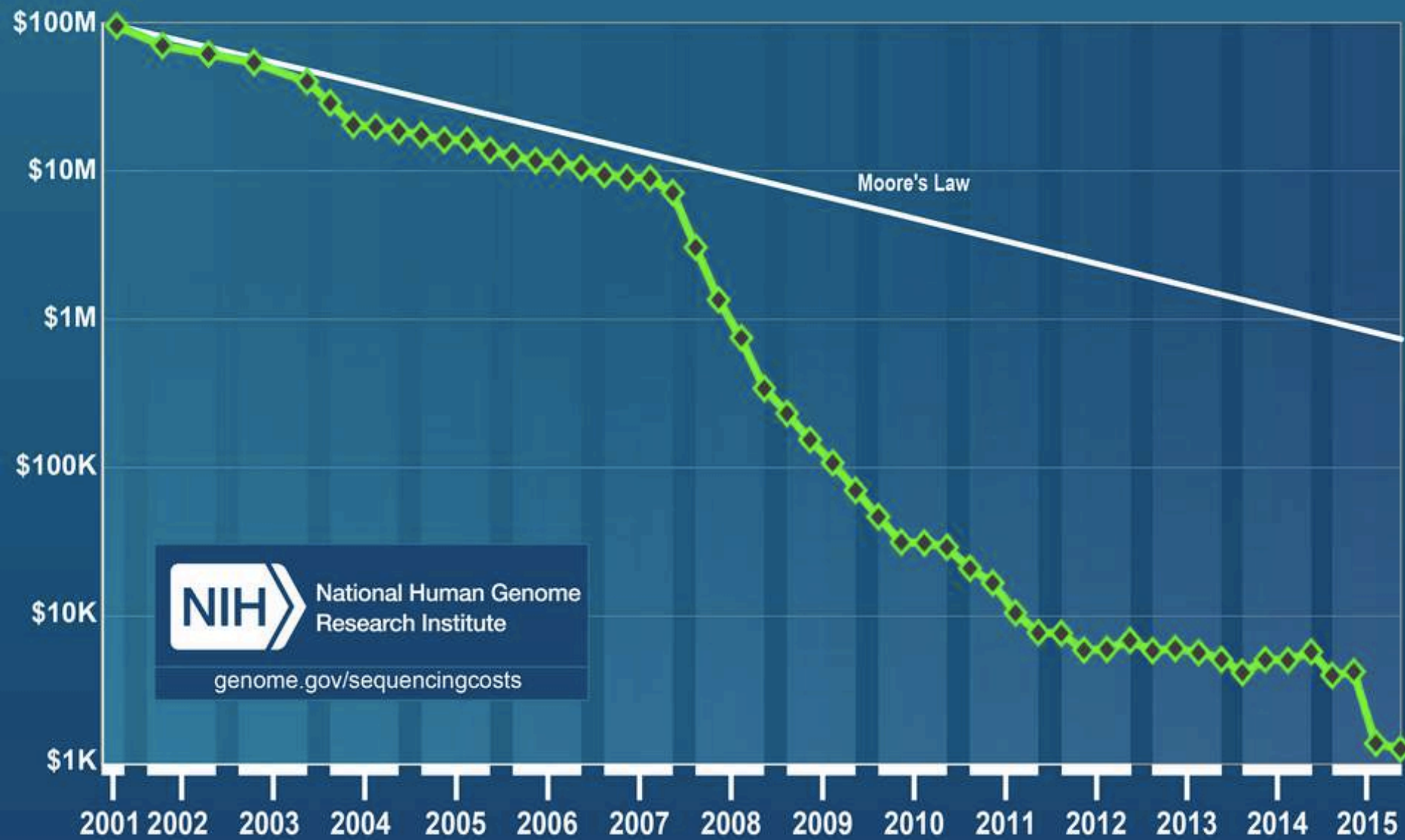
Fellow of the Information Society Project, Yale Law School

March 14th, 2016

(0)

Revolution

Cost per Genome



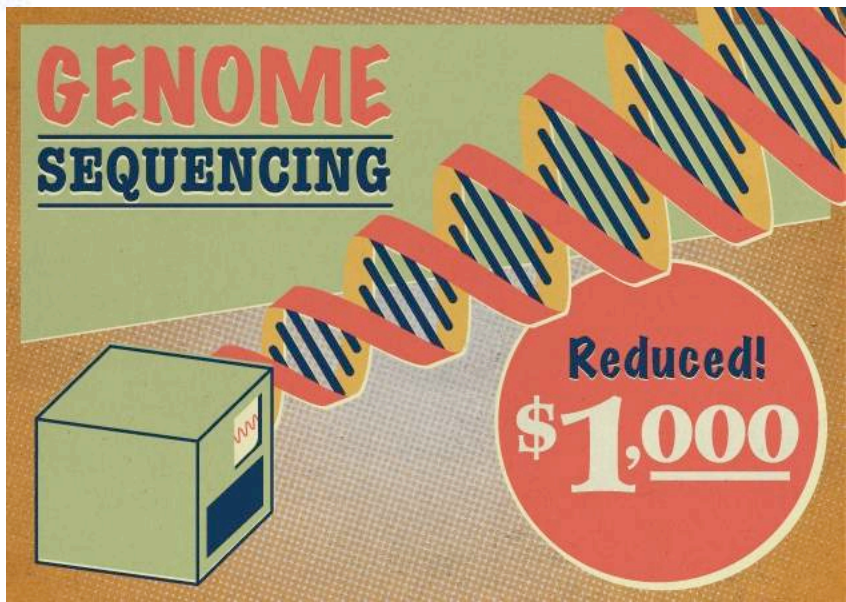


Technology: The \$1,000 genome

With a unique programme, the US government has managed to drive the cost of genome sequencing down towards a much-anticipated target.

Erika Check Hayden

19 March 2014



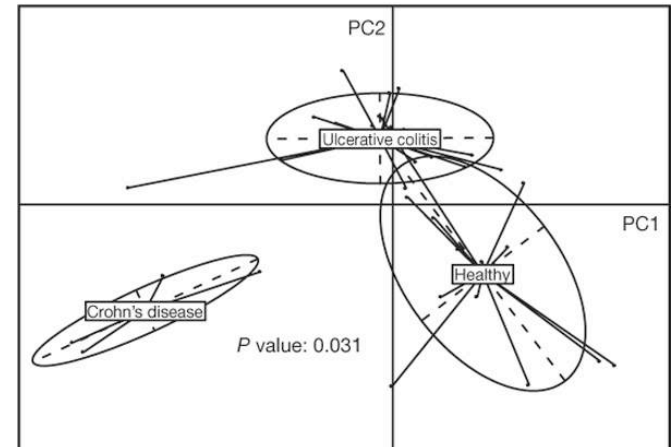
But! There is more than one genome:

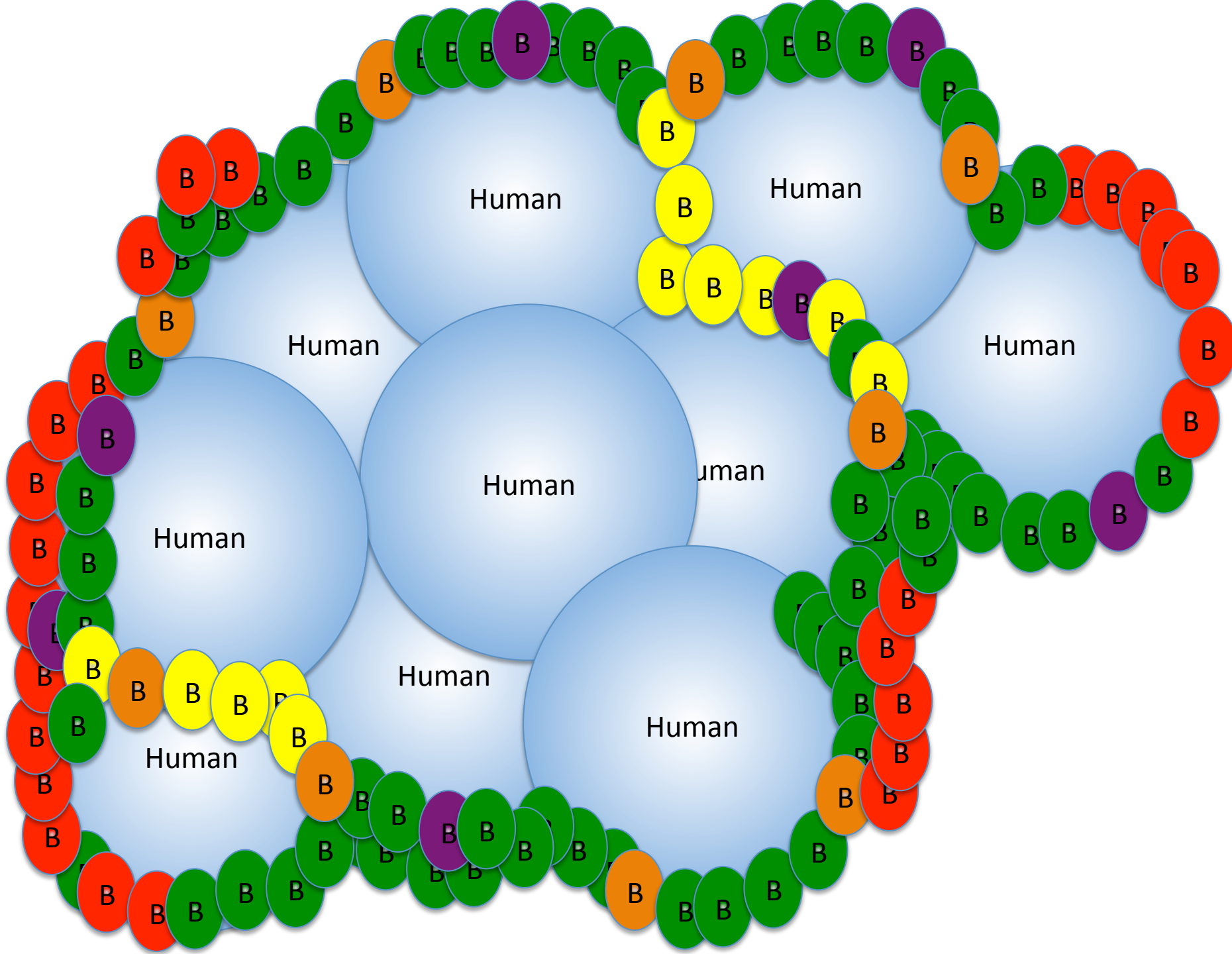
In your body's cellular democracy,

YOU are a **minority party**:

1.3-10X bacterial:human cells (*Zhu et al., 2010, Sender et al, 2016*)

150:1 bacterial:human active transcripts in the gut microbiome (*Qin et al, 2010*)





200 pounds

3-5 pounds bacteria

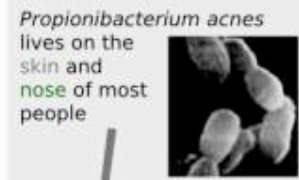
195-97 pounds human



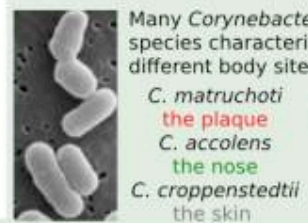
A map of diversity in the human microbiome



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



Propionibacterium acnes lives on the skin and nose of most people



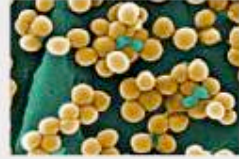
Many *Corynebacterium* species characterize different body sites:
C. matruchoti the **plaque**
C. accolens the **nose**
C. croppenstedtii the **skin**



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



Staphylococcus epidermidis colonizes external body sites



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



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



- Commensal microbes
- ☆ Potential pathogens

The four most abundant phyla

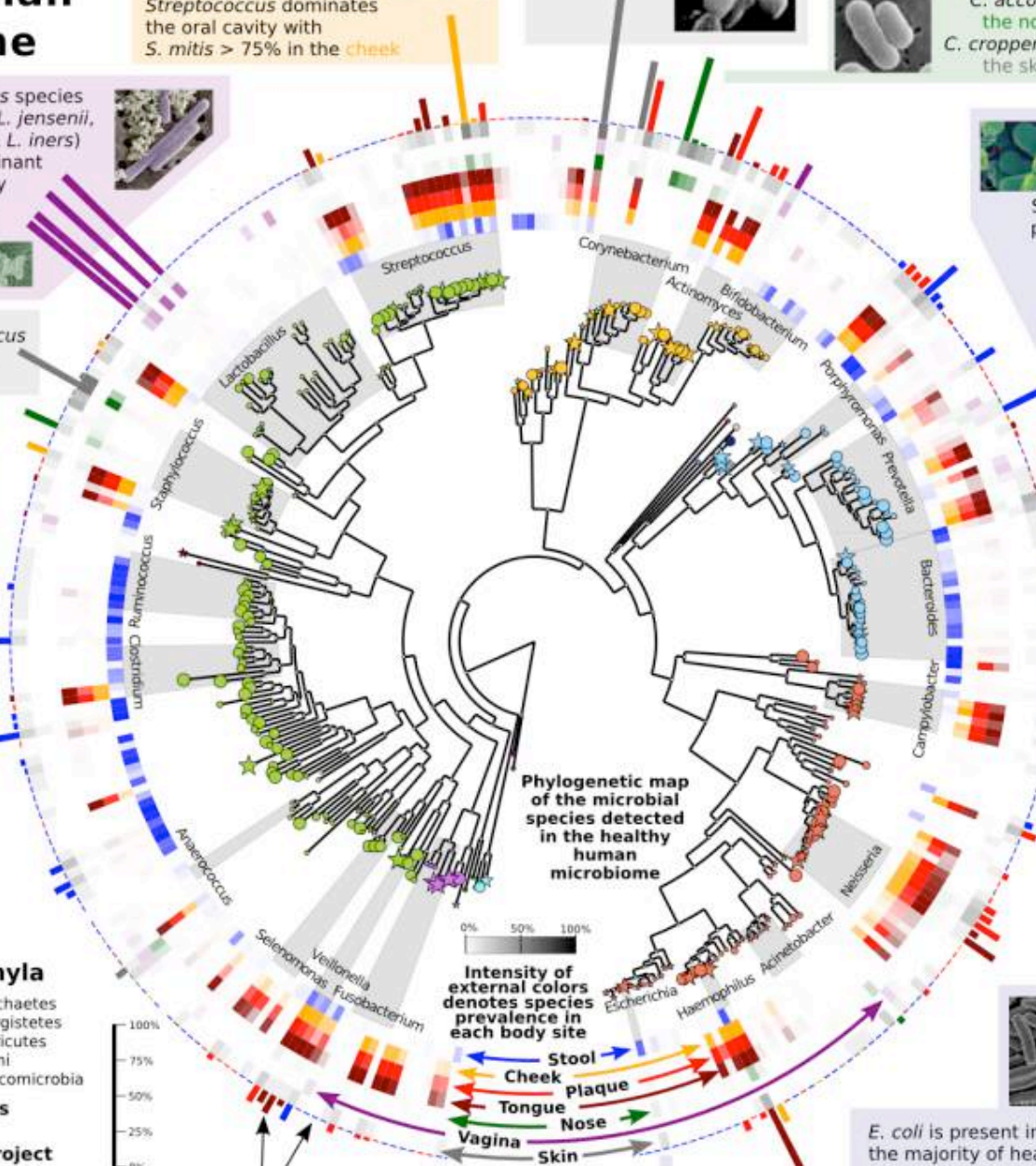
- Actinobacteria
- Bacteroidetes
- Firmicutes
- Proteobacteria

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 Circos and R packages from Bioinformatics



Phylogenetic map of the microbial species detected in the healthy human microbiome

Intensity of external colors denotes species prevalence in each body site

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

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



(1)

Microbiome

Hope

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

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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/



uman Microbiome Consortium

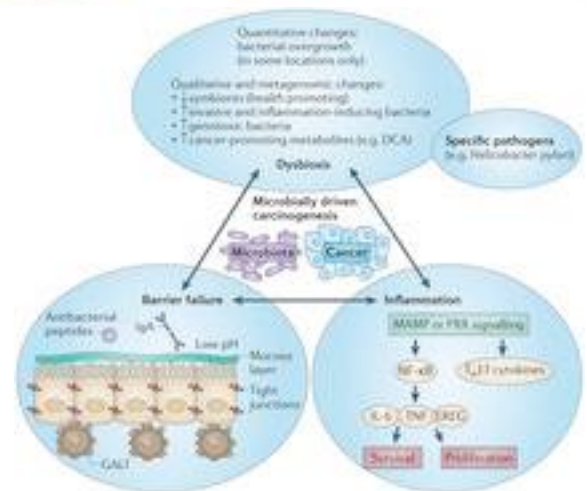
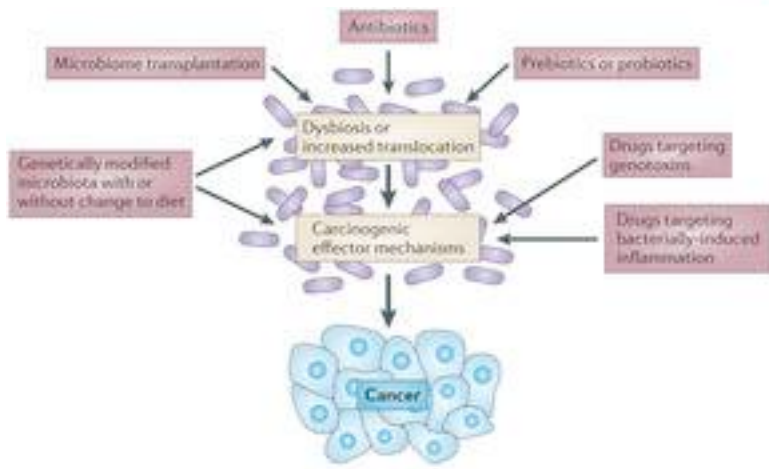
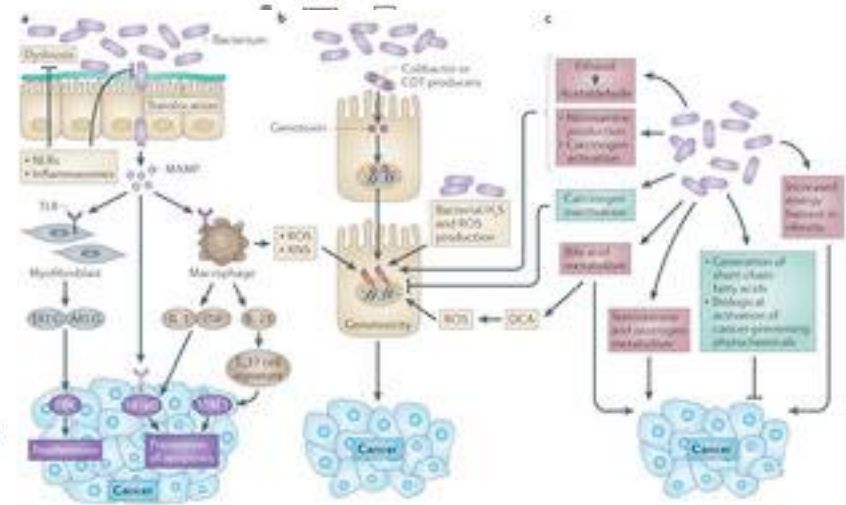
The microbiome and cancer

Robert F. Schwabe & Christian Jobin

Affiliations | Corresponding authors

Nature Reviews Cancer 13, 800–812 (2013) | doi:10.1038/nrc3610

Published online 17 October 2013



HEALTH

You Are Your Bacteria: How the Gut Microbiome Influences Health

The bacteria in our gut already plays an important role in digestion. But new studies indicate that our bacteria could play a major role in whether or not we become obese

By Veronique Greenwood | Aug. 29, 2013 | 39 Comments

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VERSION HISTORY

- 336/6086/1209 stay thin.

Published Online June 6 2012
Science 8 June 2012:
Vol. 336 no. 6086 p. 1209
DOI: 10.1126/science.1225475

EDITORIAL

Tackling the Microbiom

Leroy Hood

36%
of the small molecules
in your blood
are from the microbiome

Many organisms work on your behalf!

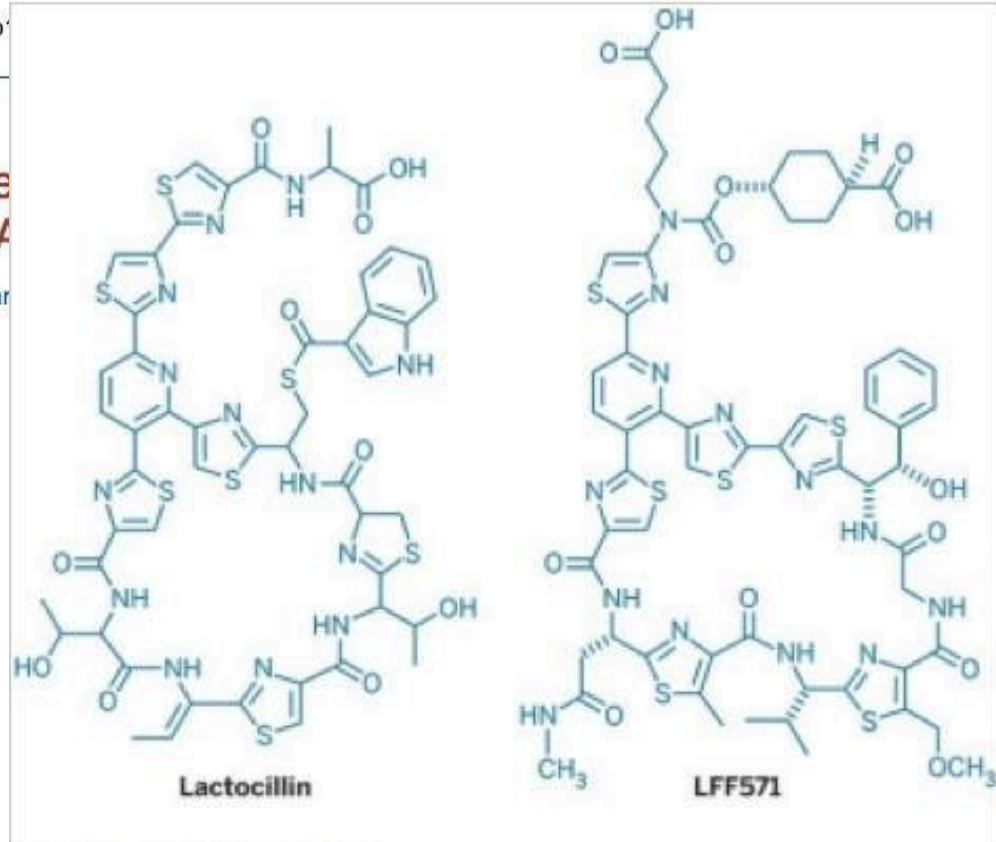
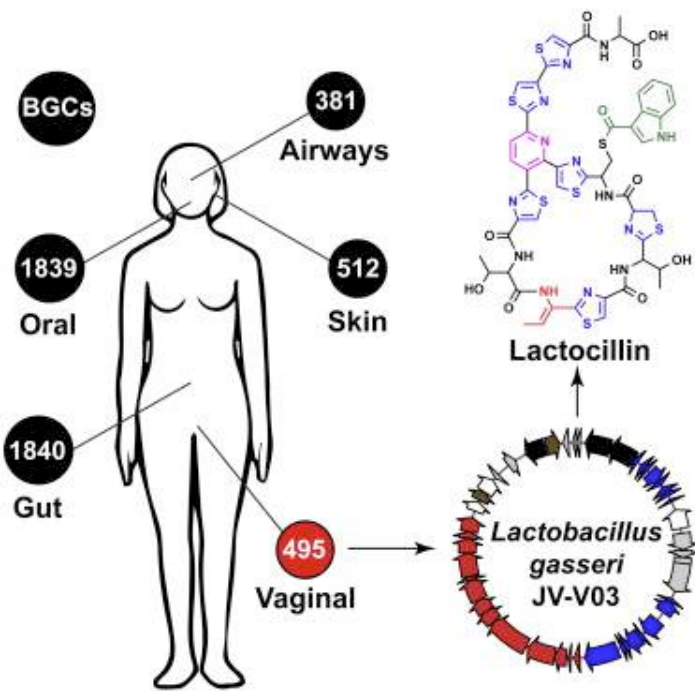
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Volume 158, Issue 6, p

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>



Microbiologist Satoshi Omura holds a news conference Monday evening at Kitasato University in Tokyo after winning the 2015 Nobel Prize in medicine for his work on debilitating diseases caused by parasitic worms. | KYODO

[NATIONAL](#) / [SCIENCE & HEALTH](#)

Japanese microbiologist Satoshi Omura shares Nobel Prize for medicine

Omura thanks his microbial helpers

“I was helped by microorganisms. I wonder if I deserve the prize,” he said.

Where do
they come
from?

We all carry a “microbiome cloud”

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Science 29 August 2014:
Vol. 345 no. 6200 pp. 1048-1052
DOI: 10.1126/science.1254529

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REPORT

Longitudinal analysis of microbial interaction between humans and the indoor environment

Simon Lax^{1,2,*}, Daniel P. Smith^{1,2,3,*}, Jarrad Hampton-Marcell^{1,2}, Sarah M. Owens^{2,4}, Kim M. Handley^{1,2}, Nicole M. Scott^{1,2}, Sean M. Gibbons^{2,5}, Peter Larsen^{6,7}, Benjamin D. Shogan⁸, Sophie Weiss^{9,10}, Jessica L. Metcalf⁹, Luke K. Ursell^{9,11}, Yoshiki Vázquez-Baeza^{9,11,12}, Will Van Treuren⁹, Nur A. Hasan^{13,14}, Molly K. Gibson^{15,16,17}, Rita Colwell^{13,14}, Gautam Dantas^{15,16,17}, Rob Knight^{9,11,18}, Jack A. Gilbert^{1,2,5,†}



Mothers Give Us a Lot (Beyond Love)

OPEN ACCESS Freely available online



Essay

Mom Knows Best: The Universality of Maternal Microbial Transmission

Lisa J. Funkhouser^{1*}, Seth R. Bordenstein^{1,2*}

1 Department of Biological Sciences, Vanderbilt University, Nashville, Tennessee, United States of America, **2** Department of Pathology, Microbiology, and Immunology, Vanderbilt University, Nashville, Tennessee, United States of America

Summary

The sterile womb paradigm is an enduring premise in biology that human infants are born sterile. Recent studies suggest that infants incorporate an initial microbiome before birth and receive copious supplementation of maternal microbes through birth and breastfeeding. Moreover, evidence for microbial maternal transmission is increasingly widespread across animals. This collective knowledge

While maternal transmission of microbes in humans has attracted considerable attention in the last few years, nearly a century's worth of research is available for vertical transmission of symbionts in invertebrates [22]. Similar to gut bacteria in humans that assist nutrient intake, many insect-associated bacteria function as nutritional symbionts that supplement the nutrient-poor diet of their host with essential vitamins or amino acids [23,24]. Since these

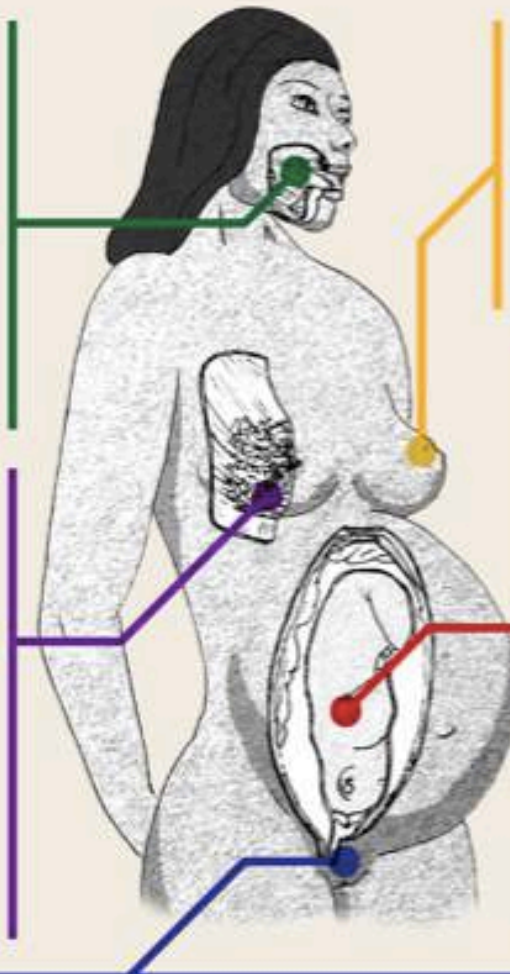
that human infants develop within a sterile environment and acquire their initial bacterial inoculum while traveling through the maternal birth canal [28]. More than a century later, the sterile womb hypothesis remains dogma, as any bacterial presence in the uterus is assumed to be dangerous for the infant. Indeed, studies of preterm deliveries have found a strong correlation between intrauterine infections and preterm labor, especially when birth occurs less than 30 weeks into the pregnancy

Mouth

- Amniotic fluid bacteria with an oral origin include *Fusobacterium nucleatum*, *Streptococcus* spp., *Bergeyella* spp., *Porphyromonas gingivalis*, *Rothia dentocariosa*, and *Filifactor alocis*.
- Oral bacteria are likely transmitted to the uterus via the blood stream, especially if gingiva inflammation is present.

Internal Breast

- Aseptically-collected breast milk contains 100-600 OTUs. Abundant genera include *Streptococcus*, *Staphylococcus*, *Serratia*, *Corynebacteria*, *Lactococcus*, *Weisella*, and *Leuconostoc*.
- An entero-mammary pathway brings gut bacteria to the mammary gland via lymph and blood circulation. External sources of milk microbes include the maternal skin and infant oral cavity.



External Breast

- The sebaceous skin of the breast is an external source of microbes for breast milk (*Staphylococcus* and *Corynebacteria*) but may also provide skin bacteria not common in milk (such as *Propionibacteria*) to the suckling infant.

Uterus

- Contrary to the "sterile womb" paradigm, bacteria are found in umbilical cord blood, amniotic fluid, fetal membranes, and meconium of healthy, term infants.
- Meconium microbiomes are dominated by Enterobacteriaceae (*Escherichia* and *Shigella*) and lactic acid bacteria (*Leuconostoc*, *Enterococcus*, and *Lactococcus*).
- Microbes likely gain access to the womb through ascension from the vagina and/or through the blood stream for bacteria of intestinal or oral origin.

Vagina

- Vaginal microbial communities vary significantly among women of different ethnicities and could influence which microbes are transferred to an infant.
- The vaginal microbiota becomes less diverse during pregnancy while certain *Lactobacillus* species become enriched.
- The initial microbiota of vaginally-born infants resembles that of their mother's vagina, while that of C-section infants is dominated by skin microbes not related to those of their mother.

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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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NATURE IMMUNOLOGY | ARTICLE

Lymphotoxin regulates commensal responses to enable diet-induced obesity

Vaibhav Upadhyay, Valeriy Poroyko, Tae-jin Kim, Suzanne Devkota, Sherry Fu, Donald Liu, Alexei V Tumanov, Ekaterina P Koroleva, Liufu Deng, Cathryn Nagler, Eugene B Chang, Hong Tang & Yang-Xin Fu

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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/>

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FMT and Inflammatory Bowel Disease

BY KRISTINA CAMPBELL ON FEBRUARY 19, 2015 · (0)

Kristina Campbell is a science writer specialising in microbiota. She writes regularly for Gut Microbiota for Health and blogs at The Intestinal Gardener. Scientists now know that the gut microbiota – the microorganisms found in the human gastrointestinal tract – have... [Read More](#)



All disease begins in the gut.
- Hippocrates

Are Antibiotics Causing a Microbiome Mass Extinction?



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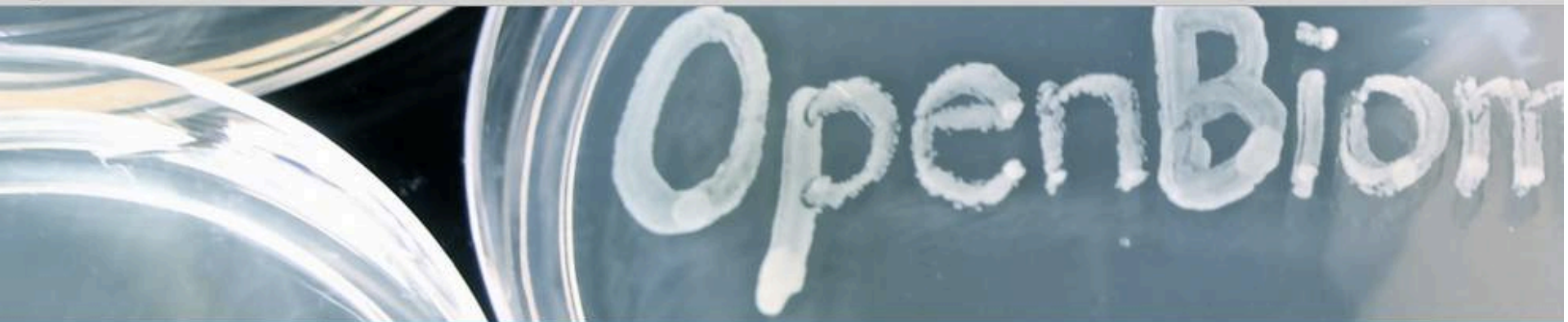
Sam's Story

BY SAMS MOTHER ON FEBRUARY 9, 2015 · (3)



Sam's mother writes this story on behalf of her 7 year old son who has recovered from Inflammatory Bowel Disease – Autistic enterocolitis, using fecal transplant. Where do you live? Michigan, USA What percentage recovered are you? 80% What was your

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



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.

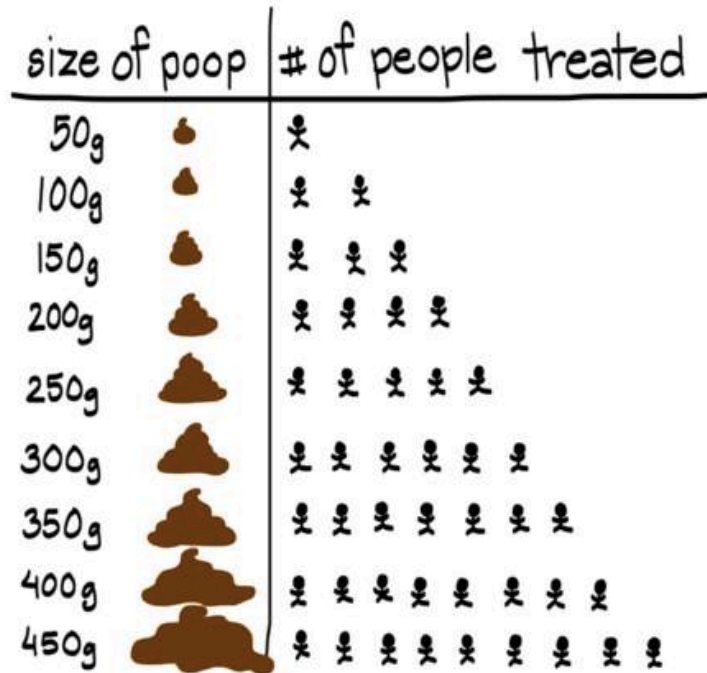
Why we're here

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



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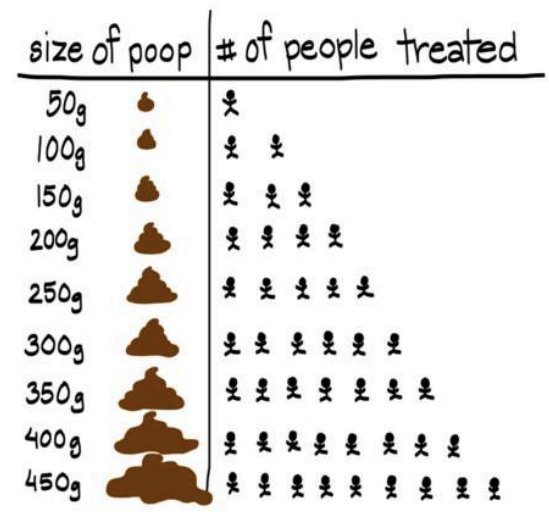
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NATURE | COMMENT



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.

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(2)

Microbiome

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Microscopic amounts of infected fecal matter can contaminate an entire pool or hot tub and make others sick if they swallow the water

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**HEALTH ADVISORY:
Avian Flu (H7N9) in China**

Updated information at
www.cdc.gov/travel









"FEAR is the main source of **SUPERSTITION,**

and one of the main sources of *crue*lty.



To conquer fear is the beginning of **wisdom.**"

– Bertrand Russell

~~FEAR~~

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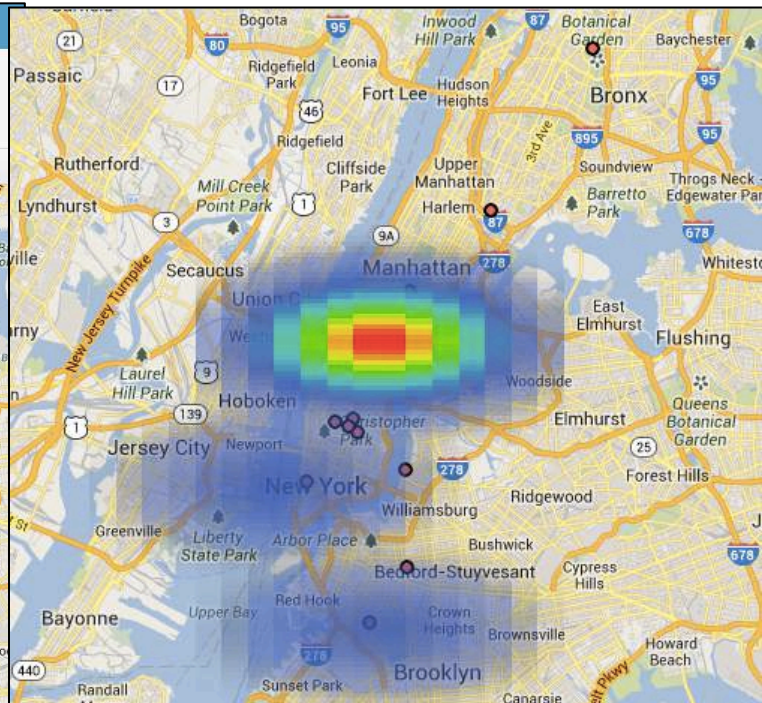
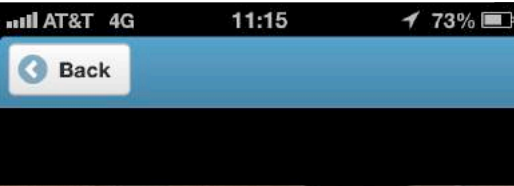




(3)

City-scale
metagenomics

Pathomap



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

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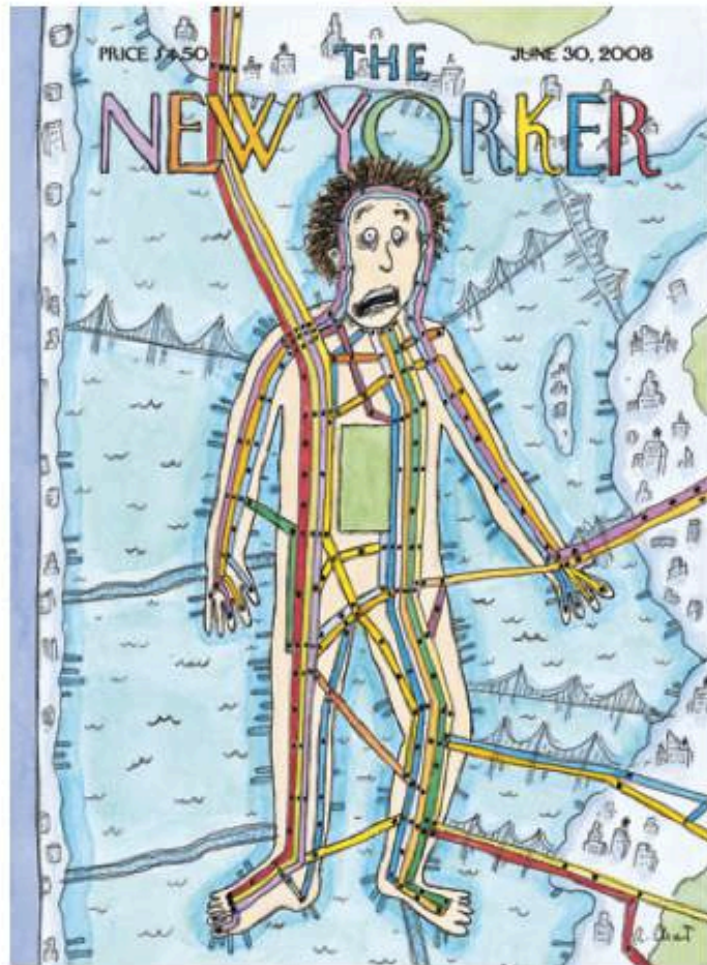
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When Weill Cornell Medical College genomicist Chris Mason would drop his 6-month-old daughter off at day care in 2011, he'd encounter more than a room filled with active toddlers. He'd step into a microbial nightmare. "Seeing how they all shared toys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

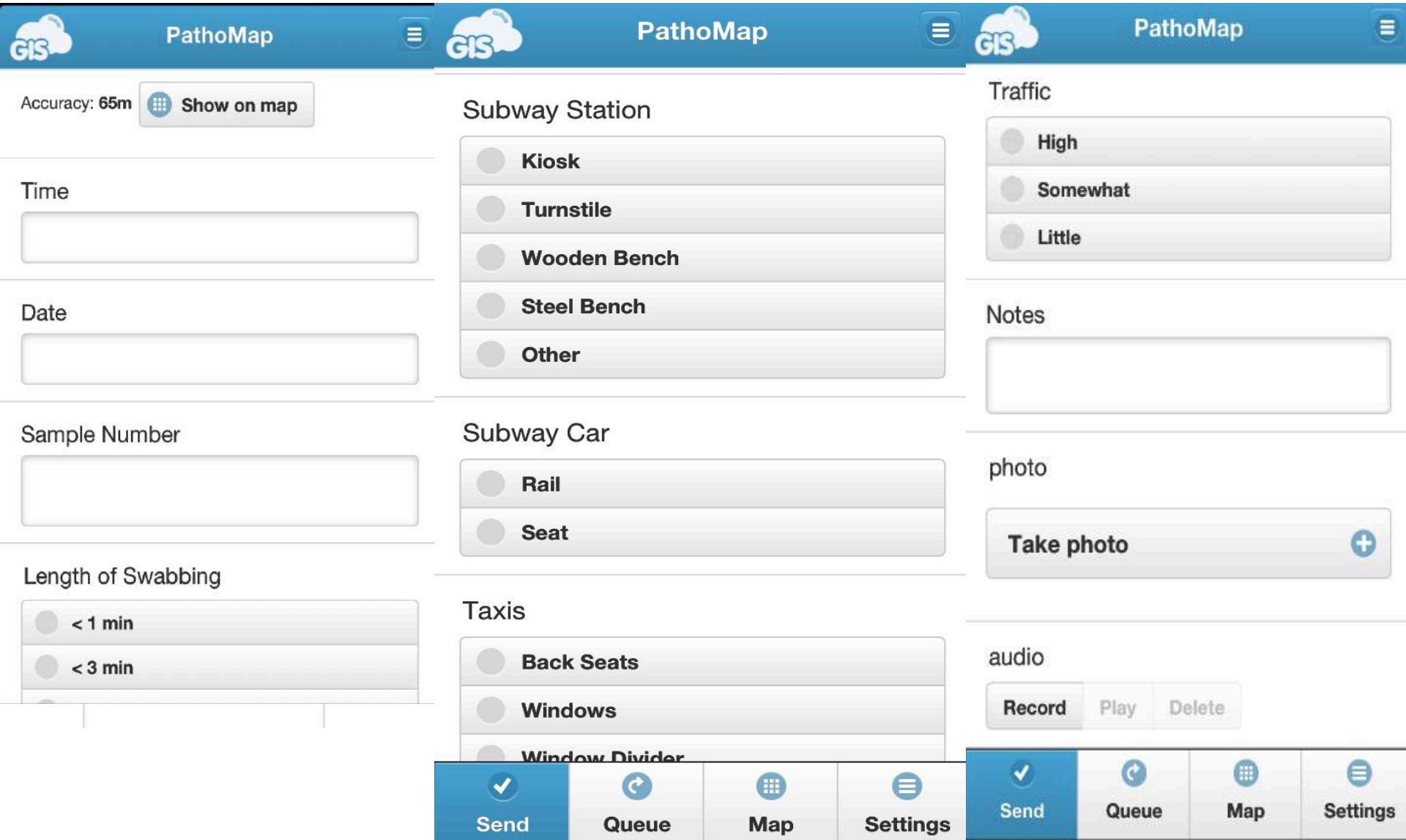
Mason learned that there was an ongoing day-care microbiome project, led by researchers at Drexel University and Brooklyn College. But he didn't necessarily want to study just the day care's microbiome. Rather, the experience sparked a bigger idea: Mason wondered if he could explore the bacterial microbiome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

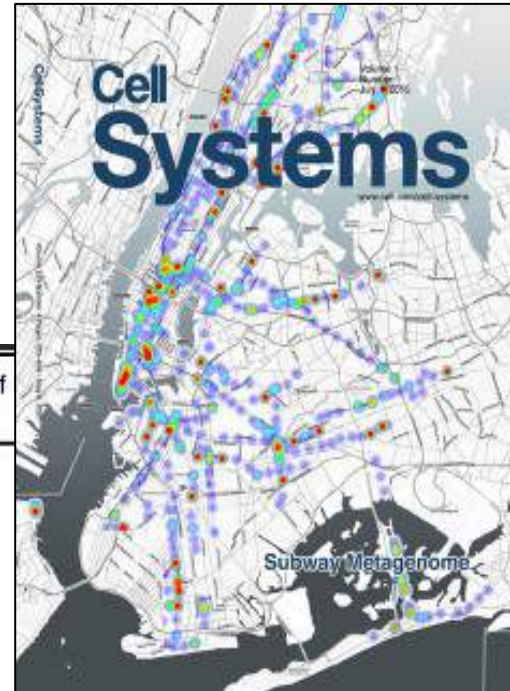
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First city-scale metagenome profile



Please cite this article in press (2015), <http://dx.doi.org/10.1016/j.chom.2015.02.001>

Resolution of

Metagenomics, CELS

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Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics

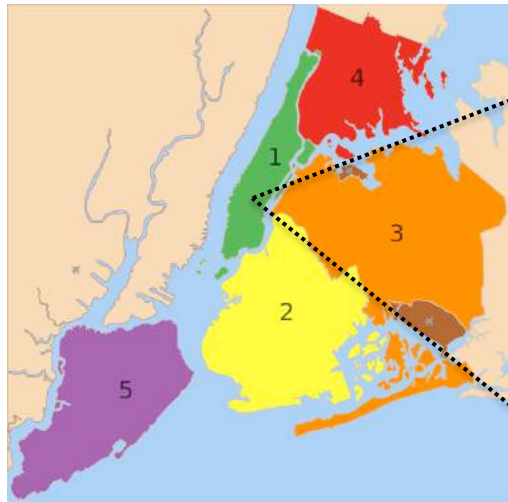
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1,427 samples from the NYC Subway:

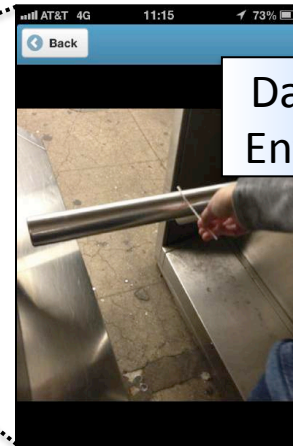
5.5 million riders/day

656 miles

468 stations

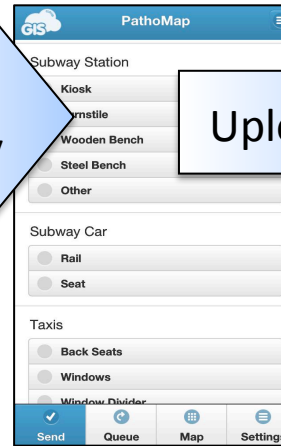


1. Swab (3 min)



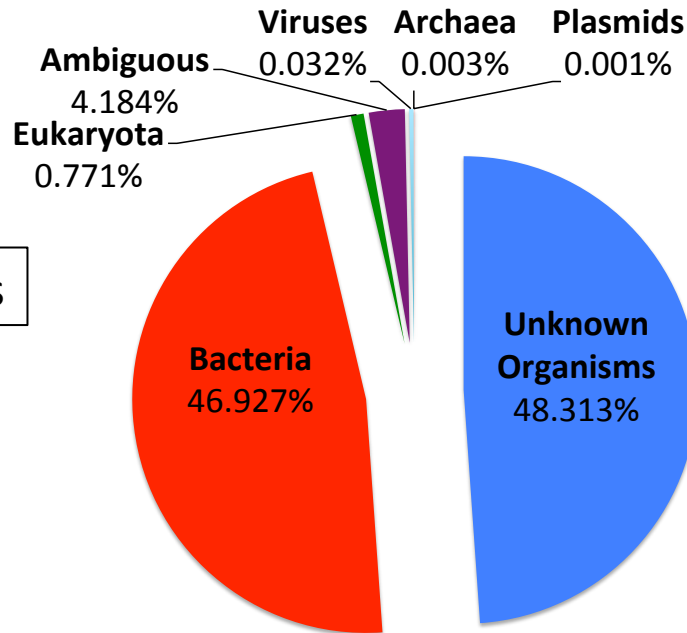
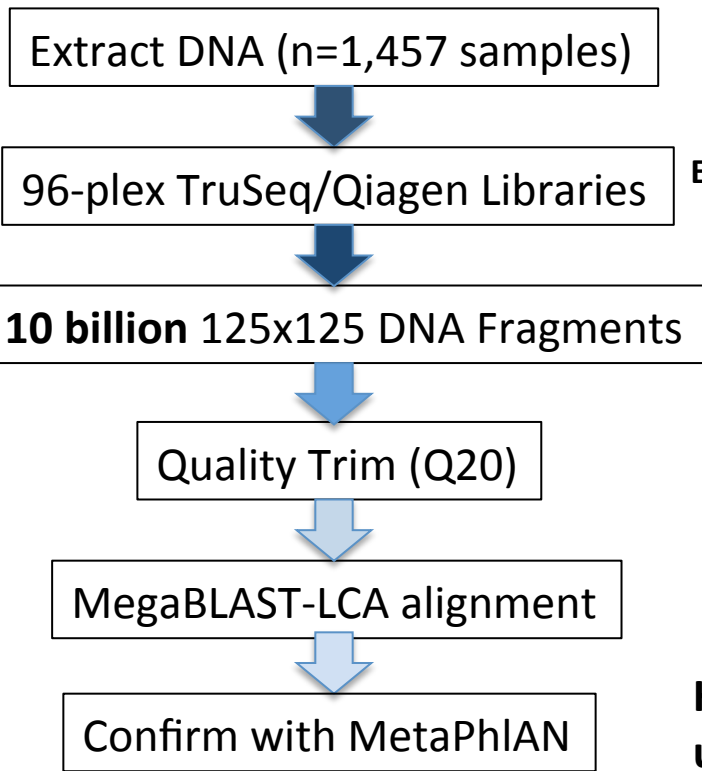
Data Entry

2. Annotate

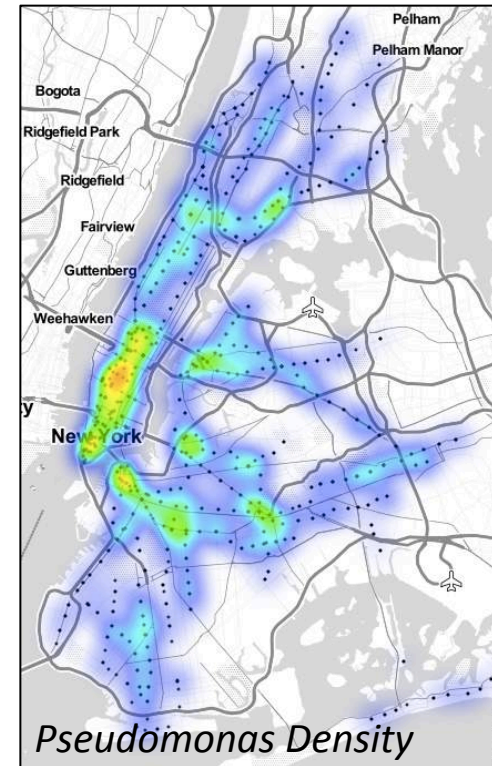


Upload

3. GPS-tag/timestamp



Half of the world under our fingertips is unknown



Explore by station

Explore by bacteria type

FIND A STATION:

Times Square-42nd St, Theater District (A, C, E, ...)

Where Certain Types of Bacteria Were Found

Select a category below to see the stations where researchers found the associated types of bacteria.

Antibiotic resistance Diarrhea Dysentery

Food poisoning Heart-valve infections

Italian cheese **Kimchi and sauerkraut**

Leuconostoc citreum

CLOSE X

Associated with **Kimchi and sauerkraut**

A species called *Leuconostoc citreum* is widely used in the fermentation of the Korean dish kimchi and is also used to ferment cabbage to make sauerkraut.

Medical-device infections Meningitis

Mozzarella cheese Oil cleanup

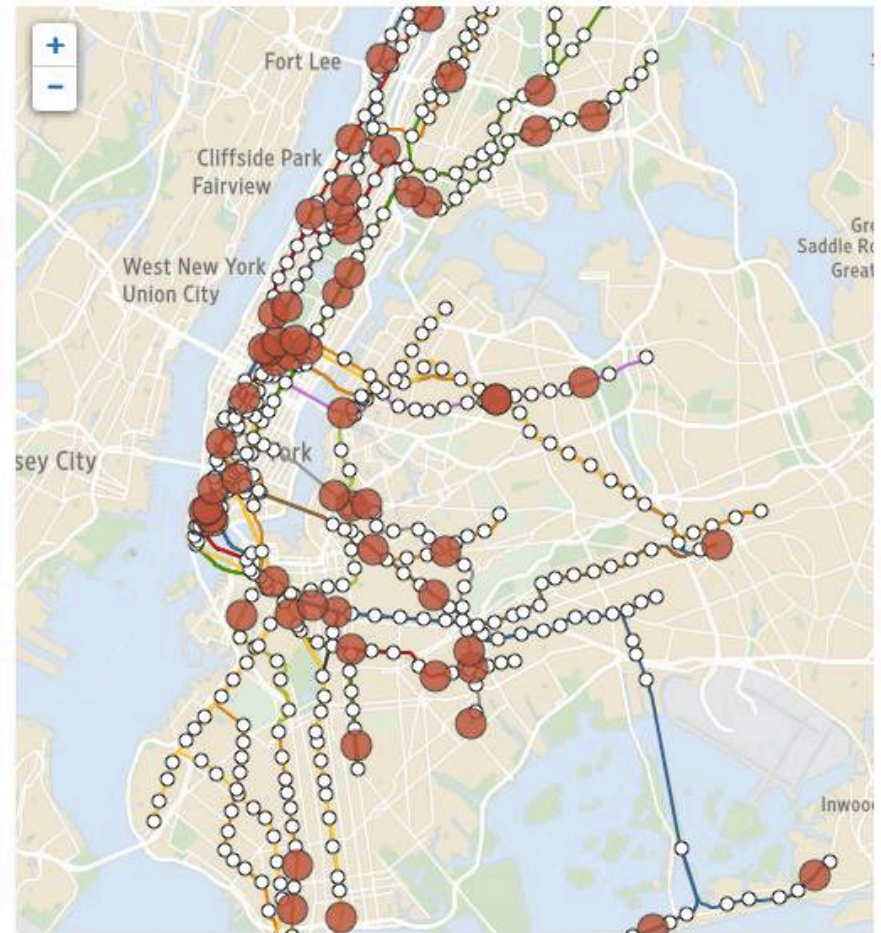
Radiation resistance Respiratory ailments

Sepsis Staph infections Sunscreen

Swiss cheese Tetanus Toxic cleanup

Urinary-tract infections

Share this view:  



Pseudomonas putida can help absorb chemicals

Explore by station

Explore by bacteria type

Share this view:



FIND A STATION:

Times Square-42nd St, Theater District (A, C, E, ...)

Where Certain Types of Bacteria Were Found

Select a category below to see the stations where researchers found the associated types of bacteria.

Antibiotic resistance

Diarrhea

Dysentery

Food poisoning

Heart-valve infections

Italian cheese

Kimchi and sauerkraut

Medical-device infections

Meningitis

Mozzarella cheese

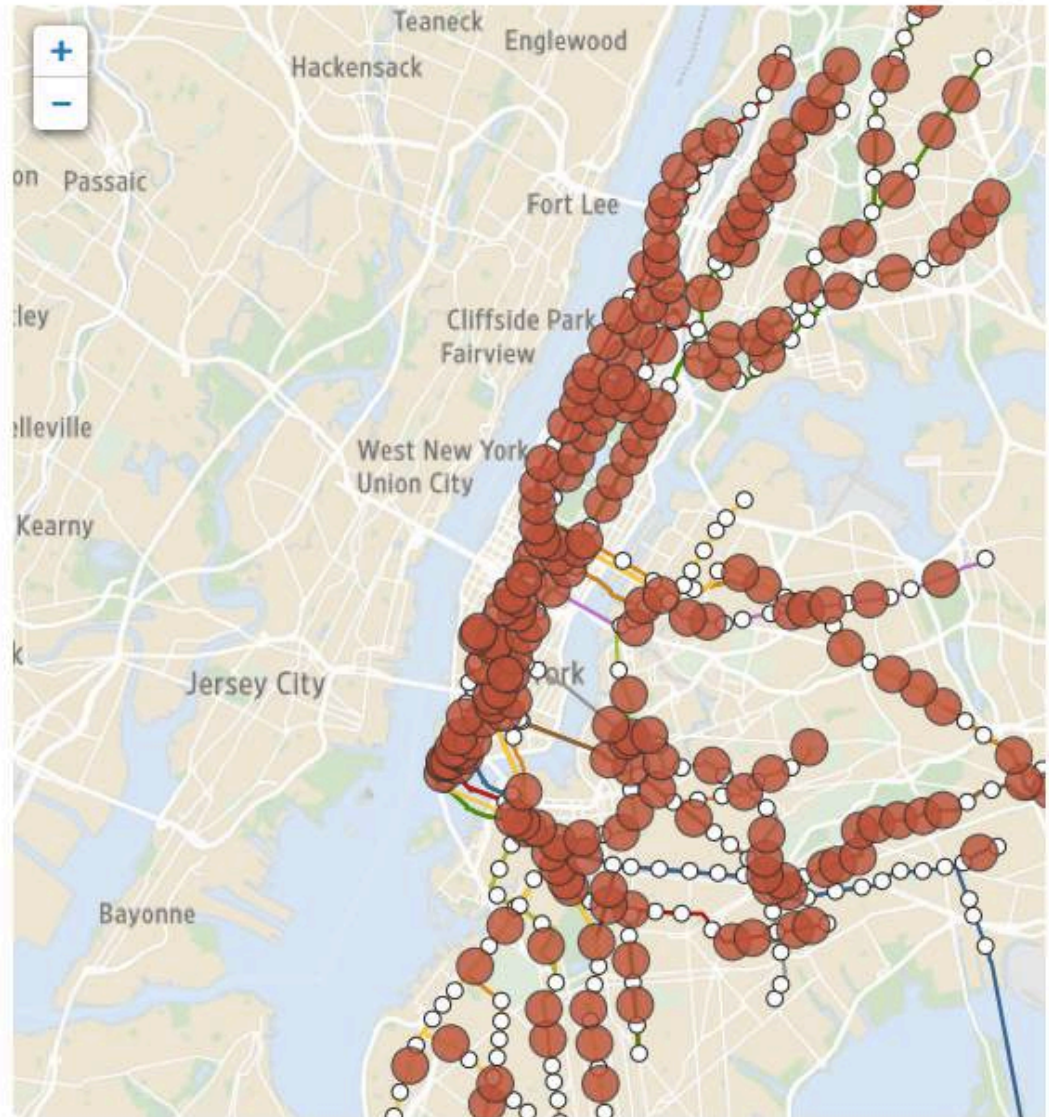
Oil cleanup

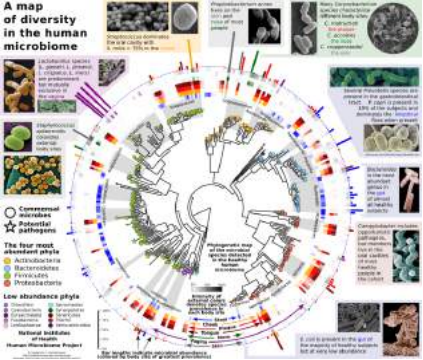
Pseudomonas putida

Associated with **Oil cleanup**

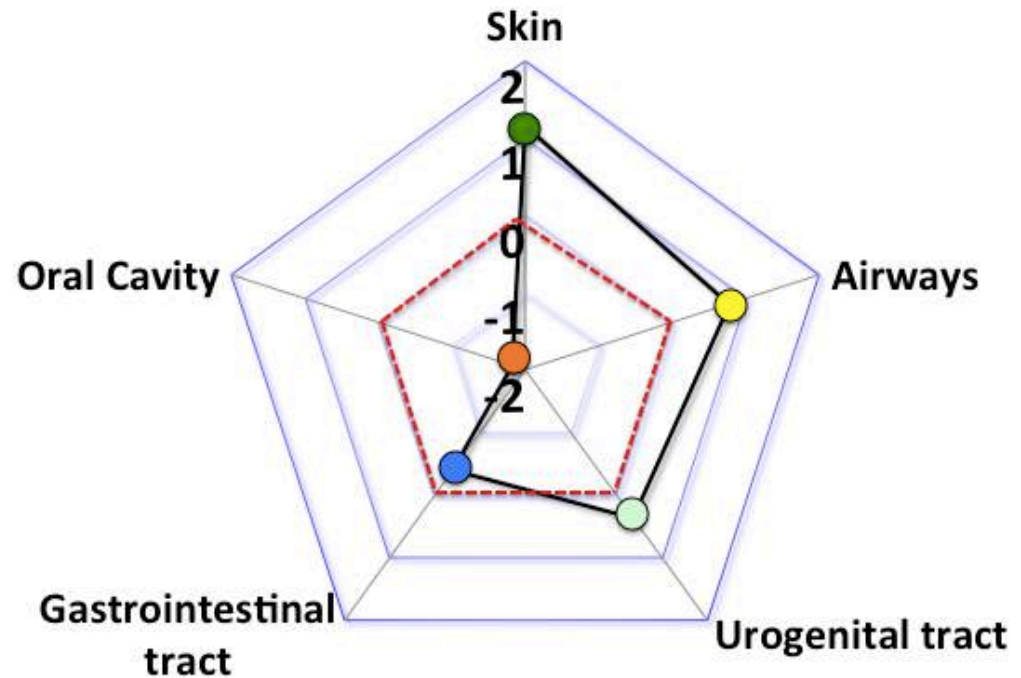
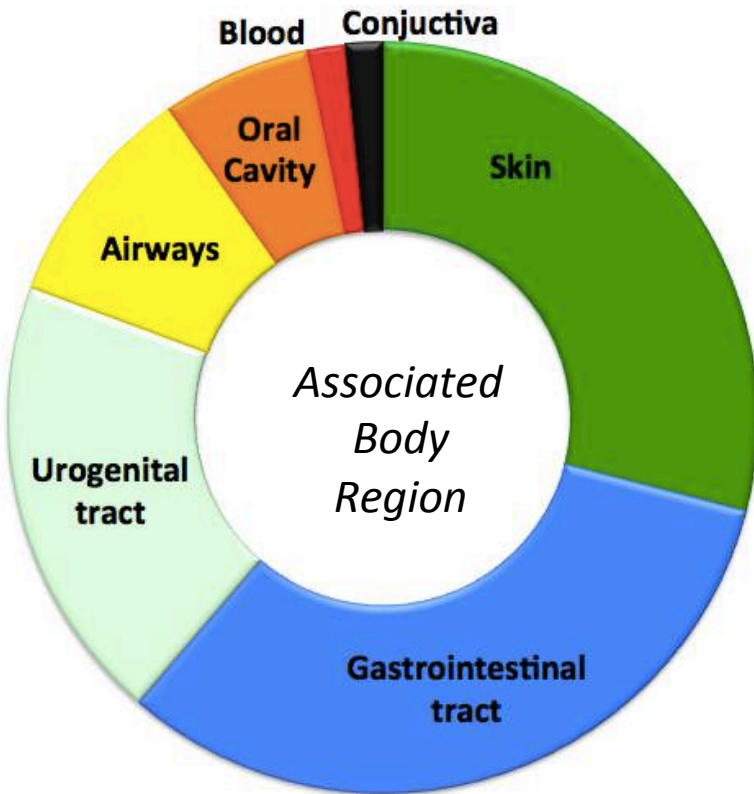
A bacteria species called *Pseudomonas putida* can break down organic pollutants such as toluene and oil. It is the first patented organism in the world, and, because the bacteria are living creatures, the patent was fought all the way up to the U.S. Supreme Court. Some strains can live on pure caffeine.

CLOSE X





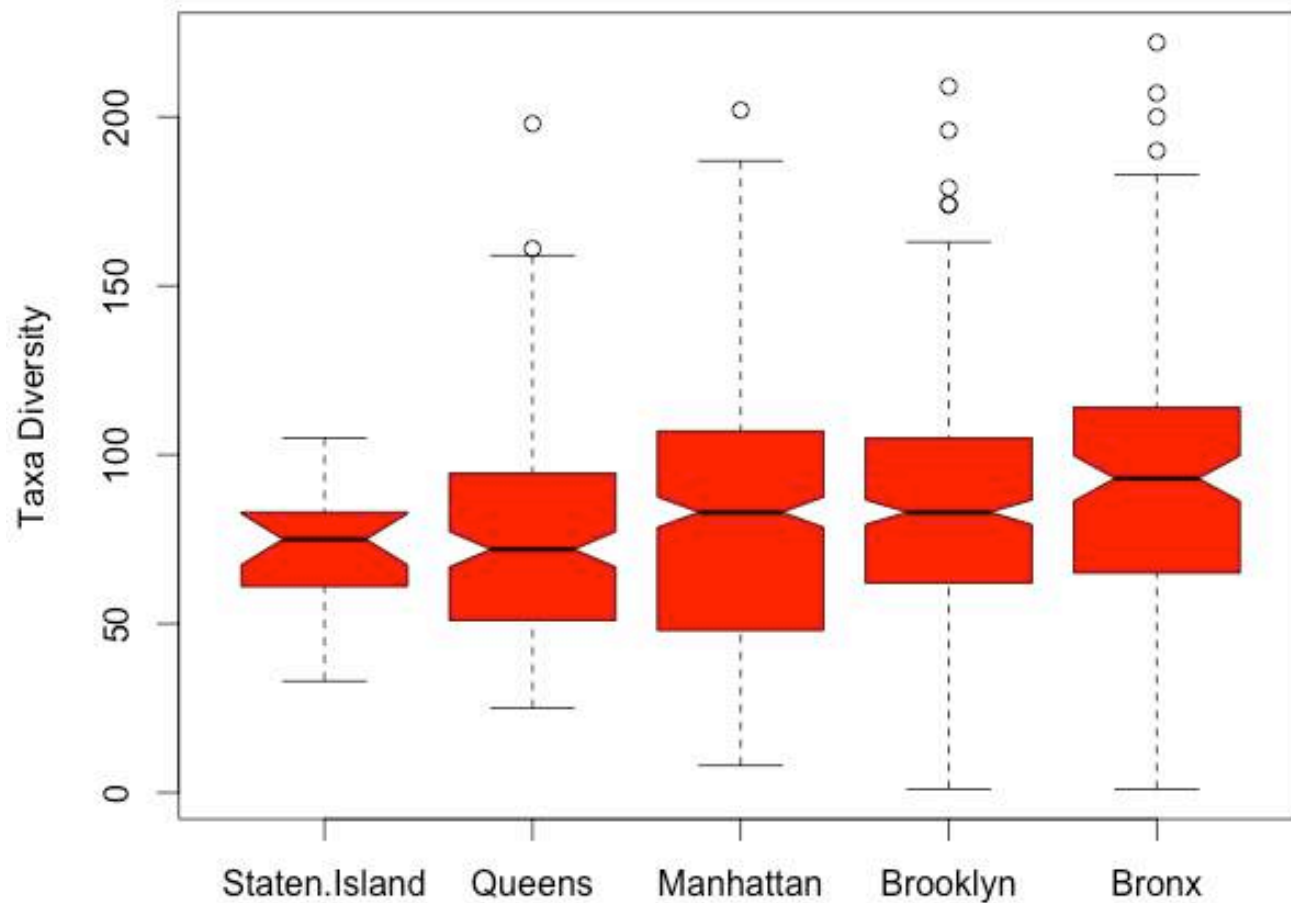
HMP Comparison Shows That the Subway “Looks Like Skin”



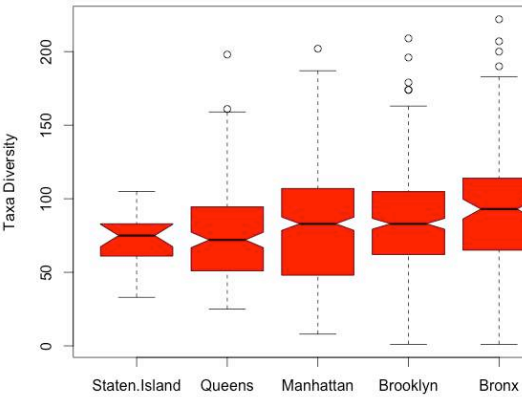
Staphylococcus epidermidis
Staphylococcus aureus
Acinetobacter radioresistens
Propionibacterium acnes

Log₂ Ratio of (Observed/Expected)

The Bronx is the most diverse!
Brooklyn comes in at #2.



This makes some sense



>600 species
ride the
subway
with you!

Mostly
harmless.

Pathogenicity
markers
absent.



Corynebacterium glutamicum

The stairwell at the **Eighth Avenue L stop** housed this tiny helper in industrial amino-acid production. Researchers also see promise for its use in bioremediation: It removes arsenic from the environment.



Spingomonas wittiehii

Turnstiles at the **Bedford Avenue L** tested positive for this bacterium discovered by scientists two decades ago, in the Elbe River in Germany, and known for its ability to digest toxic compounds sometimes found in chemical spills.



Acinetobacter radioresistens

The MTA underground (namely **turnstiles**) harbors a bacterium so robust it can resist exposure to radiation. Scientists found it on the Mars *Odyssey* orbiter before liftoff and worry it could compromise future life-detection missions.



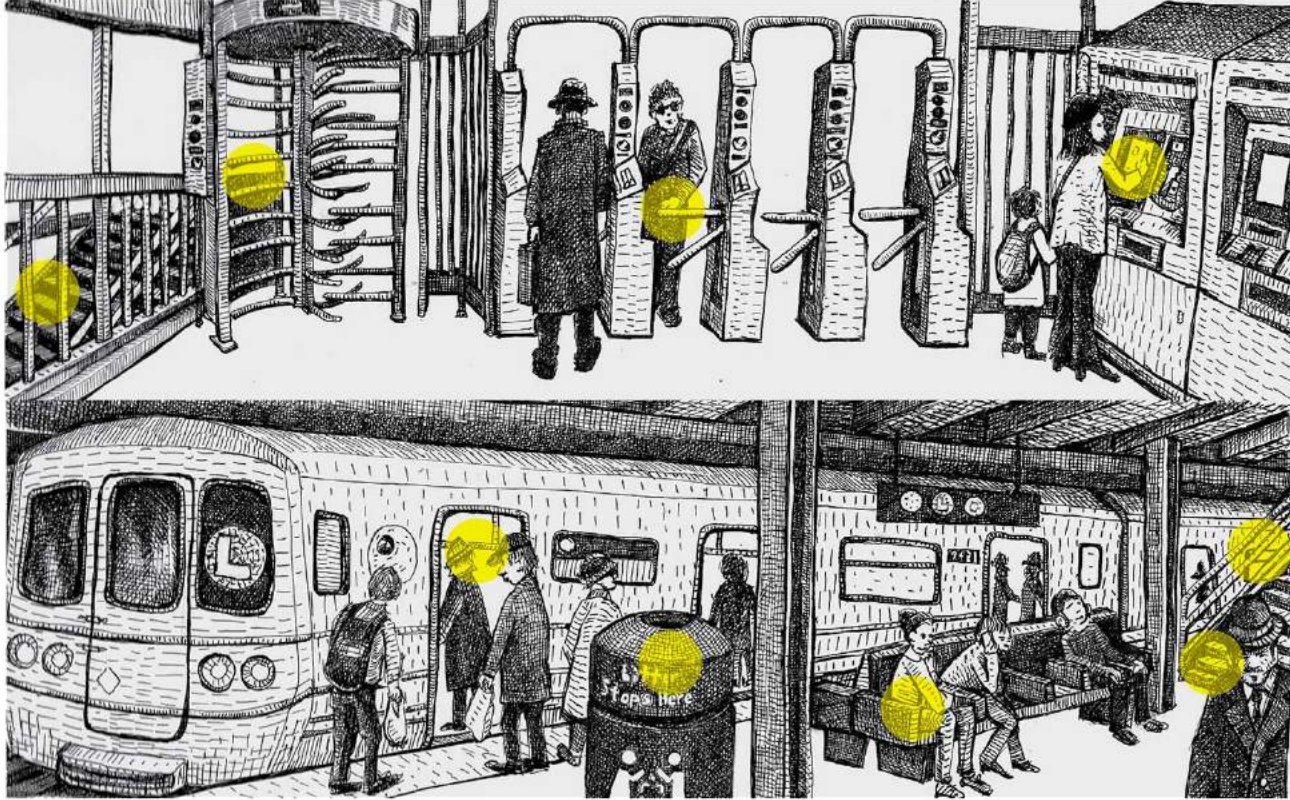
Laetobacillus sakei

A swab from a **Union Square turnstile** revealed this bacterium, which is related to the kind used to make yogurt; it's even been tested as a probiotic treatment for children with a form of the skin disease eczema.



Shigella boydii

Mason's team collected this germ, typically found in the Indian subcontinent, from a **Bedford Avenue kiosk**. It belongs to a genus of bugs responsible for shigellosis, a diarrheal disease that infects up to 800 people a year in New York State.



Lysinibacillus sphaericus

Several samples, including one from a **7 train handrail**, carried a microbe used to fight insect-borne disease; it produces a toxin that kills mosquito larvae—a useful defense against malaria and West Nile virus.



Aerococcus viridans

This bug, found on a **Beverly Road garbage can**, among other sites, preys upon weakened immune systems, has been linked to the heart disease endocarditis, and causes gaffkemia, a fatal disease for lobsters.



Exiguobacterium sibiricum

Found on a **Bedford Avenue bench**, *Exiguobacterium sibiricum* was named for Siberia, where researchers first detected it in a permafrost sample that dates back as far as 3 million years.



Enterococcus faecalis

Mason discovered this bacterium, usually found in fecal matter, in several high-traffic areas, like a **Times Square handrail**. It's behind urinary-tract infections and hospital-acquired illnesses that now show antibiotic resistance.



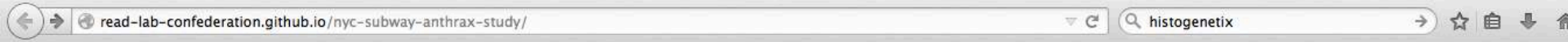
Bacillus megaterium

Doctors worldwide have this inhabitant of the **Eighth Avenue L stairwell** to thank: It produces key enzymes used to make synthetic penicillin and to test blood-glucose levels in diabetics.

Anthrax-specific fragments found by Kraken, MetaPhlAn, SURPI, BWA.

But scant pXO, no PlcR.

No strong evidence of *pathogen*. Organism is different from pathogen.



Searching for anthrax in the New York City subway metagenome.

April 23, 2015

Robert A Petit III Matthew Ezewudo Sandeep J. Joseph Timothy D. Read

Study	Number of matched 31-mers with Anthrax 31-mers
SRR1749083	0
SRR1748708	2
SRR1748707	0

Table 13: Annotated 31-mers mapped to SRR1748708.

Anthrax-specific K-mers identified from the NYC subway system SRR1748708 sample.

SNP position on the <i>B. anthracis</i> Ames ancestor genome	31-mer sequence	Number of matches
4083672	TGTGCCCATCCTGAGCATACAACCTTTATAA	2
4136672	ACATAGAACAAGTGACATTCTATCAAACGGT	2

Introduction

In January 2015 Chris Mason and his team published an in-depth analysis of metagenomic data (environmental shotgun DNA sequence) from samples isolated from public surfaces in the New York City (NYC) subway system. Along with a ton of really interesting findings, the authors claimed to have detected DNA from the bacterial bioterror pathogens *Bacillus anthracis* (which causes anthrax) and *Yersinia pestis* (causes plague) in some of the samples. This predictably led to a huge interest from the press and scientists on social media. The authors followed up with a re-analysis of the data on microbe.net, where they showed some results that suggested the tools that they were using for species identification overcalled anthrax and plague.

B. anthracis is a Gram-positive bacterium that forms tough spores as part of its lifecycle. The 5.2 M basepair (Mb) main chromosome is very similar to those of other bacteria in species informally called the '*Bacillus cereus* group' (including *B. cereus*, *B. thuringiensis* and *B. mycoides*). *Bacillus cereus* group strains in general are commonly found in soil but *B. anthracis* itself is very rare and generally associated with livestock grazing sites with a past history of anthrax.

What sets *B. anthracis* apart from close relatives is the presence of two plasmids: pXO1 (181kb), which carries the lethal toxin genes and pXO2 (94kb), which includes genes for a protective capsule. Without one of these plasmids, *B. anthracis* is considered attenuated in virulence and unable to cause classic anthrax. Other *B. cereus* group bacteria can have plasmids very similar to pXO1 and pXO2 but missing the important virulence genes. Rarely, other *B. cereus* group carry pXO1 and appear to cause anthrax-like disease. It's a confusing situation, not helped by the current overly-narrow species definitions. This recent review gives more information.

<http://read-lab-confederation.github.io/nyc-subway-anthrax-study/>

(4)

'molecular
echoes'

Some areas are more stable: Gowanus Canal

The Bell House

Search nearby: (hotels-restaurants)

The Bell House
149 7th St
Brooklyn, NY 11215
Open today 5:00 pm – 4:00 am

Directions Save

thebellhouseeny.com
(718) 643-6510

Street View 13 Photos

4.1 ★★★★★ 103 reviews · Menu · \$\$ · Bar

Big-name acts & up-and-comers play at this big bar/performance venue set in a former warehouse. - Google

Write a review · Add a photo

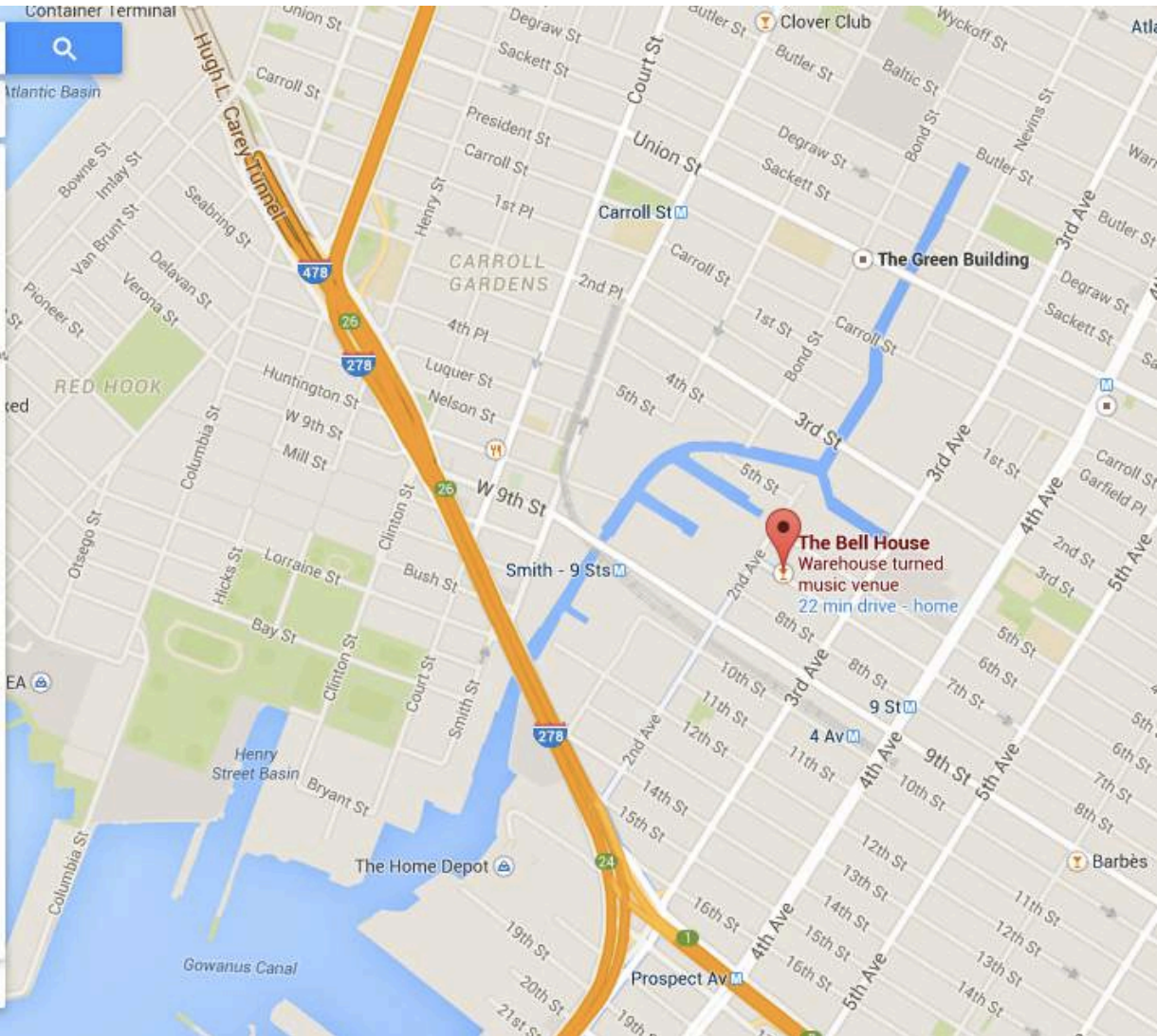
"Huge bar up front, huge performance space in back, nice outdoor patio."
15 reviewers

"Their **selection** of beer on tap made me feel like a kid in candy store."
2 reviewers

"Cool place for **comedy** club nights."
2 reviewers

Suggest an edit

Featured by Zagat





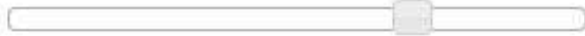
Man Swims In Gowanus Canal, Concludes "It's Not Safe To Swim In There"



Apr. 22
2015

Heatmap Data

Heatmap opacity: 70%



Heatmap radius: 25



Auto-scale radius on zoom

Fixed radius

Color scaling: 0 - 50

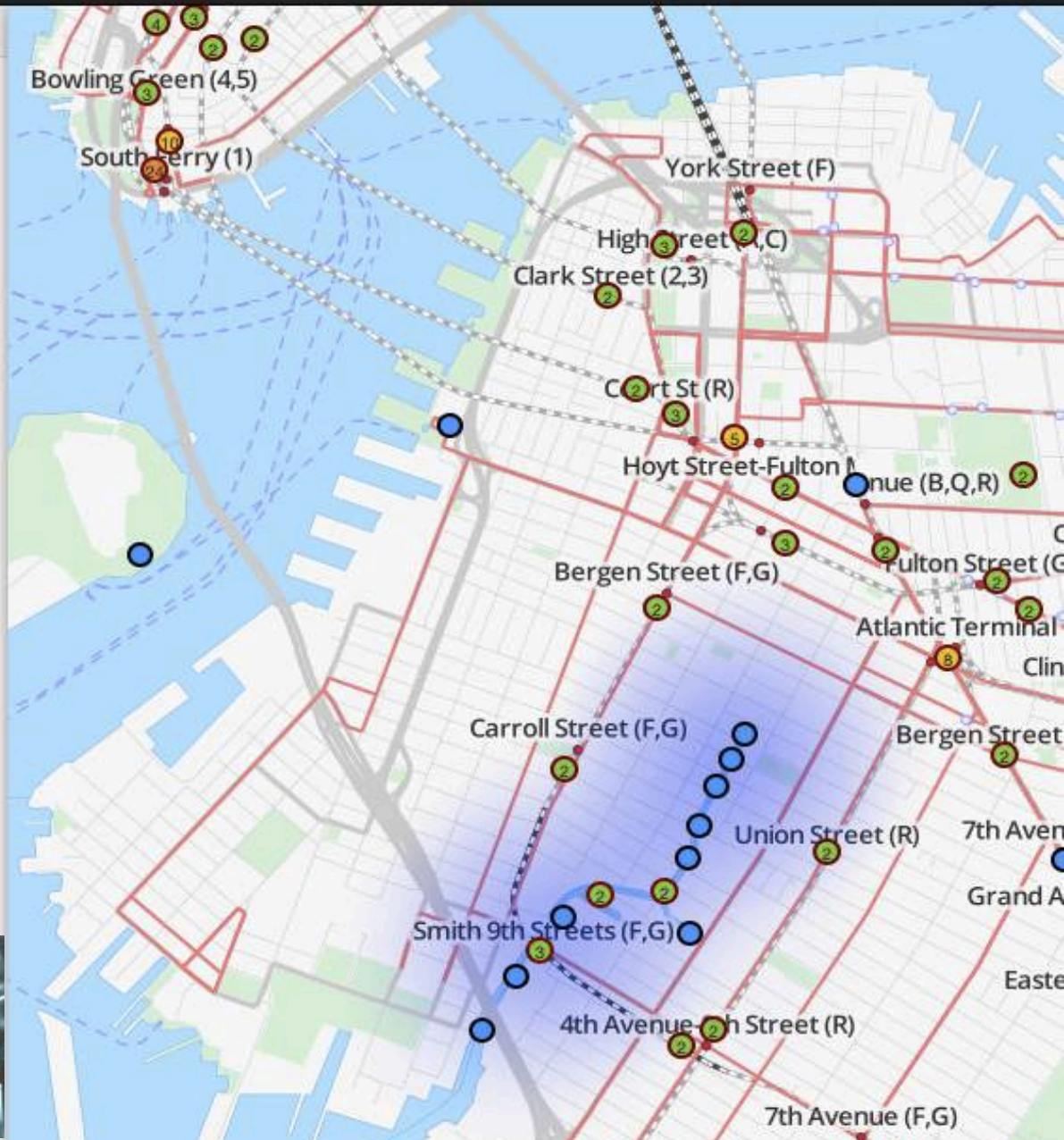
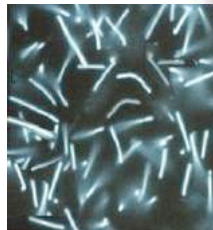


Auto-scale colors

Fixed colors

Organism

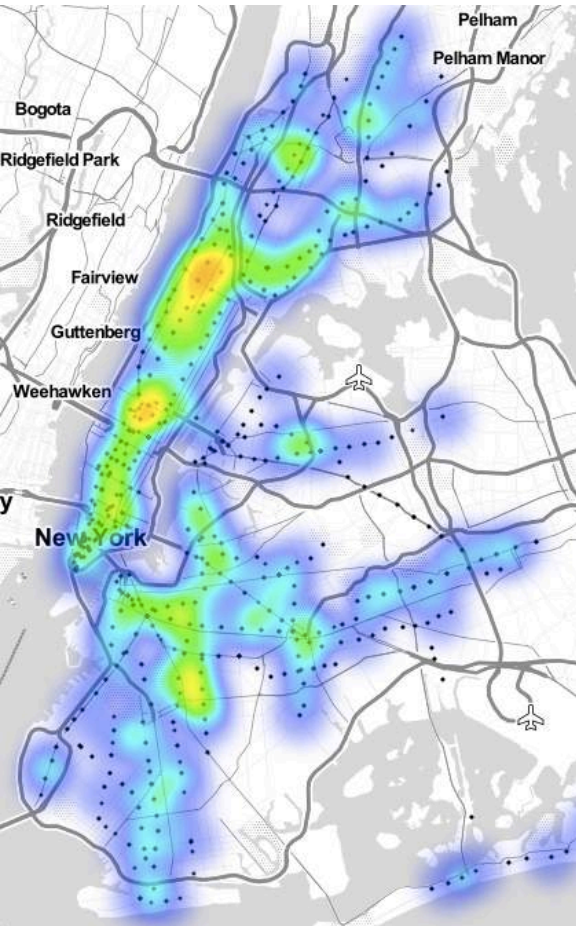
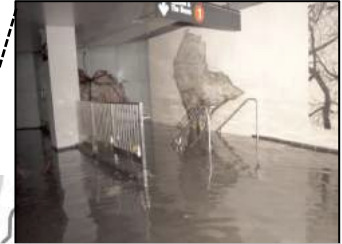
- None
- Archaea
 - Euryarchaeota
 - Methanobacteria
 - Methanobacteriales
 - Methanomicrobia
 - Methanomicrobiales
 - Methanosarcinales
 - Bacteria
 - Eukaryota
 - Ascomycota
 - Basidiomycota
 - Viruses



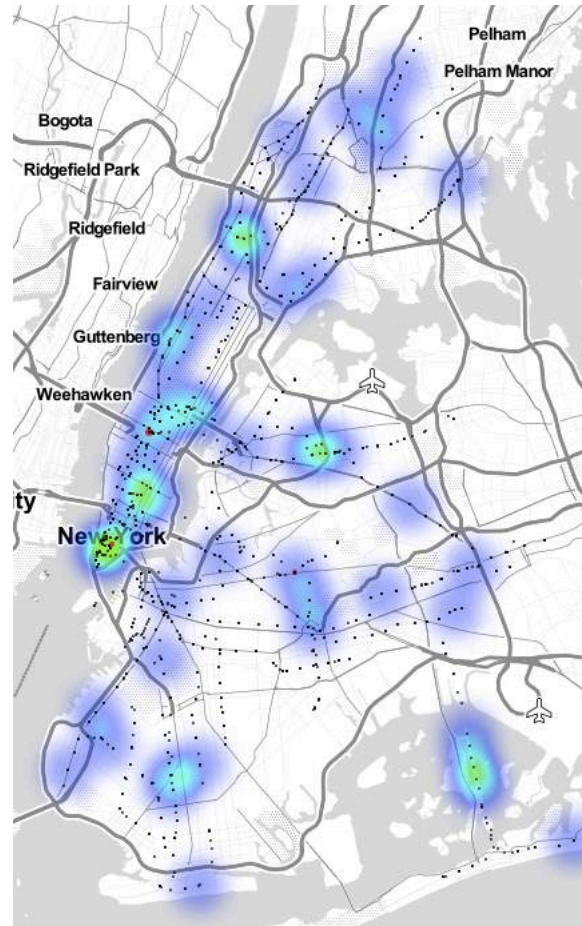
Gowanus Canal was a methanogen heaven

Species diversity varies by area of the city

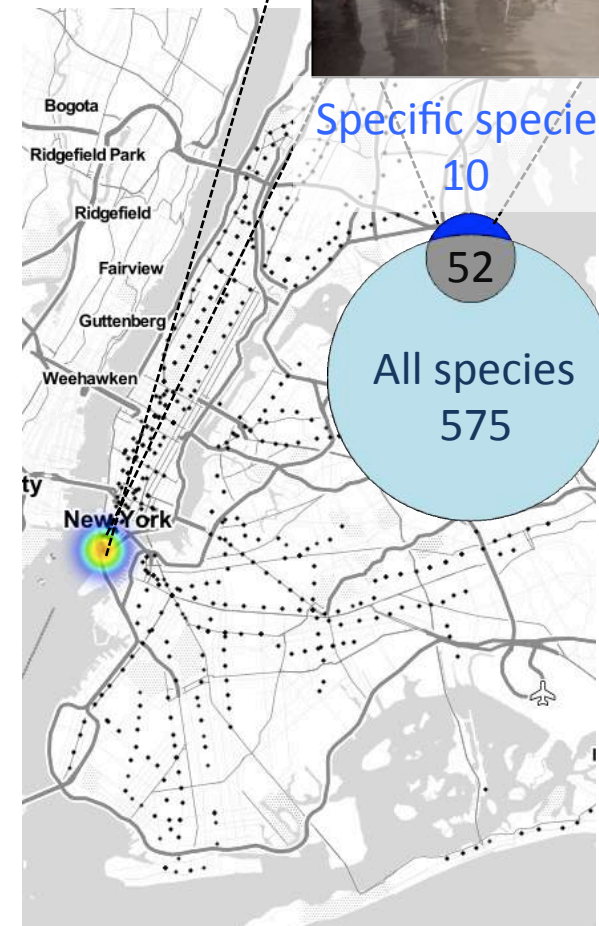
Hurricane-Flooded



Enterococcus faecium



Staphylococcus aureus



Pseudoalteromonas haloplanktis



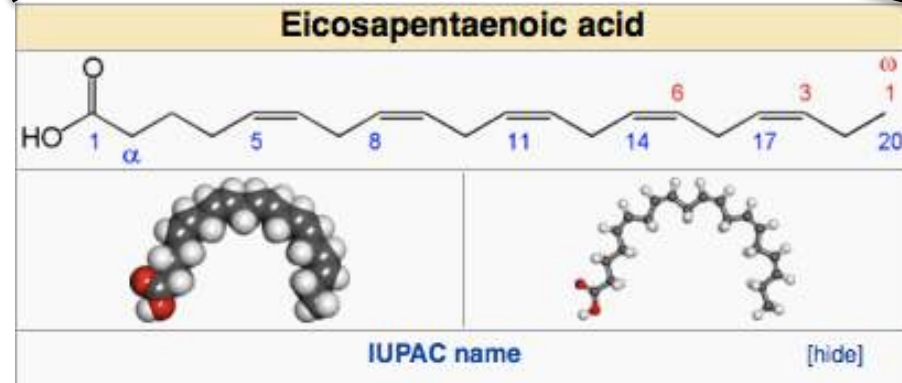
A persistent “molecular echo” of the cold, ocean water



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, salmon, menhaden and sardines.



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Biological Psychiatry
Volume 56, Issue 7, Pages 490–496, October 1, 2004

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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)

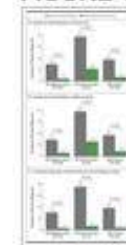
Metrics

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.

The Hygiene Hypothesis

The **hygiene hypothesis** is a **hypothesis** that states that a lack of early childhood exposure to infectious agents, symbiotic microorganisms (e.g. gut flora or probiotics), and parasites increases susceptibility to allergic diseases by suppressing the natural development of the immune system.

"Infants born by cesarean delivery are at **increased risk** of **asthma, obesity and type 1 diabetes**, whereas breastfeeding is variably protective against these and other disorders."

- Rob Knight



TEDBlog



Effects of early-life exposure to allergens and bacteria on recurrent wheeze and atopy in urban children

Susan V. Lynch, PhD,^{a*} Robert A. Wood, MD,^{b*} Homer Boushey, MD,^a Leonard B. Bacharier, MD,^c Gordon R. Bloomberg, MD,^c Meyer Kattan, MD,^d George T. O'Connor, MD,^e Megan T. Sandel, MD,^e Agustin Calatroni, MS,^f Elizabeth Matsui, MD,^b Christine C. Johnson, PhD,^g Henry Lynn, PhD,^f Cynthia M. Visness, PhD,^f Katy F. Jaffee, MS,^f Peter J. Gergen, MD,^h Diane R. Gold, MD, MPH,ⁱ Rosalind J. Wright, MD, MPH,ⁱ Kei Fujimura, PhD,^a Marcus Rauch, PhD,^a William W. Busse, MD,^j and James E. Gern, MDⁱ *San Francisco, Calif, Baltimore, Md, St Louis, Mo, New York, NY, Boston, Mass, Chapel Hill, NC, Detroit, Mich, and Madison, Wis*

Background: Wheezing illnesses cause major morbidity in infants and are frequent precursors to asthma.

Objective: We sought to examine environmental factors associated with recurrent wheezing in inner-city environments.

Methods: The Urban Environment and Childhood Asthma study examined a birth cohort at high risk for asthma (n = 560) in Baltimore, Boston, New York, and St Louis. Environmental assessments included allergen exposure and, in a nested case-control study of 104 children, the bacterial content of house dust collected in the first year of life. Associations were determined among environmental factors, aeroallergen sensitization, and recurrent wheezing at age 3 years.

Results: Cumulative allergen exposure over the first 3 years was associated with allergic sensitization, and sensitization at age 3 years was related to recurrent wheeze. In contrast, first-year exposure to cockroach, mouse, and cat allergens was negatively associated with recurrent wheeze (odds ratio, 0.60, 0.65, and 0.75, respectively; $P \leq .01$). Differences in house dust bacterial content in the first year, especially reduced exposure to specific Firmicutes and Bacteroidetes, was associated with atopy and

atopic wheeze. Exposure to high levels of both allergens and this subset of bacteria in the first year of life was most common among children without atopy or wheeze.

Conclusions: In inner-city environments children with the highest exposure to specific allergens and bacteria during their first year were least likely to have recurrent wheeze and allergic sensitization. These findings suggest that concomitant exposure to high levels of certain allergens and bacteria in early life might be beneficial and suggest new preventive strategies for wheezing and allergic diseases. (J Allergy Clin Immunol 2014;134:593-601.)

Key words: Asthma, atopy, allergen exposure, microbial exposure, inner city

Wheezing illnesses affect 35% to 50% of children by the age of 3 years^{1,2} and are a leading cause for outpatient visits and hospitalizations.^{3,4} Wheezing in nonatopic children is often transient, but recurrent wheezing in children with early allergic sensitization or other signs of atopy during the preschool years

Cockroaches are the best for young bodies?

596 LYNCH ET AL

TABLE III. Association between bedroom dust allergen expos

	No.	Unadjusted	
		Odds ratio (95% CI)	P value
Exposures (year 1)			
Cat	362	0.75 (0.61-0.92)	.005
Dog	359	1.01 (0.80-1.27)	.97
Cockroach	359	0.60 (0.45-0.80)	<.001
Mouse	366	0.65 (0.52-0.82)	<.001
Dust mite (<i>Dermatophagoides farinae</i>)	364	0.97 (0.78-1.20)	.78

(5)

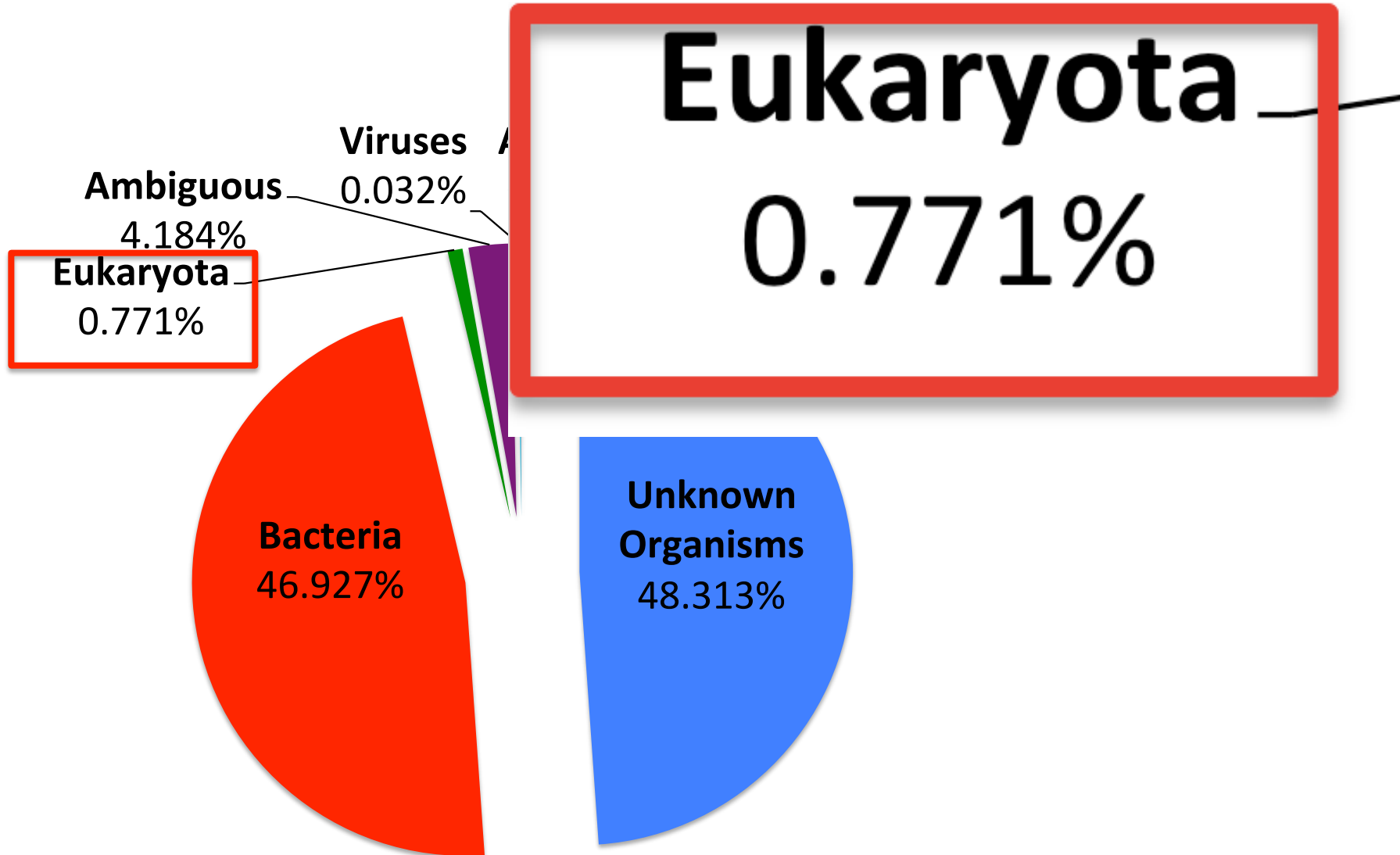
Other DNA left
behind?

Metagenomics

=

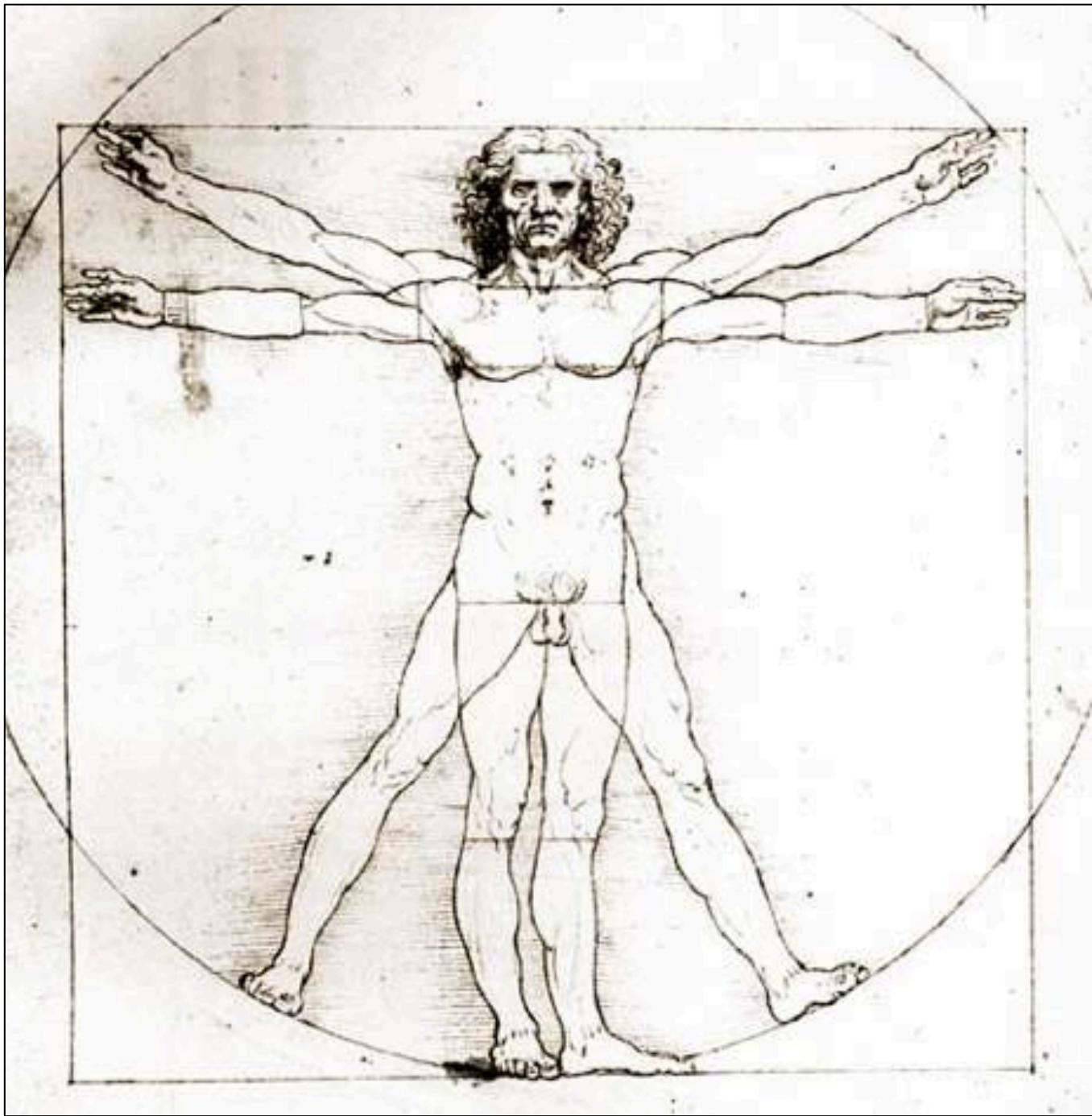
All kingdoms of life
and their DNA

What else is there?

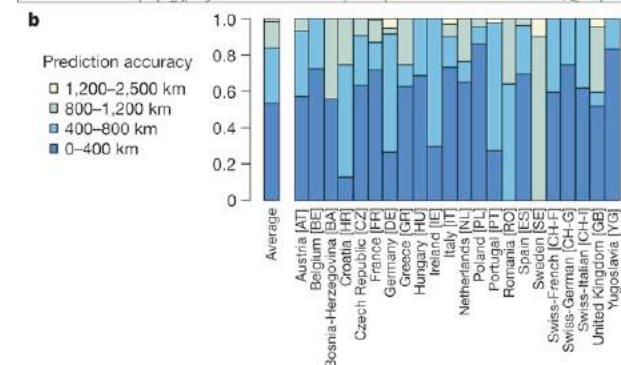
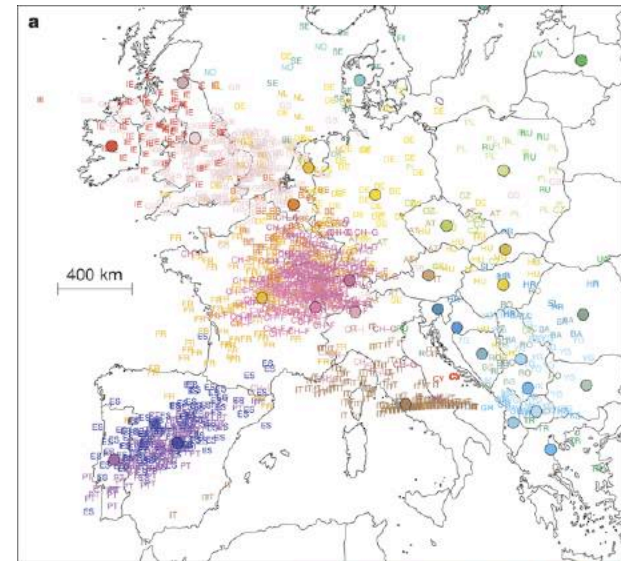
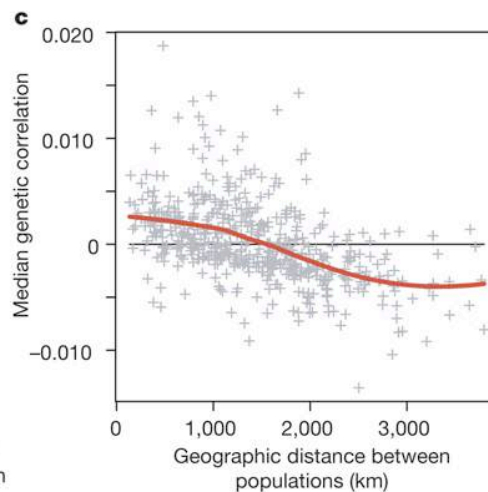
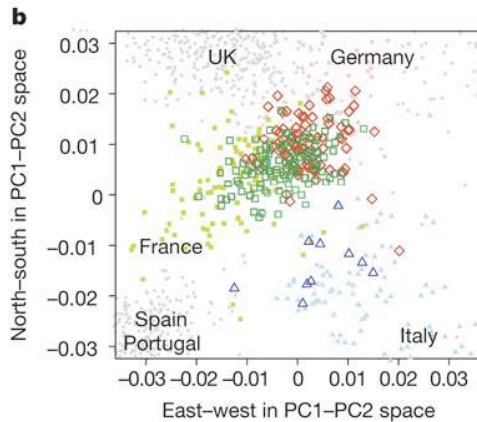
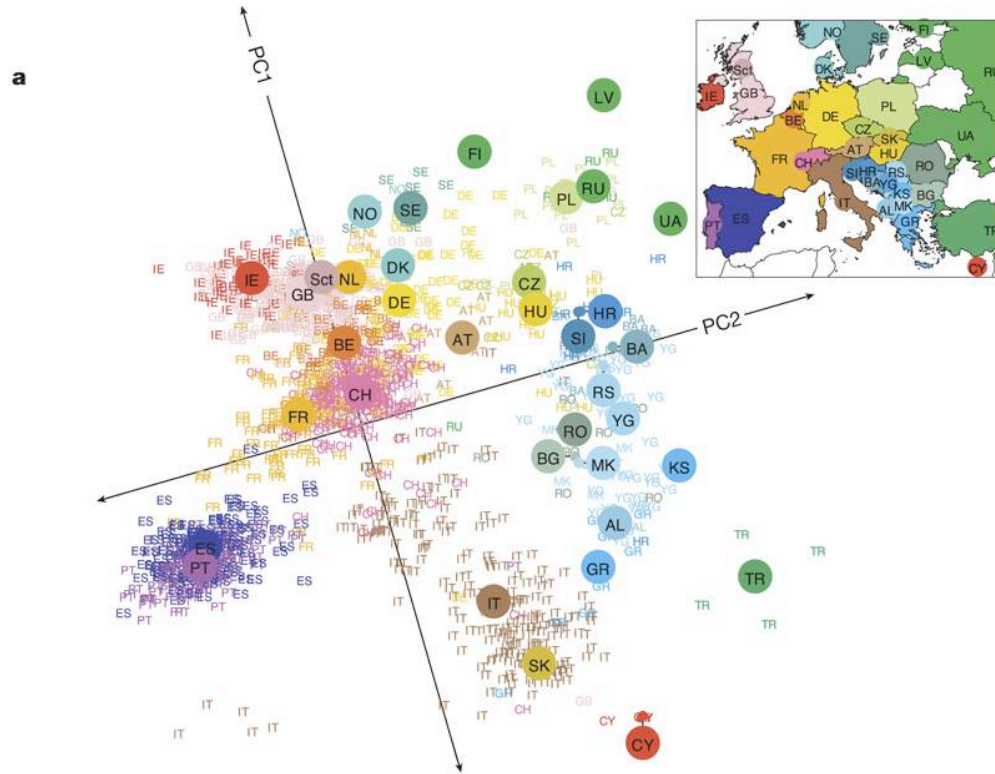


BLAST Results





Genotype data can predict your birthplace



Genes mirror geography within Europe
 Novembre *et al.*, 2008

Artist creates faces from DNA left in public

By Natalie Angley, CNN

updated 3:10 PM EDT, Wed September 4, 2013 | Filed under: **Innovations**

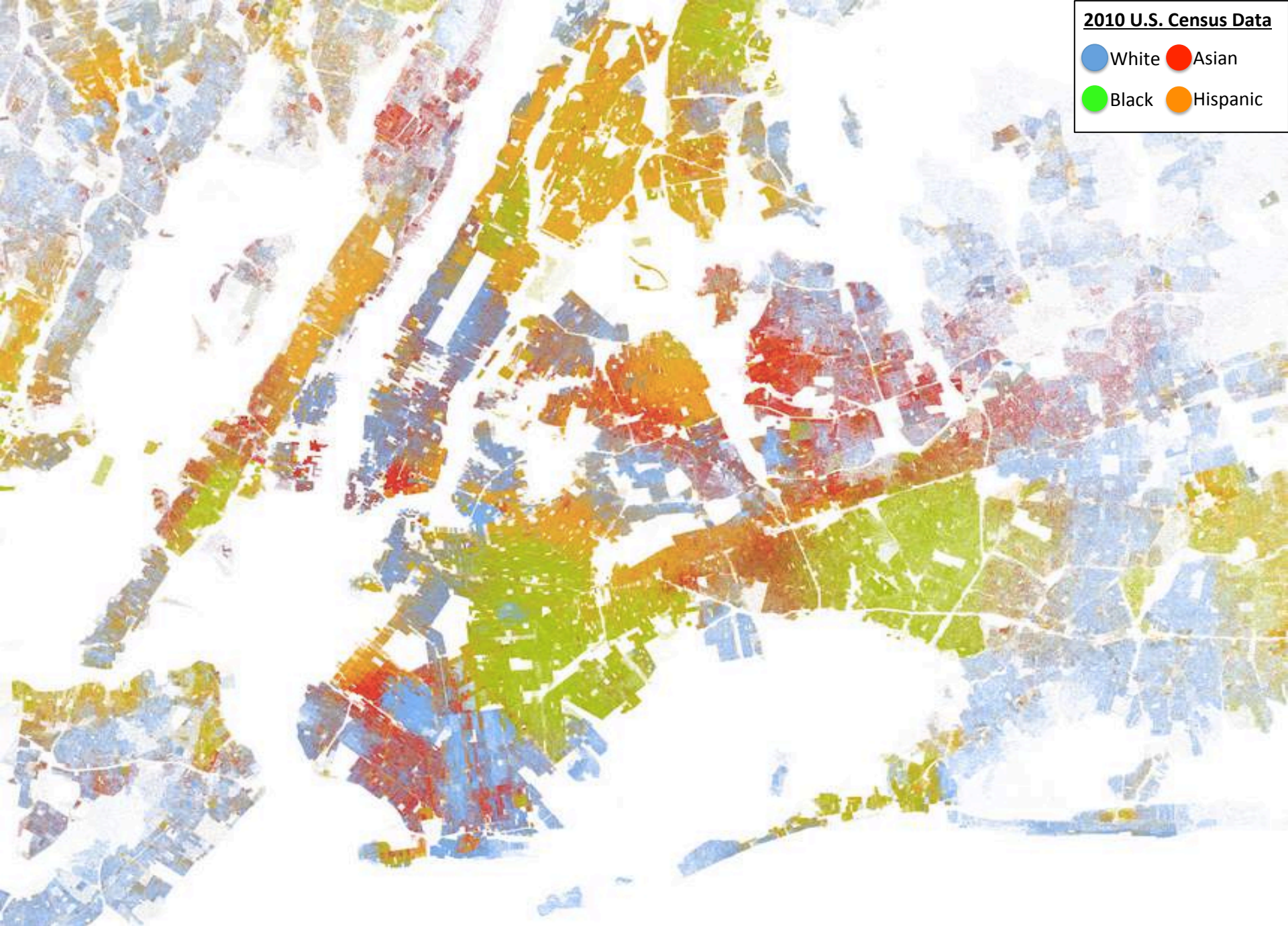


from **Heather Dewey-Hagborg's "Stranger Visions" at Genspace (Brooklyn)**

<http://www.cnn.com/2013/09/04/tech/innovation/dna-face-sculptures/>

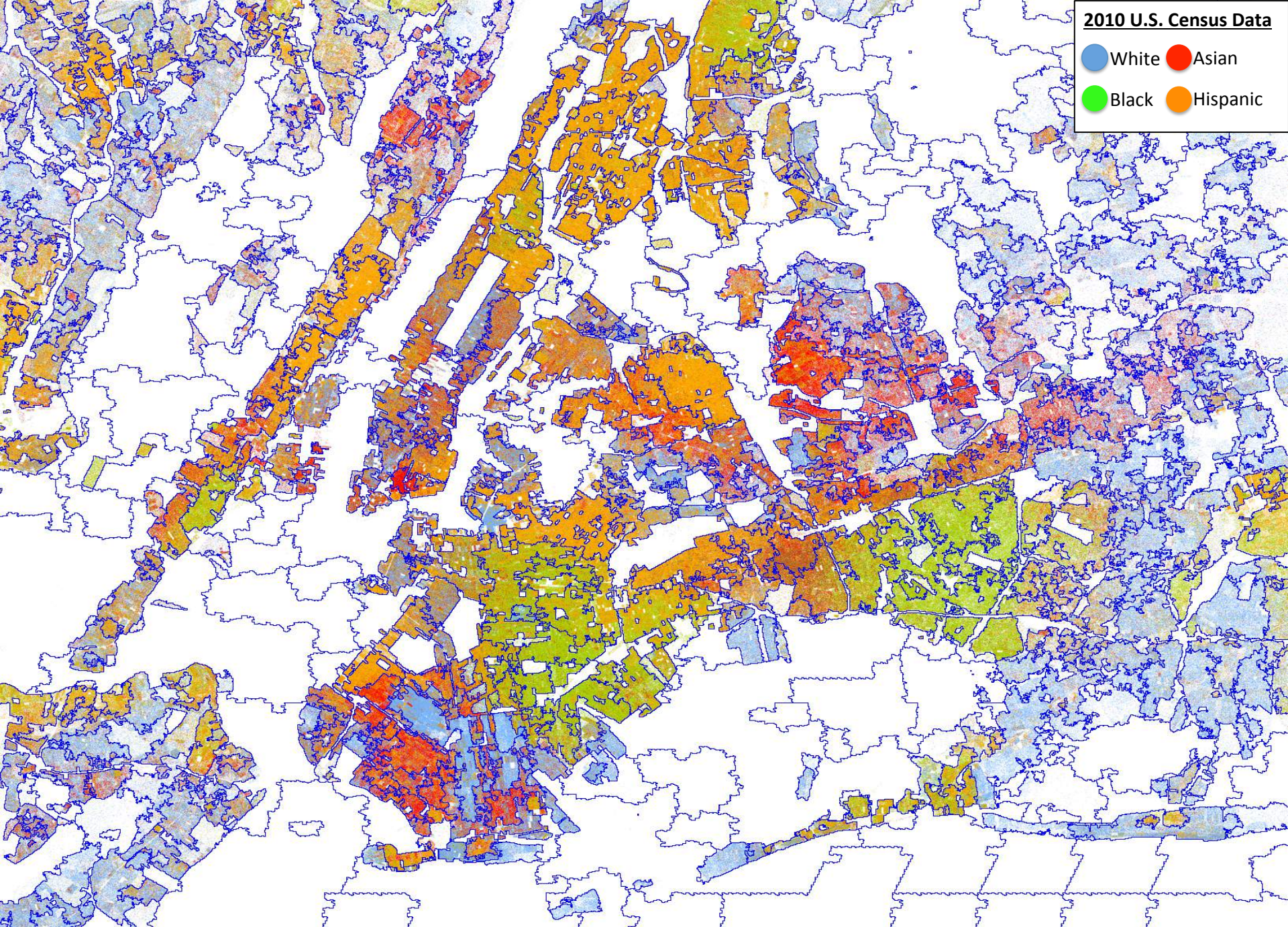
2010 U.S. Census Data

- White
- Asian
- Black
- Hispanic

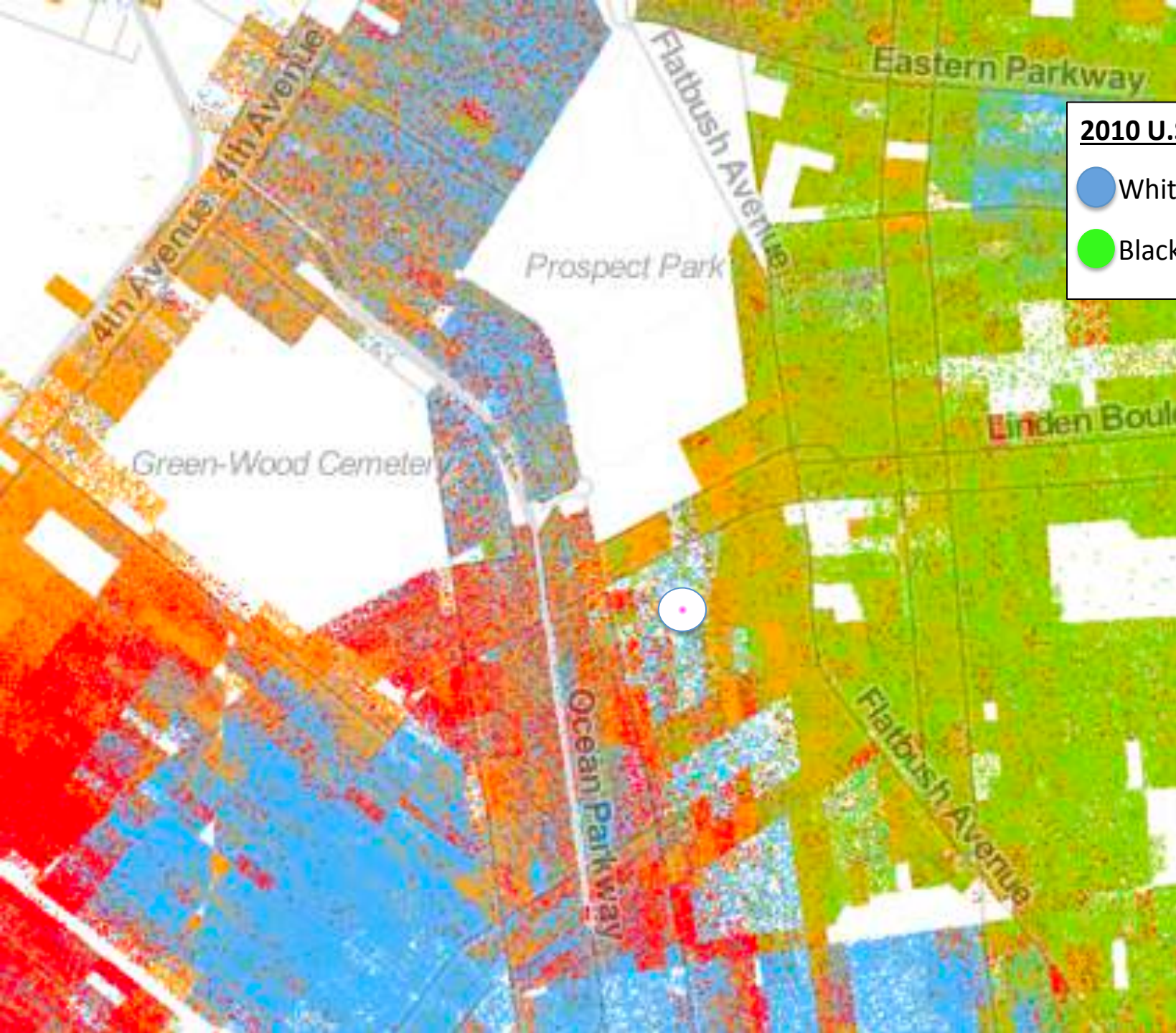


2010 U.S. Census Data

- White
- Asian
- Black
- Hispanic




Machine-learning Image Segmentation (BIS)

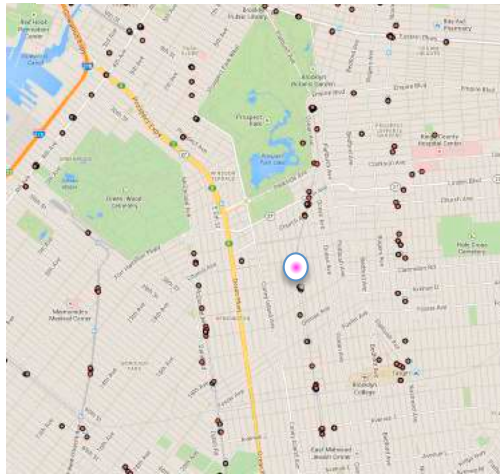


2010 U.S. Census Data

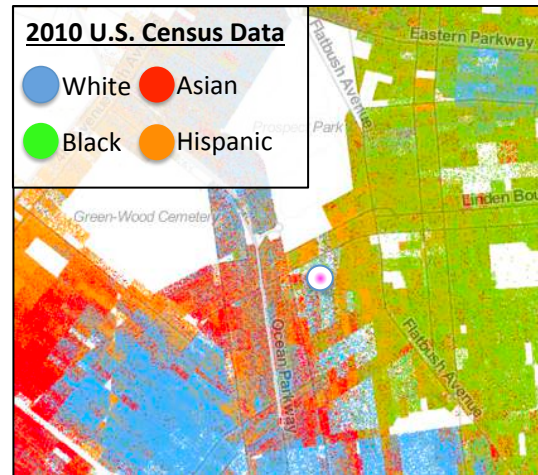
- White
- Asian
- Black
- Hispanic

Predicted Ancestry of DNA left behind can Mirror Census Data in “White” areas

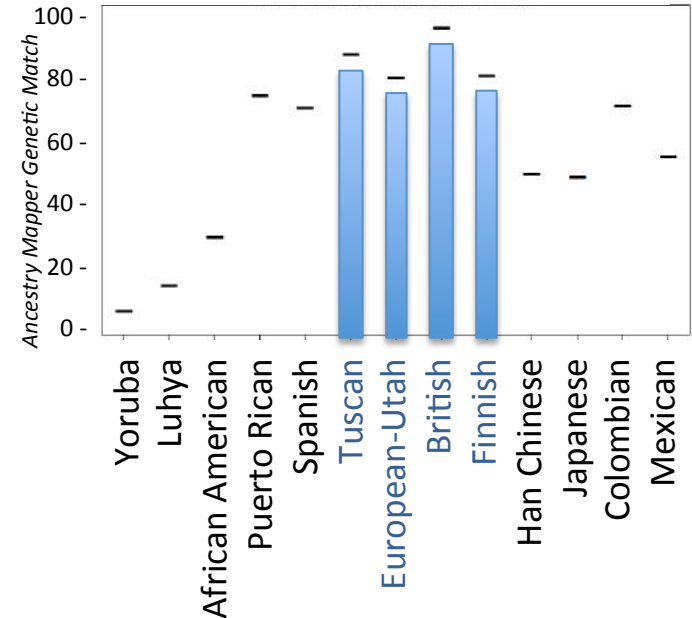
Collection Site  =P01461



Demographic data

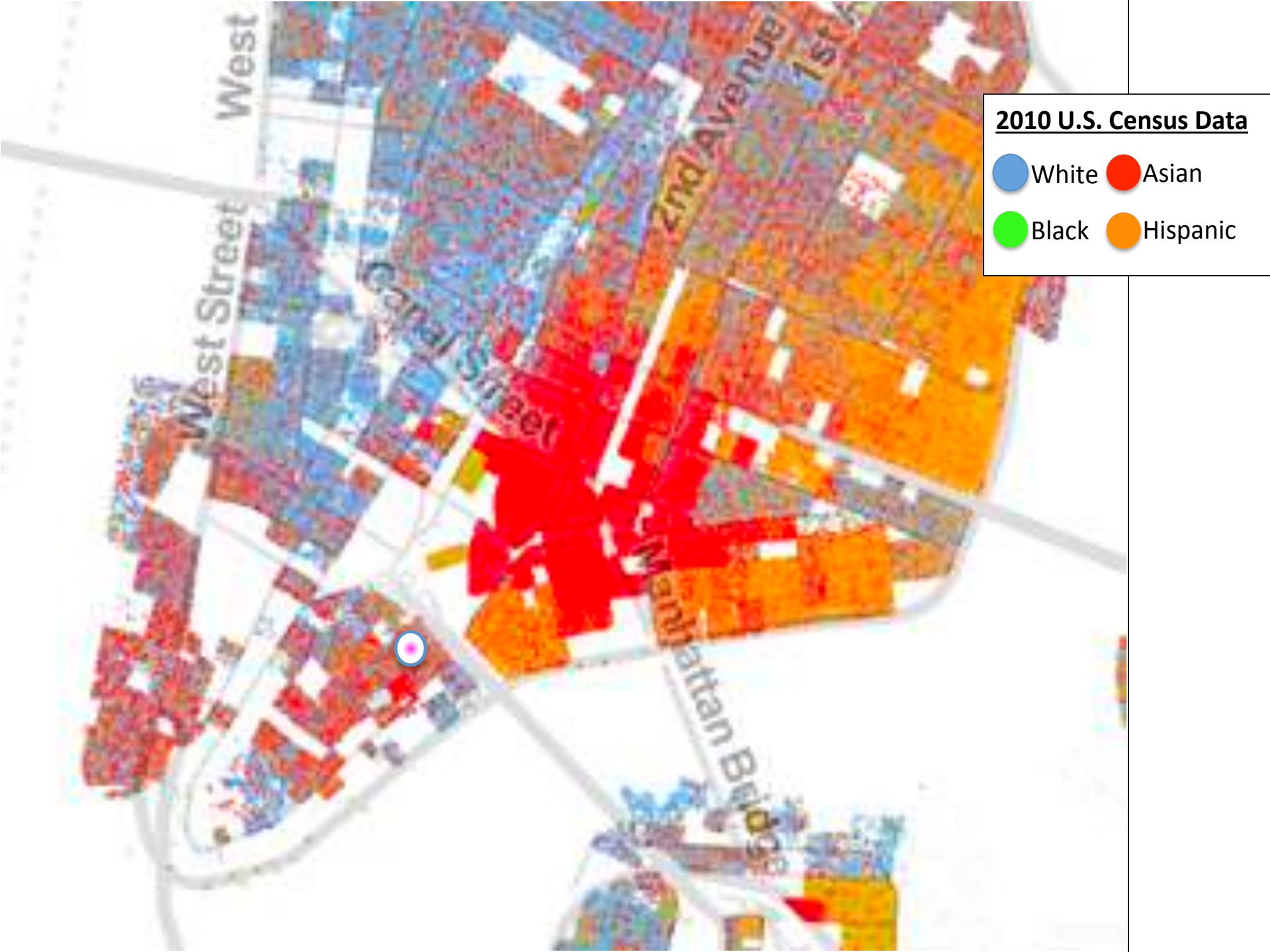


Ancestry Prediction




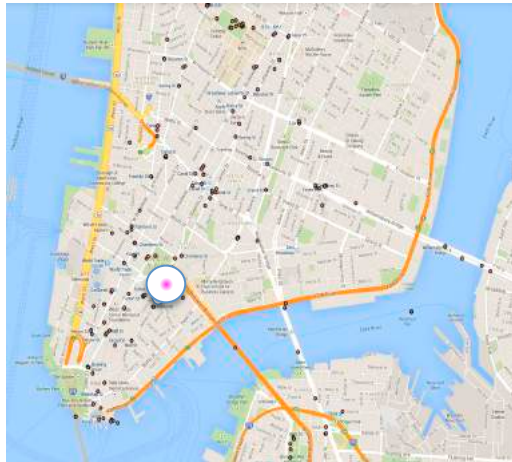
2010 U.S. Census Data

- White
- Asian
- Black
- Hispanic

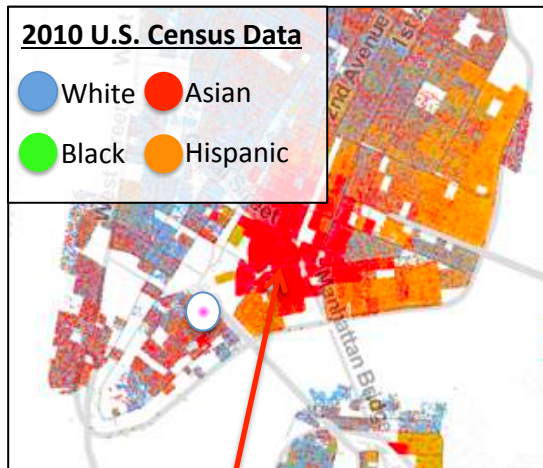


Alleles appear more Hispanic and more Asian in downtown Manhattan

Collection Site  = P00951

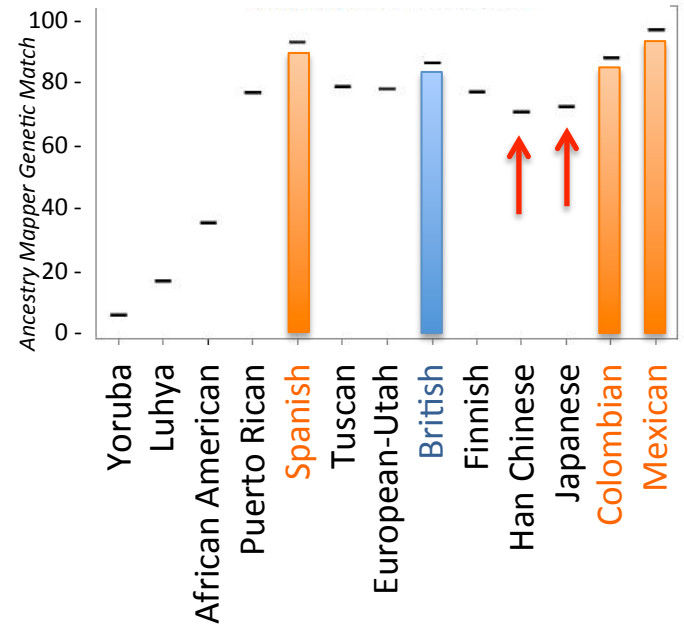


Demographic data



Chinatown

Ancestry Prediction



Hudson River

Broadway

Saint Nicholas Avenue


Dougherty Boulevard

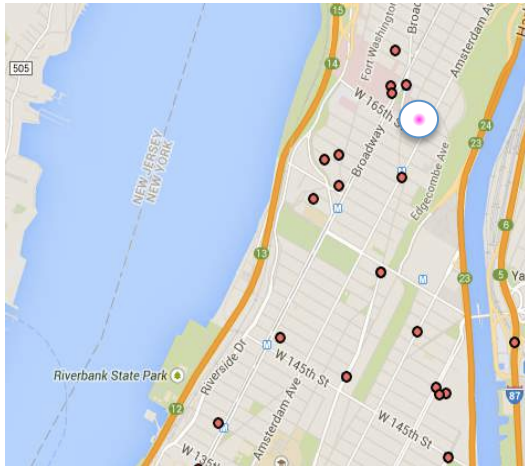
2010 U.S. Census Data

- White
- Asian
- Black
- Hispanic

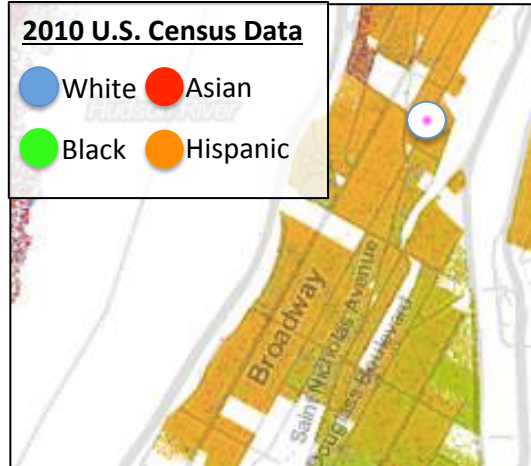


North Harlem and Washington Heights show more Yoruban alleles and Puerto Rican alleles

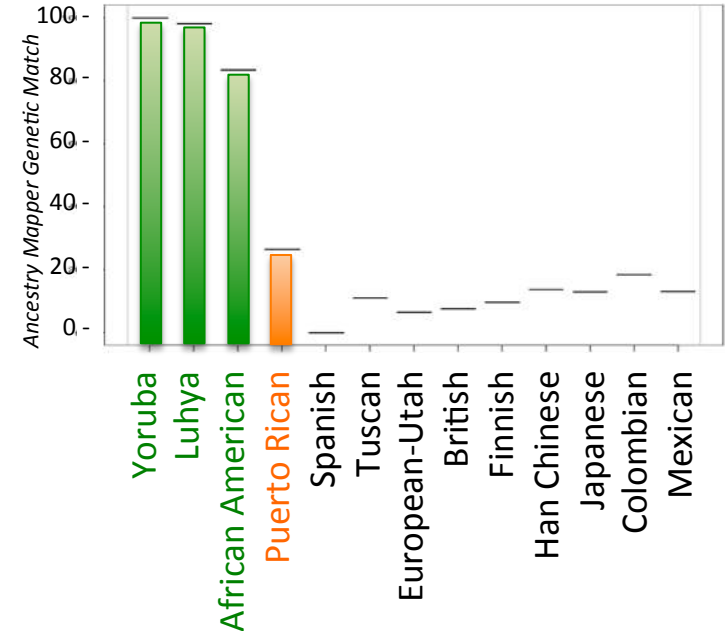
Collection Site  = P00166



Demographic data



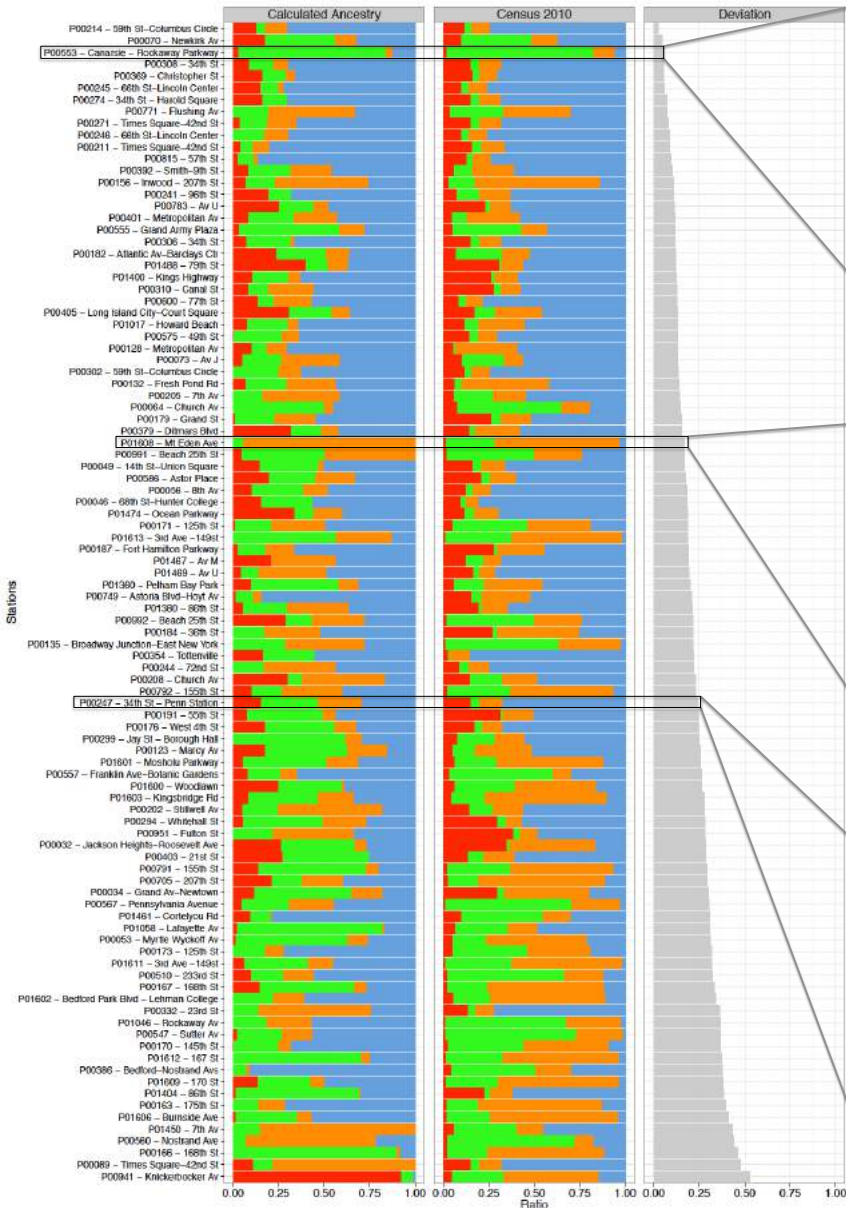
Ancestry Prediction



We can detect humans' "molecular echo"

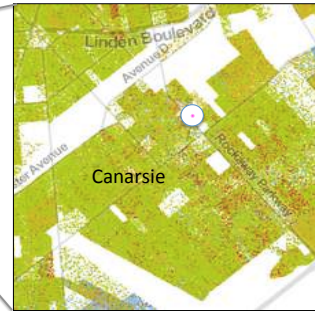
A

Admixture Proportion: ● - Asian ● - Black ● - Hispanic ● - White



B

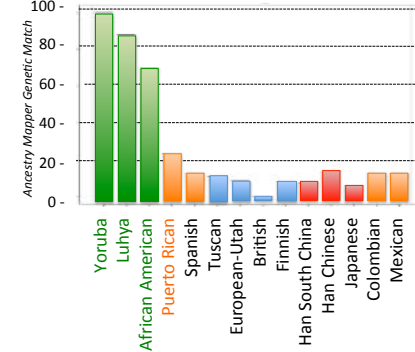
Census Demographic data



Sample = P00553

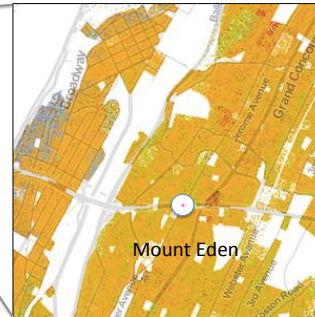
C

DNA Ancestry Calculation



D

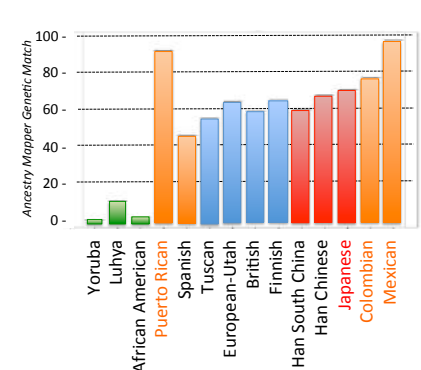
Census Demographic data



Sample = P01608

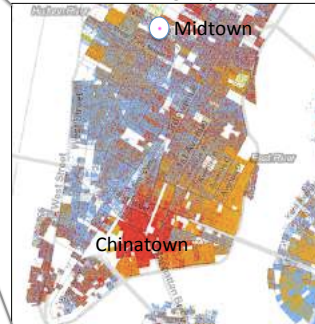
E

DNA Ancestry Calculation



F

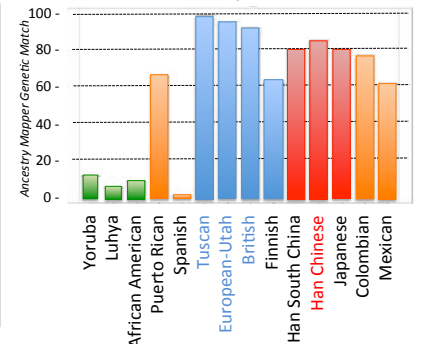
Census Demographic data



Sample = P00247

G

DNA Ancestry Calculation



NATURE | NEWS



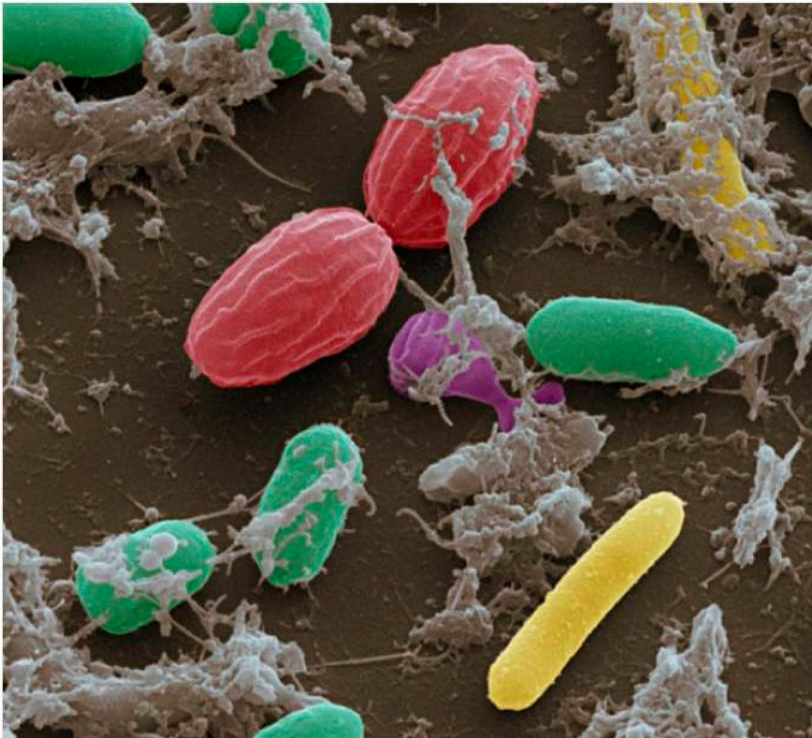
Microbiomes raise privacy concerns

DNA from microbes living on the human body can be used to identify individuals.

[Ewen Callaway](#)

11 May 2015

[PDF](#) [Rights & Permissions](#)

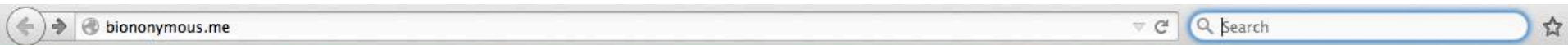


Eye of Science/Science Photo Library

DNA from bacteria in human faeces could be used as a 'gut print' to identify individuals.

Call it a 'gut print'. The collective DNA of the microbes that colonize a human body can uniquely

You can choose what DNA to leave behind



Biononymous.me

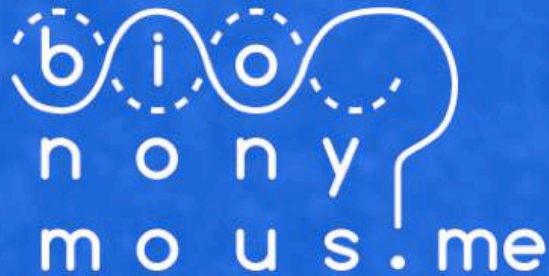
DIY Guides

Legal

Reading

Forum

Resources



**A hub for community
research into biological
privacy.**

ABOUT

Biological surveillance is the means by which biological science is used to track, monitor, analyze, and turn bodies into data.

It is the extraction of DNA and microbes from our skin, nails, hair and body fluids.

It is the analysis of identifying body parts like faces, fingerprints and irises.

It is the the tracking of life itself by body heat, pulse, perspiration, and involuntary movement.

It is the vulnerability we each face every day by the very situation of being human, by simply having a body.

We believe that privacy should be a choice.

CONTRIBUTORS

[Heather Dewey-Hagborg](#)

[Fei Liu](#)

[Aurelia Moser](#)

[Adam Harvey](#)

[Paul Vanouse](#)

[Ben Brucato](#)

[Jeremy Gruber](#)

[Claire Pentecost](#)

[Brian Holmes](#)

[Marc R. Dusseiller](#)

[Elizabeth Joh](#)

[Alondra Nelson](#)

[Ignacio Nieto](#)

Be invisible.




150

cells required to yield 1 nanogram of DNA


.5

nanograms of DNA required for standard forensic analysis


108

nanograms of DNA in a microliter of saliva


1.5

average liters of saliva a person generates each day


40

nanograms of DNA in a fingernail


.1

average millimeters a person's fingernails grow each day


5

nanograms of DNA in a single hair


50

average number of hairs a person sheds each day

(6)

Next Steps

Should I ride the
subway?

With Ice
Cream

“Yes!”

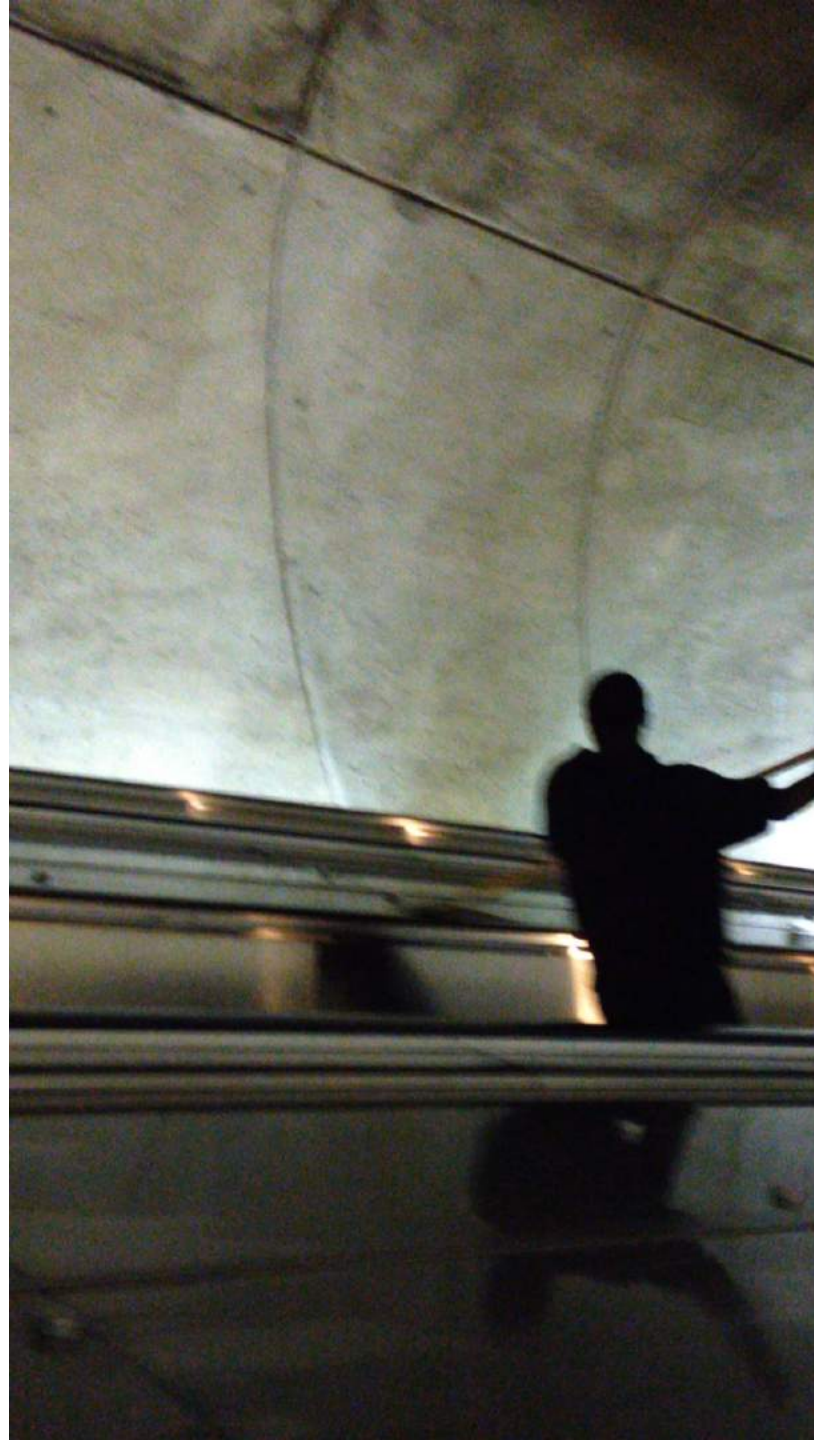








Washington
D.C.



Global Context



MetaSUB: Metagenomics & Metadesign of Subways & Urban Biomes

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[City Profiles](#)

[Interactive Map](#)

[People](#)

[Methods](#)

[Meetings](#)

[Links](#)

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Building a Molecular Portrait of Cities

Subway surfaces define the daily commute for billions of people each year, and yet there is almost nothing known about the impact of surface type, season, commuter type, or subway design on their commute. We aim to bring a molecular view of the cities to improve their design, use, and impact on health.

[Global City Sampling Day \(CSD\) slated for June 21, 2016](#)

Site	City Details								Site Principal Investigator		
	Status	City	Country	Gov't Status	Total # Stations	Transit System Length (km)	Riders / year (billions)	Population (people)	Department	University / Institute	Contact PI
1	Ongoing	Beijing	China	Pending	318	527	3.387	21,150,000	Beijing Children's Hospital	Capital Medical University	Yongli Guo / Yiming
2	Planned	Seoul	South Korea	Approved	377	464	2.563	10,117,909	Microbiology	Institut Pasteur Korea	Soojin Jang
3	Ongoing	Shanghai	China	Approved	337	548	2.519	24,150,000	Personalized Genomics	Fudan University	Leming Shi
4	Planned	Moscow	Russia	Started	196	328	2.491	11,503,501	Genomics	Institute for Physical)Chemical Medicine,	Dmitry Alexeev
5	Ongoing	Tokyo	Japan	Approved	295	316	2.351	13,185,502	Computational Biology Research Ctr.	National Institute of Advanced Science	Haruo Suzuki
6	Ongoing	Guangzhou	China	Pending	130	240	2.280	12,700,800	Systems Biology	Sun Yat-sen University	Zhi Xie
7	Ongoing	New York City	USA	Pending	468	436	1.708	8,405,837	Physiology and Biophysics	Weill Cornell Medical College	Christopher Mason
8	Ongoing	Mexico City	Mexico	Pending	195	227	1.685	8,851,080	National Institute of Public Health	IANPHI Mexico Secretariat	Celia M. Alpuche Aranda / Jesus Martinez
9	Ongoing	Hong Kong	China	Pending	87	175	1.618	7,219,700	Computer Science and Engineering	City University	Patrick Lee
10	Ongoing	Paris	France	Pending	303	214	1.527	2,273,305	Analytical Genomics	University Pierre et Marie Curie	Hugues Richard / Ingrid Lafontaine
11	Ongoing	Barcelona	Spain	Approved	131	178	1.036	4,576,394	Genomic and Epigenomic Variation	Centre for Genomic Regulation	Stephan Ossowski / Daniela Bezdán
12	Planned	Singapore	Singapore	Pending	113	153	0.922	5,399,343	Biochemistry and Molecular Biology	Pennsylvania State University	Stephan Schuster
13	Ongoing	São Paulo	Brasil	Approved	65	75	0.921	11,895,893	Genetics and Bioinformatics	University of Sao Paolo	Houtan Noushmehr / Emmanuel Dias-Neto
14	Planned	New Delhi	India	Pending	142	194	0.799	11,000,000	Computational Biology	Memorial Sloan Kettering	Sikander Hyat
15	Planned	Rome	Italy	Pending	74	60	0.279	2,627,000	Molecular Biology Section	University of Rome Sapienza	Romano Florigio Lista / Anna Anselmo
16	Ongoing	Boston	USA	Approved	51	61	0.166	4,180,000	Biostatistics	Harvard School of Public Health	Curtis Huttenhower
17	Planned	Oslo	Norway	Approved	97	86	0.083	1,502,604	Protection and Societal Security Division	Protection and Societal Security Division	Marius Dybwad
18	Ongoing	Sydney	Australia	Approved	7	15	0.031	4,576,394	Computational Metagenomics	University of Technology	Aaron Darling /Catherine Burke
19	Planned	Bogota	Colombia	Pending	144	87	0.022	6,763,000	Metagenomics	Corpogen	Carlos Ruiz / Maria Zambrano
20	Planned	Sheffield	UK	Pending	48	29	0.011	577,050	Department of Animal & Plant Science	University of Sheffield	Eran Elhaik
21	Planned	Auckland	New Zealand	Pending	42	120	0.011	1,377,000	Environmental Research Institute	Univeristy of Waikato	Christopher Dada
22	Planned	Lisbon	Portugal	Approved	55	43	0.004	530,847	Population Genetics	IPATIMUP	Manuela Oliveira

Global Swab Metagenome Festival

<http://www.metasub.org/interactive-map.html>



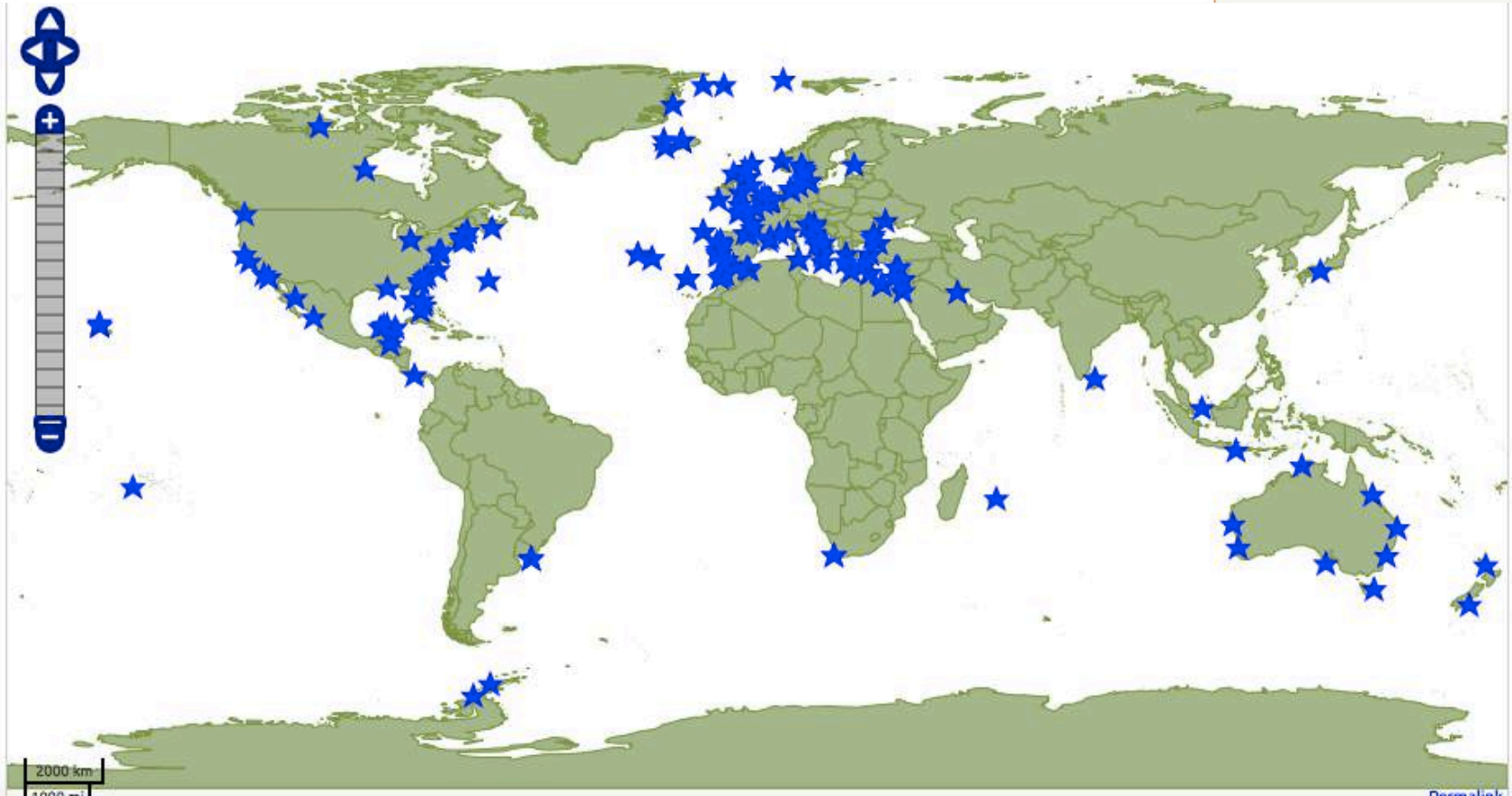


Home

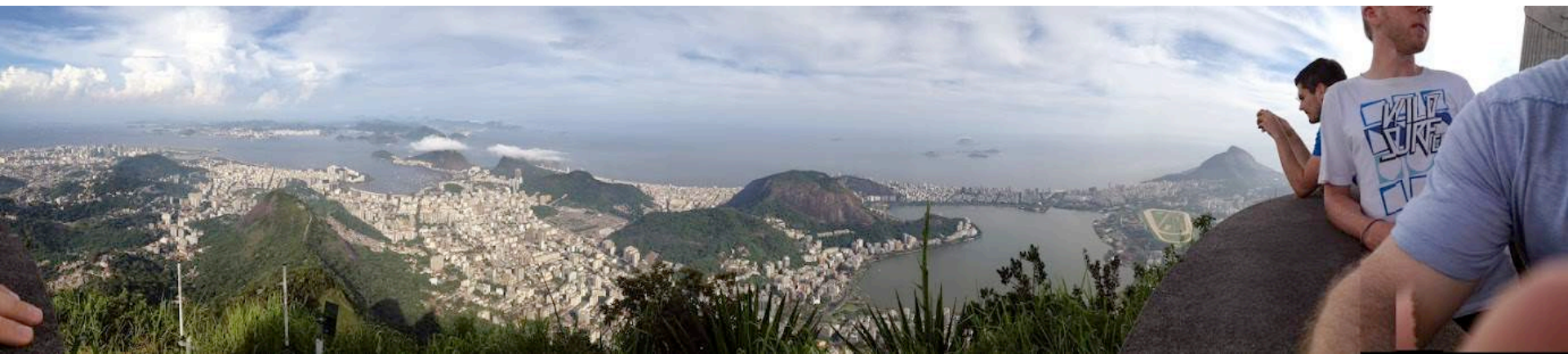
Ocean Sampling Day

Introduction to Ocean Sampling Day (OSD)

Follow us

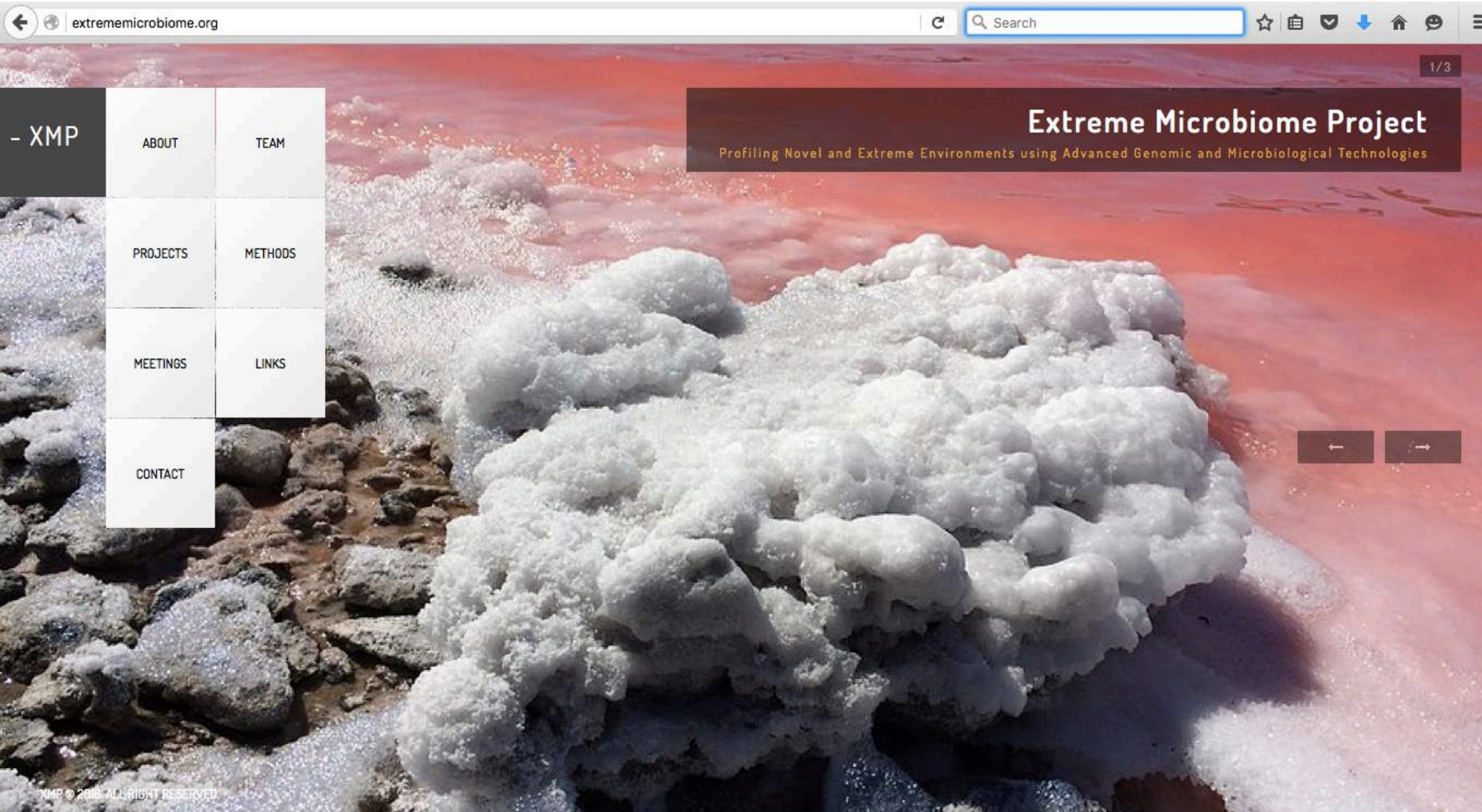


The Olympiome – Rio 2016 Before, During, and After



Extreme Context

Extreme Microbiomes for New Biology and Drug Discovery

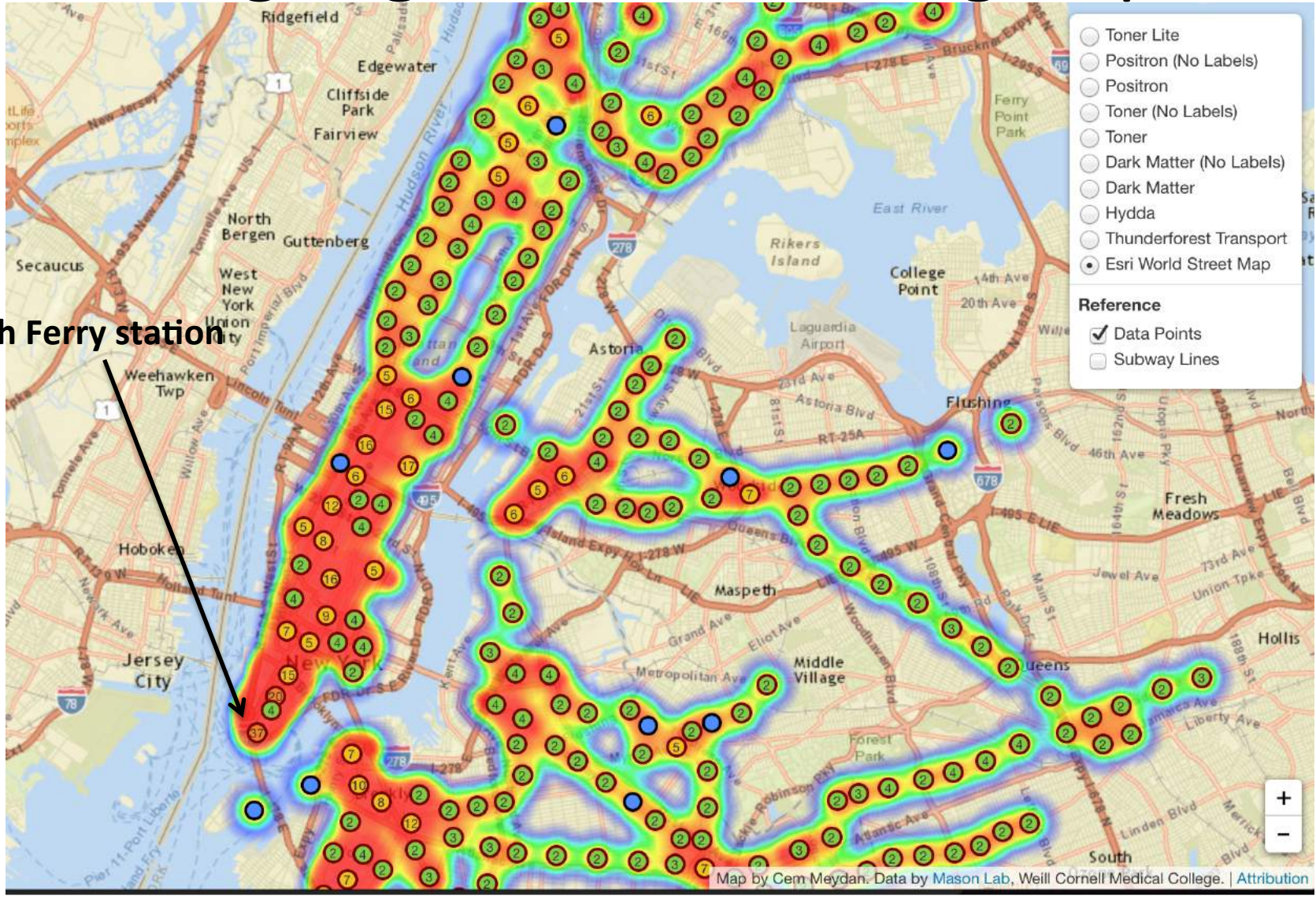


<http://www.extrememicrobiome.org>



Biosynthetic Gene Clusters show new drugs right under our fingertips

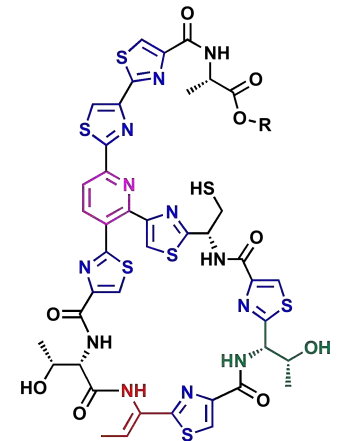
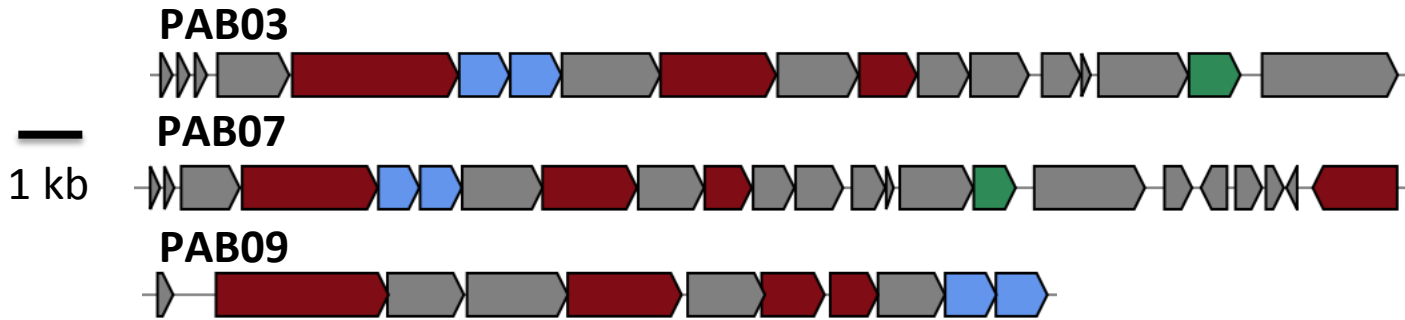
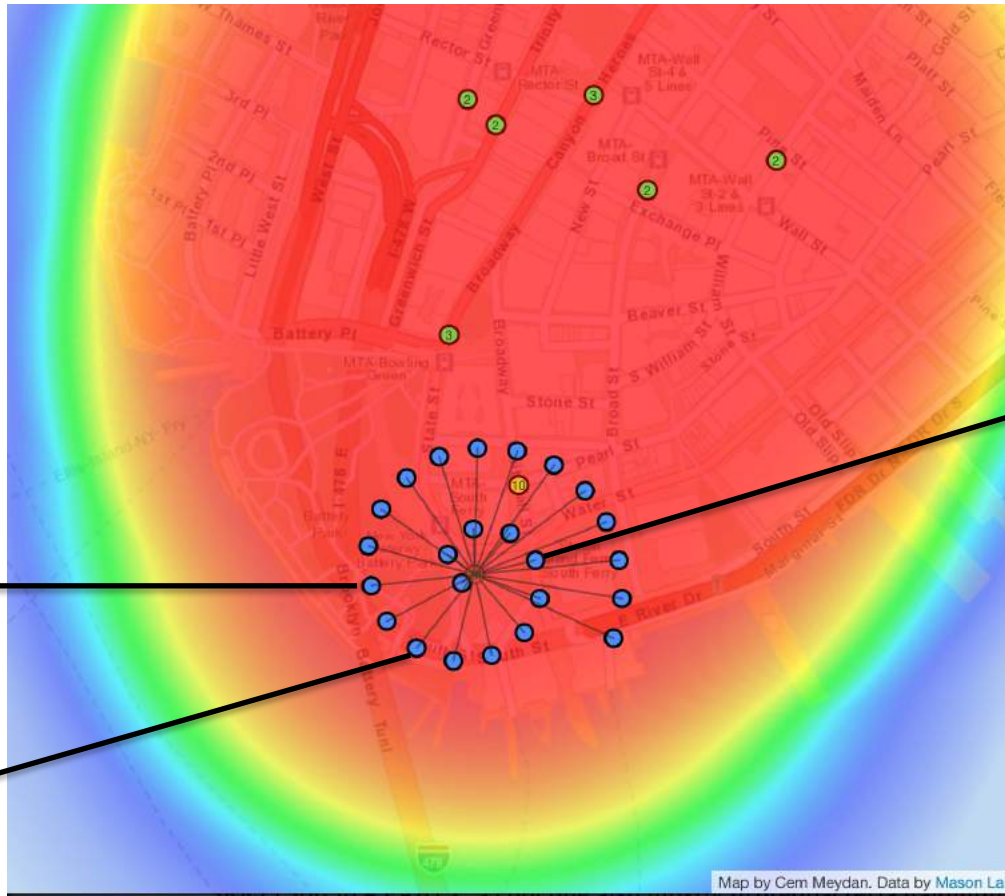
South Ferry station



PAB09
Metal stairway rail

PAB07
Plastic sign

PAB03
Metal payphone



(7)

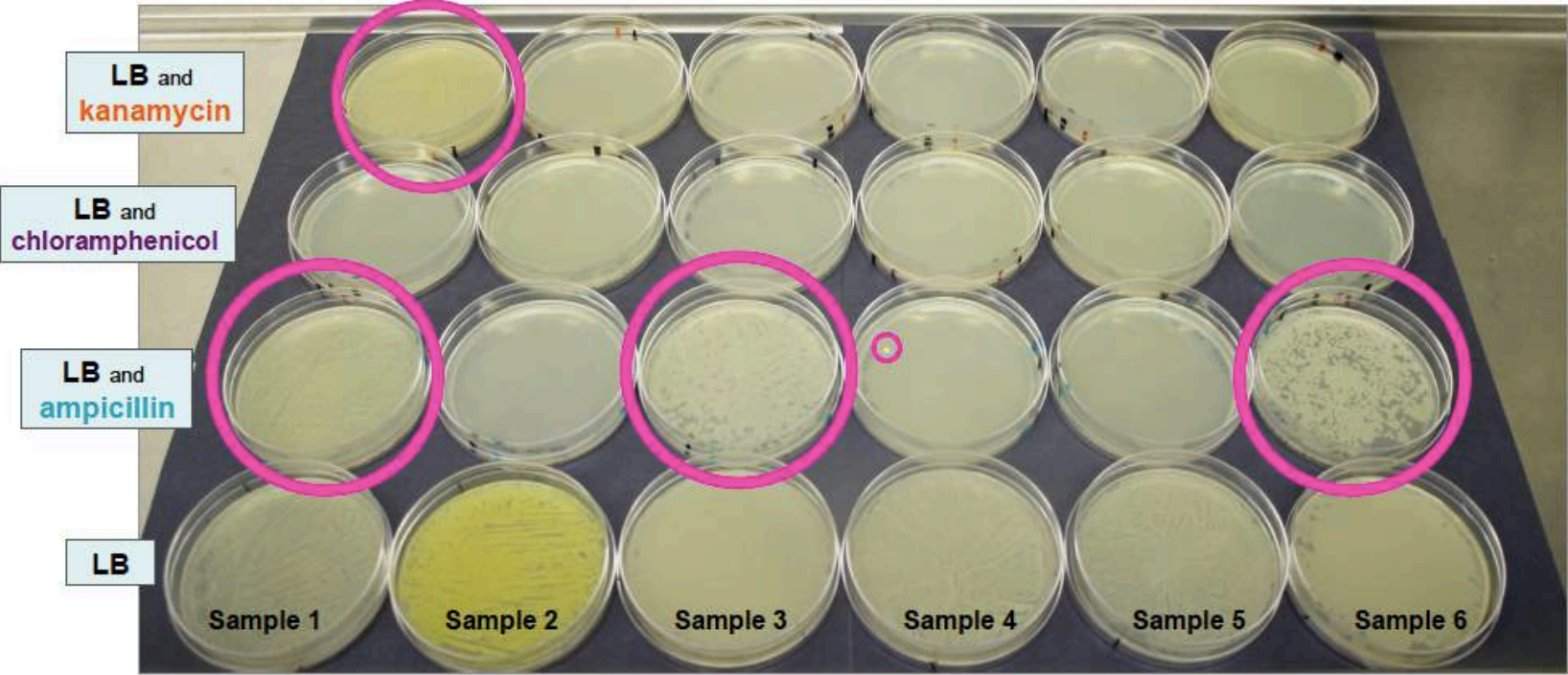
Precision

Metagenomics

Evidence of live & antibiotic resistant bacteria

Bacterial Growth from Subway Station Samples on Antibiotic Plates

	Sample 1 63 rd St.	Sample 2 63 rd St.	Sample 3 68 th St.	Sample 4 96 th St.	Sample 5 77 th St.	Sample 6 77 th St.
LB + kanamycin	growth	no growth	no growth	no growth	no growth	no growth
LB + chloramphenicol	no growth	no growth	no growth	no growth	no growth	no growth
LB + ampicillin	growth	no growth	growth	one colony	no growth	growth
LB	growth	growth	growth	growth	growth	growth



Examine hospital settings – at Chicago (Jack Gilbert) and now at WCMC

[Home](#) [Goals](#) [Overview](#) [Design](#) [Timeline](#) [Consortium](#) [Findings](#) [Affiliations](#)

Hospital *Microbiome*

This study aims to collect microbial samples from surfaces, air, staff, and patients from the University of Chicago's new hospital pavilion in order to better understand the factors that influence bacterial population development in healthcare environments.

[Study Design](#)



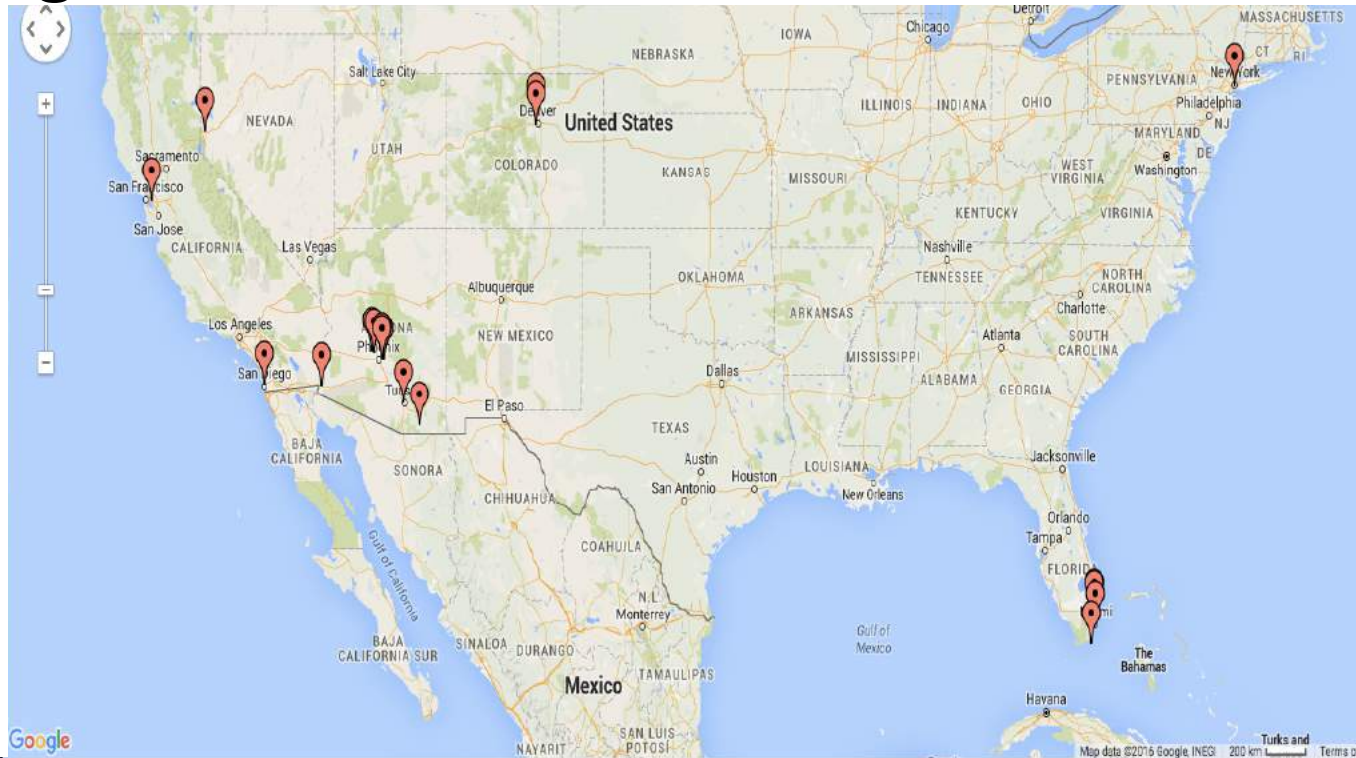
What if wasn't the hospital that carried the infection?

- Currently conducting pilot study in ambulances across the US.
- Building HAI/AAI genomic database and backend.
- Developing new data analysis pipelines.



Current Ambulance Pilot Study

- 1407 samples collected from ambulances across the US.
- 137 ambulances, in 20 cities, 6 states and 5 regions.



(8)

Designer and

Borrowed

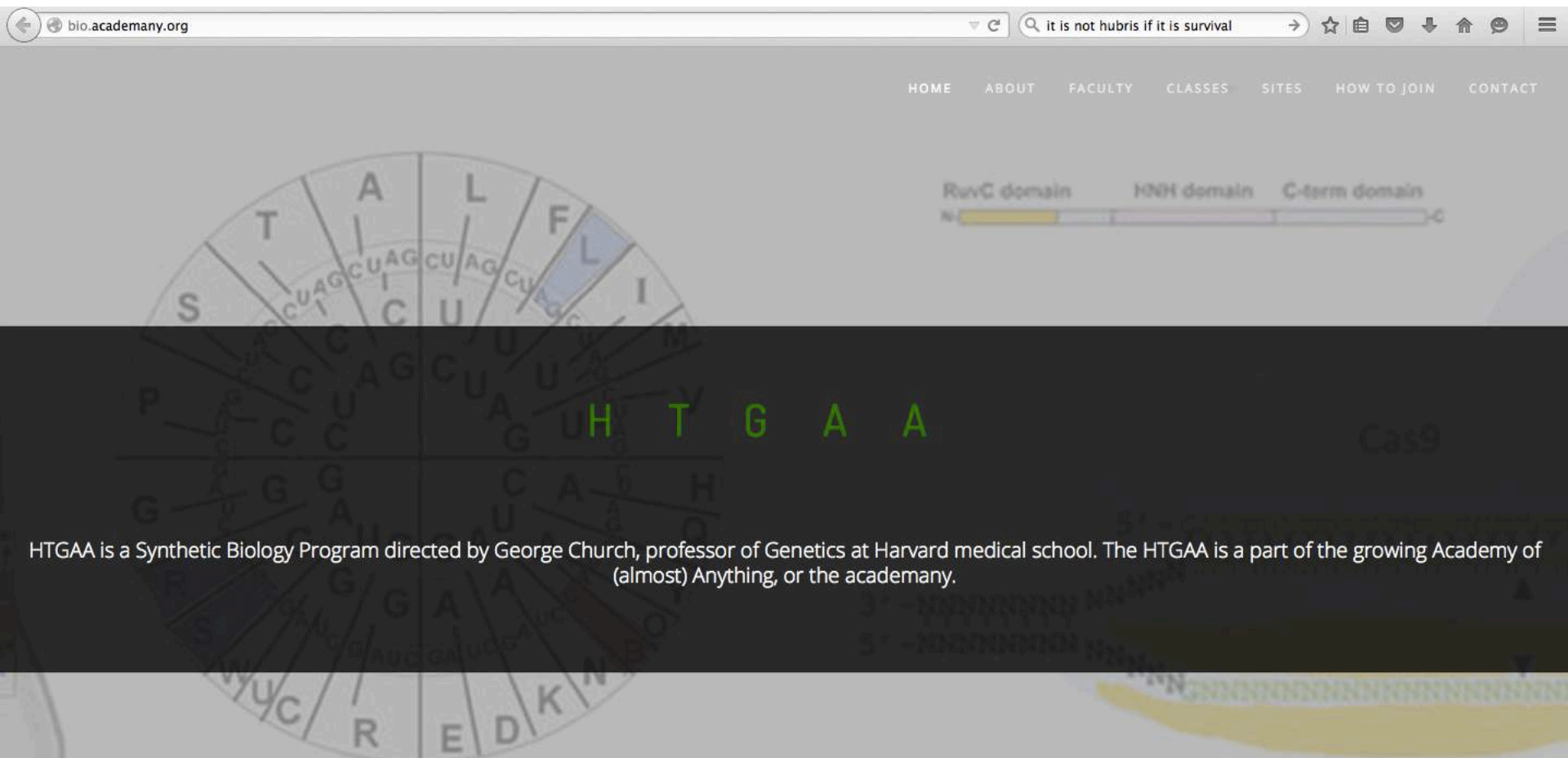
Metagenomics

Understanding
of biology

is measured by

the ability to engineer it
and predict the outcome.

How to Grow Almost Anything, HTGAA, including synthetic genomes and your modified microbiome



http://bio.academany.org/labs/new_york



The BK BioReactor

A Mobile Research Library for the Unseen
Microbiology of the Gowanus Canal

A screen for an experiential lecture in spatial context is designed and fabricated for the BK BioReactor. The screen displays a 3D visualization of the canal's microbiology.

The BK BioReactor is a mobile research library for the unseen microbiology of the Gowanus Canal. It is a mobile research library for the unseen microbiology of the Gowanus Canal. It is a mobile research library for the unseen microbiology of the Gowanus Canal.

The BK BioReactor is a mobile research library for the unseen microbiology of the Gowanus Canal. It is a mobile research library for the unseen microbiology of the Gowanus Canal. It is a mobile research library for the unseen microbiology of the Gowanus Canal.

- 1. BK BioReactor
- 2. Smart Dock
- 3. Spatial Catalyst
- 4. Mapping Modes
- 5. Functional Metabolic Pathways

The BK BioReactor

A mobile research library for the unseen microbiology of the Gowanus Canal.

The BK BioReactor is a mobile research library for the unseen microbiology of the Gowanus Canal. It is a mobile research library for the unseen microbiology of the Gowanus Canal.

MAPPING MODES

Geospatial: Environmental Information

Geospatial: Environmental Information. This mode displays a 3D map of the Gowanus Canal area, showing the location of the BK BioReactor and the Smart Dock. It also displays environmental data such as water quality and air pollution levels.

Genetic: Evolutionary Relationships

Genetic: Evolutionary Relationships. This mode displays a phylogenetic tree showing the evolutionary relationships between different microbial species found in the Gowanus Canal. The tree is color-coded to show different clades and is interactive, allowing users to explore specific lineages.

Functional: Metabolic Pathways

Functional: Metabolic Pathways. This mode displays a network of metabolic pathways, showing the flow of information and energy between different genes and proteins. The pathways are color-coded and interactive, allowing users to explore specific metabolic processes.

SPATIAL CATALYST

A screen for an experiential lecture in spatial context is designed and fabricated for the BK BioReactor. The screen displays a 3D visualization of the canal's microbiology.

Smart Dock

A mobile research library for the unseen microbiology of the Gowanus Canal. It is a mobile research library for the unseen microbiology of the Gowanus Canal. It is a mobile research library for the unseen microbiology of the Gowanus Canal.

A mobile research library for the unseen microbiology of the Gowanus Canal. It is a mobile research library for the unseen microbiology of the Gowanus Canal. It is a mobile research library for the unseen microbiology of the Gowanus Canal.





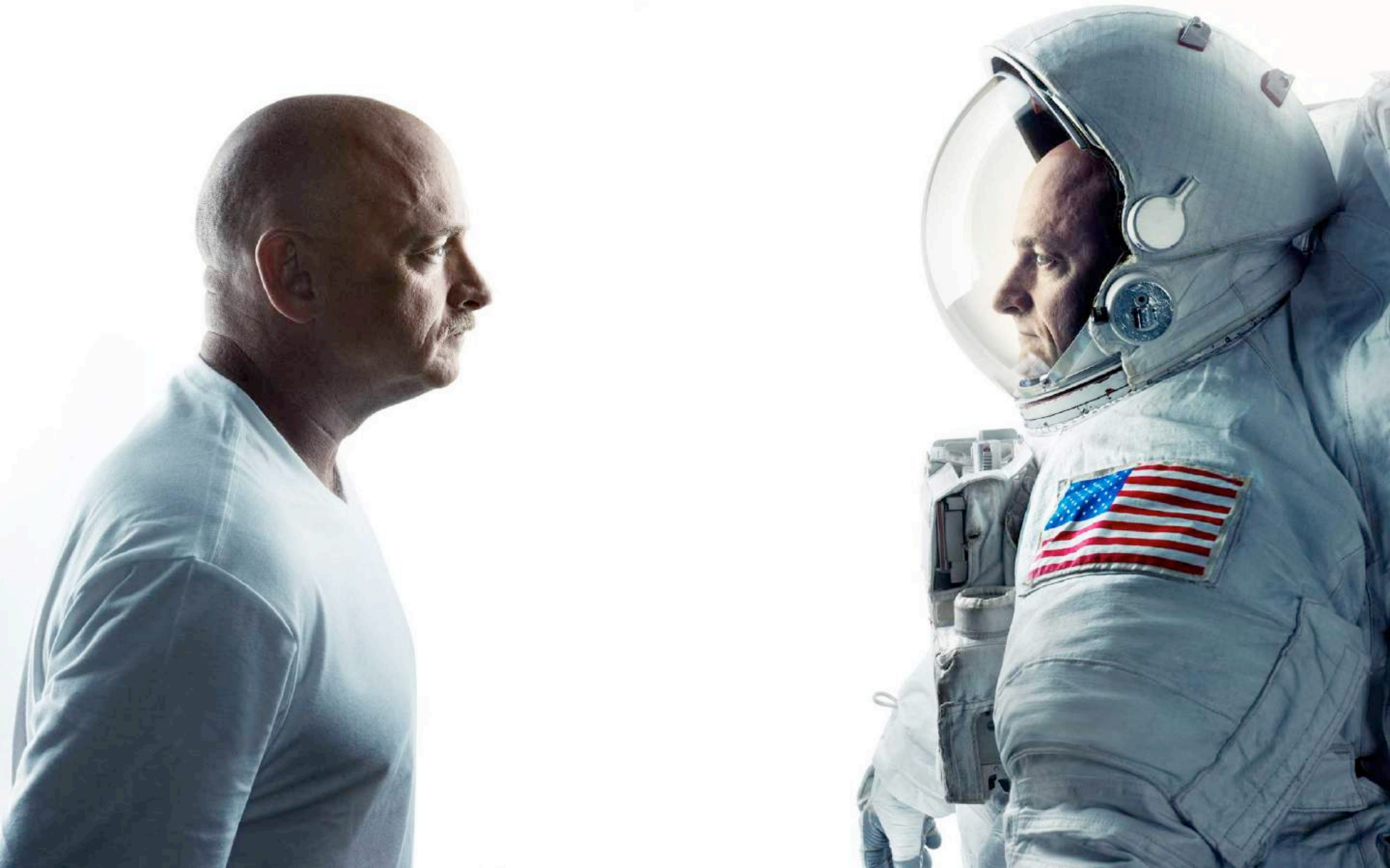
ISS009E2877

**ISS Medical Project:
Science Implementation on the
International Space Station**





Participatory Medicine with Twin Astronauts



Longitudinal, Integrative Systems Biology



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News, features & press releases

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- Exploration: Beyond Earth**
- International Space Station
 - Commercial Space Transportation
 - Crew Vehicle and Launch System
 - Human Health and Safety
 - Analog Missions and Field Testing
 - Human Exploration Technology
 - Multimedia
 - News & Media Resources
 - All NASA Missions

Text Size

NASA Selects 10 Proposals to Explore Genetic Aspects of Spaceflight **March 7, 2014**

Only one set of twins has ever been into space, and now those twins are providing an unprecedented opportunity for scientists to understand better the effects of microgravity on the human body.

NASA's Human Research Program (HRP) will fund 10 short-term, first-of-its-kind investigations into the molecular, physiological and psychological effects of spaceflight in a continuous effort to reduce the health impacts of human space exploration. The National Space Biomedical Research Institute is partnering with HRP to provide genetic counseling and assisting in the management of the research.

This unique opportunity is made possible by NASA's decision to fly veteran astronaut Scott Kelly aboard the International Space Station for one year, beginning March 2015, while his identical twin brother, retired astronaut Mark Kelly, remains on Earth.

This study will focus in part on the comparison of blood samples collected from Scott and Mark at regular intervals before, during and after the one-year mission. Physiological and psychological testing also will be conducted on the brothers before, during and after the mission.

Scientific and technical experts from academia and government reviewed 40 proposals submitted in response to the research announcement "Human Exploration Research Opportunities - Differential Effects on Homozygous Twin Astronauts Associated with Differences in Exposure to Spaceflight Factors." The following 10 selected proposals, which are from 10 institutions in seven states, will receive a combined \$1.5 million during a three-year period:

"All the News
That's Fit to Print"

The New York Times

Late Edition

Today, mostly cloudy, snow showers, windy, colder, high 40. Tonight, evening flurries, clearing, cold, low 26. Tomorrow, mostly sunny, high 44. Weather map is on Page C8.

VOL. CLXIV . . . No. 56,819 +

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NEW YORK, SATURDAY, MARCH 28, 2015

\$2.50

PILOT CONCEALED MENTAL ILLNESS, AUTHORITIES SAY

SCRUTINY AFTER CRASH

In Screening, Onus Is
on Employees to Be
Forthcoming

This article is by Melissa Eddy,
Dan Bilefsky and Nicola Clark.

DÜSSELDORF, Germany — Andreas Lubitz, the pilot at the controls of the Germanwings jetliner that crashed into the French Alps on Tuesday, had a mental illness but kept the diagnosis hidden from his employer, the authorities said Friday.

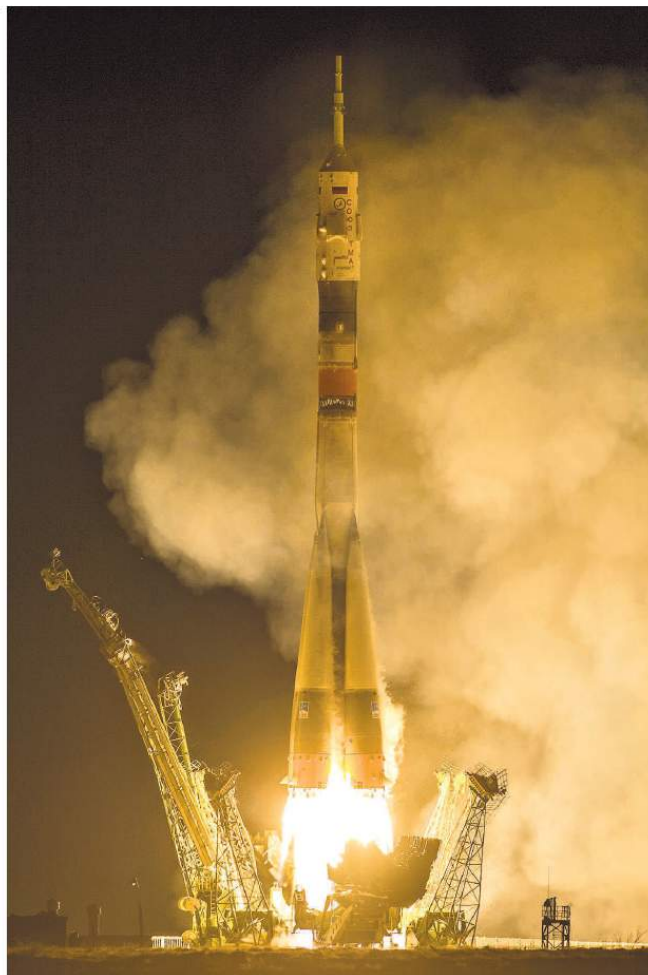
A psychiatric diagnosis might explain why Mr. Lubitz, a 27-year-old German, did not disclose his full medical record to Germanwings and its parent company, Lufthansa. Lufthansa company policy requires notification of conditions that could affect flying or a pilot's license.

Prosecutors said Friday that among the items found at Mr. Lubitz's home were several doctors' notes stating that he was too ill to work, including on the day of the crash; one of the notes had been torn up. These documents "support the preliminary assessment that the deceased hid his illness from his employer and colleagues," the prosecutors said in a statement.

But there remained considerable confusion about the precise nature and severity of his psychiatric condition. A German hospital said it had evaluated Mr. Lubitz twice in the past two months but added that he had not been there for assessment or treatment of depression.

The crash killed Mr. Lubitz and the other 149 people on board the Airbus A320 jetliner bound from Barcelona, Spain, to Düsseldorf, Germany, on Tuesday morning.

Airlines and their regulatory agencies have longstanding processes to screen for pilots whose



BILL INGALLS/NASA

Getting a Lift to 2016

A NASA astronaut, Scott J. Kelly, and two Russians left Saturday from Kazakhstan in a Soyuz TMA-16M spacecraft, headed to the International Space Station. Mr. Kelly will stay about a year.

Venture Capital Firm Prevails in Bias Case Riveting Silicon Valley

Sweeping Victory for Kleiner Perkins in Suit on Diversity in Tech Industry

By DAVID STREITFELD

SAN FRANCISCO — One of Silicon Valley's most famous venture capital firms prevailed on Friday over a former partner in a closely watched suit claiming gender discrimination, but hardly got away unscathed.

The plaintiff, Ellen Pao, had accused the firm, Kleiner Perkins Caufield & Byers, of discriminating against her in the course of her employment and eventual dismissal.

The decision handed Kleiner a sweeping victory in a case that had mesmerized Silicon Valley with its salacious details while simultaneously amplifying concerns about the lack of diversity in the technology industry.

Even with her loss in the case, Ms. Pao's suit succeeded in prompting debate about women in technology and venture capital, said Deborah Rhode, a law professor at Stanford University.

"This case sends a powerful signal to Silicon Valley in general and the venture capital industry in particular," Ms. Rhode said. "Defendants who win in court sometimes lose in the world outside it."

Kleiner and its lawyers did little to celebrate the win, with the lawyer Lynne C. Hermle saying that it "never occurred to me for a second that a careful and attentive jury like this would find either discrimination or retaliation." Kleiner issued a statement saying it was committed to supporting women.

Ms. Pao waved to the jury as she left the courtroom for the last time, a smile fixed on her face. "If I've helped to level the playing field for women and minorities in venture capital, then the battle was worth it," she said in a brief



JUSTIN SULLIVAN/GETTY IMAGES

Ellen Pao brought the suit against her former employer.

news conference.

Her suit, filed in Superior Court here, claimed that Kleiner did not promote her because of her gender, that it retaliated against her for complaining, that it failed to prevent gender discrimination and that it fired her in 2012 for complaining.

The suit asked \$16 million in compensatory damages plus punitive damages. Ms. Pao is now interim chief of the social media news site Reddit.

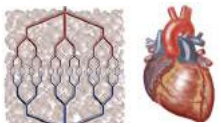
After the jurors rejected each of her four claims, they were found to be a vote short on a claim about her termination. For two hours, doubt reigned, the media unspooled possible outcomes and the jury went back to work. In the end, the problem seemed more juror confusion than anything else, and the claim went down with the others.

The jurors said in interviews they did not take on the role of "conscience of this community,"

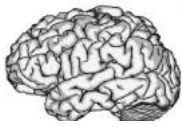
Continued on Page A3

In Defeat, Some Gains

Ellen Pao got people talking about the status of women, Farhad Manjoo writes. Page B1.



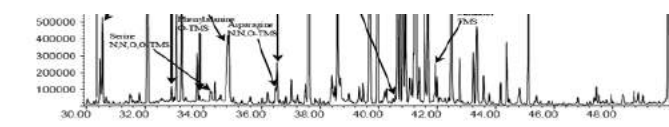
Vasculature



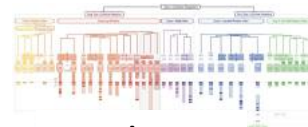
Cognition



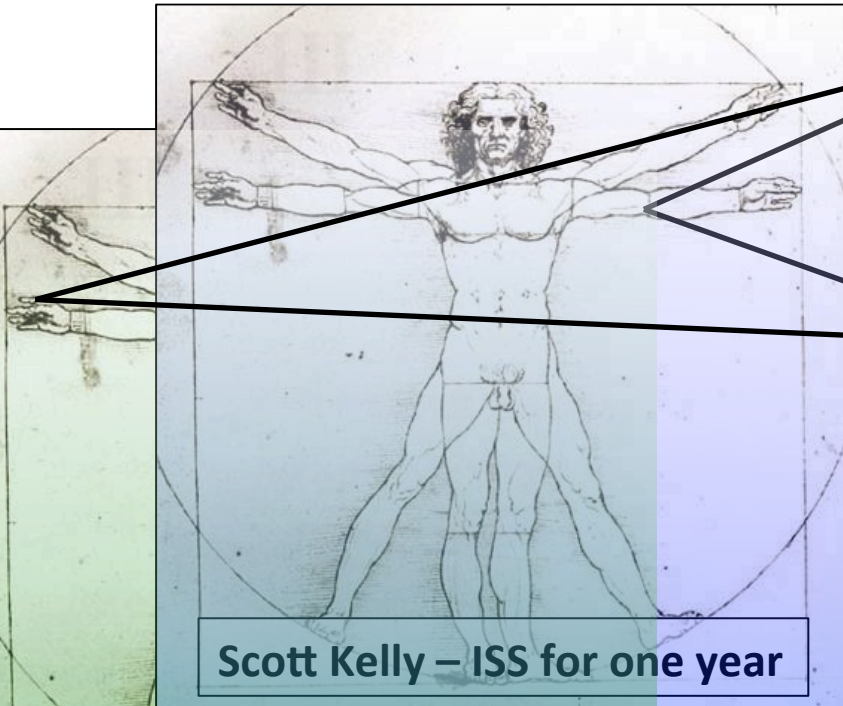
Microbiome



Targeted and Global Metabolomics



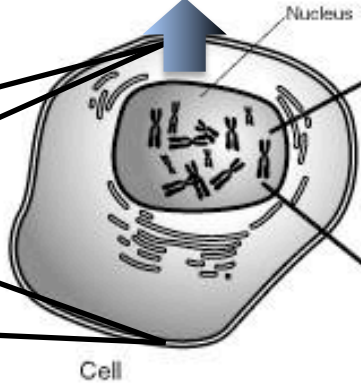
Cytokines



Scott Kelly - ISS for one year

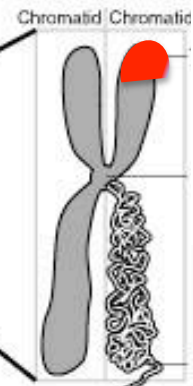


Mark Kelly - Earth control



Cell

Chromosome



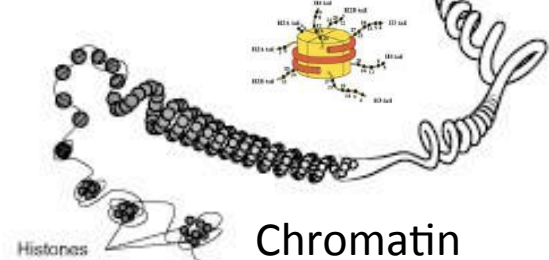
Chromatid Chromatid

Telomere Length

B-cells / T-cells

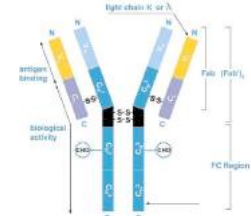


Antibody Titers

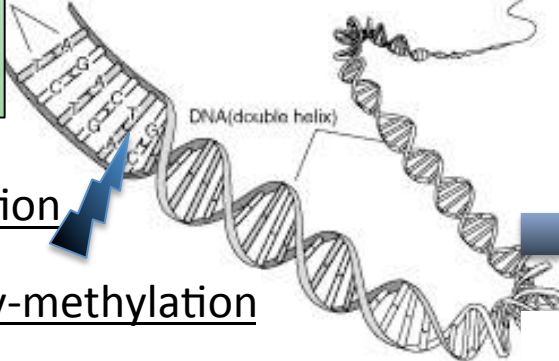


Histones

Chromatin

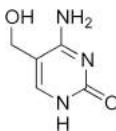


DNA Mutations & Structural Variation

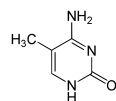


DNA(double helix)

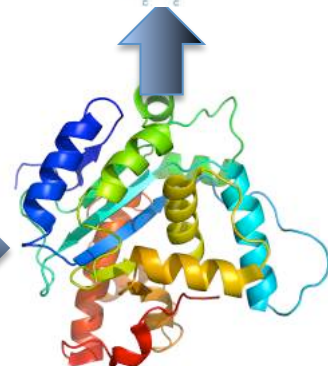
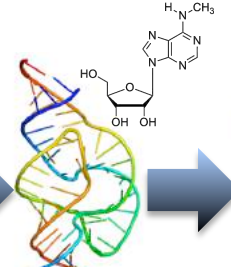
DNA Hydroxy-methylation



DNA Methylation



RNA expression & RNA Methylation (large and small)



Proteomics

Protocol Planning

NASA asks,
“What’s your terrestrial protocol?”

Two Options:

1. Bring Samples Back

- Frozen

- Ambient

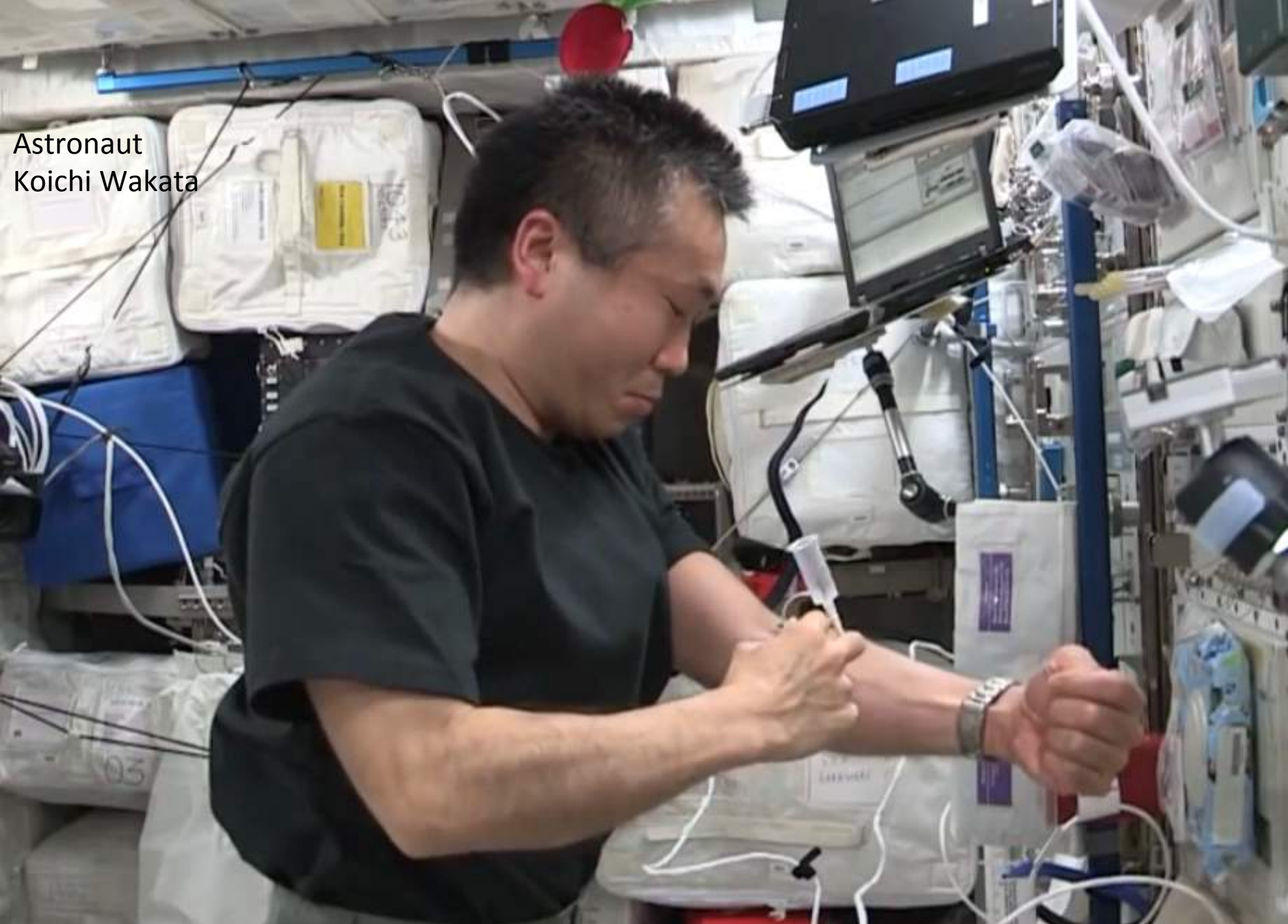
2. Sequence in Space



<http://www.youtube.com/watch?v=0ODYdyLy9Tg>



Astronaut
Koichi Wakata



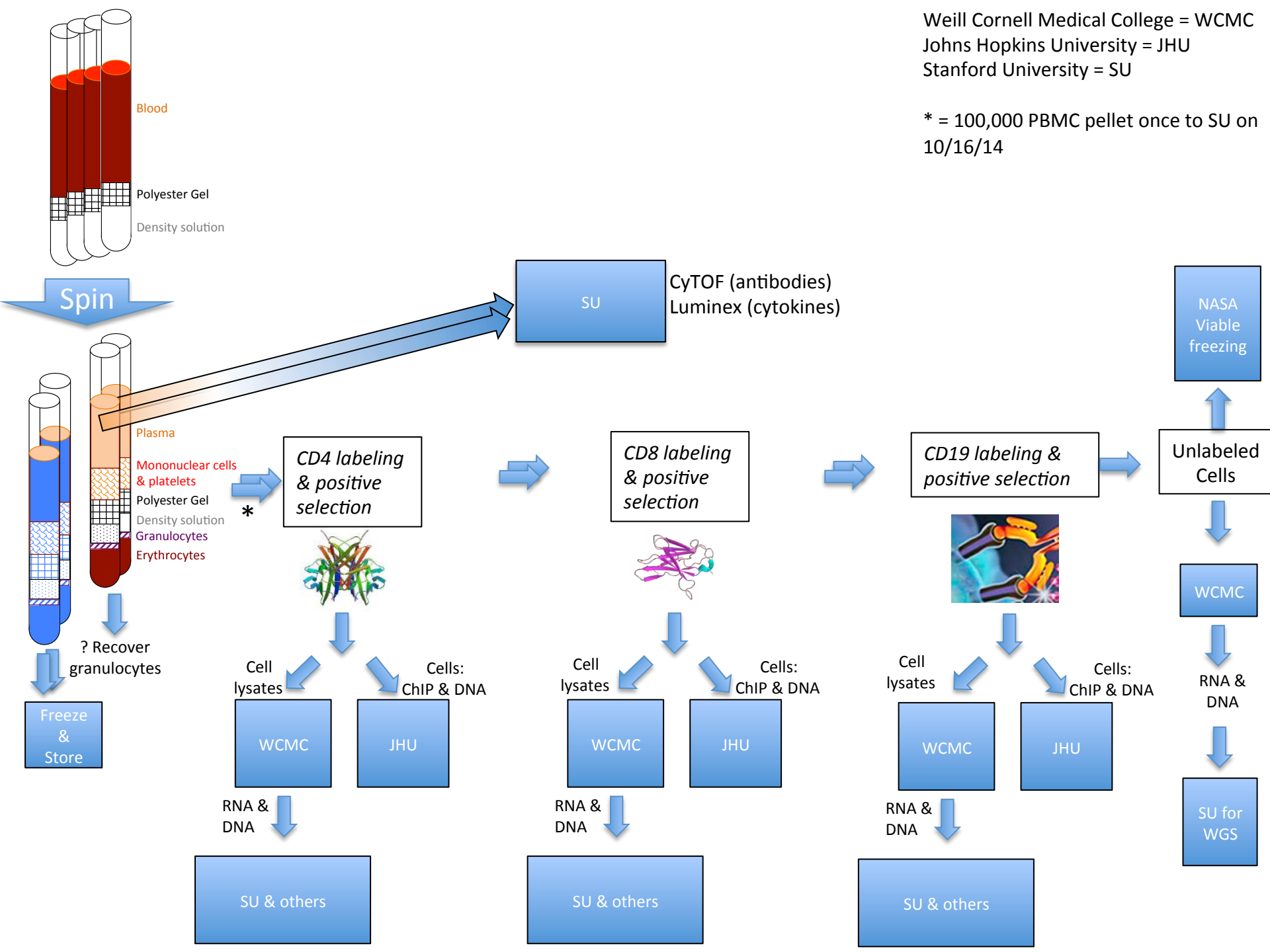
<http://www.youtube.com/watch?v=VmhEtPN5u9Y>



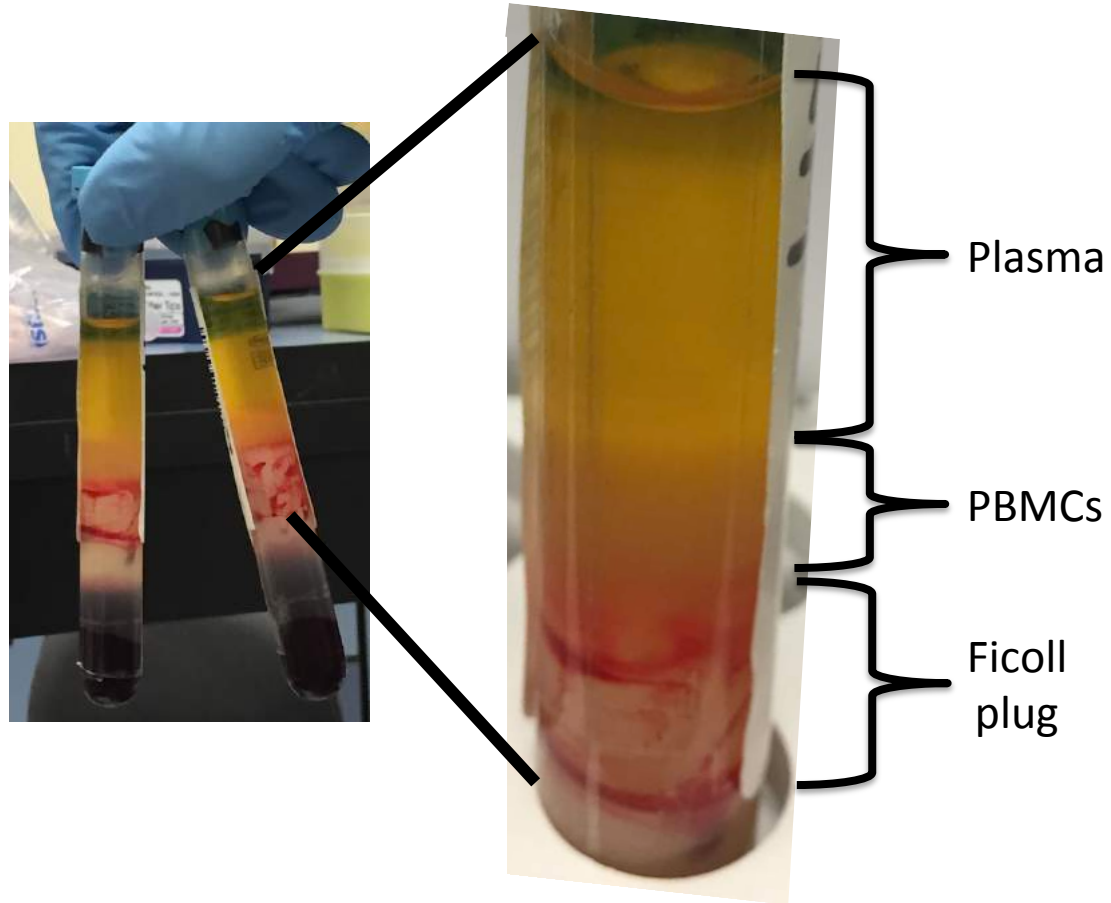


Weill Cornell Medical College = WCMC
Johns Hopkins University = JHU
Stanford University = SU

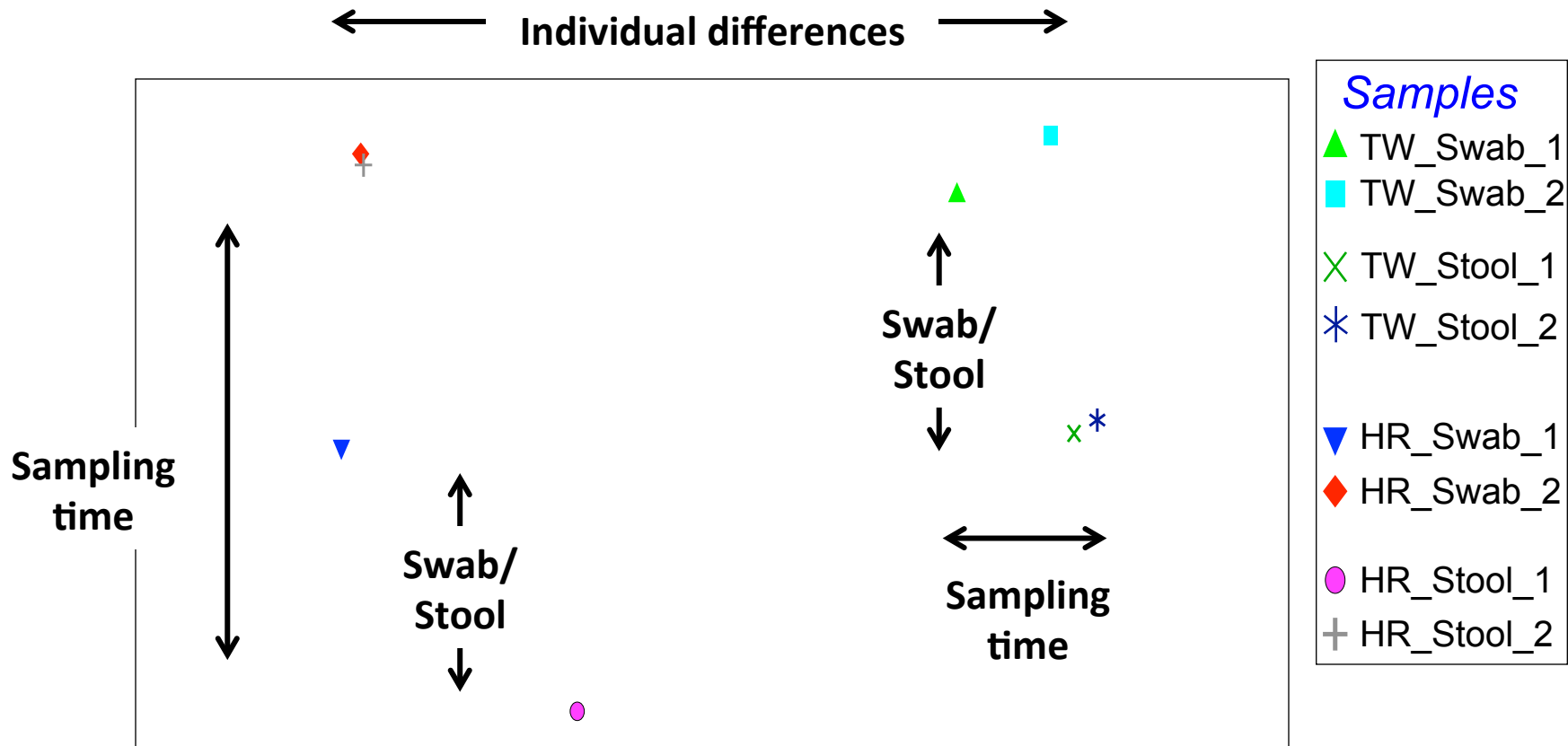
* = 100,000 PBMC pellet once to SU on 10/16/14



Only 36 hours prior – in space!



We can already see differences in the twins



- A shift in community structure was observed between time points one and two in both individuals.

Two Options:

1. Bring Samples Back

- Frozen
- Ambient

2. Sequence in Space

MinION sequencer (v5 chemistry)

Launch planned for June 2016

www.nasa.gov/mission_pages/station/research/experiments/2181.html

ISS biomolecular sequencer



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Biomolecule Sequencer (Biomolecule Sequencer) - 03.10.16

[Overview](#) | [Description](#) | [Applications](#) | [Operations](#) | [Results](#) | [Publications](#) | [Imagery](#)

ISS Science for Everyone

Science Objectives for Everyone

Living organisms contain DNA, or deoxyribonucleic acid, and sequencing DNA is a powerful way to understand how they respond to changing environments. The Biomolecule Sequencer investigation seeks to demonstrate, for the first time, that DNA sequencing is feasible in an orbiting spacecraft. A space-based DNA sequencer could identify microbes, diagnose diseases and understand crew member health, and potentially help detect DNA-based life elsewhere in the universe.

Science Results for Everyone

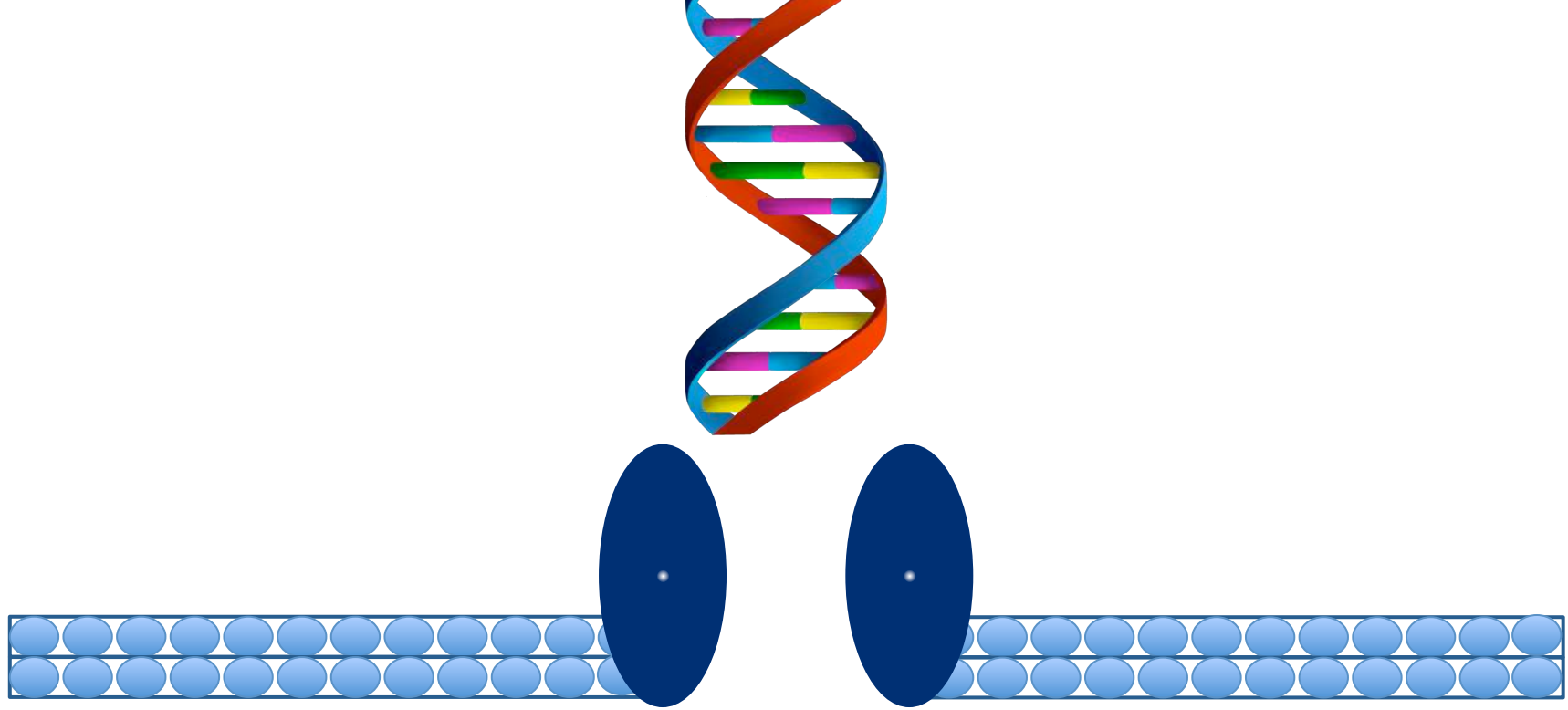
Information Pending

The following content was provided by Aaron Burton, Ph.D., and is maintained in a database by the ISS Program Science Office.

Experiment Details

OpNom: Biomolecule Sequencer





Zero-G Pipetting: Hardest Lab Job Ever



Dr. Andrew Feinberg

Zero-gravity genomics passes first test

Two experiments demonstrate sample transfer and sequencing in a low-gravity environment.

[Chris Cesare](#)

13 October 2015

[Rights & Permissions](#)

After 160 swoops in NASA's zero-gravity aeroplane, researchers have the first evidence that genetic sequencing can be done in space.





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- Med Ed Webinars

Selected Areas of Concentration (AOC) Summaries and Contact Information

Listed below are some selected Areas of Concentration that have been established. Many others are in different stages of development by the faculty. Students are encouraged to consider developing their own Area of Concentration.

Updated January 26, 2016

Addiction and Trauma in Special Populations

Addiction Medicine

Aerospace Medicine, Space Genetics and Technology

Autoimmune and Inflammatory Disease

Cancer Biology and Therapy

Cardiometabolic Disease and Prevention

Community and Public Health

- AOC Home
- List of AOCs
- Scholarly Project
- Core Activities
- Timelines

-
- AOC Canvas Page
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HOME

ABOUT US

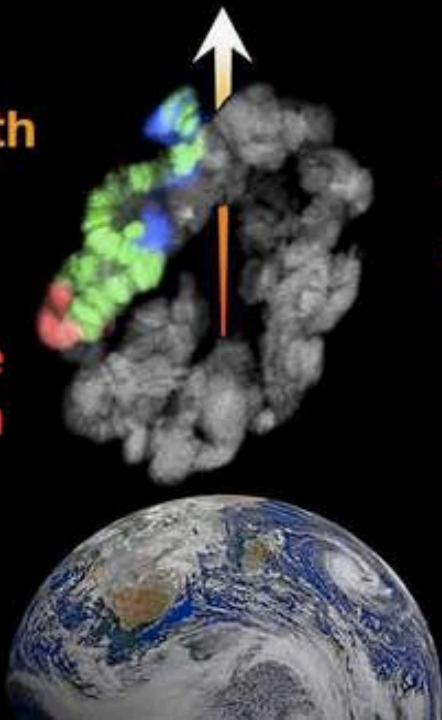
FACULTY

CONTACT US

**To Protect
Human Health**

**To Promote
Exploration**

**To Sustain
Our Planet**

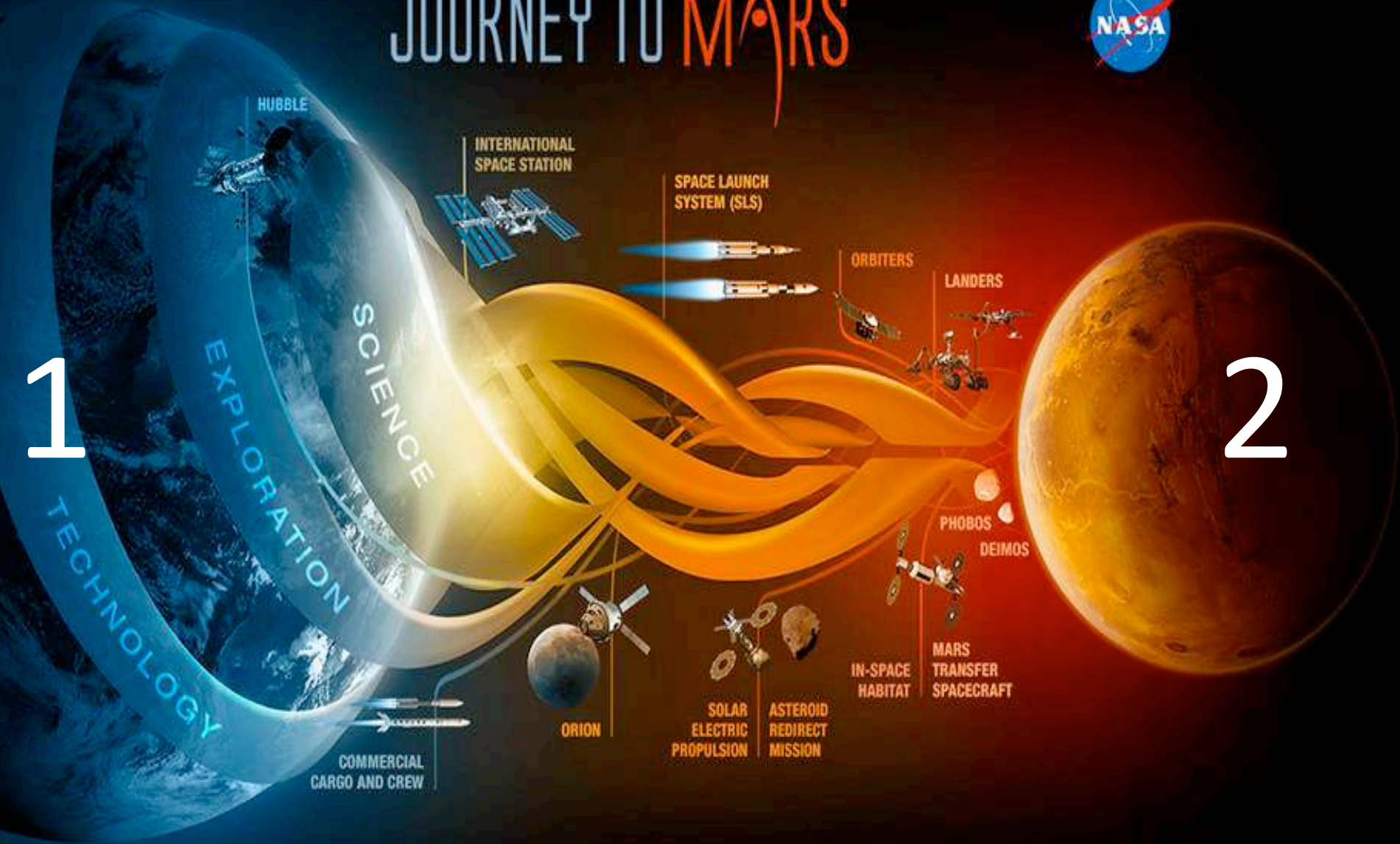


JOURNEY TO MARS



1

2



Conclusions

- The subway is safe
- Forensics applies across all kingdoms of life
- Multi-disciplinary science is fantastic
- Space is Hard
- First demonstration of zero-gravity sequencing
 - Some optimization of the current and input is needed, but indeed we could potentially sequence on Mars or the ISS

These People are Awesome





INTERNATIONAL
SPACE STATION
EXPEDITION XLV
THE SCIENCE CONTINUES

Thanks to the Swabbing Teams! www.pathomap.org/people/



Weill Cornell Medical College



Mount Sinai



AMERICAN MUSEUM OF NATURAL HISTORY



Queens College



New York University



York College



John Jay College



Fordham University



Brooklyn College

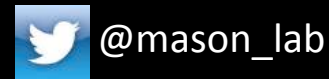


State University of New York (SUNY) Downstate



City University of New York (CUNY)

Gratitude to Many People and Places



Mason Lab

Ebrahim Afshinnekoo
Sofia Ahsanuddin
Noah Alexander
Pradeep Ambrose
Marjan Bozinoski
Dhruva Chandramohan
Sagar Chhangawala
Shanin Chowdhury
Jorge Gandara
Francine Garrett-Bakelman
Elizabeth Hénaff
Sheng Li
Alexa McIntyre
Cem Meyden
Lenore Pipes
Darryl Reeves
Yogesh Saletore
Priyanka Vijay

HudsonAlpha

Shawn Levy

NYU

Jane Carlton
Julia Maritz



Cornell/WCMC

Jason Banfelder
Scott Blanchard
Selina Chen-Kiang
Olivier Elemento
Yariv Houvras
Samie Jaffrey
Ari Melnick
Margaret Ross
Adam Siepel
Epigenomics Core

FDA/SEQC/Fudan Univ.

Leming Shi

NIH/UDP/NCBI

Jean & Danielle Thierry-Mieg

Icahn/MSSM

Eric Schadt, Andrew Kasarskis,
Joel Dudley, Ali Bashir,
Bobby Sebra

UMMS

Maria E Figueroa

Horner Lab

Stacy Horner

Yale University

Nenad Sestan
Sherman Weissman

ABRF

George Grills
Scott Tighe
Don Baldwin

Univ. Chicago

Yoav Gilad



Illumina

Gary Schroth
Marc Van Oene

Baylor

Jeff Rogers

MSKCC

Christina Leslie
Ross Levine

AMNH

George Amato
Mark Sidall

