“Revealing the Dynamics of an Individual’s Gut Microbiome Dynamics”

Invited Seminar
Gordon Lab at WashU Medicine
Washington University in St. Louis
May 13, 2025

Dr. Larry Smarr
Founding Director Emeritus, California Institute for Telecommunications and Information Technology;
Distinguished Professor Emeritus, Dept. of Computer Science and Engineering
Jacobs School of Engineering, UCSD
http://lsmarr.net

UC San Diego

Abstract

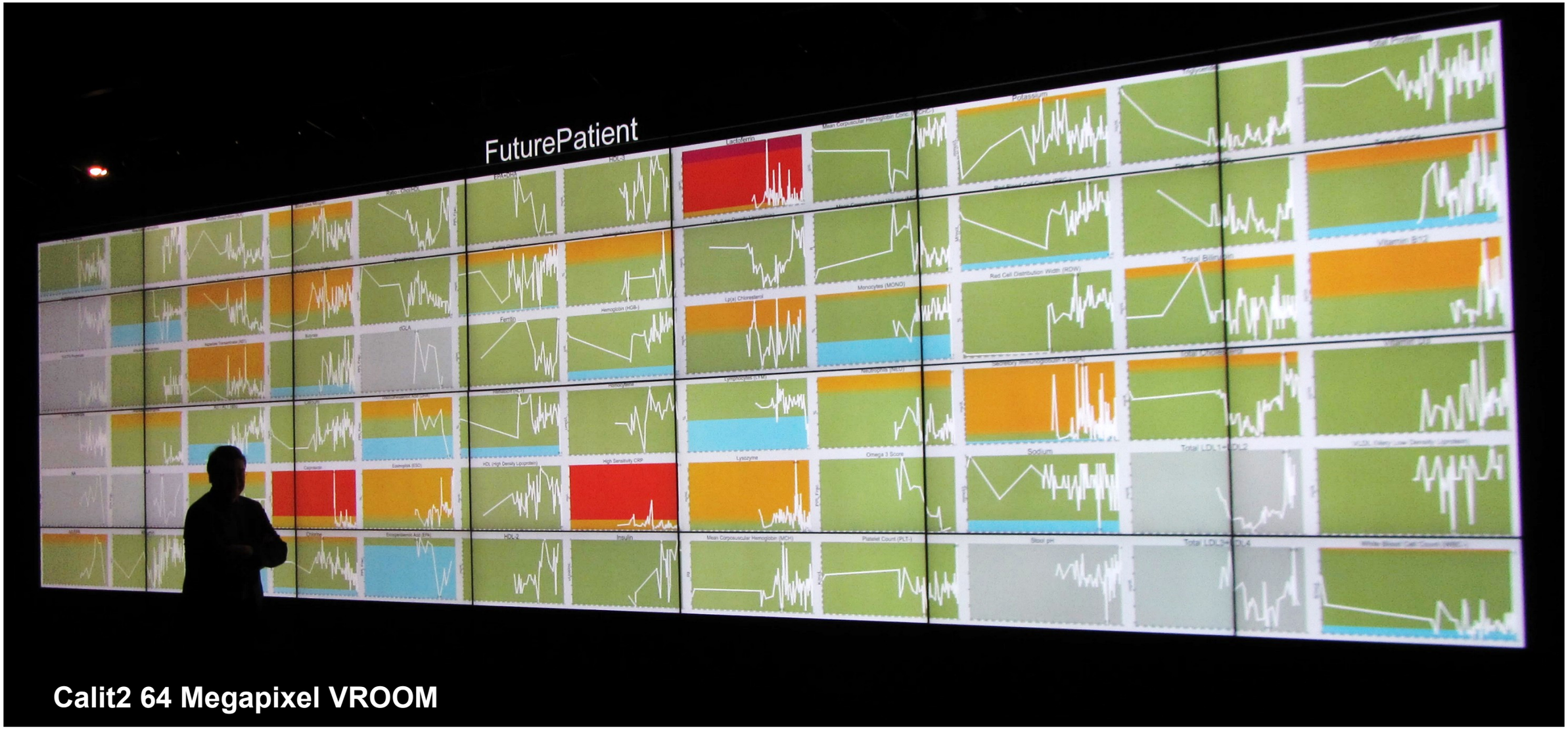
I will describe my decade-long experiment in collecting 700 daily samples of my stool, which are genomically analyzed in the UCSD Knight Lab, using 16s and short and long read metagenomics.

Machine learning reveals the microbiome's ecological dynamics under a variety of medical interventions and dietary shifts.

Computational models uncover the highly dynamic metabolite production of the gut microbiome and its coupling to other organs.

UC San Diego

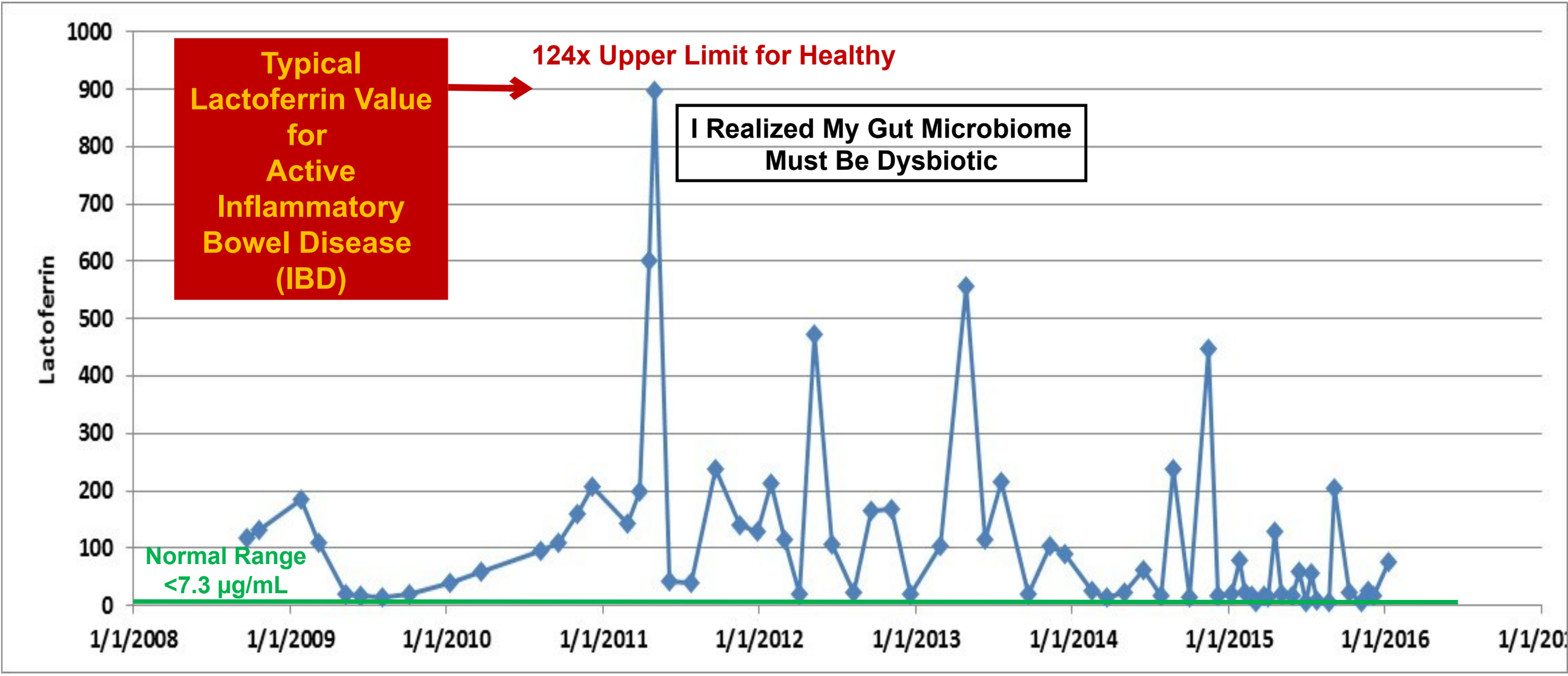
For the Last a Decade I Have Been Exploring the Application of Data Science to My Blood and Stool Biomarkers Time Series in a Clinical Setting



Calit2 64 Megapixel VROOM

UC San Diego

I Discovered An Antibacterial Human Immune Protein from My Stool Exhibited Dynamic Behavior

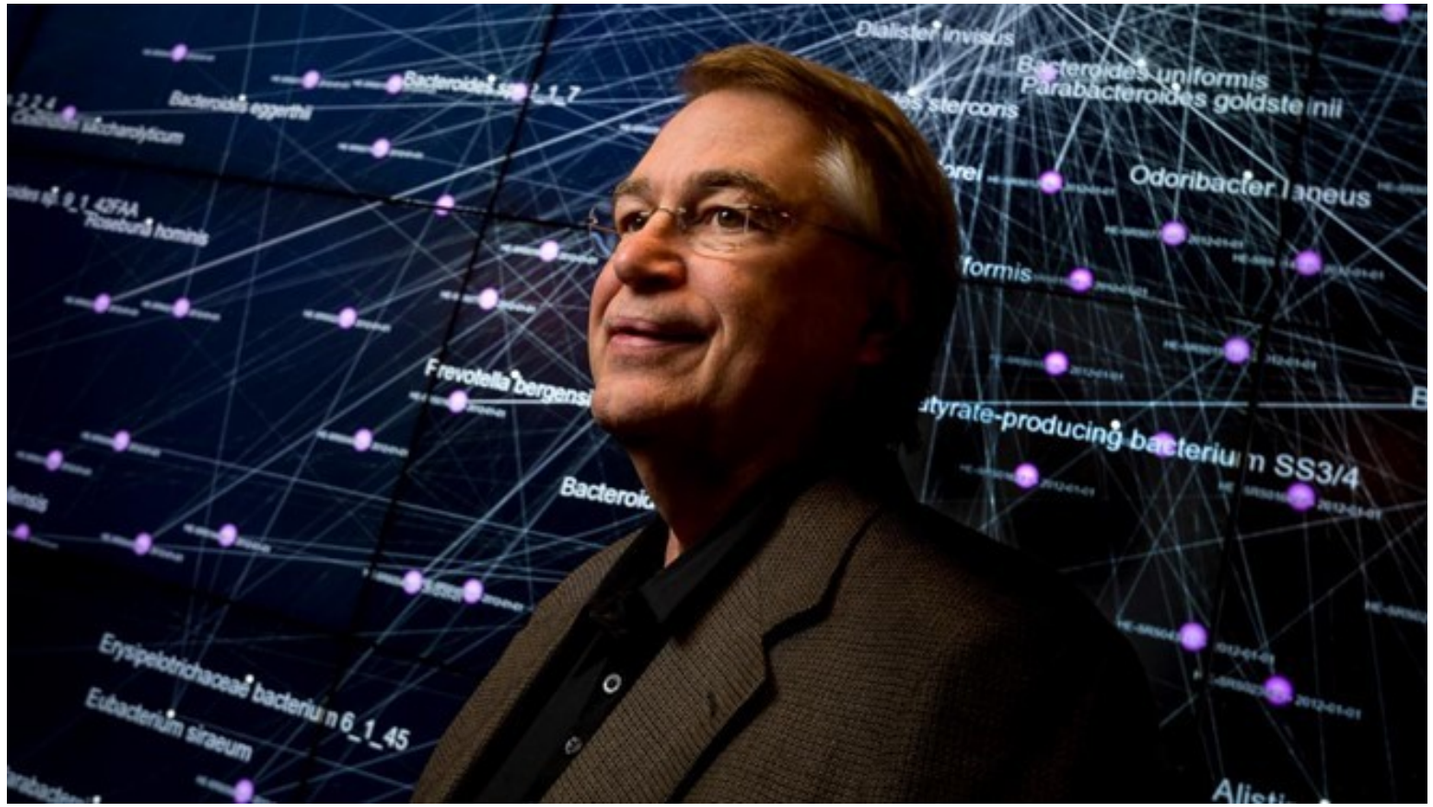


UC San Diego

Lactoferrin is a Protein Shed from Neutrophils - An Antibacterial that Sequesters Iron

This Led to the "Future Patient" Project: An N=1 High Time-Frequency Multi-Variable Time Series

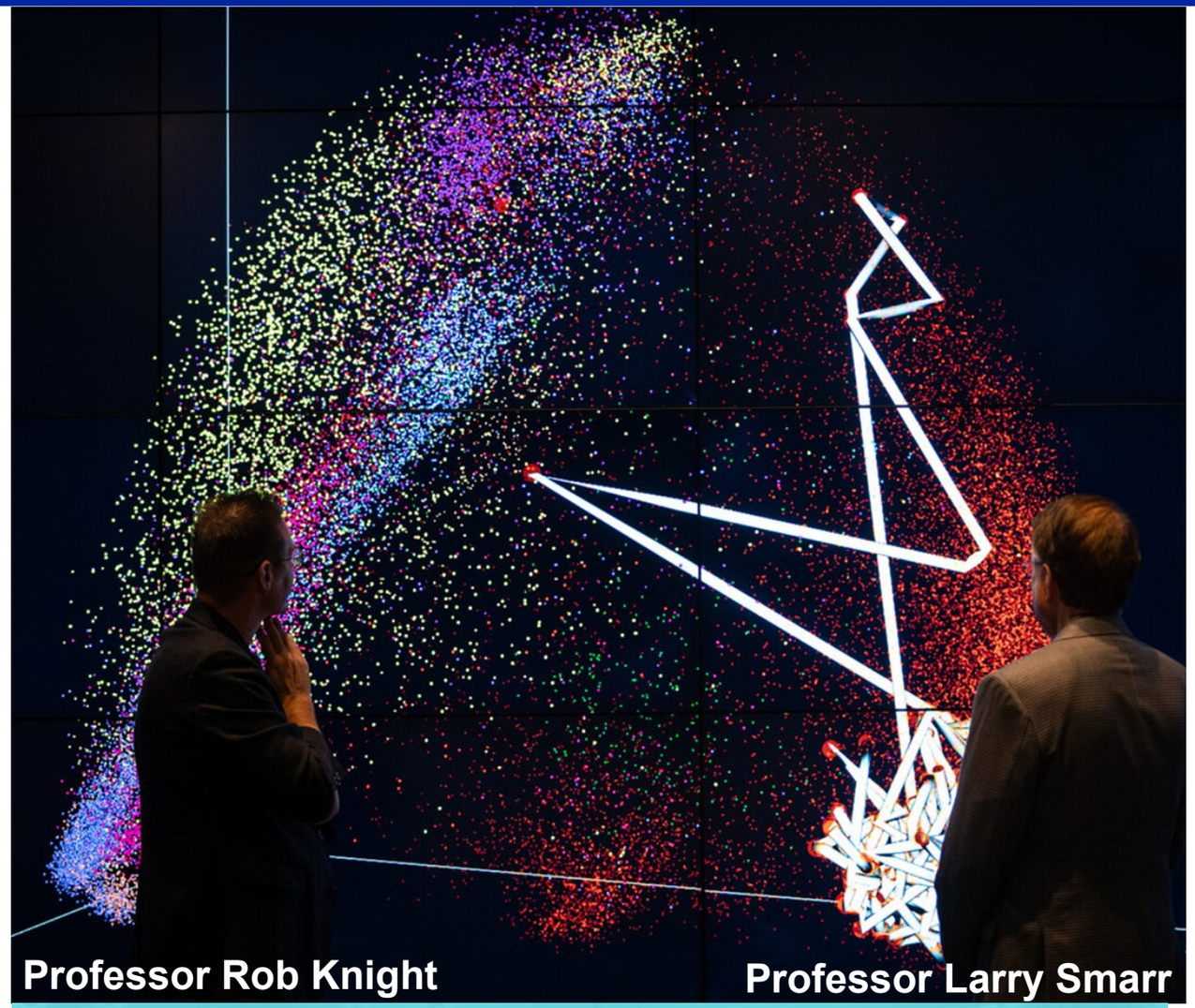
- **Over 700 Daily Frozen (-80°) Stool Samples From One Individual Over 11 Years**
  - ~420 16S Sequenced Samples
  - ~80 Metagenomics Sequenced Samples
  - ~8 Metaproteomic Mass Spec Samples
  - Stored and Sequenced in the UCSD Knight Lab
- **~167 Days of Stool Lab Results**
  - Immune/Inflammatory Biomarkers
  - SCFA
- **~155 Days of Blood Samples**
  - ~200 Biomarkers
- **A lot of dietary/medical history**
- **...and more!**



UC San Diego

For the Last Decade, Analysis of My Personal Microbiome Ecology Dynamics Has Been Done in Rob Knight's UCSD Center for Microbiome Innovation

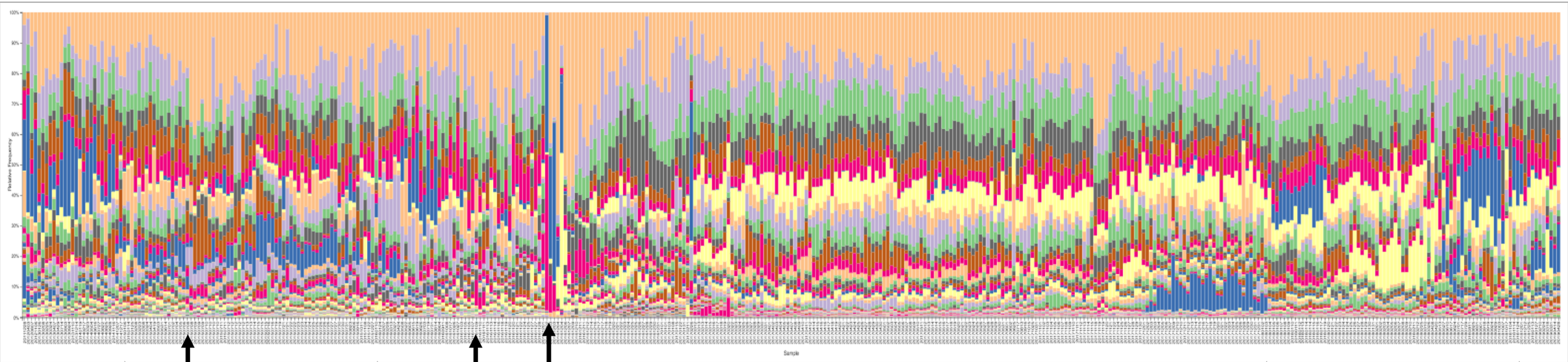
- 1995 Carl Woese, UIUC
- 2005 Moore Foundation CAMERA
- 2012 JCVI Sequencing
- 2014 Recruiting Rob Knight



UC San Diego

Gut Microbiome Ecological Dynamics Revealed by 16S Genomic Sequencing of ~400 Smarr Daily Stool Samples Over 8 Years

Taxonomic Stacked Bar Plot of 16S Relative Abundance (Colors Represent Different Genus)



2015

2016

2017

2018

Colonoscopy
(July 7, 2015)

Resection Surgery
(November 29, 2016)

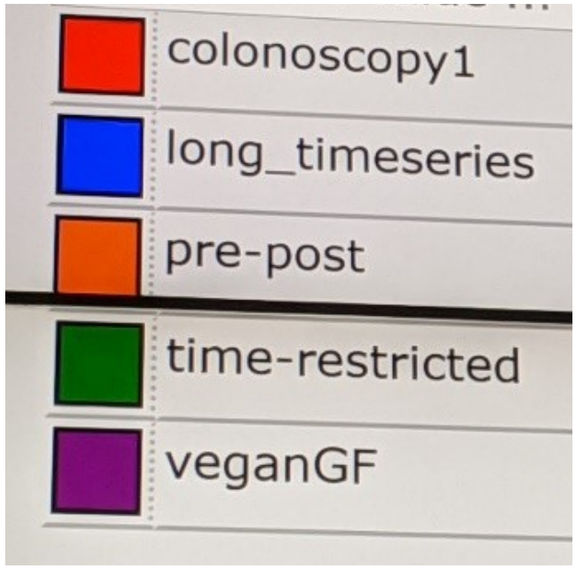
Colonoscopy
(November 8, 2016)

December 28, 2011

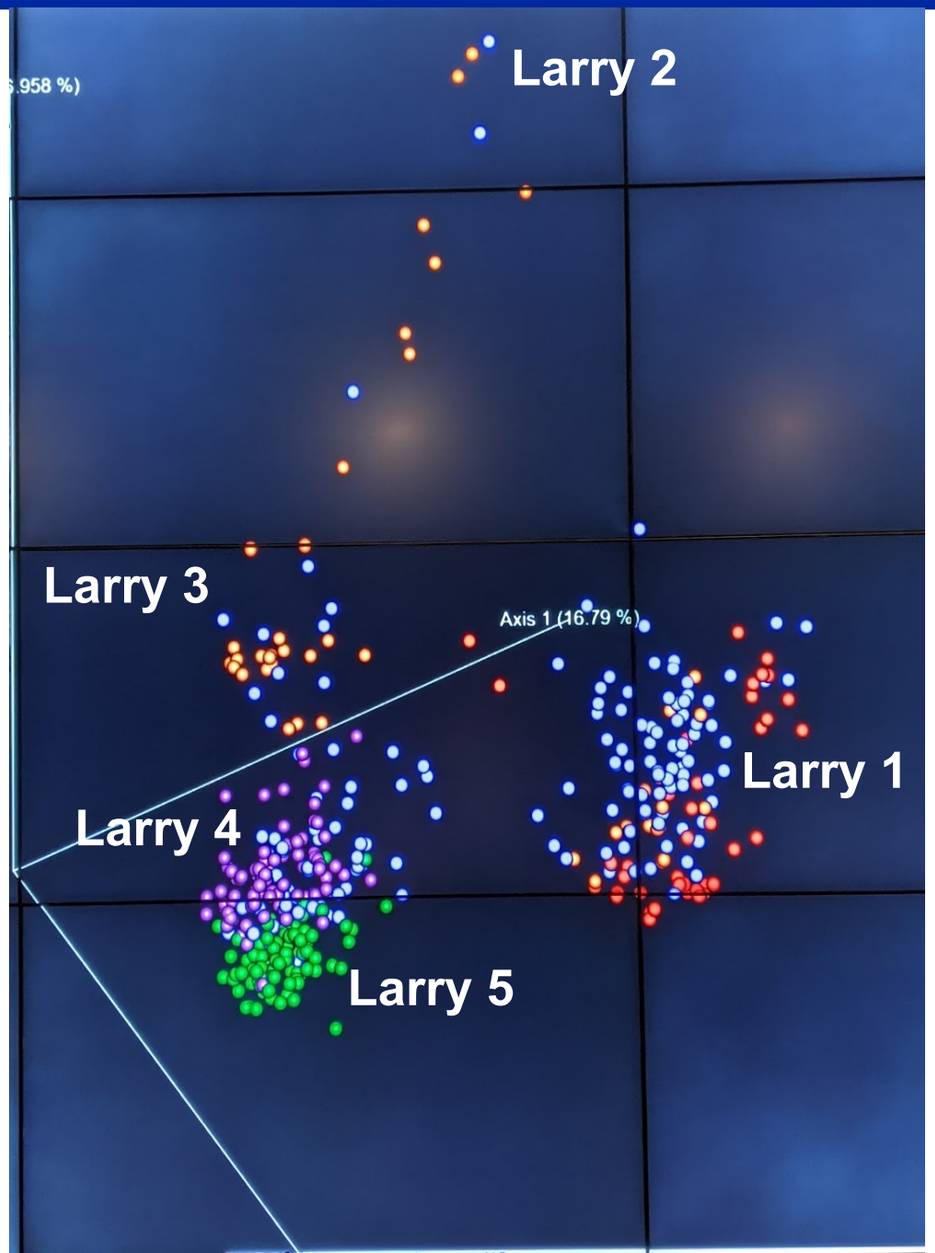
April 28, 2019

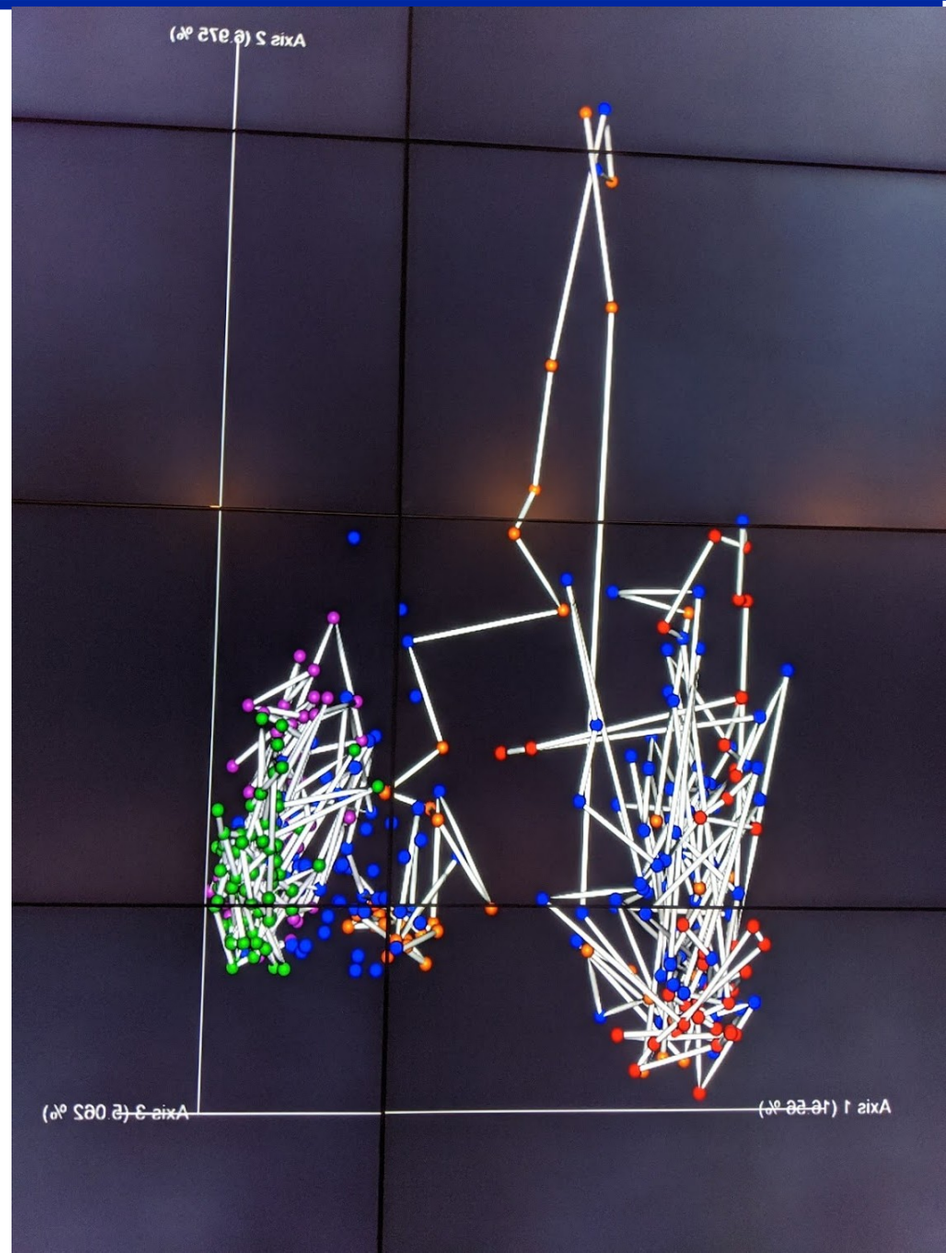
UC San Diego

16S Machine Learning (PCA) Reveals I Became Five Different People Over 8 Years: First Three Were IBD Pre- and Post Surgery, Last Two From Dietary Changes



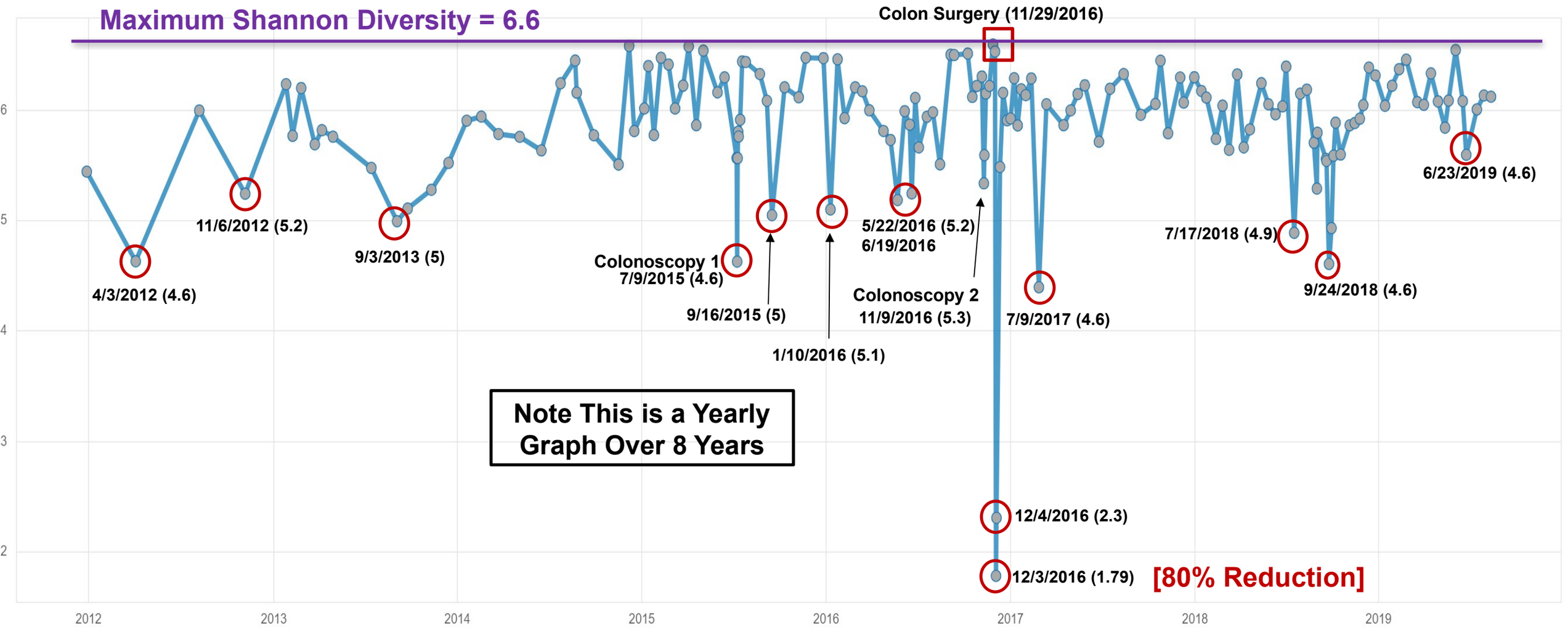
Note: Each Dot is a Single Day with a Full Gut Microbiome Ecology Consisting of 50 Genus, Each with a Relative Abundance





UC San Diego

The Shannon Diversity of My Gut Microbiome Ecology Has Many Abrupt Drops-Some Caused by Medical Interventions



UC San Diego

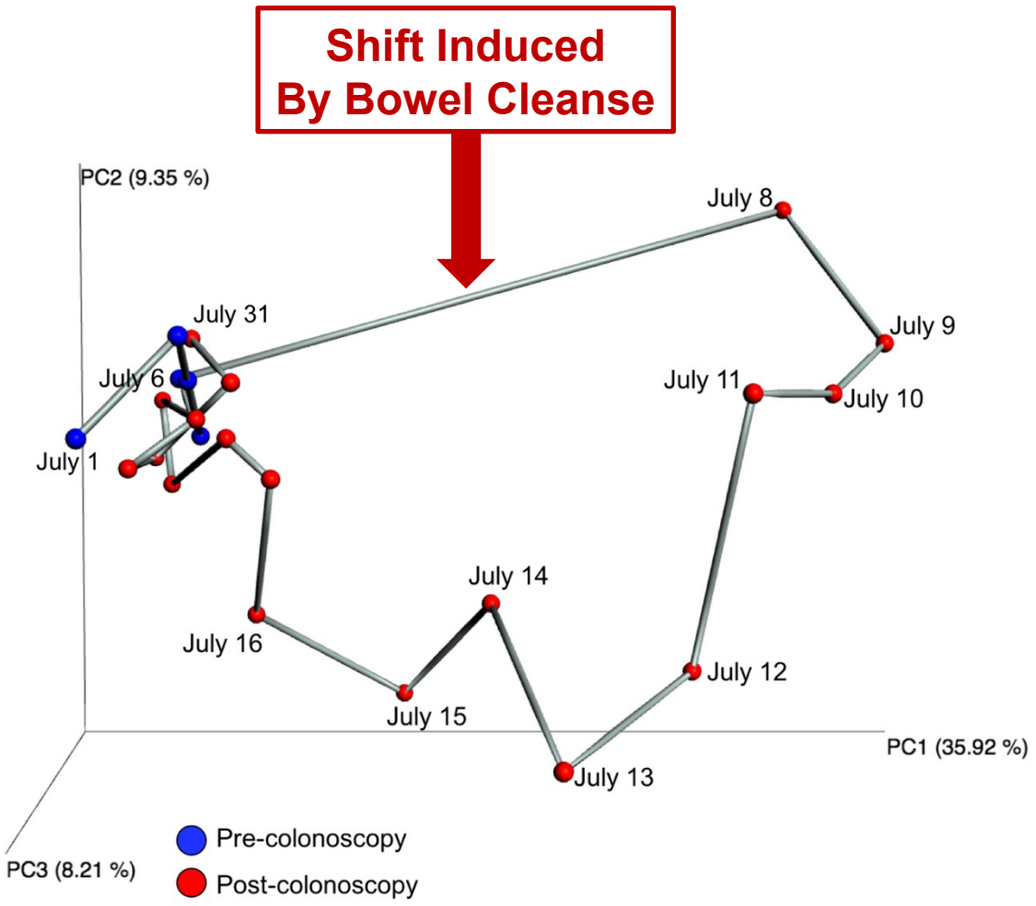
Previous Graph

Experiment #1
Discovering Impact of Colonoscopy on Gut Microbiome Ecology

UC San Diego

My Microbiome Ecology Was Highly Disrupted by a Common Medical Intervention, But Eventually Returned to the Prior State

July 2015 Colonoscopy



Tracking Human Gut Microbiome Changes Resulting from a Colonoscopy

Larry Smarr[1,2,5]; Embriette R. Hyde[4]; Daniel McDonald[4]; William J. Sandborn[2,3]; Rob Knight[2,4,5]

[1]University of California San Diego, Calit2, La Jolla, CA, USA; [2]University of California San Diego, Center for Microbiome Innovation, La Jolla, CA, USA; [3]University of California San Diego, Gastroenterology, San Diego, CA, USA; [4]University of California San Diego, Pediatrics, La Jolla, CA, USA; [5]University of California San Diego, Computer Science and Engineering, La Jolla, CA USA

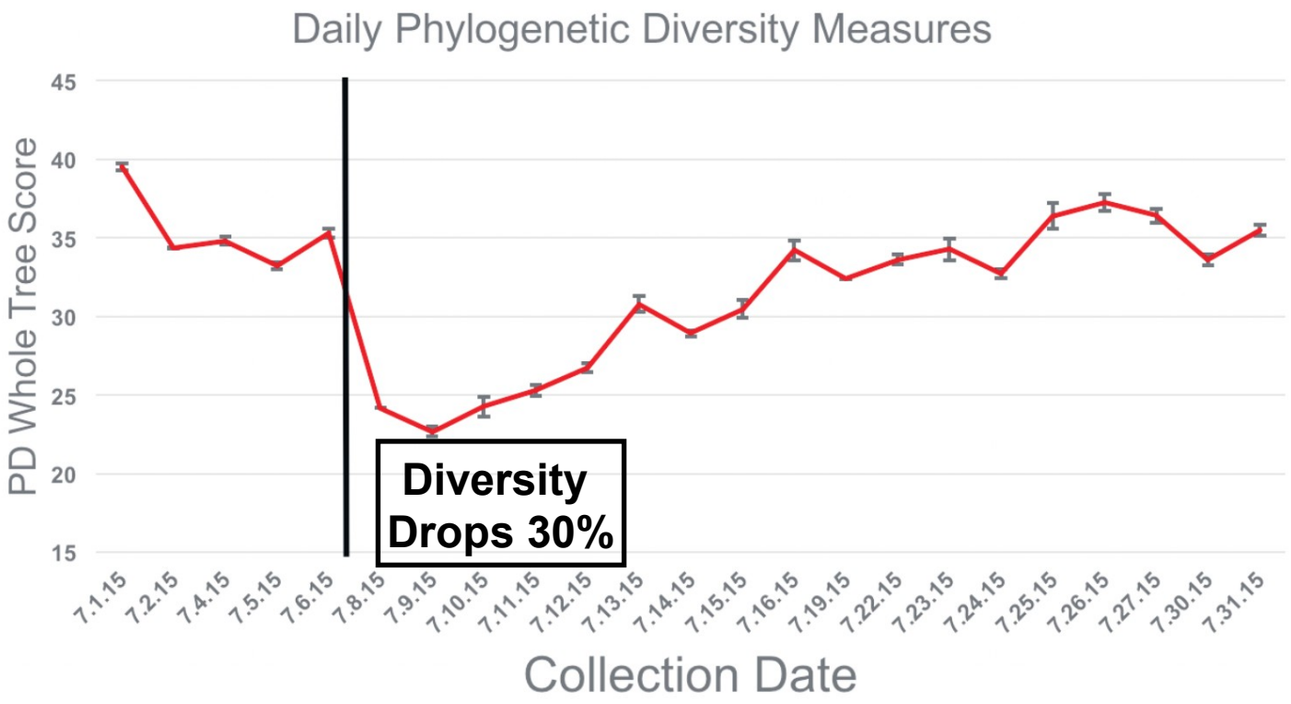
Methods Inf Med. 56, 442-447 (2017)

Machine Learning Principal Component Analysis: Each Dot is a Single Day with a Full Gut Microbiome Ecology Consisting of 50 Genus, Each with a Relative Abundance

UC San Diego

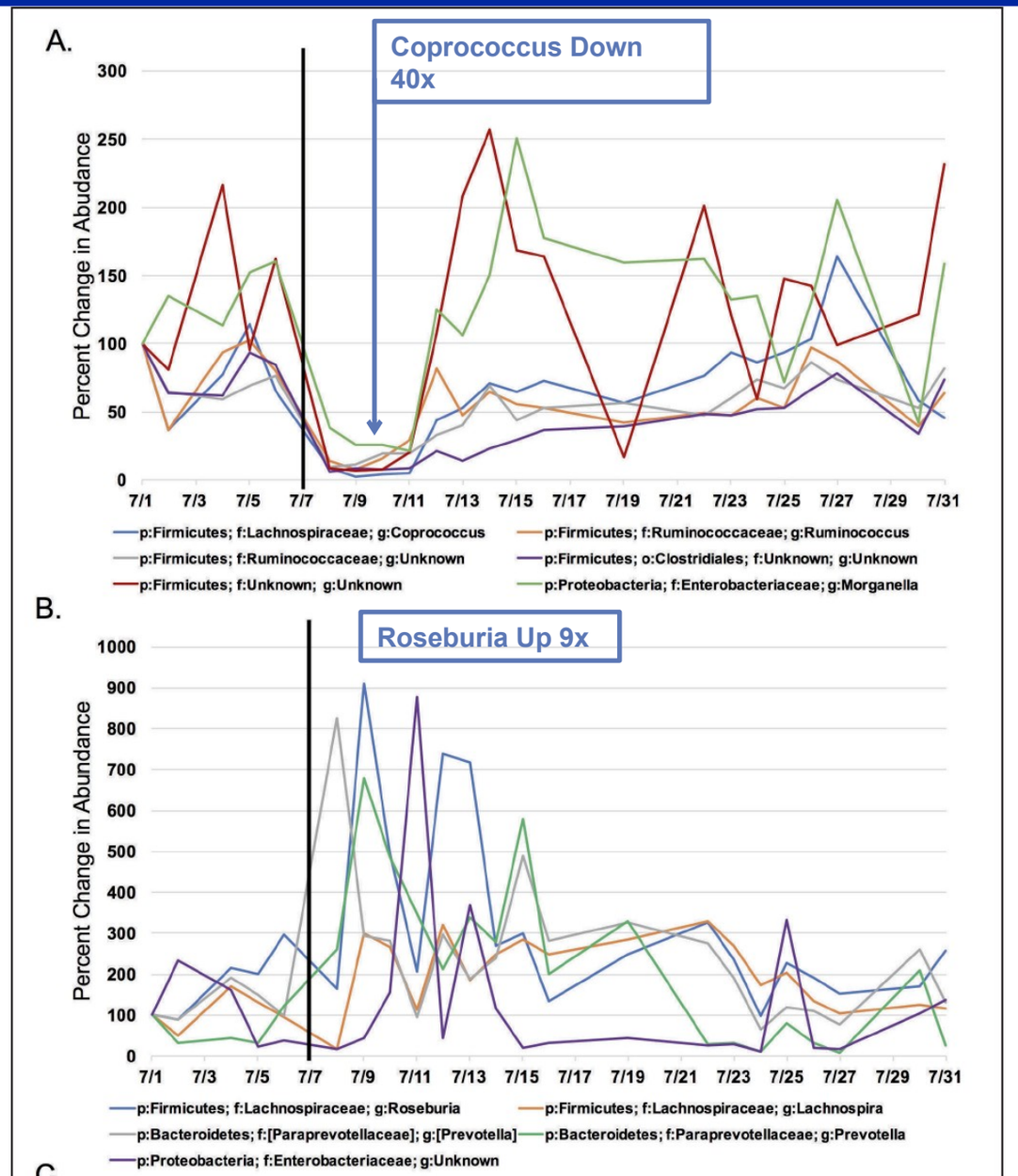
In the 2-3 Days Following Colon Cleanse There is a 50% Drop in Ecological Diversity and Major Changes in Microbial Genus Relative Abundance

Prior Literature Concluded:
"Changes in Taxon Relative Abundance Up to 3X Were Observed Post-Colonoscopy"



Diversity Drops 30%

15 Million Colonoscopies Are Performed in the US Each Year

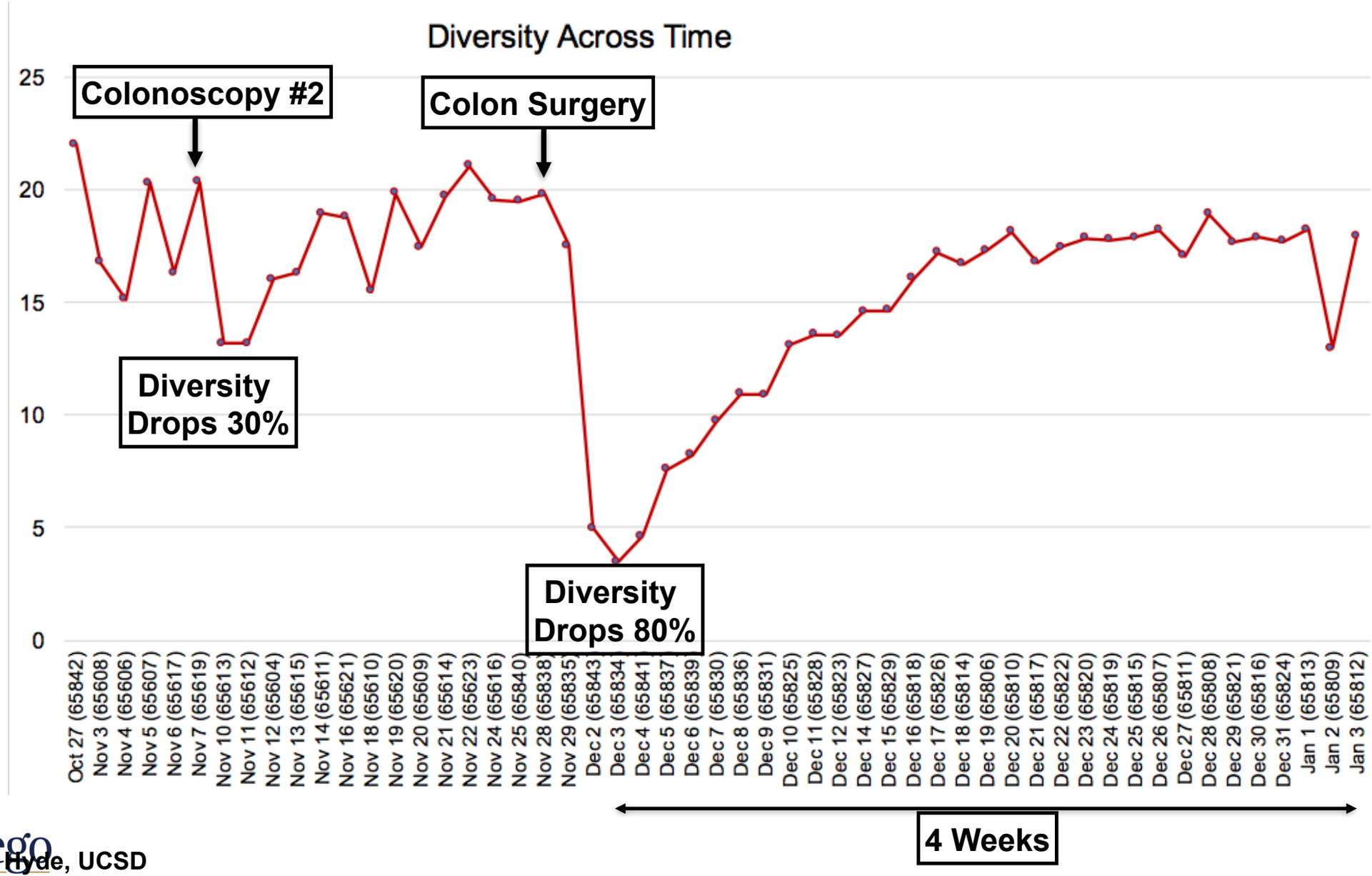


UC San Diego

Experiment #2
Discovering Impact of Colon Surgery on Gut Microbiome Ecology

UC San Diego

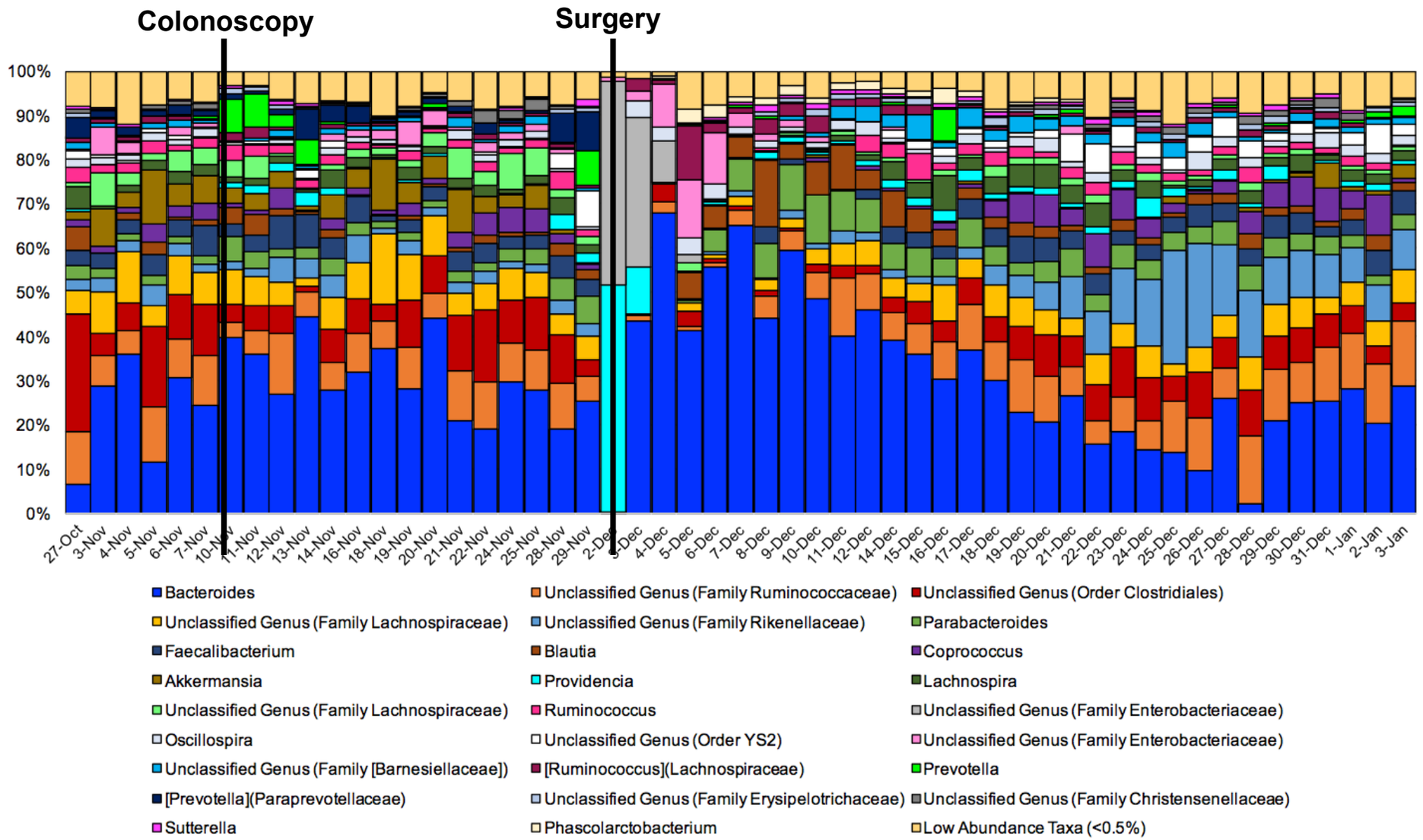
Sigmoid Colon Resection Surgery Wiped Out My Gut Microbiome Ecological Diversity: It Slowly Recovered Over a Month, But To a New State



UC San Diego

Source: Embriette Hyde, UCSD

Major Gut Microbiome Drop in Diversity Seen from 16S Genus Profiles: Daily Samples Before and After Abdominal Surgery

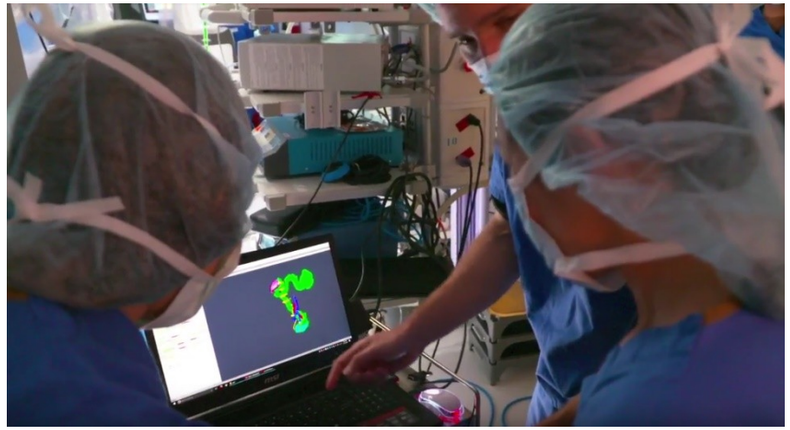


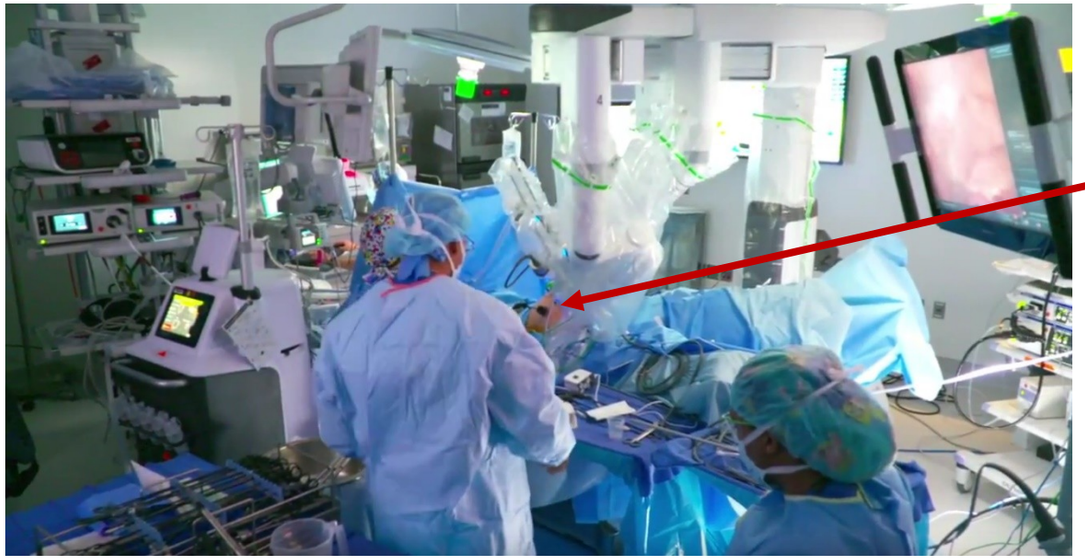
UC San Diego

Source: Embriette Hyde, UCSD

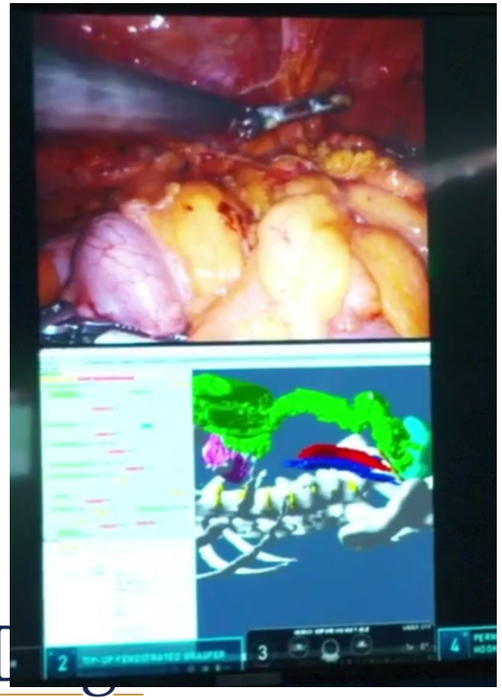
Dr. Ramamoorthy Used Calit2 Interactive 3D Anatomy To Guide Her Surgical Team During My Sigmoid Colon Resection on November 29, 2016

Dr. Schulze Rotating 3D Organs To Match Up With da Vinci Arms and Internal Camera



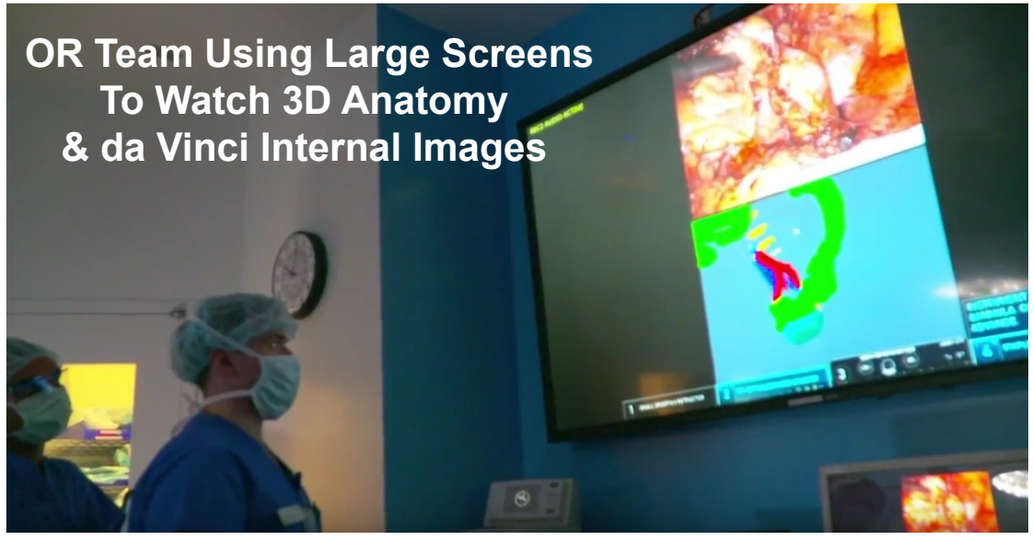


Patient Smarr With da Vinci Robot Arms Inside Him





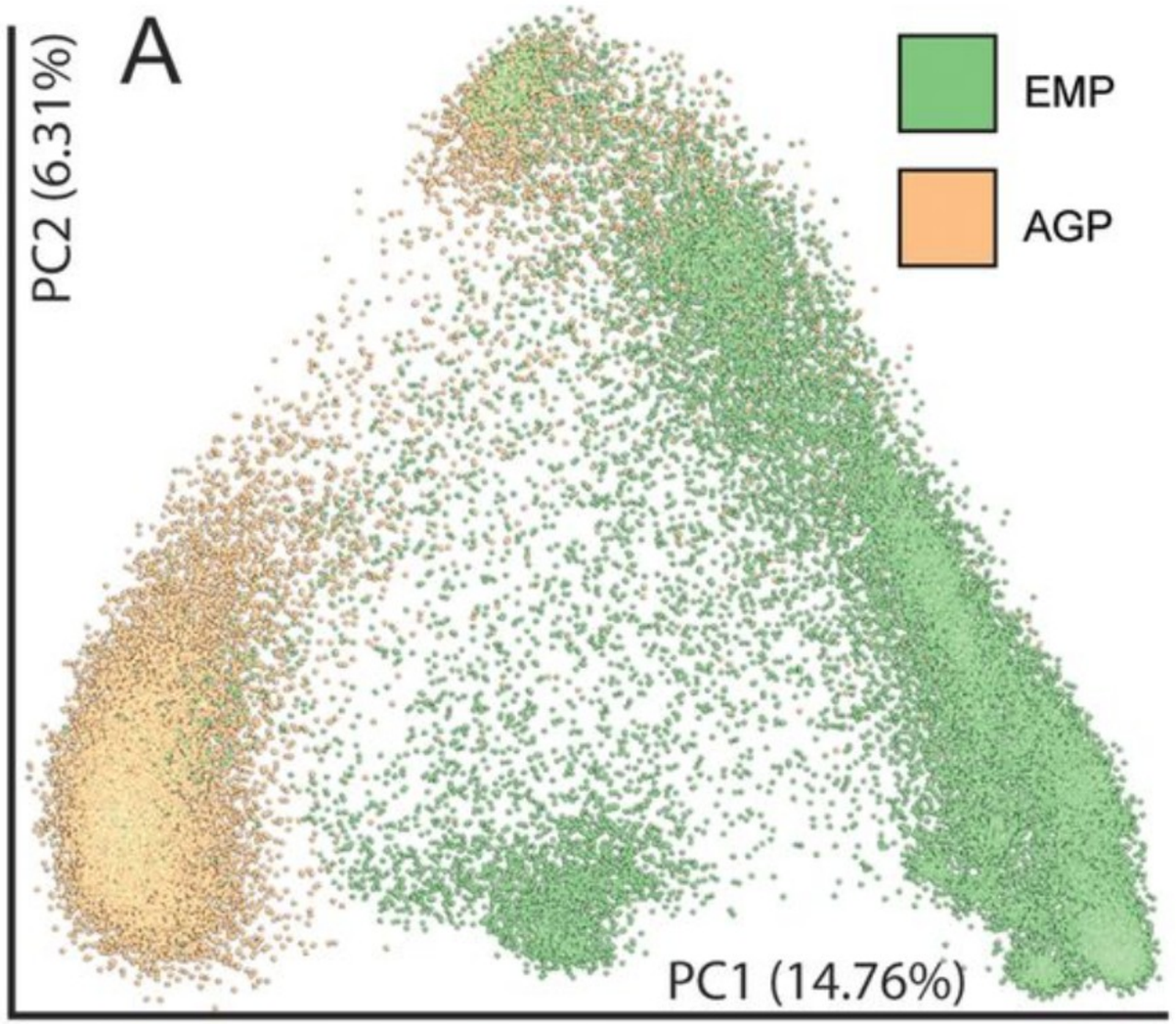
Dr. Ramamoorthy Operating da Vinci Xi Robot During Surgery

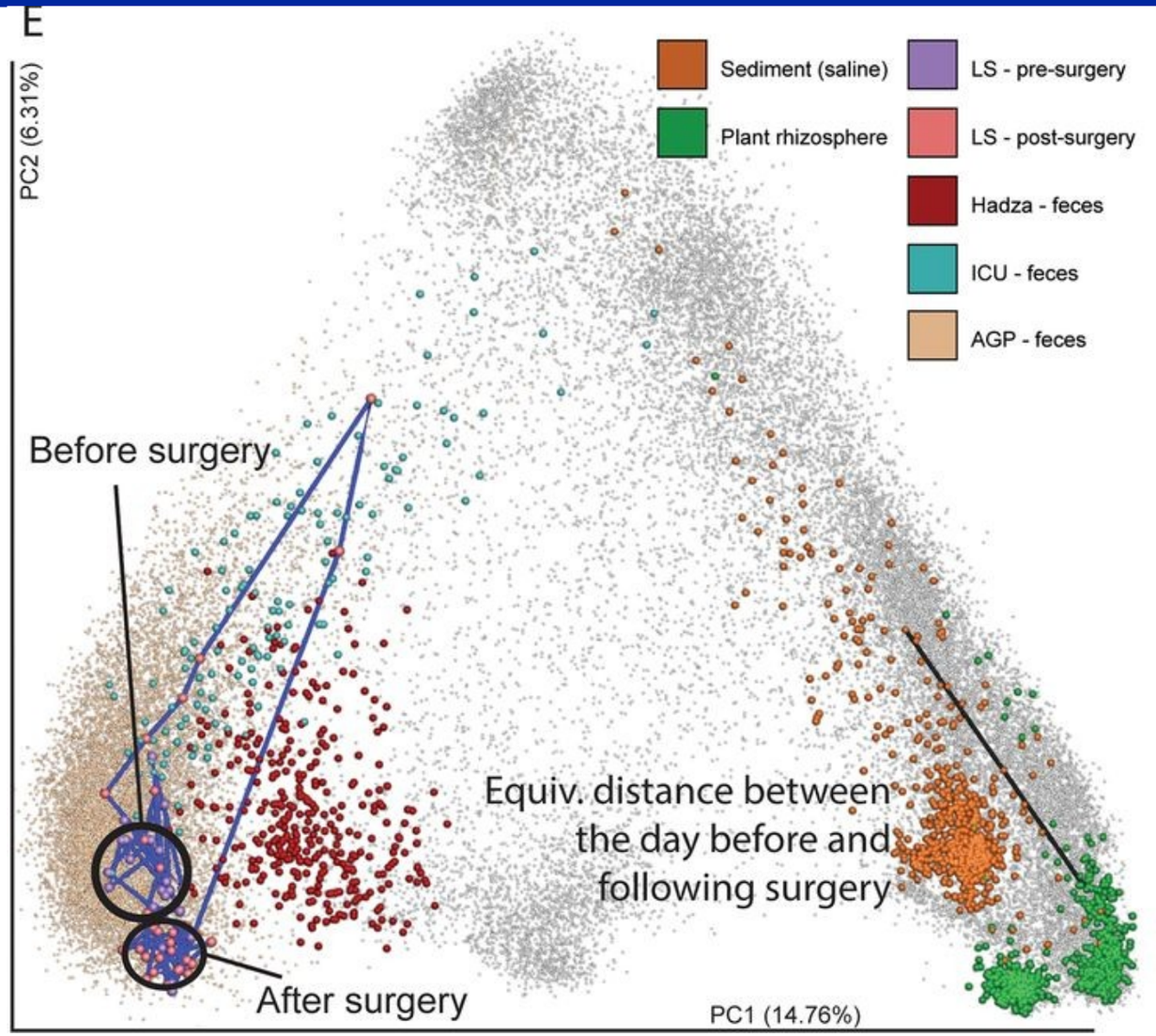


https://lsmarr.net/look-twice-cut-once/

UC San D

My Gut Microbiome Changed More After Colon Resection Surgery Than the Difference Between 10,000 Individuals in the American Gut Project!





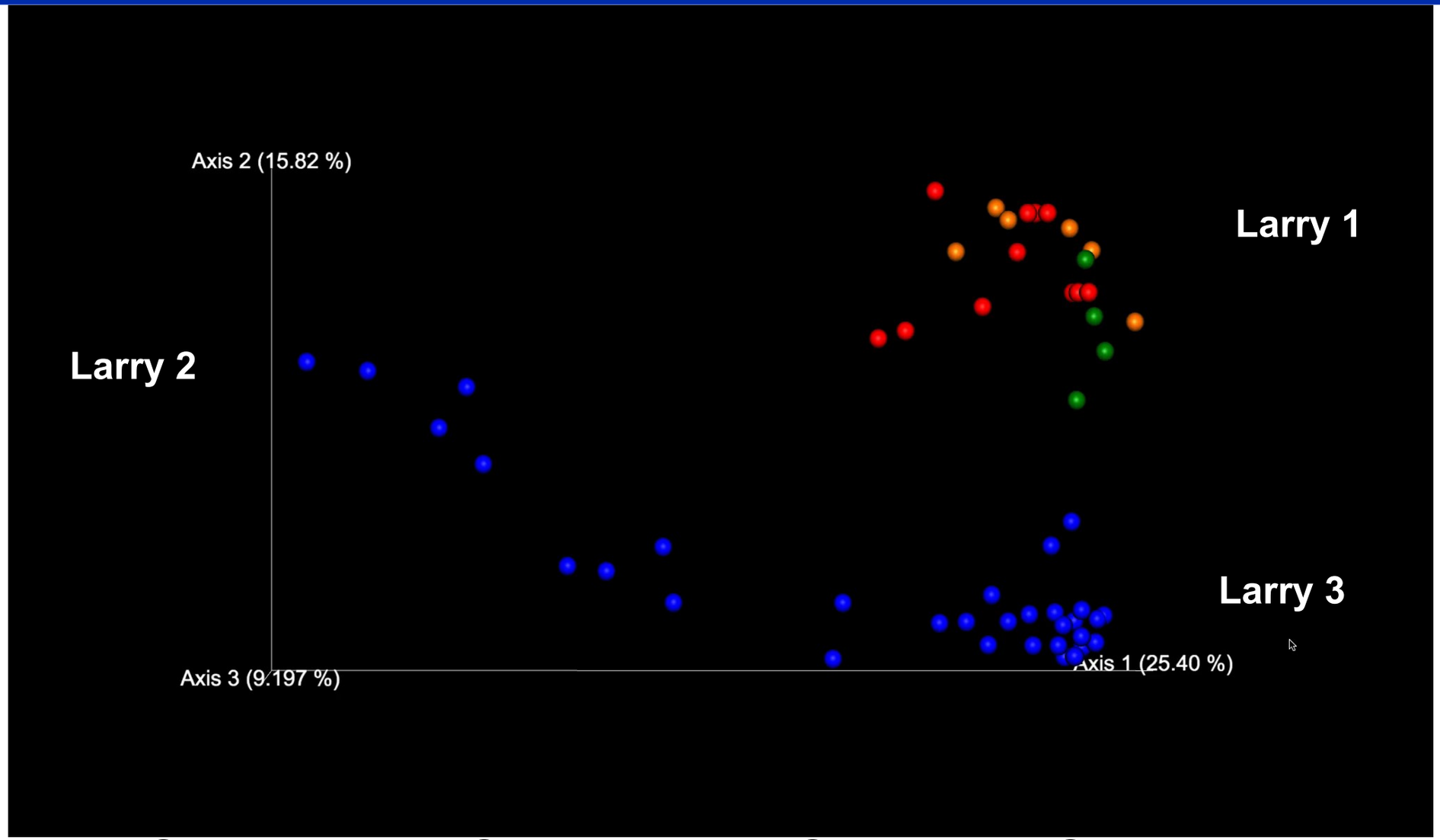
AMERICAN SOCIETY FOR MICROBIOLOGY | mSystems®

American Gut: an Open Platform for Citizen Science Microbiome Research

Daniel McDonald et al. mSystems 2018;
doi:10.1128/mSystems.00031-18

Principal Component Analysis (PCA) Reveals Major Shift in Gut Microbiome Ecology Following Abdominal Surgery With Return to Different Equilibrium State

Each Dot is That Day's Microbiome Ecology Projected Into 3-Space Using PCA Dimensional Reduction to Reveal Clusters Of Similar Ecologies



58 Samples
10/27/2016 - 1/3/2017

Inflamed Disease State

⇩

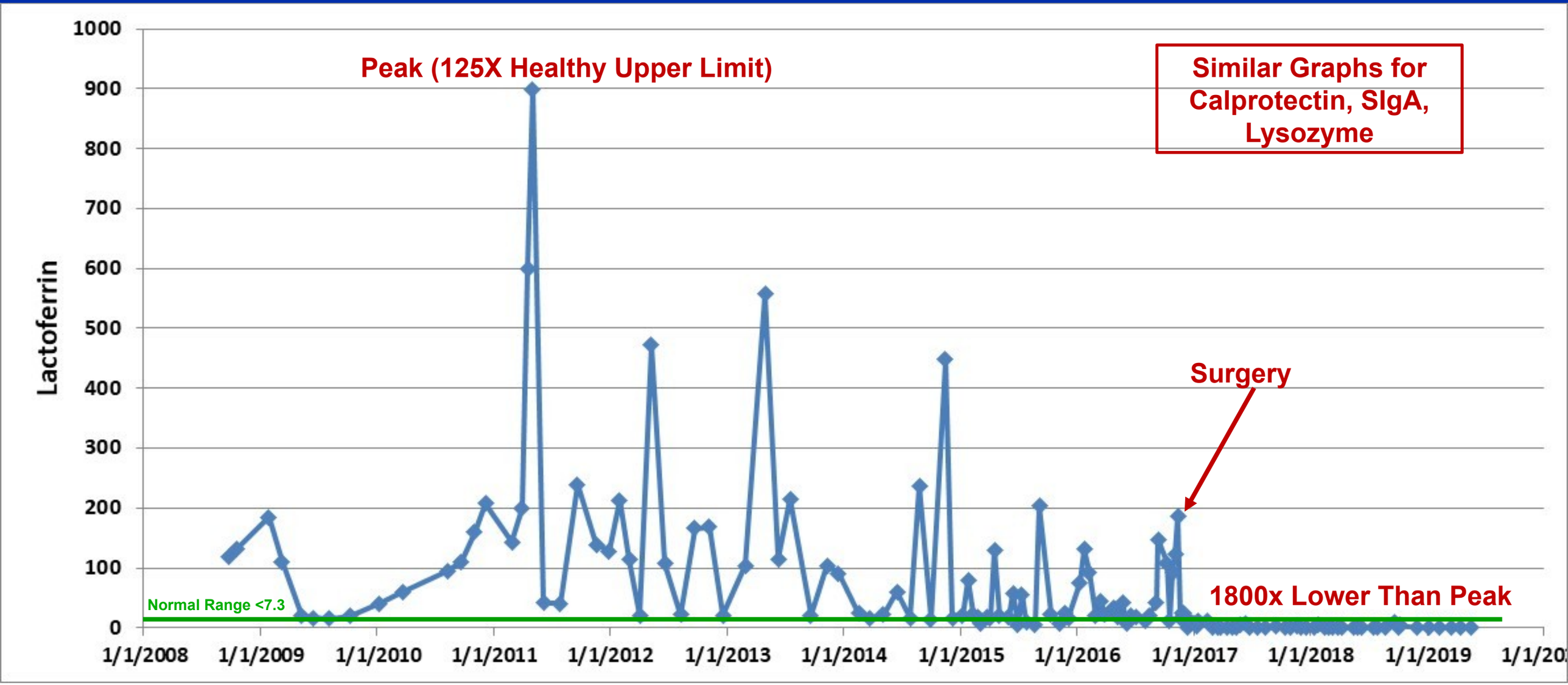
Healthy Post-Surgery State

Pre-colonoscopy Post-colonoscopy Pre-surgery Post-surgery

UC San Diego

Source: Embriette Hyde, Yoshiki Vázquez Baeza, Knight Lab, UCSD

Colonic Inflammation:
Abrupt Shift to Healthy Following Surgical Resection



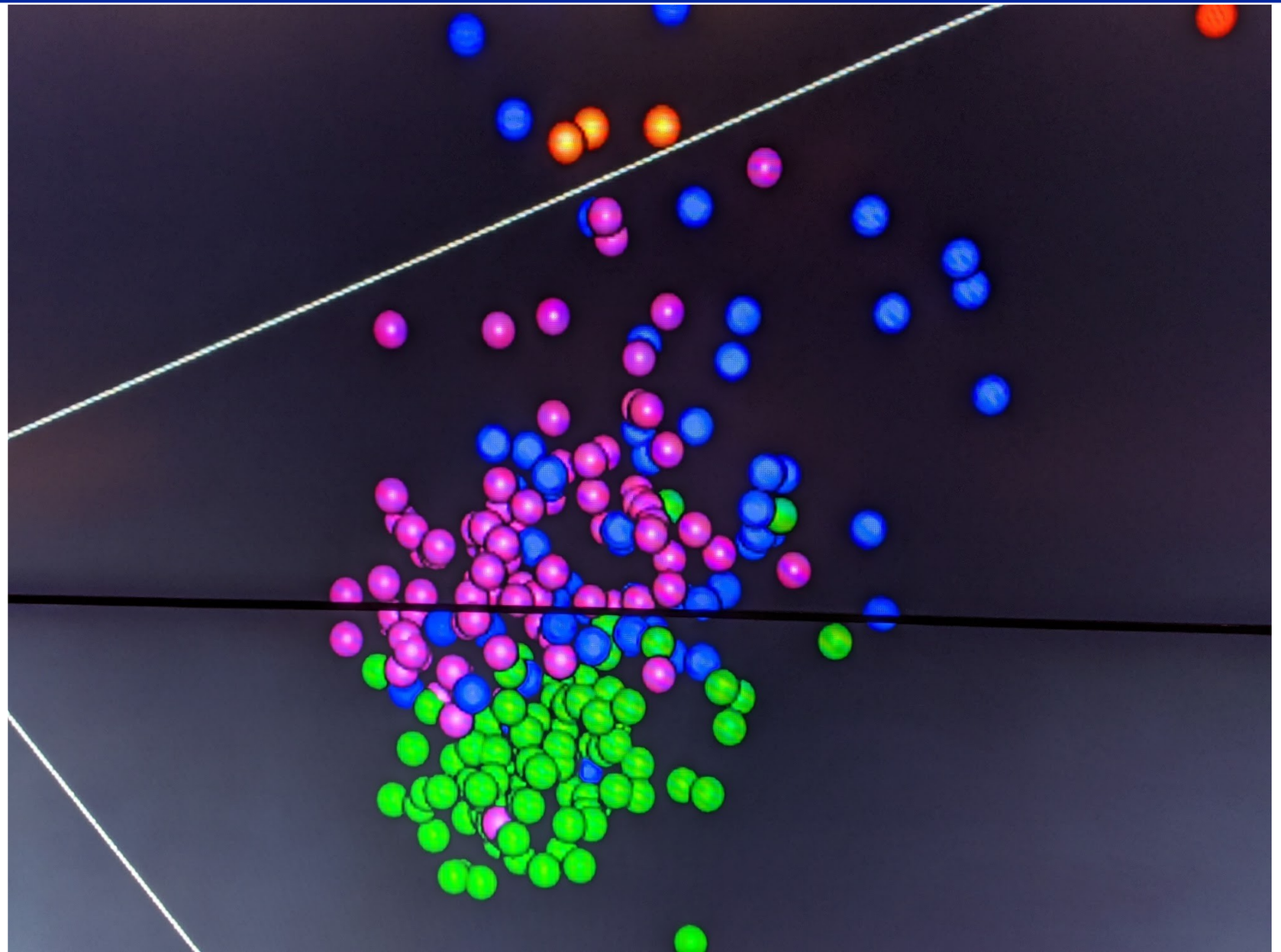
UC San Diego

Experiment #3
Discovering Microbiome Ecology Diagnostics From Dietary Intervention

UC San Diego

Closeup of Switch to Vegan and Then Time Restricted Eating with Green Smoothies

Using PCA ML Reveals Clusters Indicating Major Microbiome Ecological Shifts With Dietary Interventions



UC San Diego

Adding Vegetable Fiber to the Diet Seems to Counter Obesity By Increasing Microbiome Diversity

Cell Host & Microbe 10 January 2018

Fiber-Mediated Nourishment of Gut Microbiota Protects against Diet-Induced Obesity by Restoring IL-22-Mediated Colonic Health

Jun Zou, Benoit Chassaing, Vishal Singh, Michael Pellizzon, Matthew Ricci, Michael D. Fythe, Matam Vijay Kumar, Andrew T. Gewirtz[5],



The more different types of plants a person eats, the higher their gut microbiome diversity.

mSystems. 2018 May 15;3(3)

UC San Diego

Can I Increase My Microbiome Diversity By Consuming ~60 Plant Species Per Day?





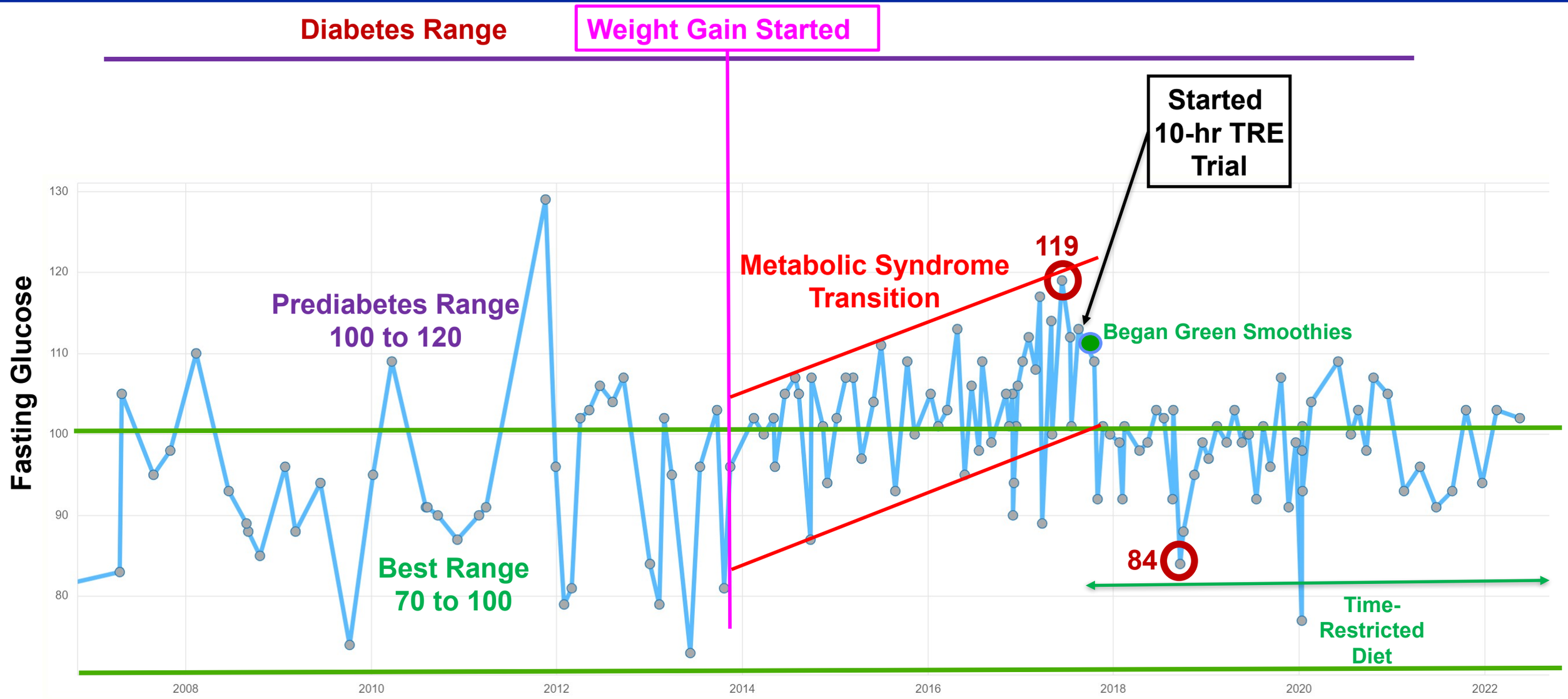


UC San Diego's Rob Knight Lab is Currently Sequencing 100 Days of My Stool Samples

I Also Have Time-Stamped Annotated Photos of Everything I Consumed

UC San Diego

15 Years of Blood Draws Created a Fasting Glucose Time Series Which Revealed An Abrupt Drop After Start of Green Smoothies and Time-Restricted Diet

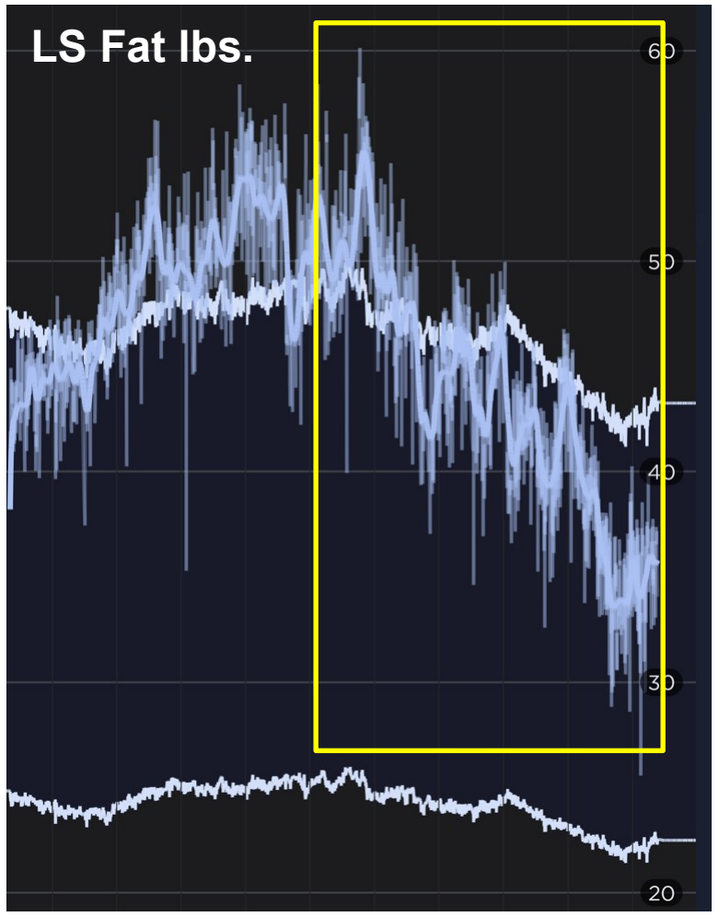


UC San Diego

My Body Fat and Visceral Fat Was Also Dramatically Reduced Since 2017

Peak
60 lbs
10/8/17

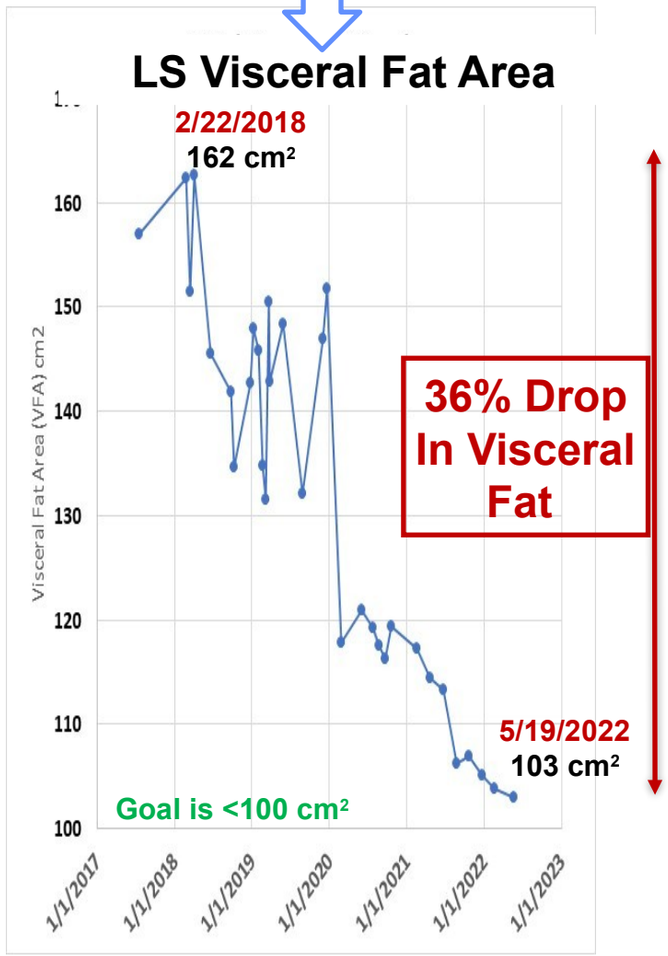
Same Time Scale



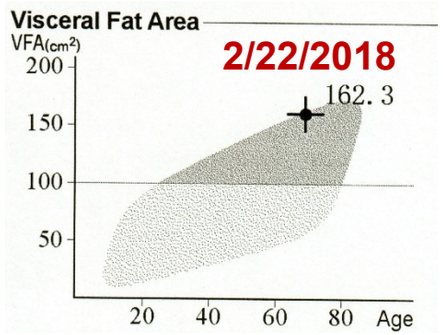
Start
45 lbs
5/6/22

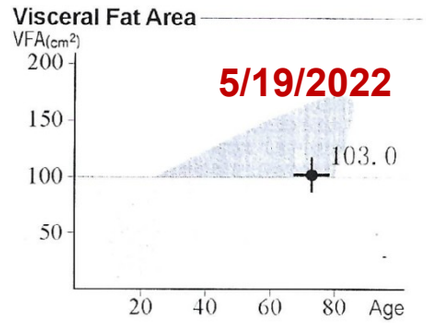
Now
35 lbs
6/5/22

42% Drop In Total Fat



36% Drop In Visceral Fat





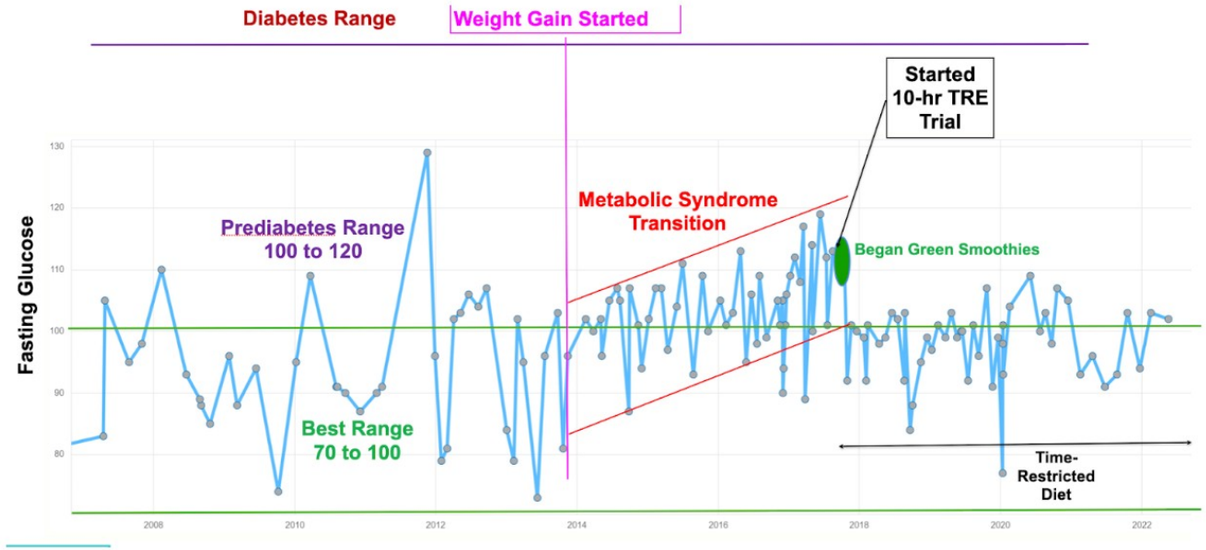
$17,000 InBody 770 Scale

$100 Home Withings WiFi Scale

Visceral Fat Area is based on the estimated amount of fat surrounding abdominal internal organ. It's recommended <100 cm² for

UC San Diego

LS Gut Microbiome Diversity Shifted Following High Plant Diversity Intake



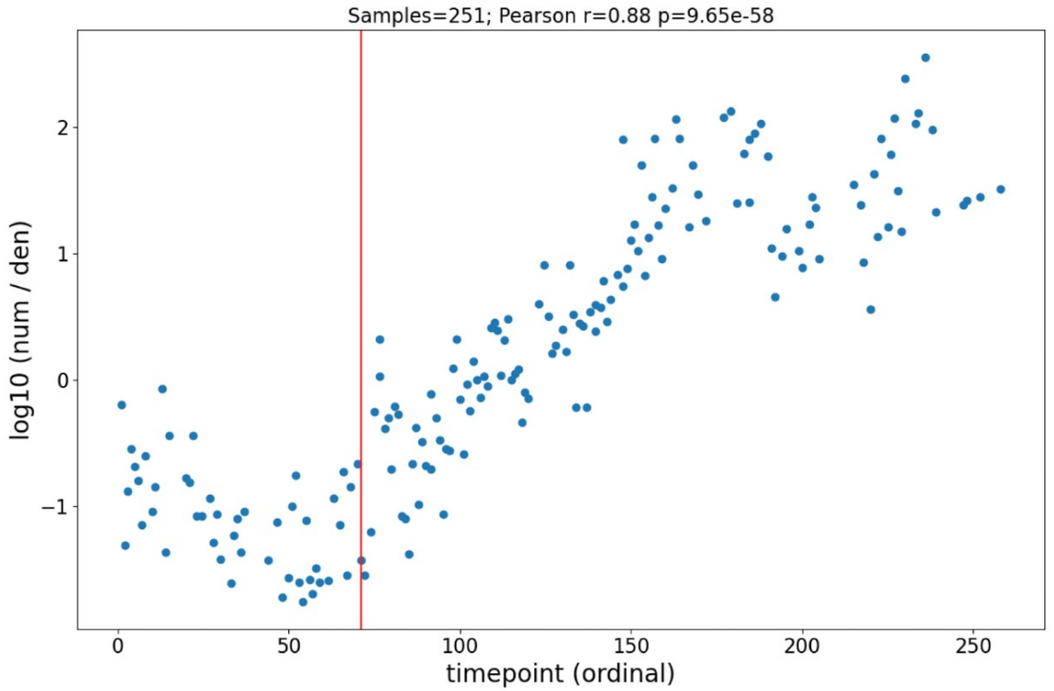
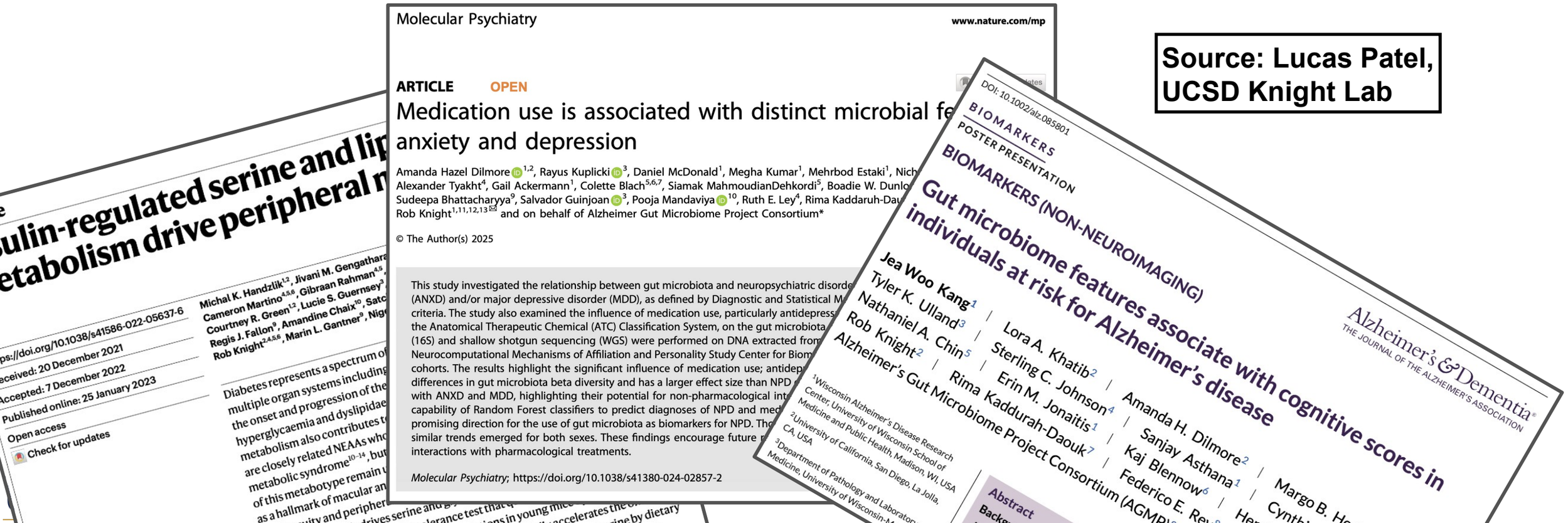


Figure XC. Correlation of the log ratio from BIRDMAn with the time series. The red line indicates when the TRE and smoothie consumption trial began.

UC San Diego

BIRDMAn is a Bayesian differential abundance technique

- **What it is: A Bayesian statistical framework designed specifically for microbiome differential abundance analysis that leverages Stan under the hood**
- **Core function: Applies principled Bayesian modeling to microbiome count data, handling the high variability and sparsity typical in metagenomic datasets**
- **Practical utility: Helps researchers identify differentially abundant microbes across conditions while accounting for uncertainty, overdispersion, and varying sequencing depths common in microbiome studies**

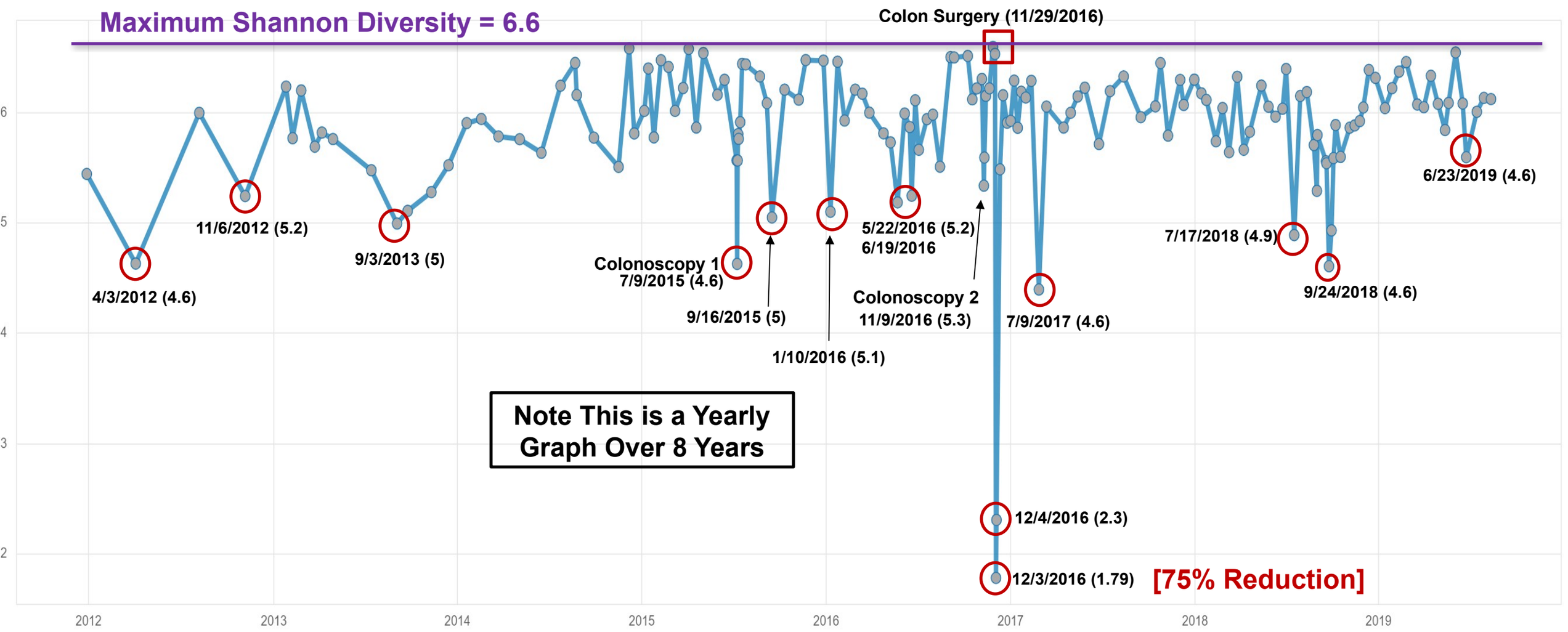


Source: Lucas Patel, UCSD Knight Lab

Experiment #4
Discovering Impact of Single Species Blooms on Gut Microbiome Ecology

UC San Diego

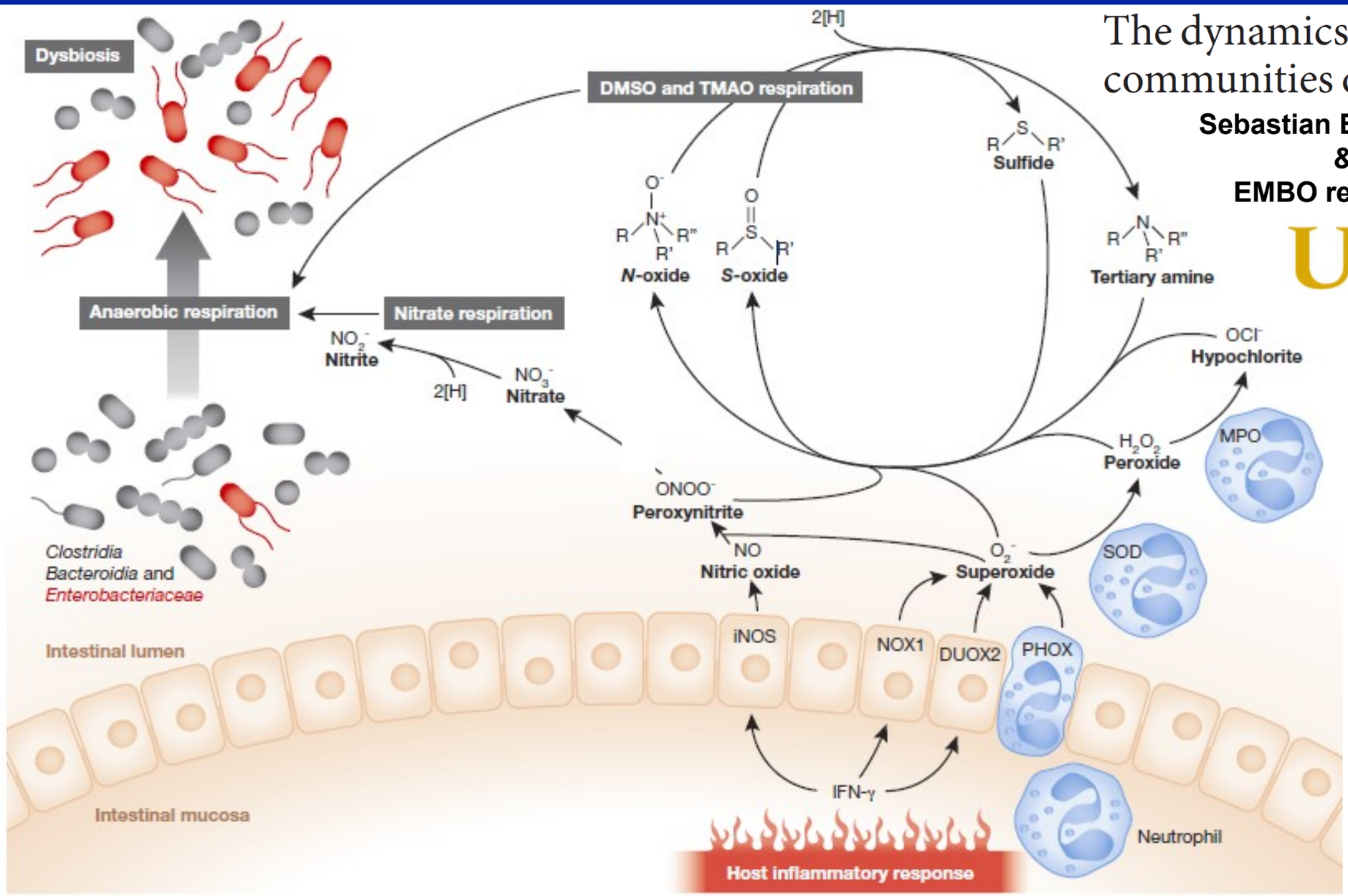
What Causes the Shannon Diversity of My Gut Microbiome Ecology Dips? Other Than Colonoscopy Cleanse and Surgery?



UC San Diego

Previous Graph

Inflammation Enables Anaerobic Respiration Which Leads to Dysbiosis: Phylum-Level Shifts in the Gut Microbiome Ecology

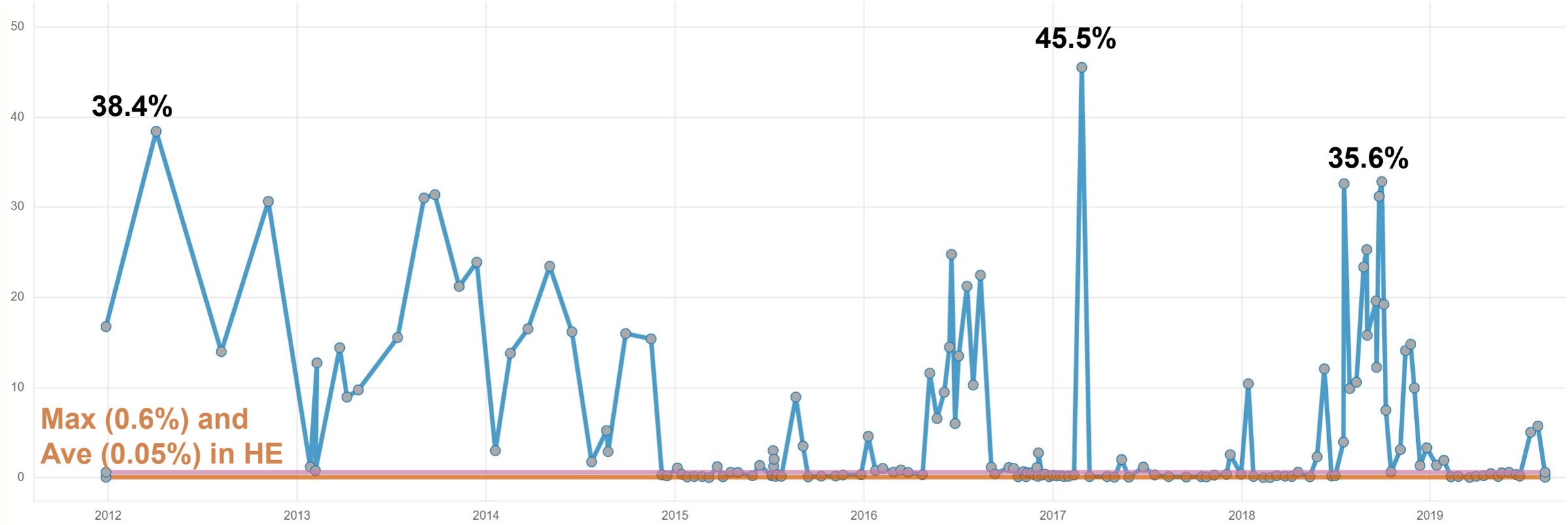


The dynamics of gut-associated microbial communities during inflammation

Sebastian E. Winter, Christopher A. Lopez & Andreas J. Bäumler,
EMBO reports v.14, p. 319-327 (2013)

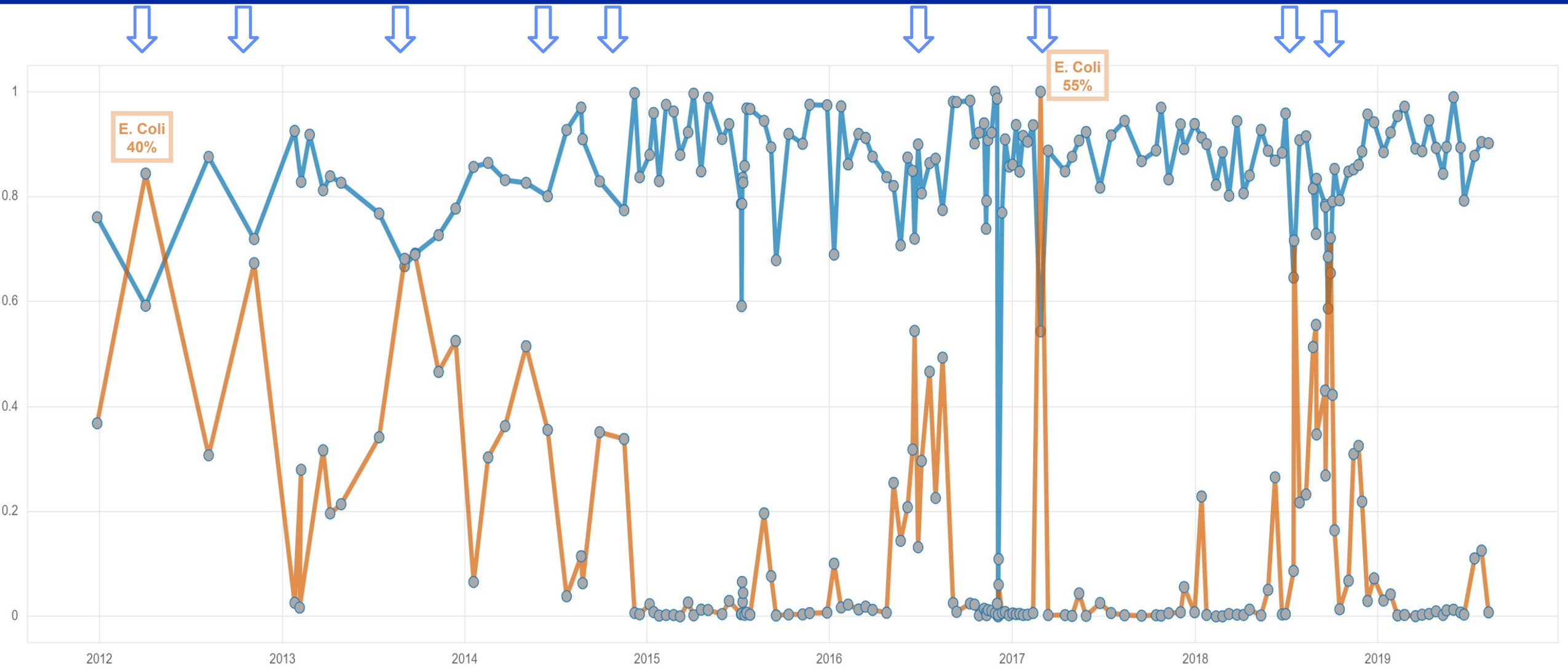
UCDAVIS

There Are Repeated Blooms of E. coli in LS Gut Microbiome



UC San Diego

A Number of Shannon Diversity Dips Are Associated with E. coli blooms



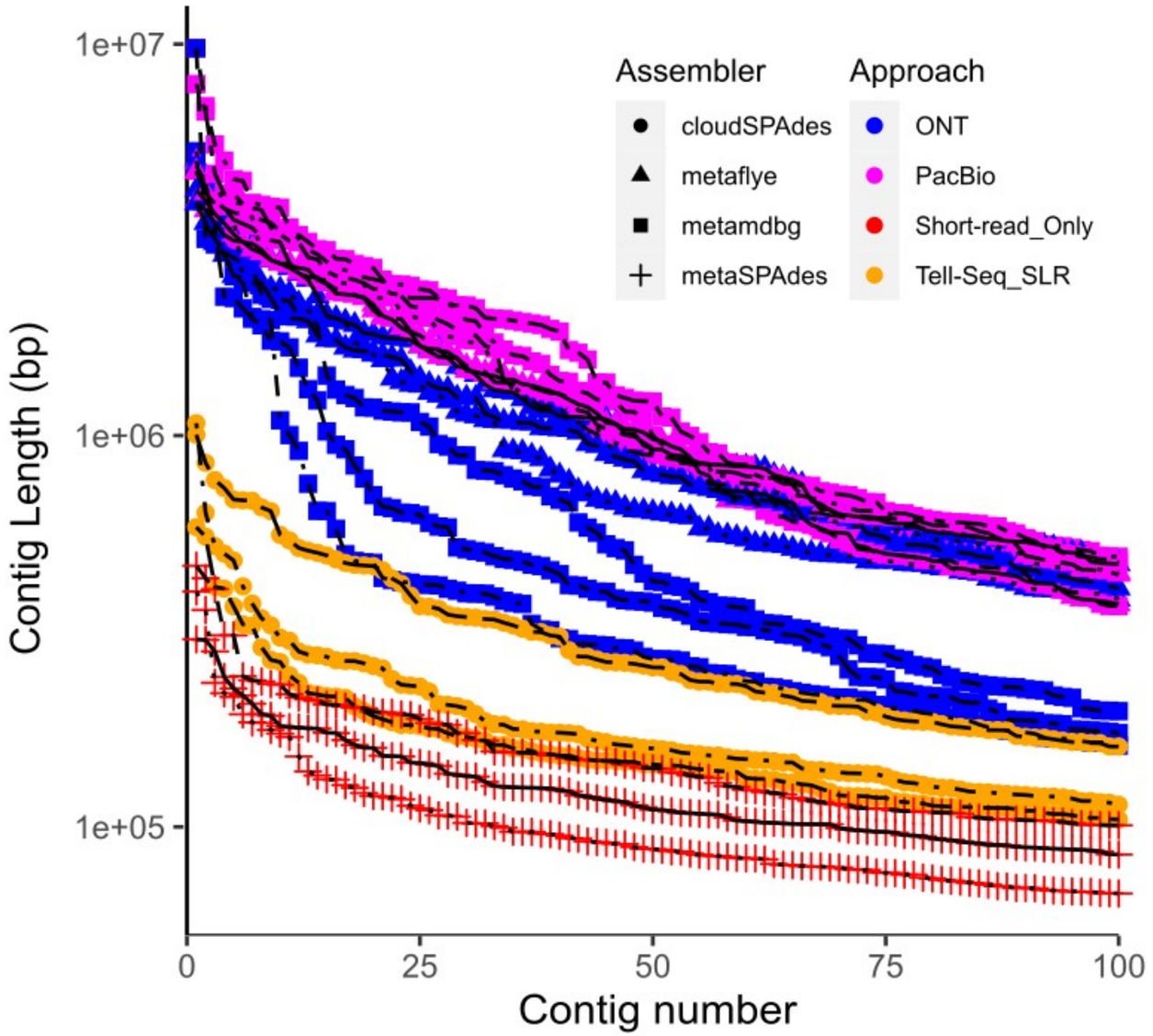
UC San Diego

Experiment #5
Discovering Absolute Strain Level Gut Microbiome Dynamics

UC San Diego

Omar Din
Postdoctoral Scholar
Knight Lab, UCSD

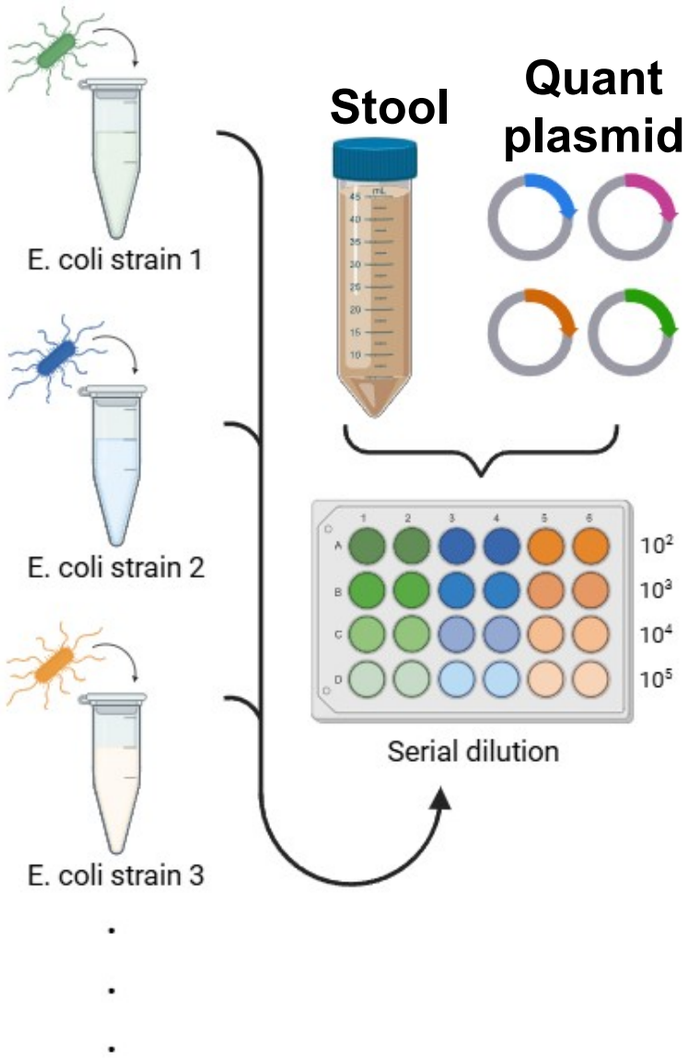
Dramatically Increased Genome Resolution with Longer Assemblies



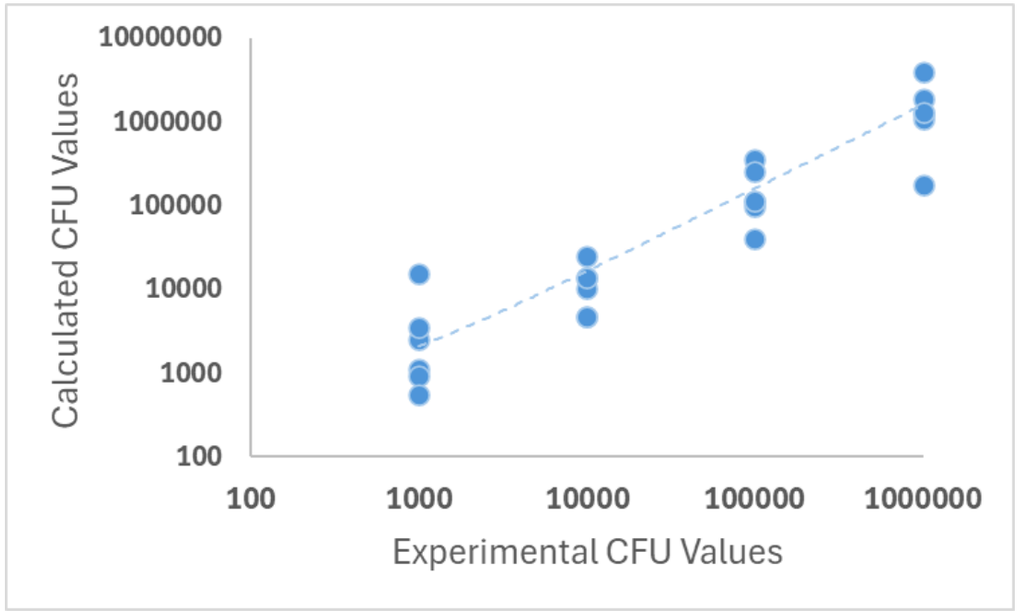
UC San Diego

Research by Omar Din, UCSD Knight Lab

Quantitative LR Metagenomics Can Accurately Estimate Cell Numbers



- Using various strains of Enteropathogenic E. coli as a proof-of-concept, various experimental CFUs were spiked into stool and LR metagenomics sequenced
- Using *only* sequencing data, we are able to determine the CFU amounts for each strain
- Possibly the first demonstration of accurate CFU estimation with long read metagenomics

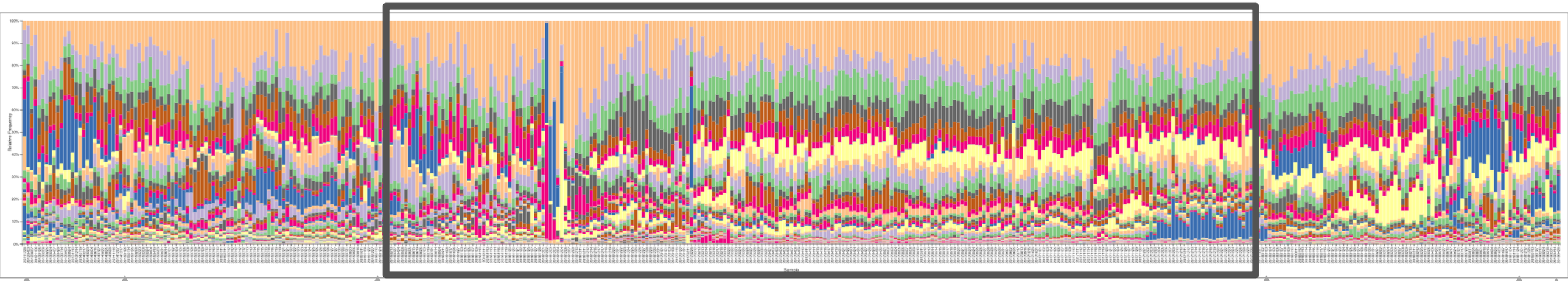


UC San Diego

Research by Omar Din, UCSD Knight Lab

Knight Lab Currently Applying PacBio Long-Read Metagenomics with Newly Developed Absolute Quantification to LS Stool Time Series

Omar Din is Initially Processing LS Samples in this Time-Range (Species and Strain Level Quantification!)



2015 | 2016 | 2017 | 2018

Bar Graph of 16S Taxonomy Relative Abundances

December 28, 2011

April 28, 2019

UC San Diego

Research by Omar Din, UCSD Knight Lab

Experiment #6
Discovering Gut Microbiome Metabolite Dynamics

UC San Diego

Toward a "Digital Twin" Computational Model of the Human Host/Gut Microbiome System

Longitudinal flux balance analyses of a patient with episodic colonic inflammation reveals microbiome metabolic dynamics

Arianna Basile[a,b], Almut Heinken[b,c], Johannes Hertel[d], Larry Smarr[e], Weizhong Li[f], Laura Treu[a], Giorgio Valle[a], Stefano Campanaro[a§], and Ines Thiele[b,c,g,h§]

[a]Department of Biology, University of Padova, Padua, Italy; [b]School of Medicine, University of Galway, Galway, Ireland; [c]Ryan Institute, University of Galway, Galway, Ireland; [d]Department of Psychiatry and Psychotherapy, University Medicine Greifswald, Greifswald, Germany; [e]Department of Computer Science and Engineering, University of California, San Diego, La Jolla, CA, USA; [f]J. Craig Venter Institute, San Diego, La Jolla, CA, USA; [g]Discipline of Microbiology, University of Galway, Galway, Ireland; [h]APC Microbiome Ireland, University College Cork, Cork, Ireland

GUT MICROBES
2023, VOL. 15, NO. 1, 2226921
https://doi.org/10.1080/19490976.2023.2226921

OPEN ACCESS

UC San Diego

What are Genome-Scale Metabolic Reconstructions?

Literature review



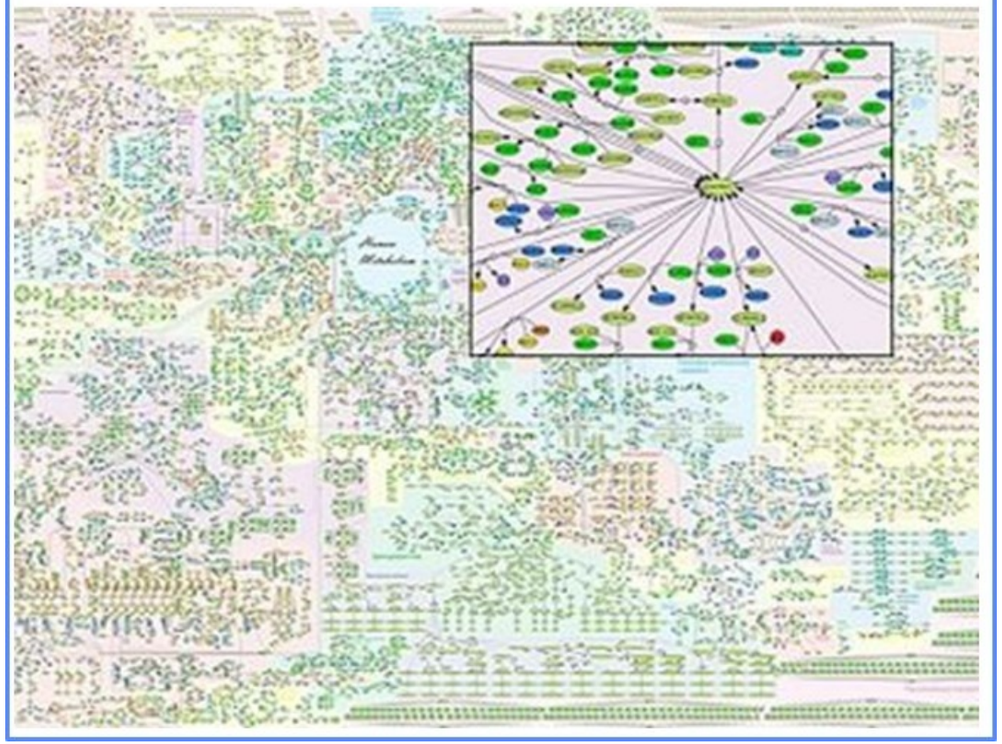
Genome annotation



Knowledge base

Computational model

Metabolic map

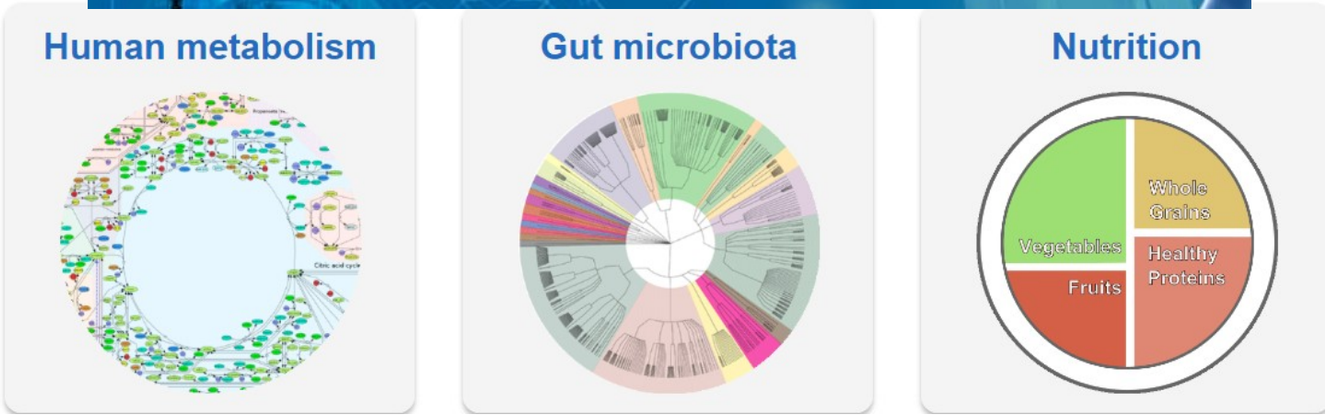


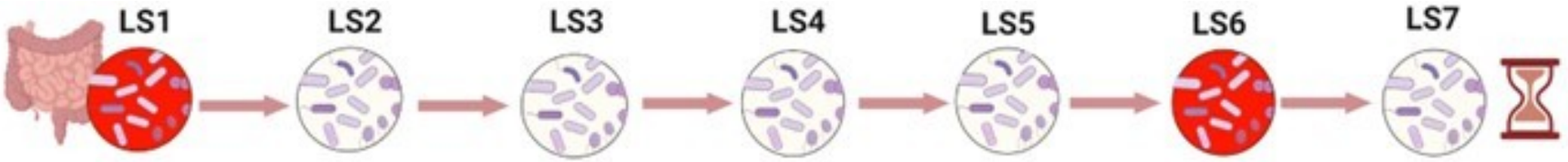
UC San Diego

My Initial Seven Gut Microbiome Metagenomic Sequenced Stool Samples Hav Been Analyzed by the Virtual Metabolic Human Team

Collaboration with
Professor Ines Thiele,
National University of Ireland, Galway
PI, Molecular Systems Physiology Group
www.thielelab.eu/



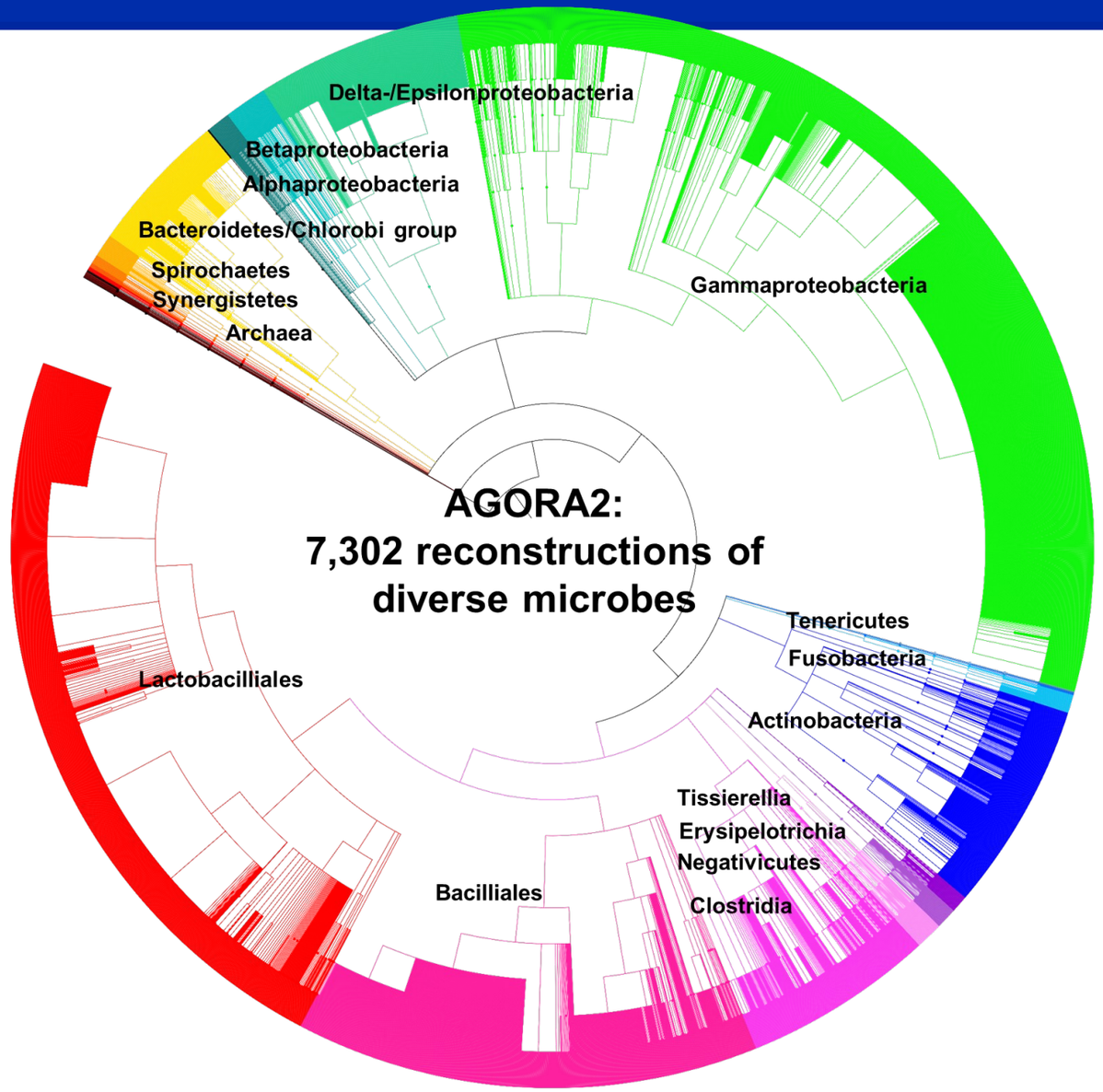




	LS1	LS2	LS3	LS4	LS5	LS6	LS7
Date	28/12/2011	03/04/2012	07/08/2012	06/11/2012	26/01/2013	08/02/2013	25/02/2013
Inflammation	Yes	No	No	No	No	Yes	No
Blood CRP (mg/dL)	27.1	2.8	3	4.3	3.2	26.3	3.7
Antibiotic treatment	None	Yes	None	None	None	None	None
Alpha diversity	74.86	77.86	76.85	77.11	74.50	80.18	77.46
Microbes	76	125	102	91	87	101	106
Reactions	142,358	253,294	185,468	140,923	115,612	173,610	141,914
Metabolites	126,065	222,120	164,170	126,108	104,972	154,198	129,276

UC San Diego

AGORA2: Reconstruction Resource of Human Microbes Accounting for Drug Metabolism



- 7,302 strains
- 1,734 species
- 422 genera
- 24 phyla

- **Biochemistry**: 732 papers and >8,000 pages of textbooks
- **Drug metabolite structures**: 73 papers and databases
- **Comparative genomic analyses** for up to 5,438 strains and 35 metabolic subsystems
- *Special focus:* drug metabolism for 25 genes, the subcellular localization, and 12 drug-transporter

Article | Open access | Published: 19 January 2023

Genome-scale metabolic reconstruction of 7,302 human microorganisms for personalized medicine

Almut Heinken, Johannes Hertel, Geeta Acharya, Dmitry A. Ravcheev, Malgorzata Nyga, Onyedika Emmanuel Okpala, Marcus Hogan, Stefanía Magnúsdóttir, Filippo Martinelli, Bram Nap, German Preciat, Janaka N. Edirisinghe, Christopher S. Henry, Ronan M. T. Fleming & Ines Thiele

Nature Biotechnology **41**, 1320–1331 (2023) | Cite this article

UC San Diego

My First Seven Stool Samples Sequenced by JCVI Are Input to the AGORA2 Metabolic Model

Table 1. Information about the species filtering performed through AGORA2 mapping.

Features	LS1	LS2	LS3	LS4	LS5	LS6	LS7	HeAve
Total number of strains identified	1,041	1,055	1,532	1,110	1,037	1,112	1,039	939
Strains covered in the *in silico* microbial community models	76	125	102	91	87	101	106	198
Fraction of total abundance covered	0.923	0.937	0.902	0.904	0.926	0.925	0.923	0.98
Alpha diversity	74.86	77.86	76.85	77.11	74.5	80.18	77.46	75.56

The total number of strains identified, and the strains covered by the AGORA2 mapping are reported. The abundance based on AGORA2 mapping, using a cutoff threshold abundance of 0.0001 is reported as well, together with the alpha diversity of the samples. For details on the calculation of the Alpha diversity, please refer to the method section.

- **7 LS Time Series Gut Microbiome Community Models**
- **1 'Healthy Average' Gut Microbiome Community Model Based on Average Gut Microbiome Abundances from 34 Patients**
- **Community Models linked to Host Multi-Organ Models**
- **Average European Diet**
- **Flux Balance Analysis Performed on These 8 Microbiota-Personalised Models**

UC San Diego

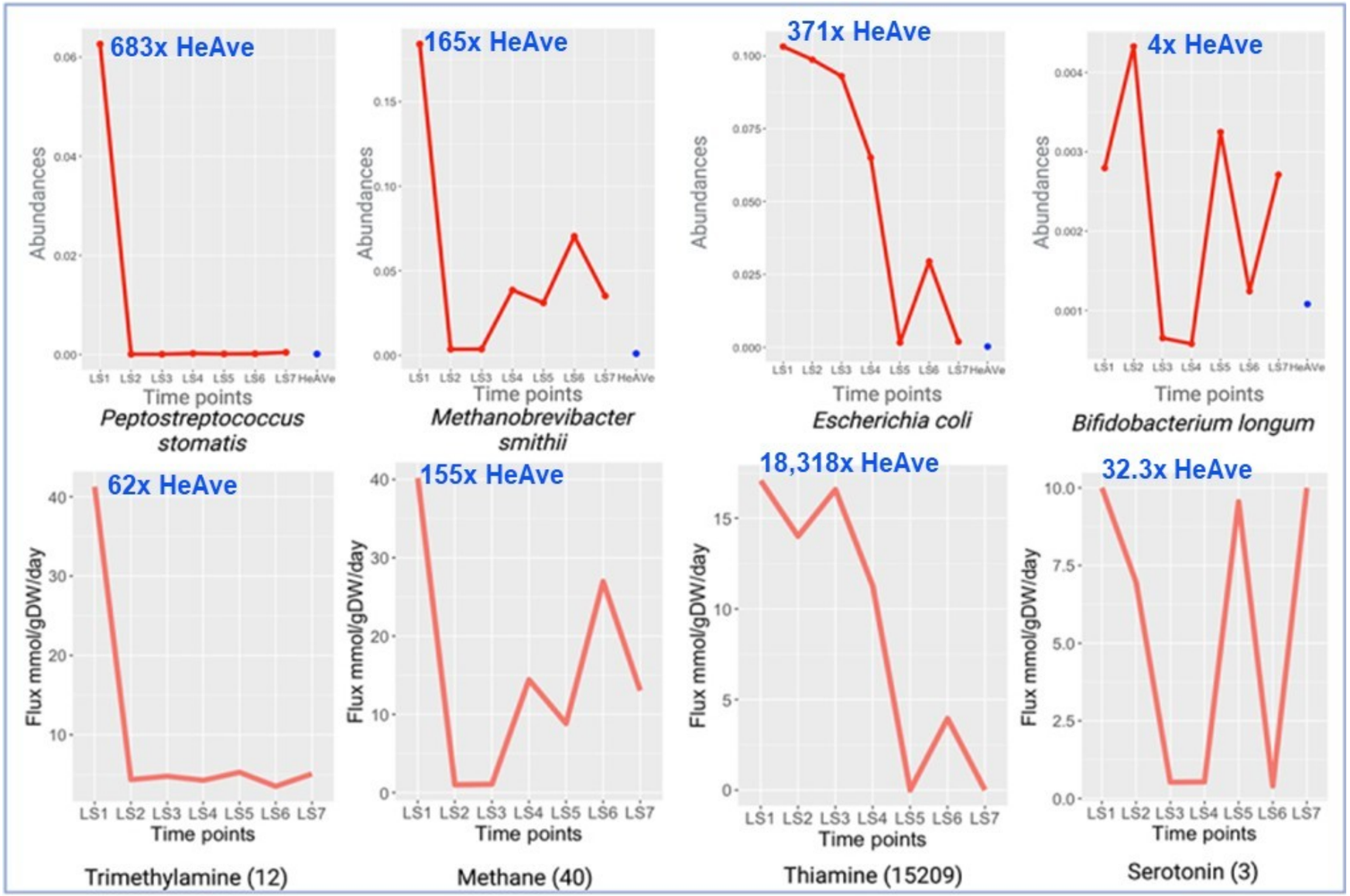
Surprising Result from the Thiele Lab Model

We found that LS's major gut microbiome
taxonomic shifts over time
led to correspondingly large
Flux Balance Analysis (FBA) metabolic shifts
from the personalized microbial community models.
Since we also computed the metabolite production
from each of the 34 healthy controls' microbiome,
we could compare LS's metabolite production at each time point to the average value (HeAve) of the healthy controls.

The results of our models showed that
several biologically important metabolites
***were highly (10–10,000×) overproduced*, compared to HeAve**,
at various time points in LS's samples,
including oxygen, methane, thiamine, formaldehyde,
trimethylamine N-oxide, folic acid, serotonin, histamine, and tryptamine.

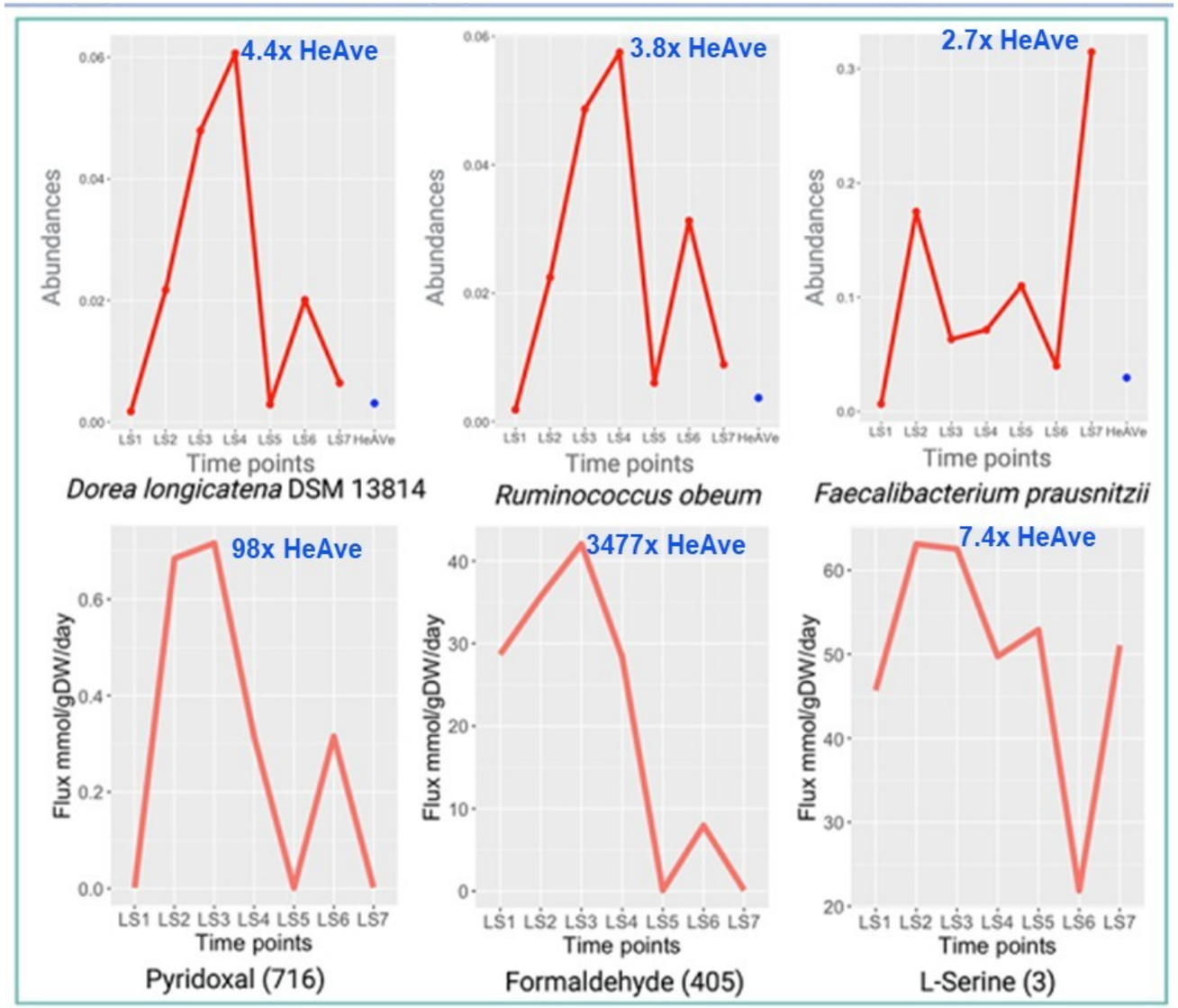
UC San Diego

Time-Correlated Microbial Species and Metabolites Reveal (10–10,000×) Overproduction of Biologically Important Metabolites



Basile A et al., Gut Microbes, 2023

Time-Correlated Microbial Species and Metabolites



Healthy Average
LS samples

UC San Diego

Basile A et al., Gut Microbes, 2023

Toward a Human Digital Twin Next Steps: Collaboration of Knight Lab, Thiele Lab, with Smarr Time Series

- **Step One is Done:**
  - **Seven Stool Samples Over 13 Months**
  - **Published in Gut Microbes July 2023**
- **Step Two is Underway:**
  - **Fifty Stool Samples Over 2.5 Years**
  - **Stool Sample Metagenomics From Knight Lab**
  - **Thiele AGORA2 Computations Are Done**
  - **Planning Comparison with Dorrestein Lab Metabolomics**
- **Step Three Has Begun:**
  - **500 Stool Samples Over a Decade**
  - **Knight Lab Has Done 16S on Time Series**
  - **Starting on Long Read Metagenomics**
  - **Coupling That into AGORA2 Next Step**

Experiment #7
Discovering Microbiome Ecology Diagnostics Between Healthy and IBD Subtypes

UC San Diego

Human Genomics Imply Three Groups of IBD:
~35,000 IBD Patients Genotyped in 16 Countries in Europe, North America, and Australasia

Lancet 2016; 387: 156–67

Inherited determinants of Crohn's disease and ulcerative colitis phenotypes: a genetic association study

Isabelle Cleynen, Gabrielle Boucher*, Luke Jostins*, L Philip Schumm, Sebastian Zeissig, Tariq Ahmad, Vibeke Andersen, Jane M Andrews, Vito Annese, Stephan Brand, Steven R Brant, Judy H Cho, Mark J Daly, Marla Dubinsky, Richard H Duerr, Lynnette R Ferguson, Andre Franke, Richard B Gearry, Philippe Goyette, Hakon Hakonarson, Jonas Halfvarson, Johannes R Hov, Hailang Huang, Nicholas A Kennedy, Limas Kupcinskas, Ian C Lawrance, James C Lee, Jack Satsangi, Stephan Schreiber, Emilie Théâtre, Andrea E van der Meulen-de Jong, Rinse K Weersma, David C Wilson, International Inflammatory Bowel Disease Genetics Consortium†, Miles Parkes, Severine Vermeire, John D Rioux, John Mansfield, Mark S Silverberg, Graham Radford-Smith, Dermot P B McGovern*, Jeffrey C Barrett*, Charlie W Lees**

Our data support a continuum of disorders within inflammatory bowel disease, much better explained by three groups (ileal Crohn's disease, colonic Crohn's disease, and ulcerative colitis) than by Crohn's disease and ulcerative colitis as currently defined.

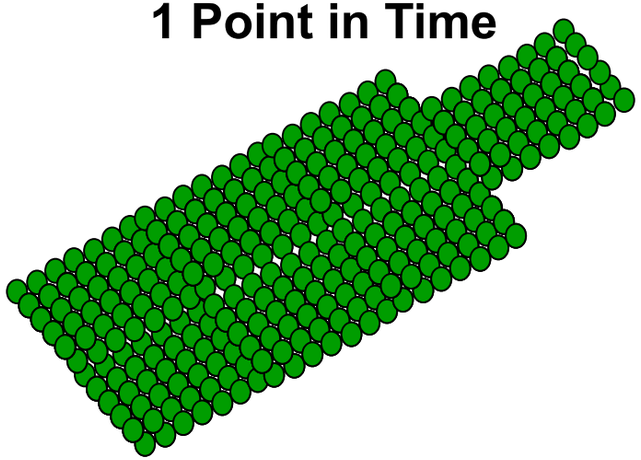
UC San Diego

THE LANCET

I Decided to Carry Out an Initial Deep Metagenomics Study of the Variation of the Human Gut Microbiome Between Healthy Individuals and IDB Patients

"Healthy" Individuals

250 Subjects
1 Point in Time

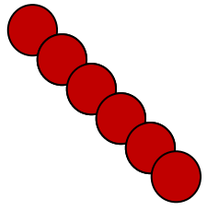


Downloaded from NIH HMP

Inflammatory Bowel Disease (IBD) Patients

Larry Smarr
(Colonic Crohn's)

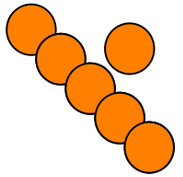
7 Points in Time



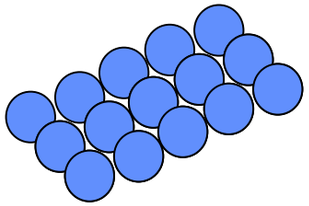
LS 7 samples sequenced by JCVI

J. Craig Venter INSTITUTE

2 Ulcerative Colitis Patients,
6 Points in Time



5 Ileal Crohn's Patients,
3 Points in Time



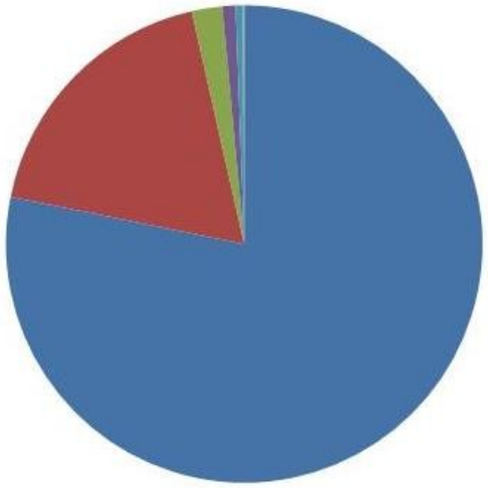
Each Sample Has 100-200M Illumina Short Reads (100 bases)
Total of 27 Billion Reads
or 2.7 Trillion Bases

UC San Diego

Larry Smarr, Weizhong Li, Sitao Wu, UCSD
Graphic Source: Jerry Sheehan, Calit2

We Found Major State Shifts in Microbial Ecology Phyla Between Healthy and Two Forms of IBD

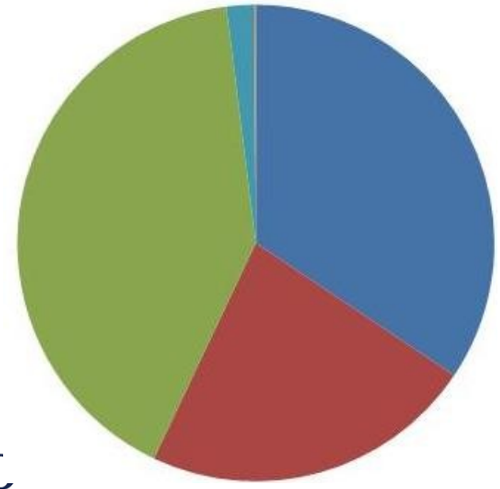
Average HE



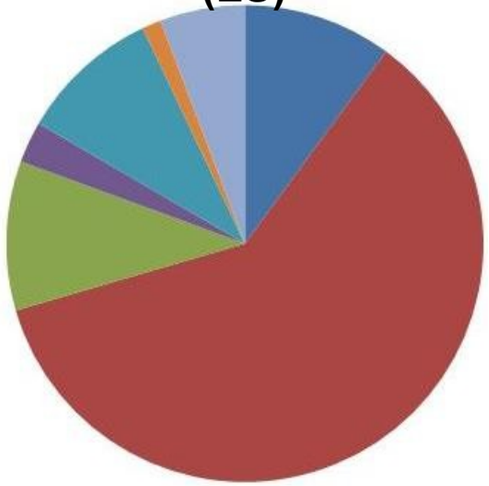
Most Common Microbial Phyla

- Bacteroidetes
- Firmicutes
- Proteobacteria
- Verrucomicrobia
- Actinobacteria
- Fusobacteria
- Euryarchaeota

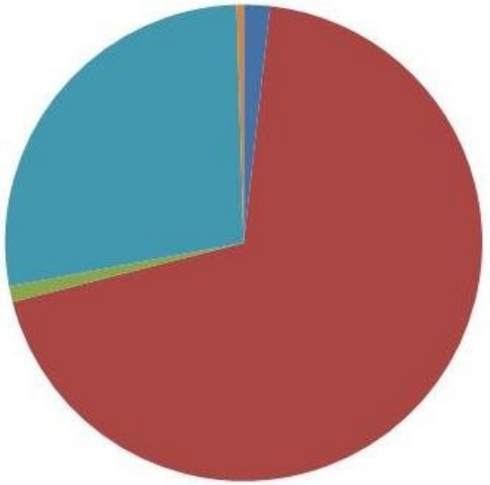
Average Ulcerative Colitis



Average Colonic Crohn's Disease (LS)

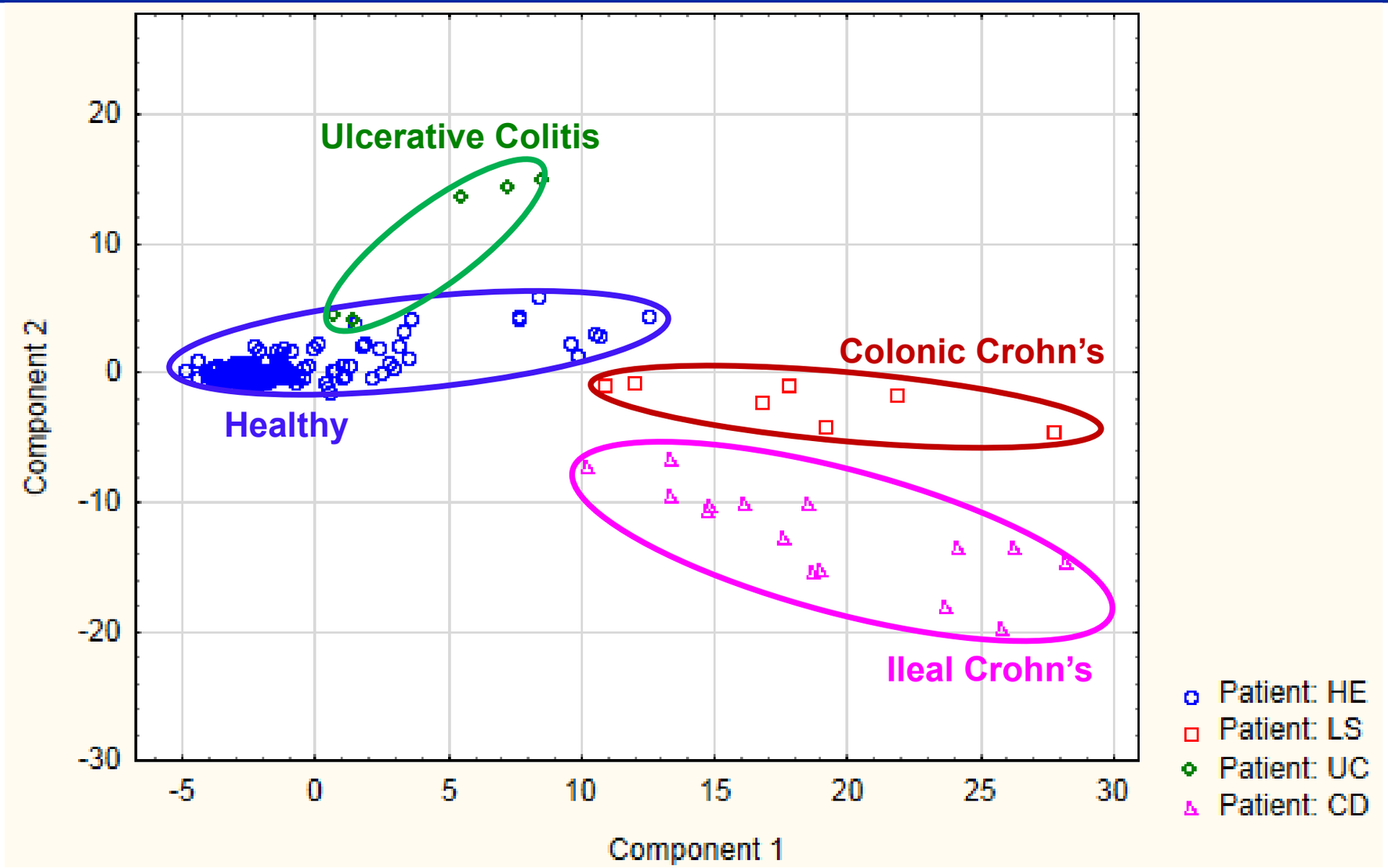


Average Ileal Crohn's Disease



UC San Diego

Machine Learing on the Metagenomic Sequencing of the Stool of Our 300 Patients Clustered into 3 Disease Types as Well



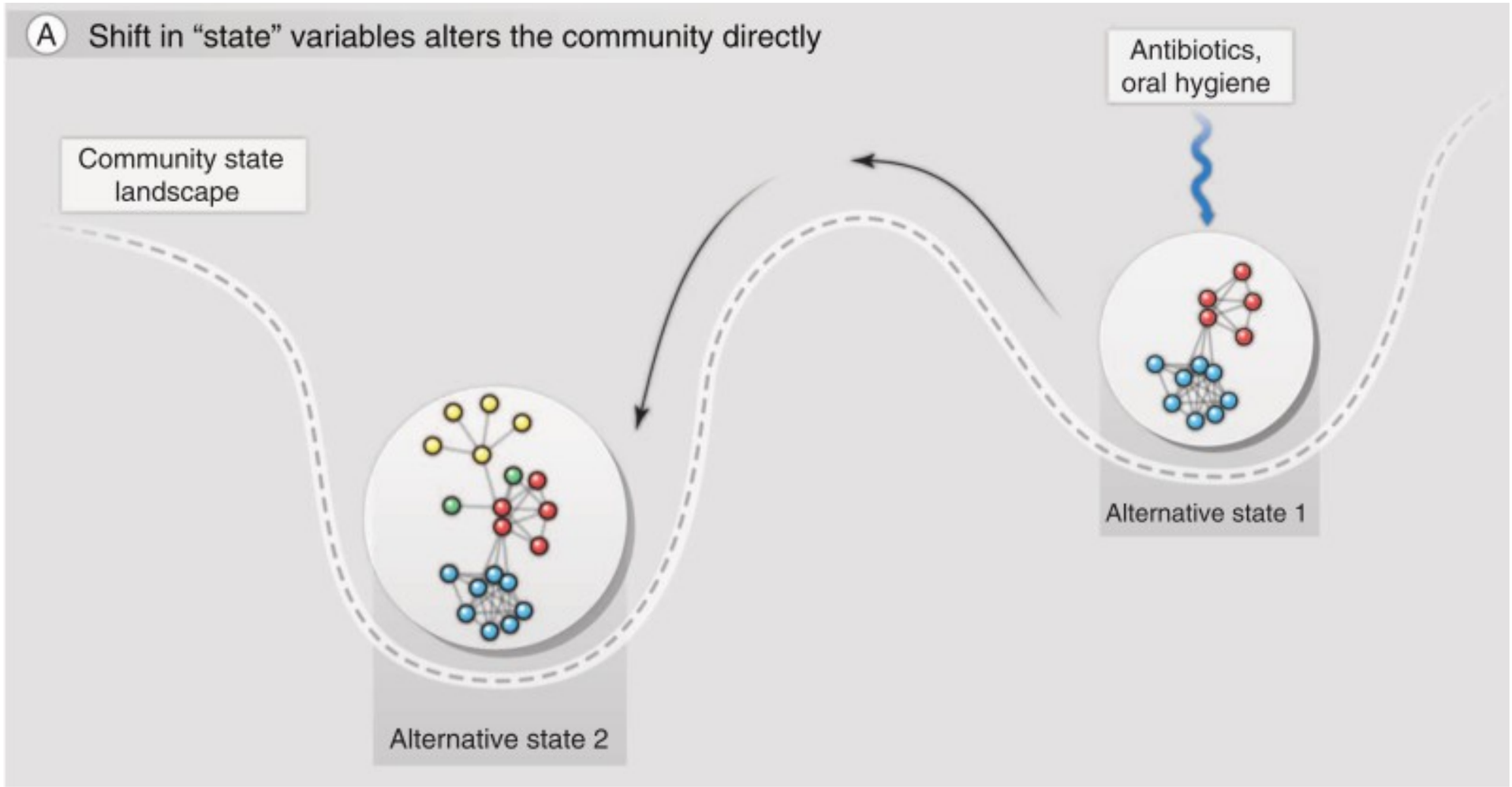
Source: Thomas Hill, Ph.D.
Executive Director Analytics
Dell | Information Management Group, Dell Software

UC San Diego

Experiment #8
Discovering Ecological Replacements Using Metagenomics

UC San Diego

Lessons from Ecological Dynamics I: Gut Microbiome Has Multiple Relatively Stable Equilibria



"The Application of Ecological Theory Toward an Understanding of the Human Microbiome," Elizabeth Costello, Keaton Stagaman, Les Dethlefsen, Brendan Bohannan, David Relman Science 336, 1255-62 (2012)

UC San Diego

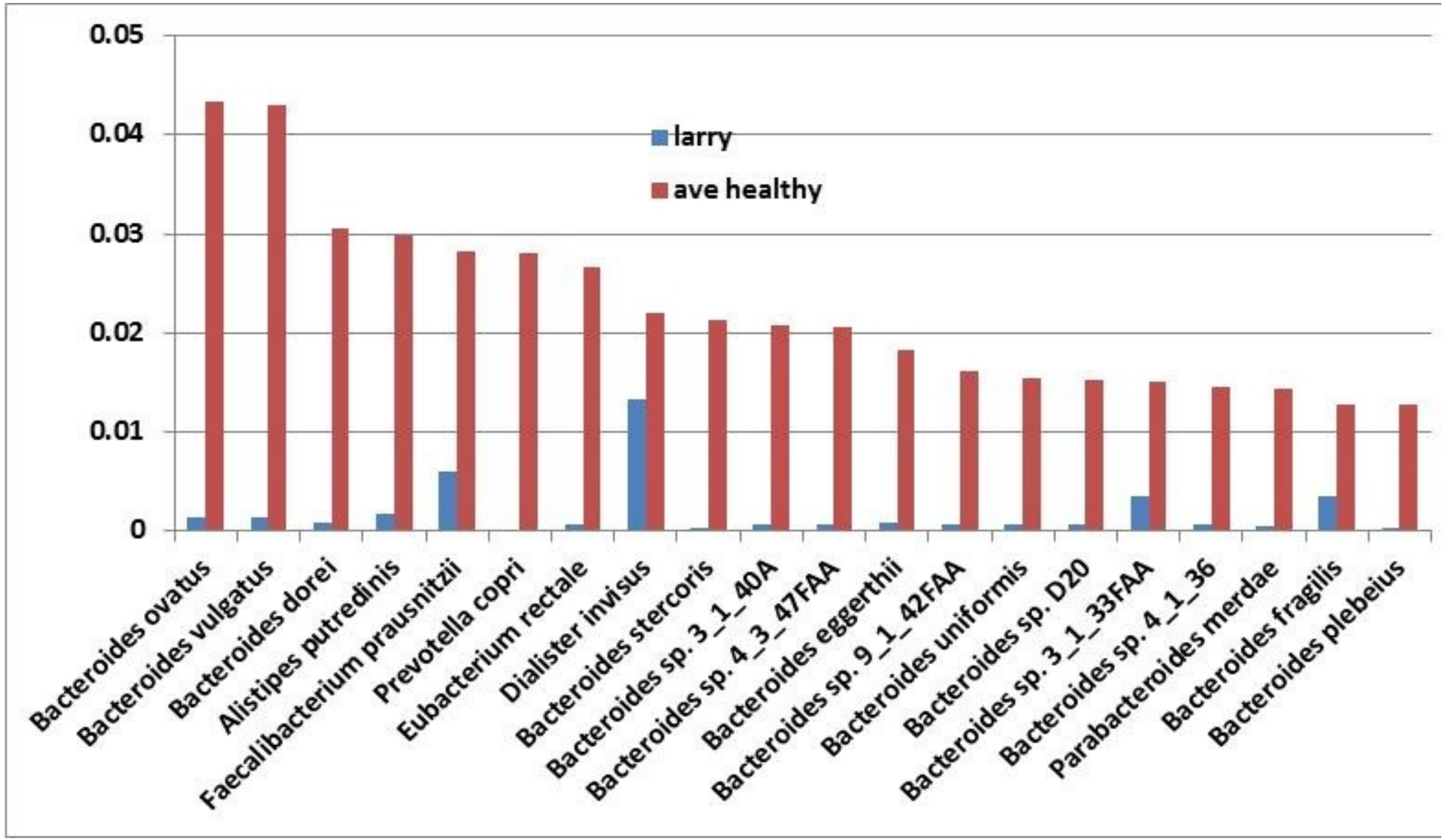
Lessons From Ecological Dynamics I:
Invasive Species Dominate After Major Species Destroyed



”In many areas following these burns invasive species are able to establish themselves, crowding out native species.”

Source: Ponderosa Pine Fire Ecology
http://cpluhna.nau.edu/Biota/ponderosafire.htm

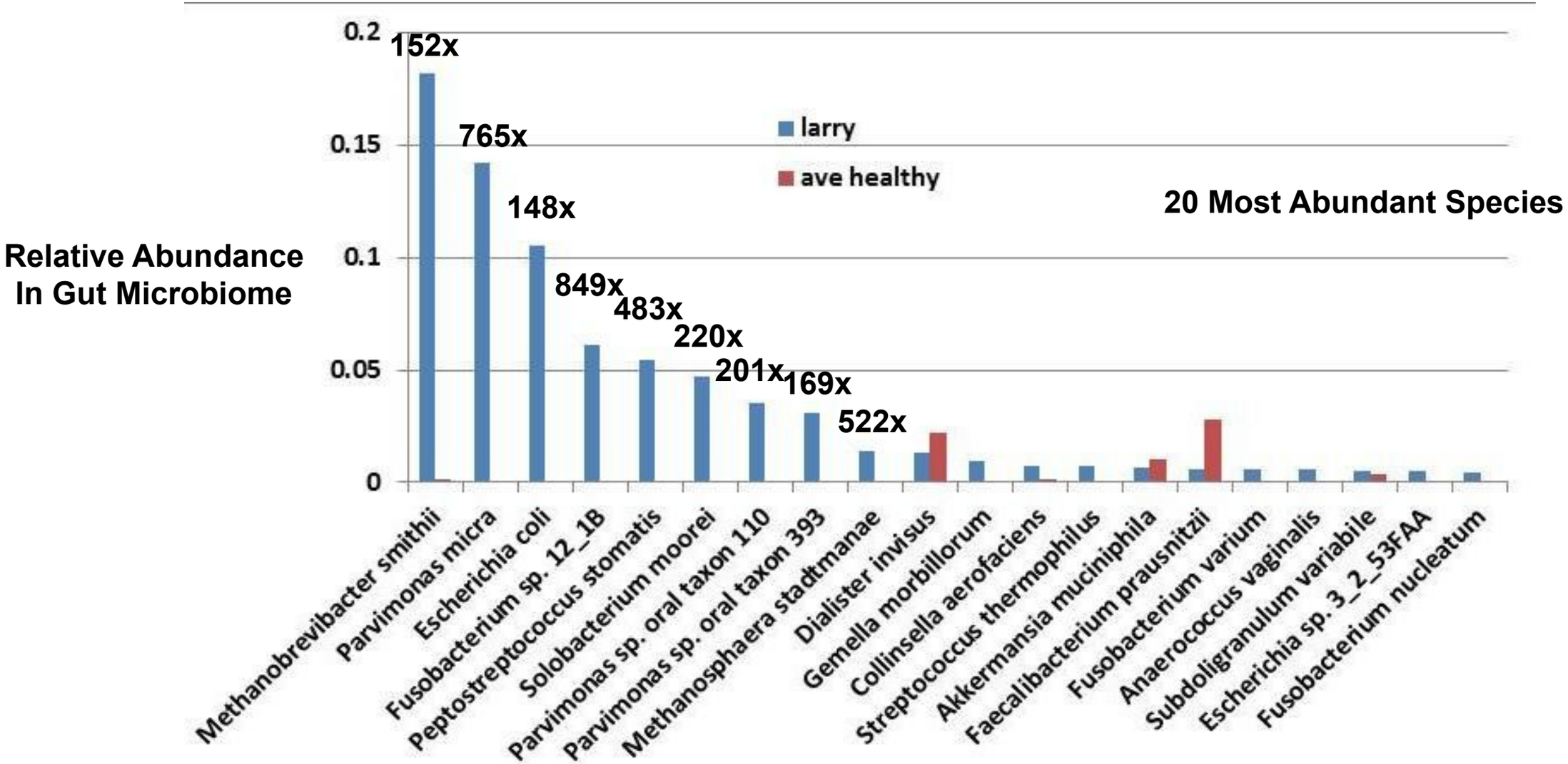
Almost All Abundant Species (≥1%) in Healthy Subjects Are *Severely Depleted* in Larry's LS01 Gut Microbiome



Source: Sequencing JCVI; Analysis Weizhong Li, UCSD
LS01 December 28, 2011 Stool Sample

UC San Diego

Invasive Species Take Over Gut Microbiome in Disease State



UC San Diego

Source: Sequencing JCVI; Analysis Weizhong Li, UCSD
LS01 December 28, 2011 Stool Sample

Experiment #9
Discovering Ecological Shifts Within Phyla Using Metagenomics

UC San Diego

Metagenomically Sequencing Long Time Series Stool Samples to Reveal Patient Gut Microbiome Ecology Dynamics During Disease

frontiers in Microbiology

Metagenomics-Based, Strain-Level Analysis of *Escherichia coli* From a Time-Series of Microbiome Samples From a Crohn's Disease Patient

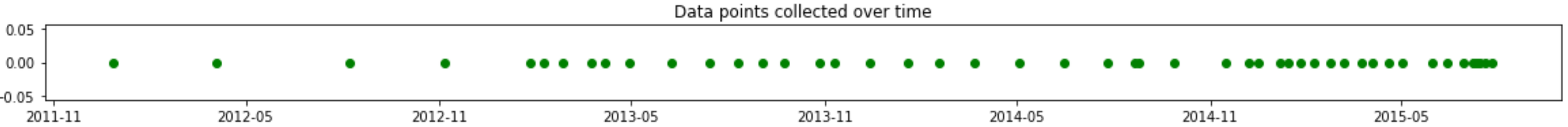
October 2018

Xin Fang[1], Jonathan M. Monk[1], Sergey Nurk[2], Margarita Akseshina[3], Qiyun Zhu[4], Christopher Gemmell[5], Connor Gianetto-Hill[5], Nelly Leung[6], Richard Szubin[1], Jon Sanders[6], Paul L. Beck[7], Weizhong Li[8,9], William J. Sandborn[10,11], Scott D. Gray-Owen[6], Rob Knight[4,12,13], Emma Allen-Vercoe[5], Bernhard O. Palsson[1,2,13,14] and Larry Smarr[12,13,15]**

UC San Diego

Metagenomically Sequencing Long Time Series Stool Samples to Reveal Patient Gut Microbiome Ecology Dynamics During Disease

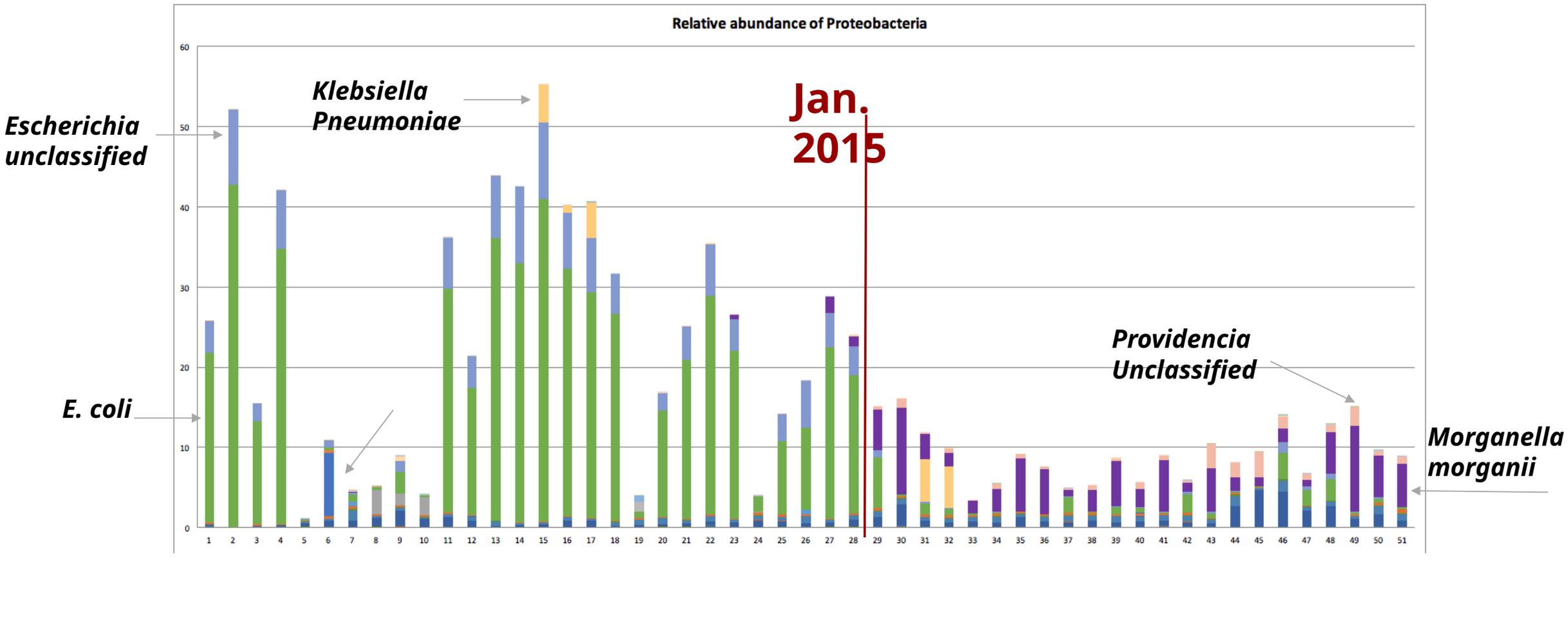
- **51 Stool Samples Collected from Dec. 2011 - July 2015**
- **Metagenomics Sequencing of Each Sample**
  - **# of Reads per Sample Range from 6M to 46M;**
  - **Average: 30M Paired Reads**



UC San Diego

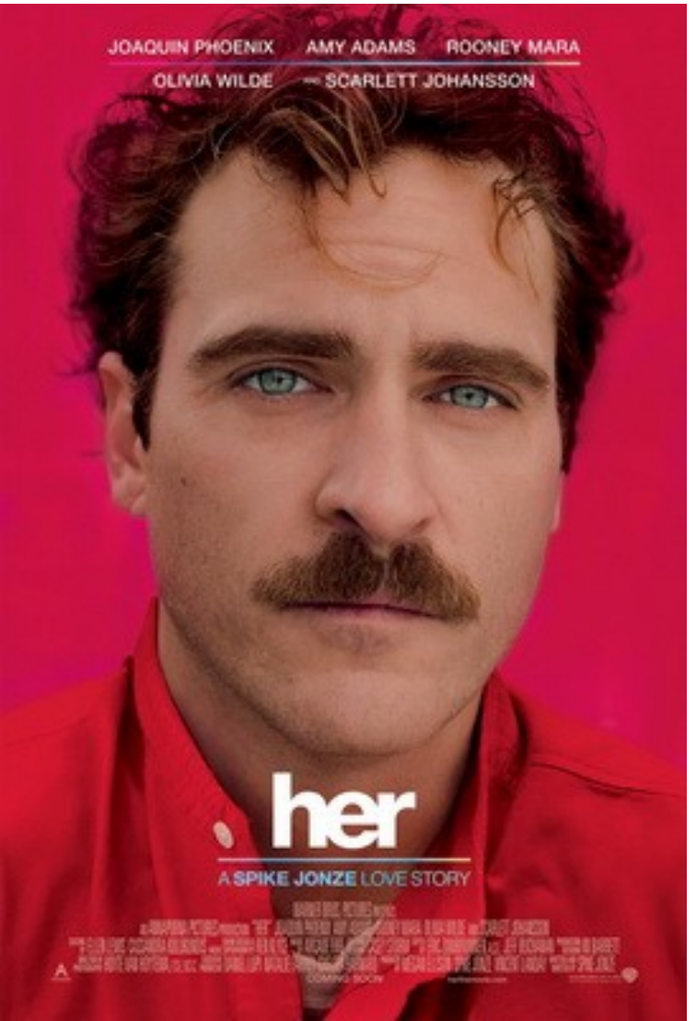
Source: Xin Fang

Proteobacteria Community Structure Changed Dramatically - Microbiome Metagenomics



UC San Diego

Coupling Human Digital Twins with Personal Digital Assistants: A Vision for Healthcare in the Coming Decades



Using this data, the planetary computer will be able to build a computational model of your body and compare your sensor stream with millions of others. Besides providing early detection of internal changes that could lead to disease, cloud-powered voice-recognition wellness coaches could provide continual personalized support on lifestyle choices, potentially staving off disease and making health care affordable for everyone.

ESSAY | The New York Times | Science

An Evolution Toward a Programmable Universe

By LARRY SMARR

Published: December 5, 2011