

# **Microbiomes of Pregnancy and Infancy: Implications for Child Health Outcomes**

Sarah S. Comstock  
Michigan State University

# Overview

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The microbiome

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Microbiome collection efforts in ECHO

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ECHO-wide microbiome results

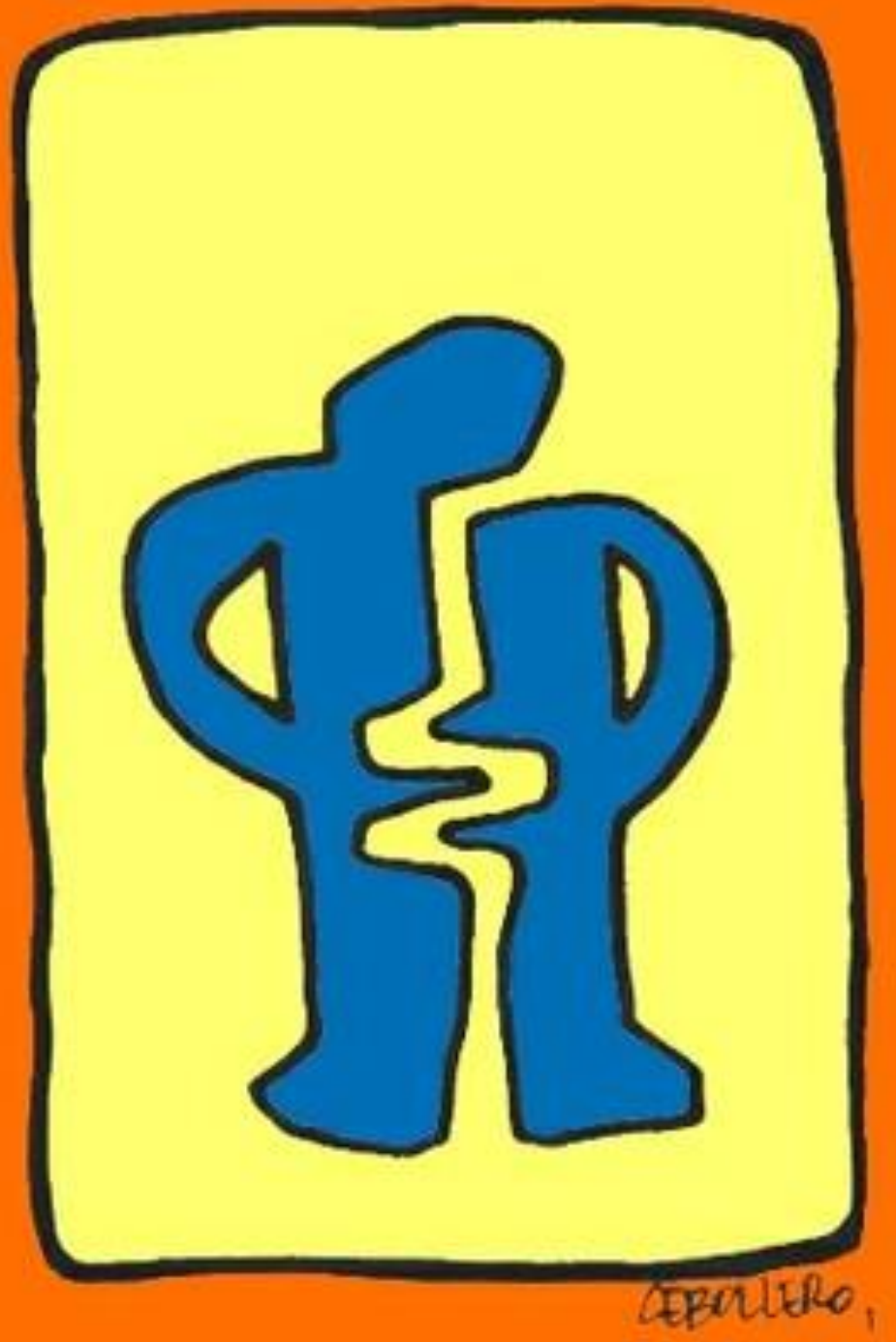
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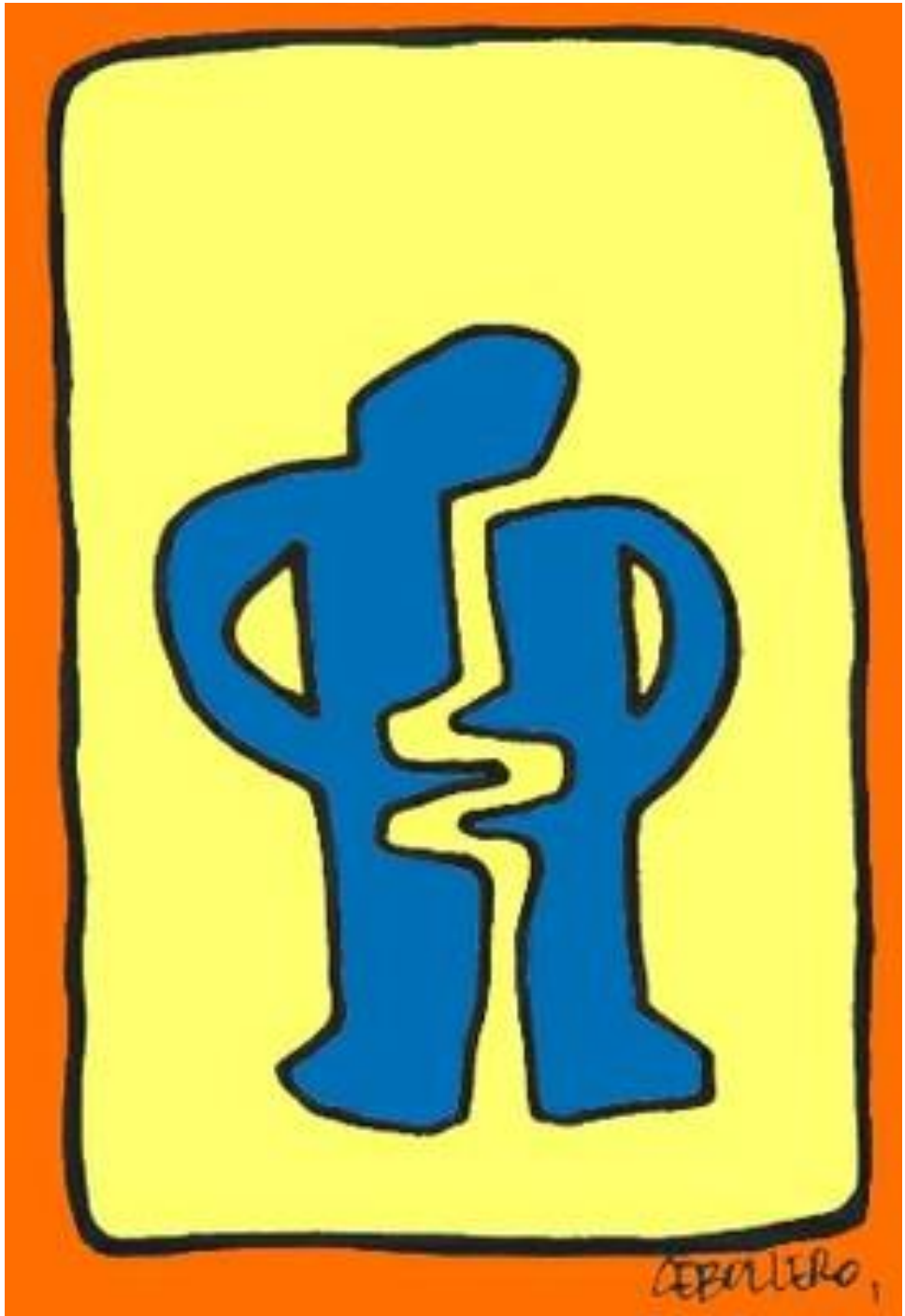
Cohort-specific microbiome results

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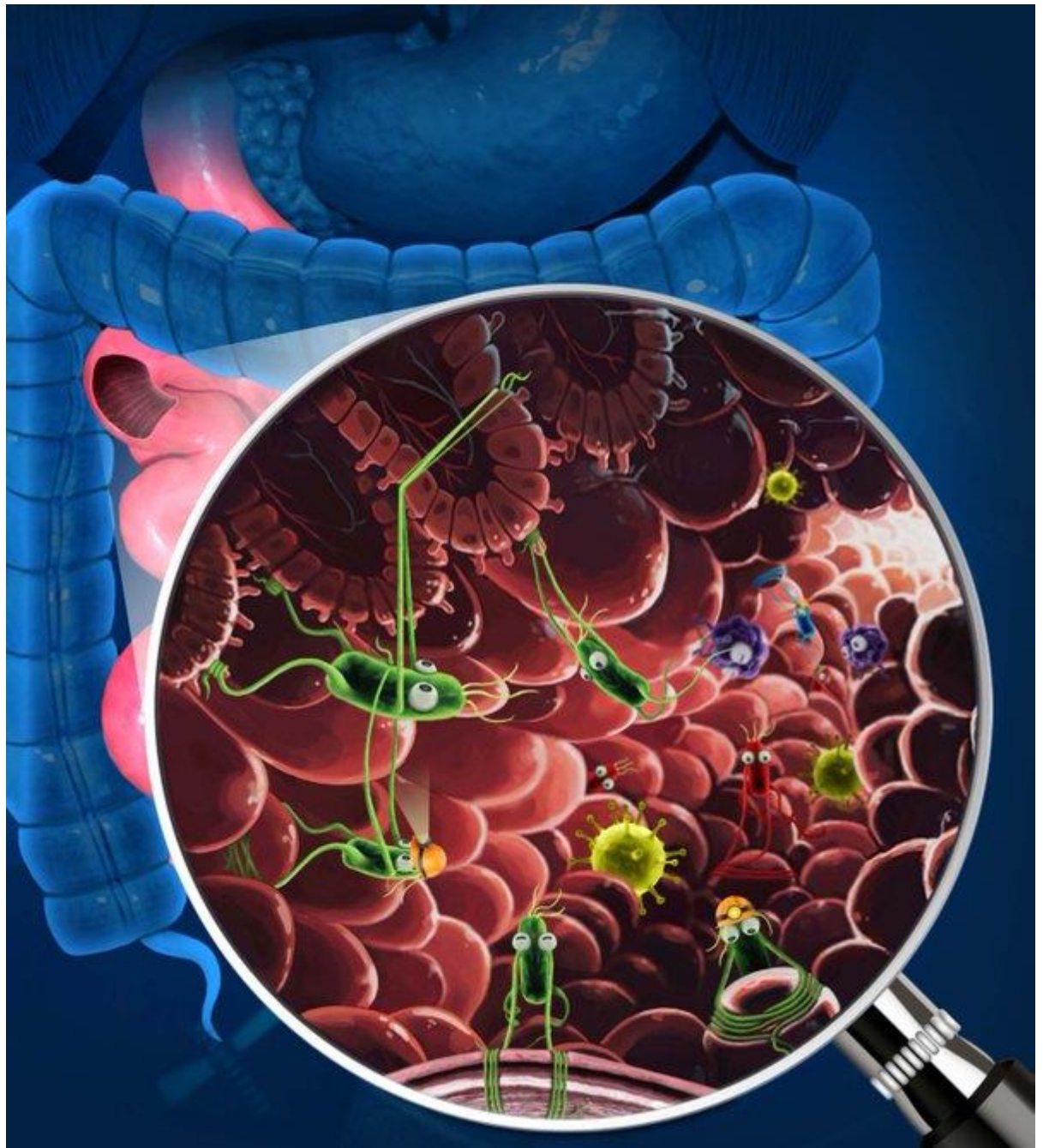
Summary & Outlook

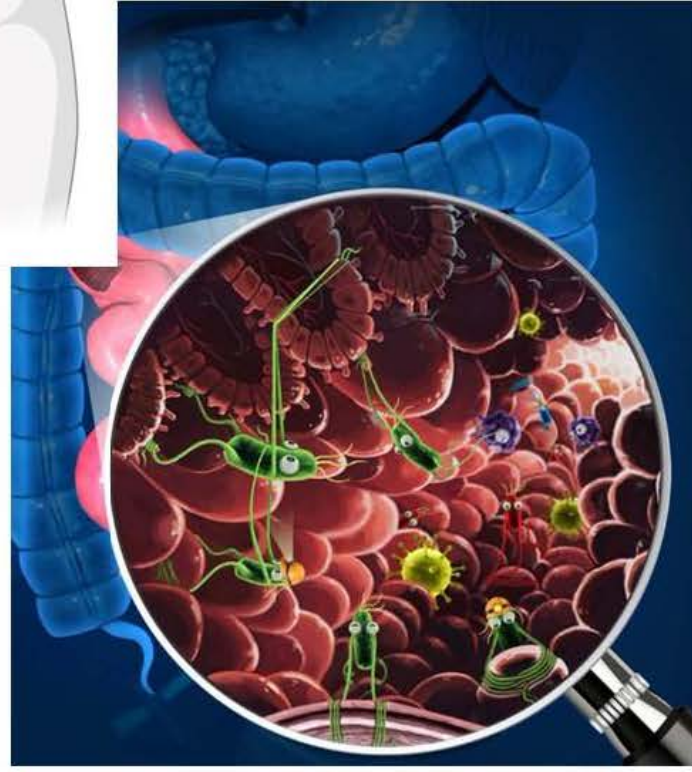
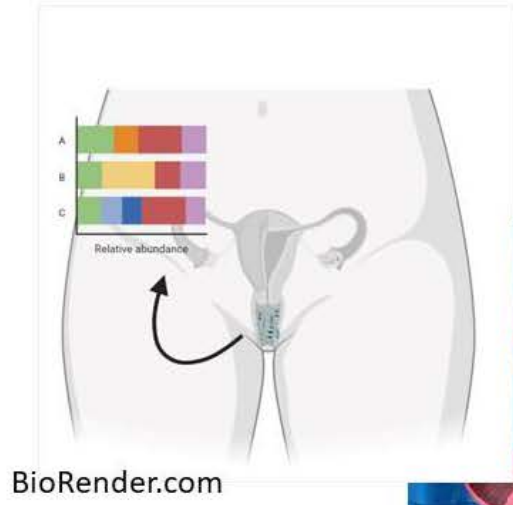
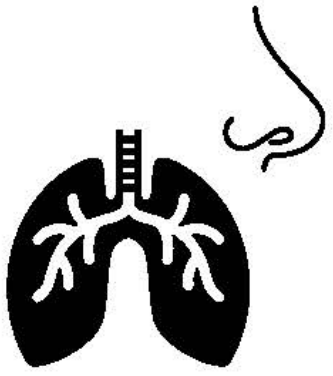
# The Intestinal Tract





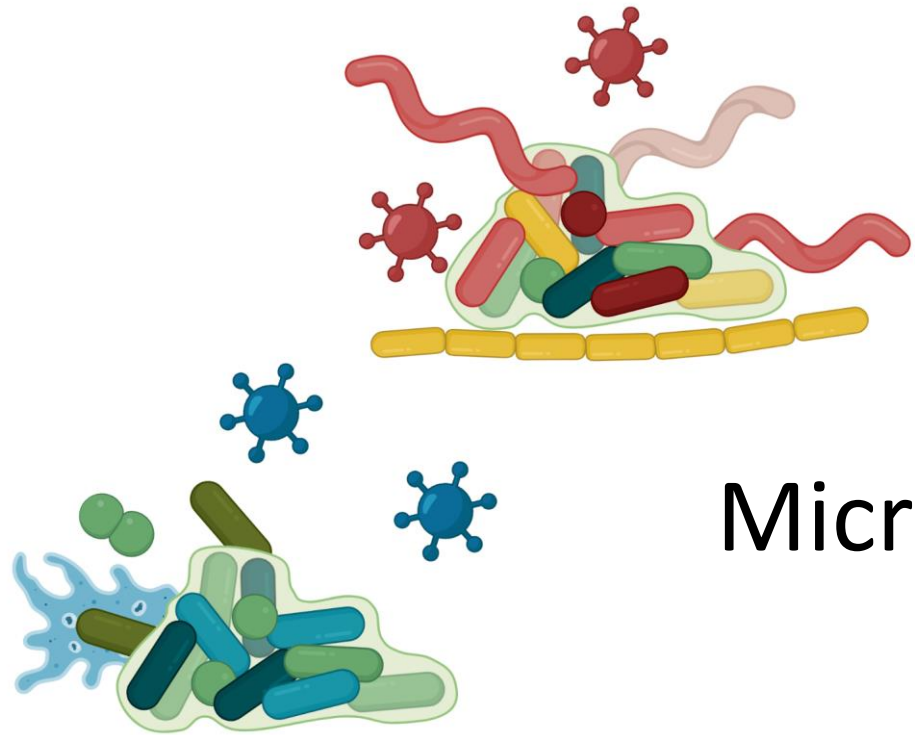
# The Microbiome



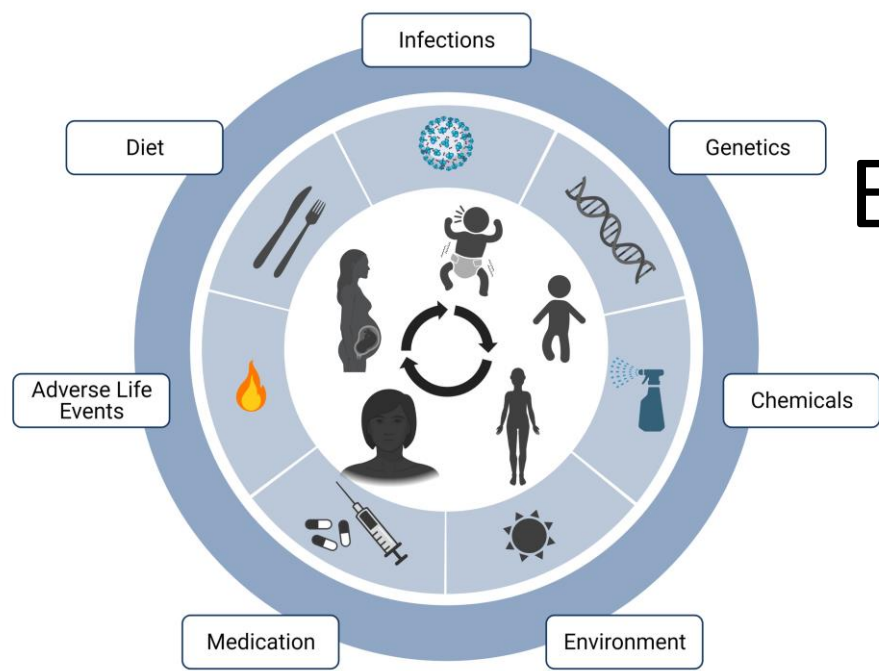


# Microbiomes

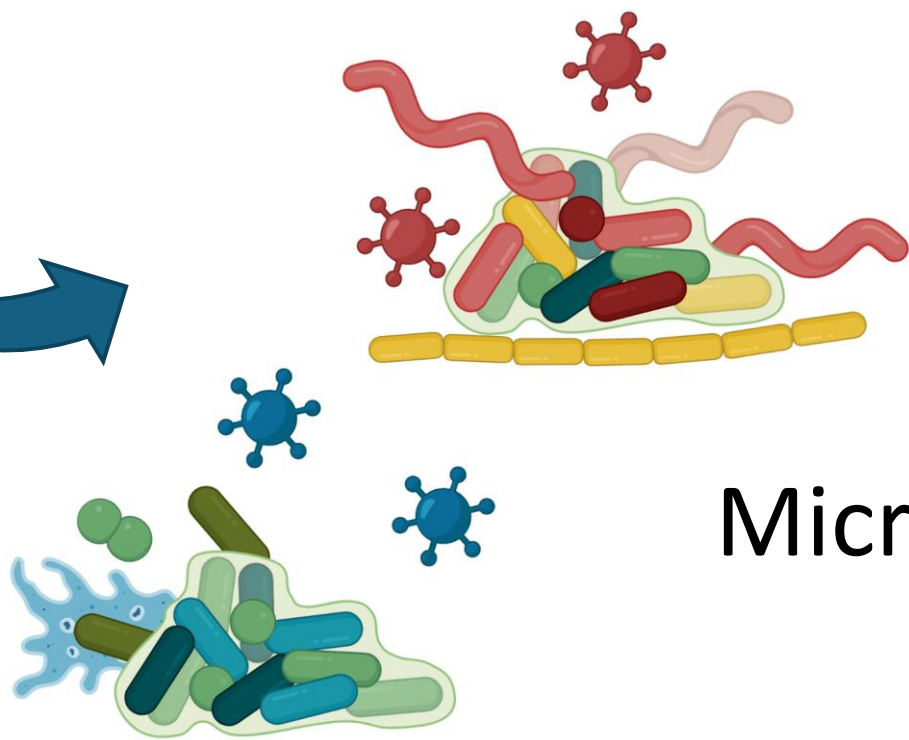




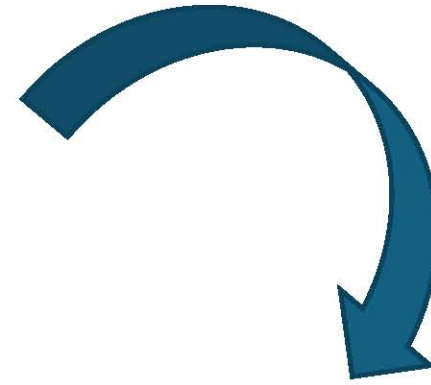
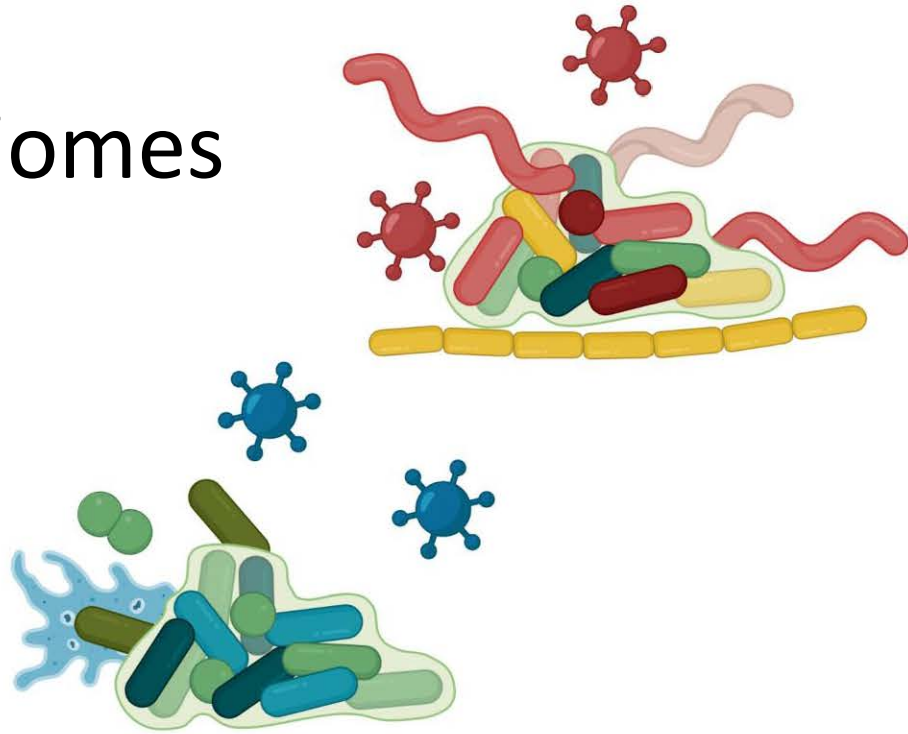
Microbiomes



# Exposures



# Microbiomes



# Outcomes



PRE-, PERI-,  
AND POSTNATAL  
(pregnancy and birth)



UPPER AND  
LOWER AIRWAY  
(breathing)



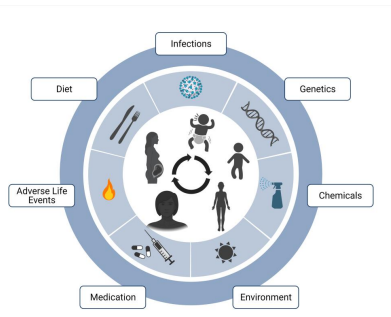
OBESITY  
(body weight)



NEURODEVELOPMENT  
(brain development)



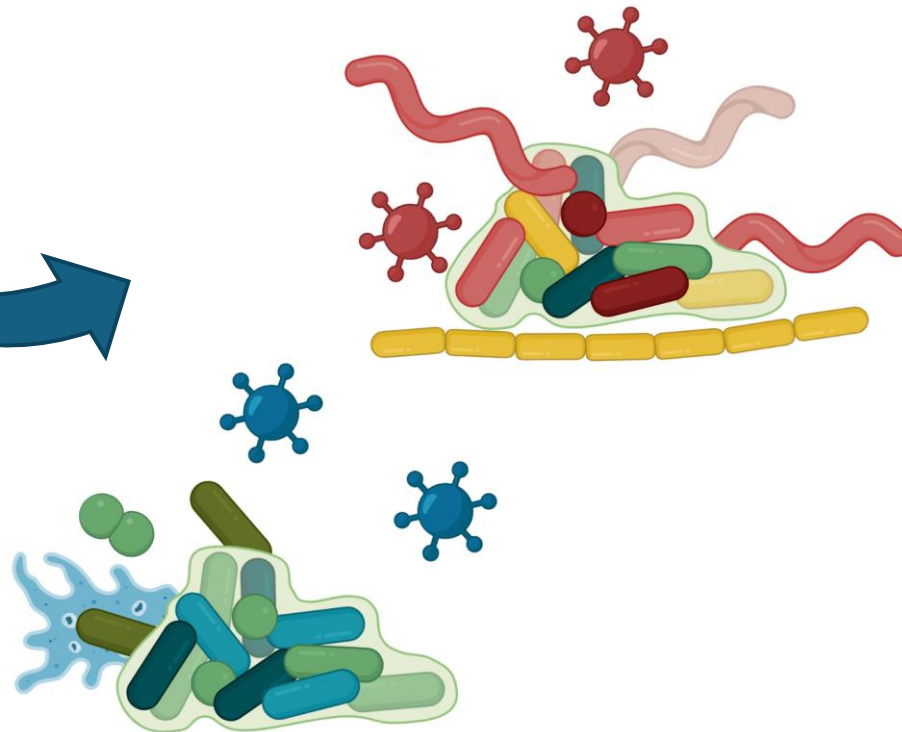
POSITIVE HEALTH  
(well-being)



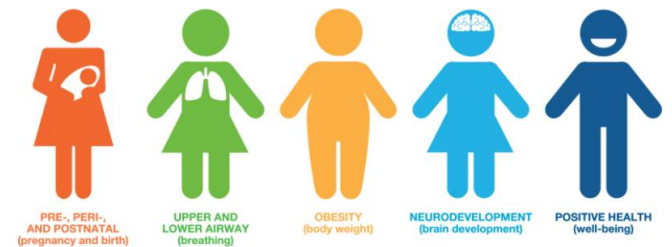
# Exposures



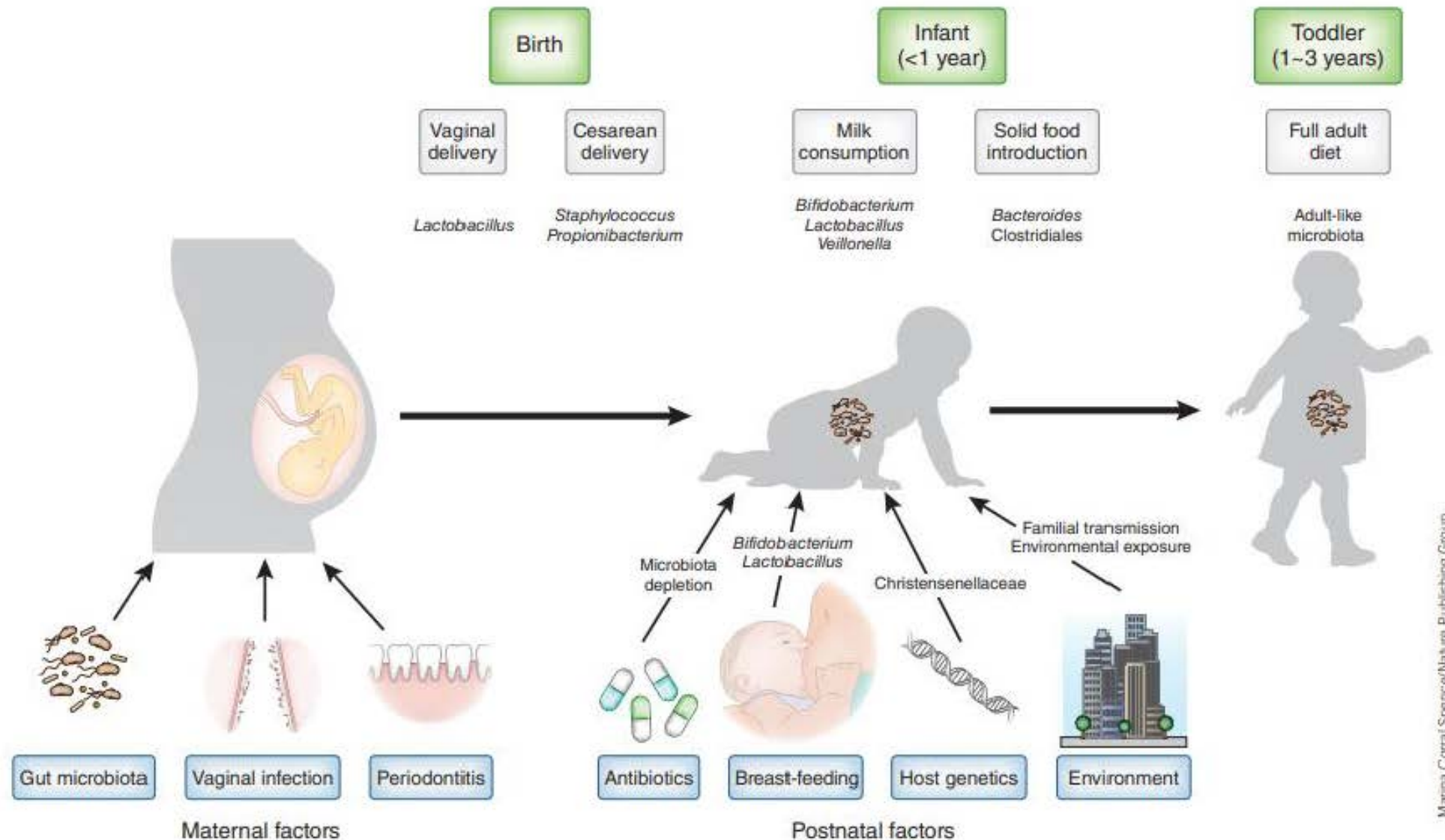
# Microbiomes



# Outcomes



# Exposures which Influence the Gut Microbiome



# What We Can Do in ECHO

Determine which exposures build host-associated microbiomes that ensure appropriate child development.



# The Power of a Longitudinal Pregnancy, Birth, and Pediatric Cohort

- Unique study design that collects information on exposures before outcomes are known



Preconception and birth



Infancy



Preschool age



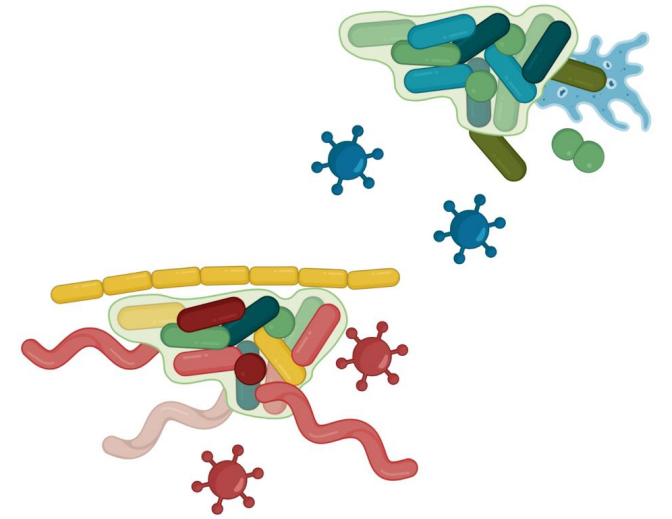
Adolescence



Adulthood

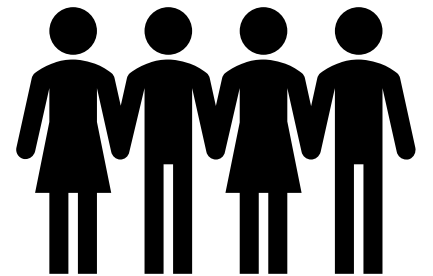
# ECHO Microbiome

- Extant data
  - Prenatal vaginal, prenatal fecal, child fecal, child airways
- Existing biospecimens
  - human milk, stool, saliva, nasal mucus
- New biospecimen collections ECHO-wide
- New biospecimen collections through specialized protocols



# ECHO Extant Data – Microbiota (16S)

- 16 cohort sites
- ~7,000 participants
  - Pregnant people
  - Children
- Over 16,000 samples



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	People	Samples
Vaginal – Prenatal	770	780
Fecal - Prenatal	700	770
Fecal – Child	3300	7000
Airways - Child	2900	6900



# ECHO Extant Biospecimens

	Prenatal	Infant: Perinatal	Infancy	Early Childhood	Middle Child- hood	Adolescence
Meconium/Stool	560	350	690	1000	400	500
Human Milk		500				
Nasal Mucus			100	500		
Saliva	13,400		1,600	5,000	4,500	2,300

# ECHO Collections in Cycle 2

- ECHO wide

- Child stool 0-5mos



- Obesity Specialized Protocol

- Prenatal 3<sup>rd</sup> trimester stool
- Child stool at: 6-11mos, 12-23mos, 24-35mos, 3-5yr, 6-10yr, 11-17yr, 18-20yr



- Airways Specialized Protocol

- Nasal airway mucosal sample (brush &/or filter) 0-11 mos (preferably 0-5mos) and 6 years



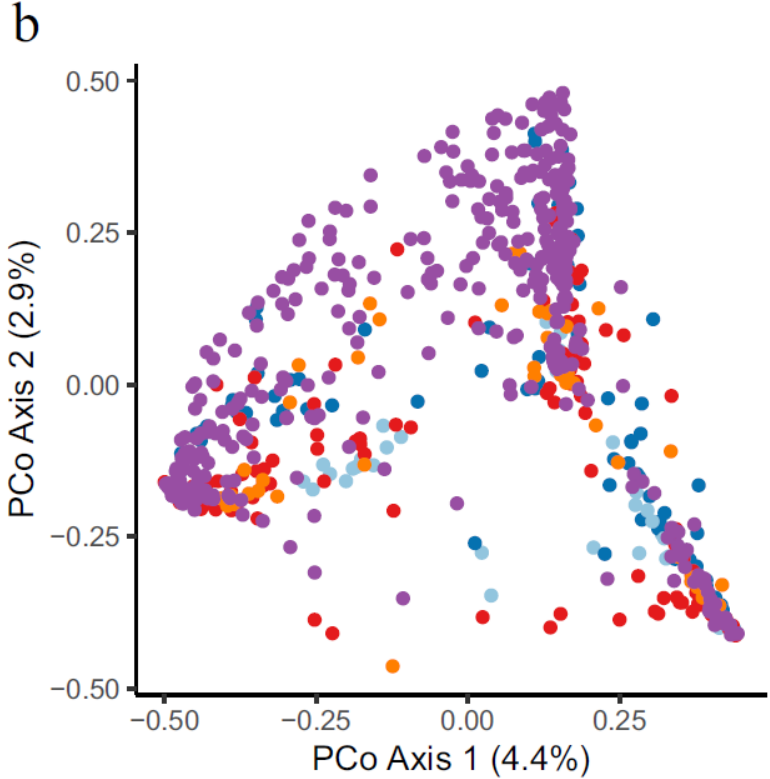
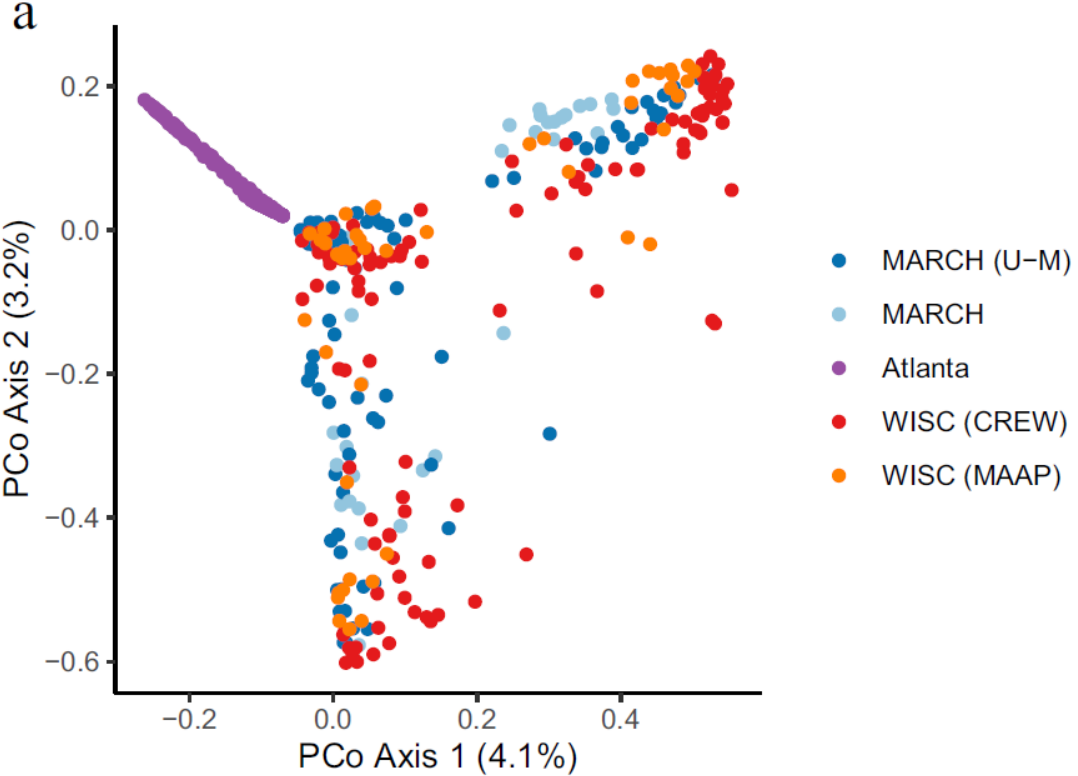
- Lifestyle Specialized Protocol

- Human milk



# ECHO-Wide Analyses with Extant Data

# Phylogenetic Placement of ASVs on a Reference Tree Removed a Large Degree of Variation by Site



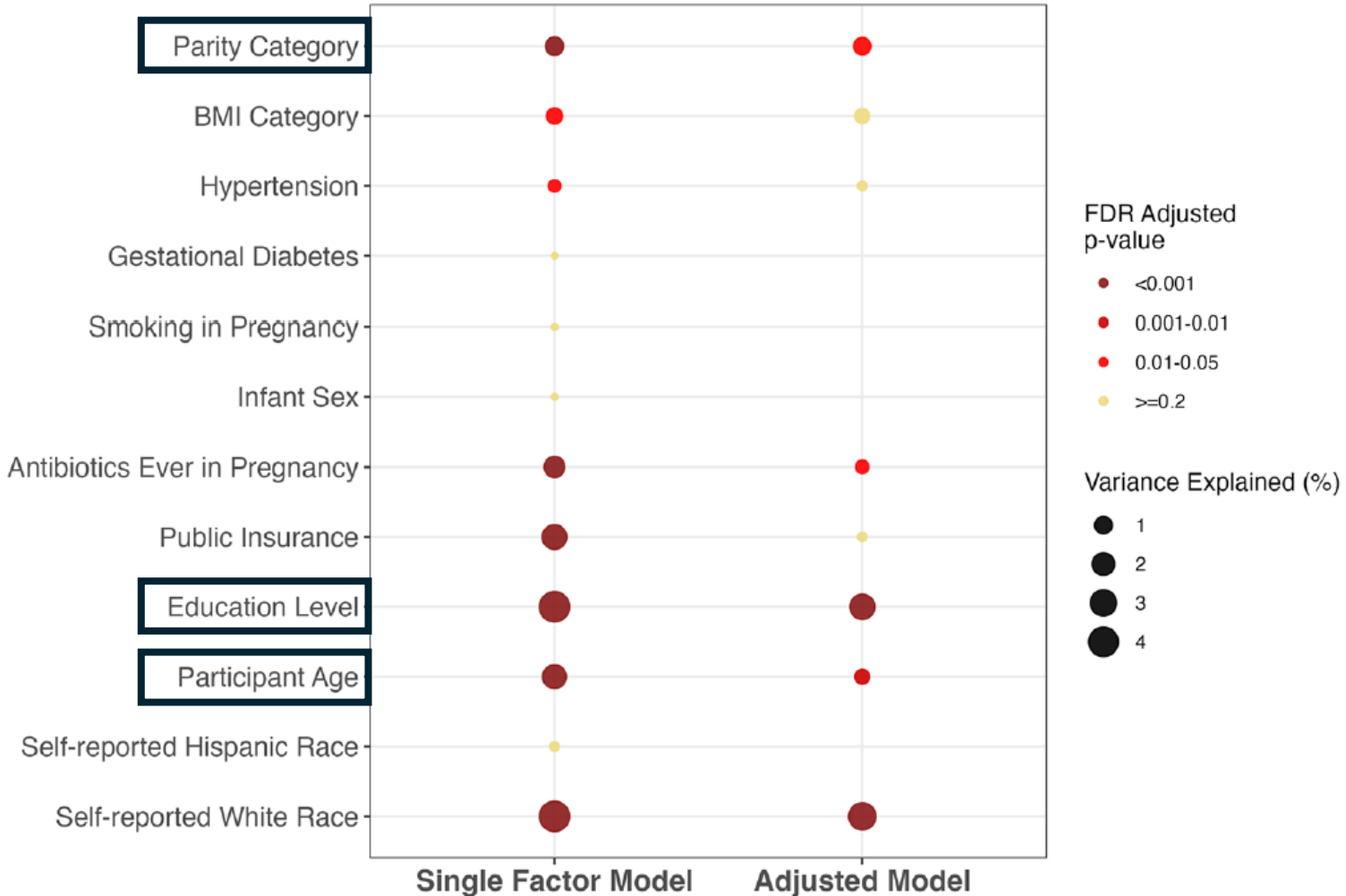
Jonathan Golob



Kimberly McKee

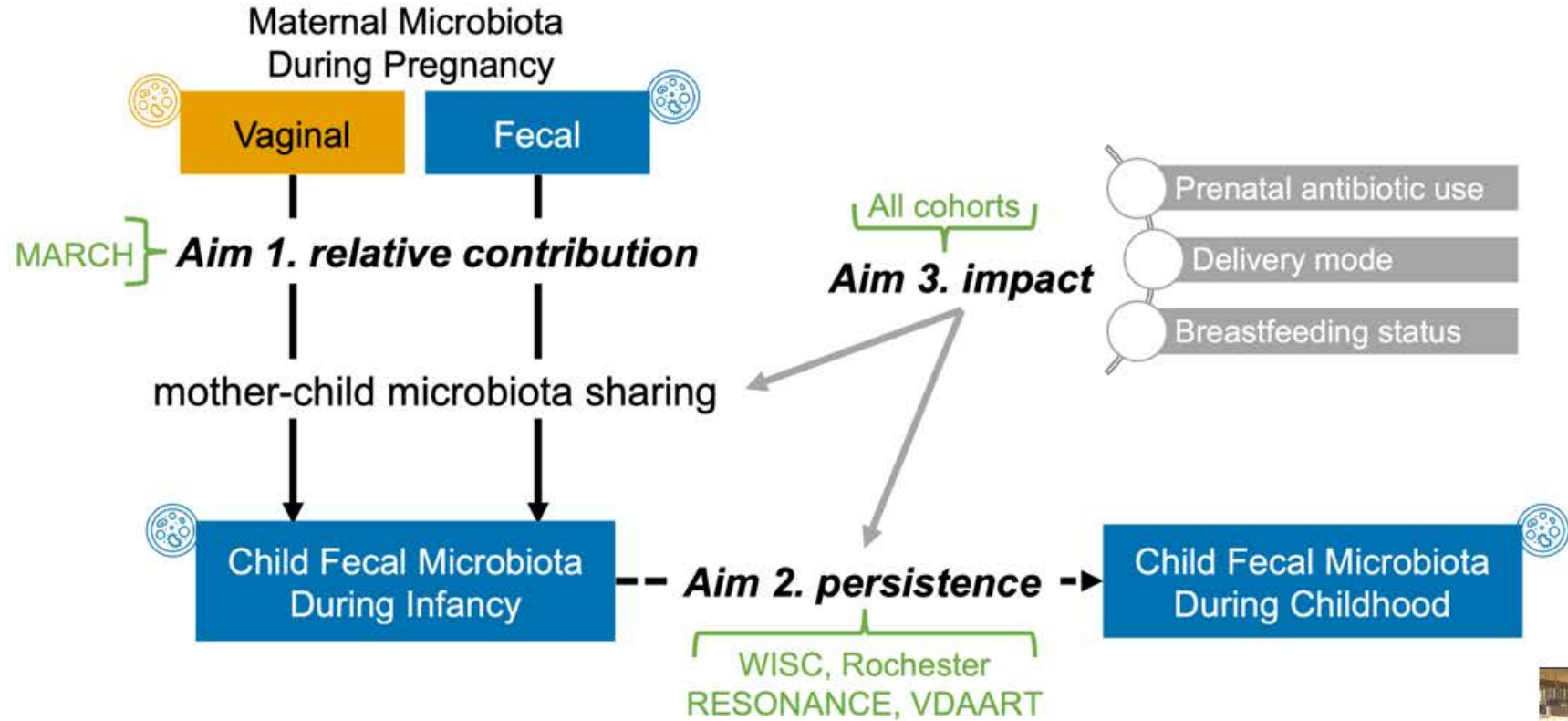
Bray-Curtis, Vaginal Microbiota

# Factors Associated with Vaginal Community Structure in Pregnancy

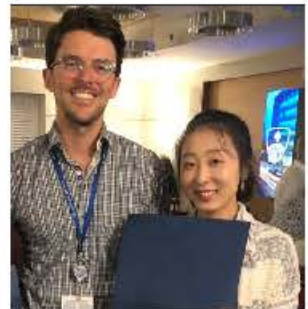


# Contributions of the Pregnancy Vaginal & Fecal Microbiota to Offspring Fecal Microbiota Development

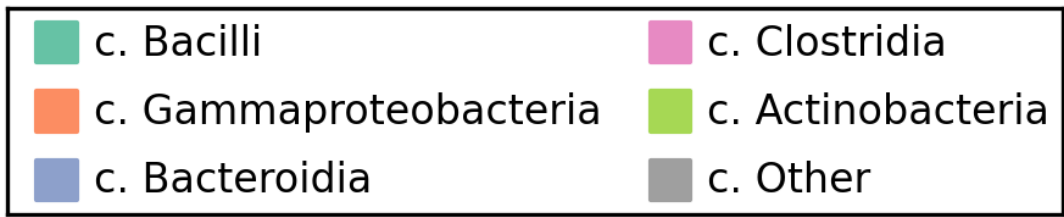
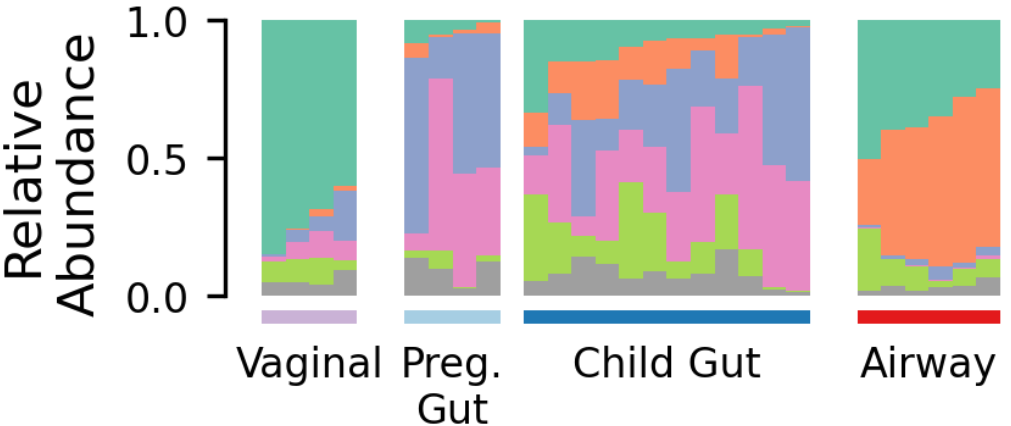
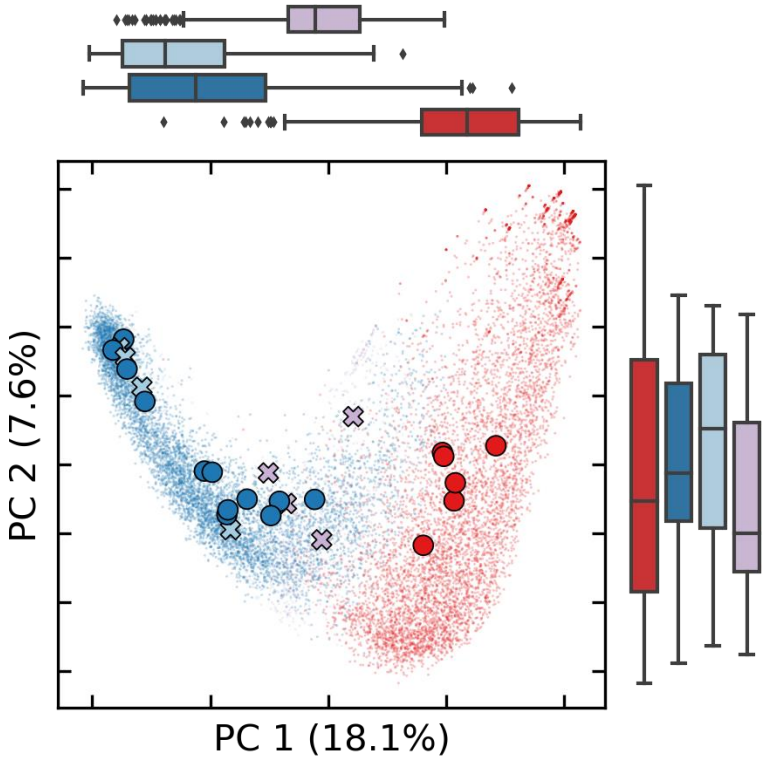
Study Aims



Noel Mueller  
Tiange Liu



# Microbiota Community Composition Differs by Body Site

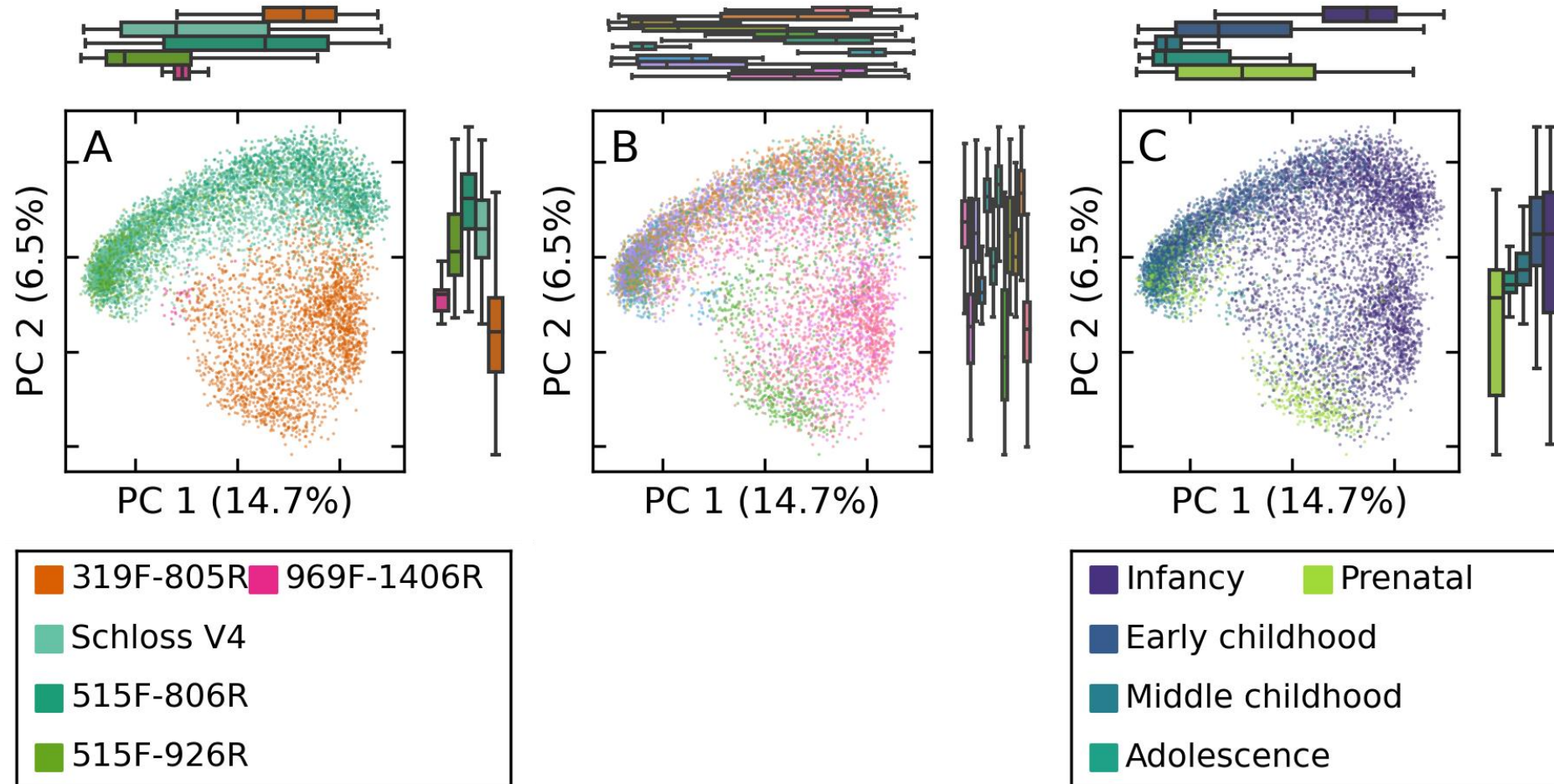


Vaginal      Gut      Airway  
 Pregnant Person      ×      ×  
 Child      ●      ●



Justine Debelius  
DAC

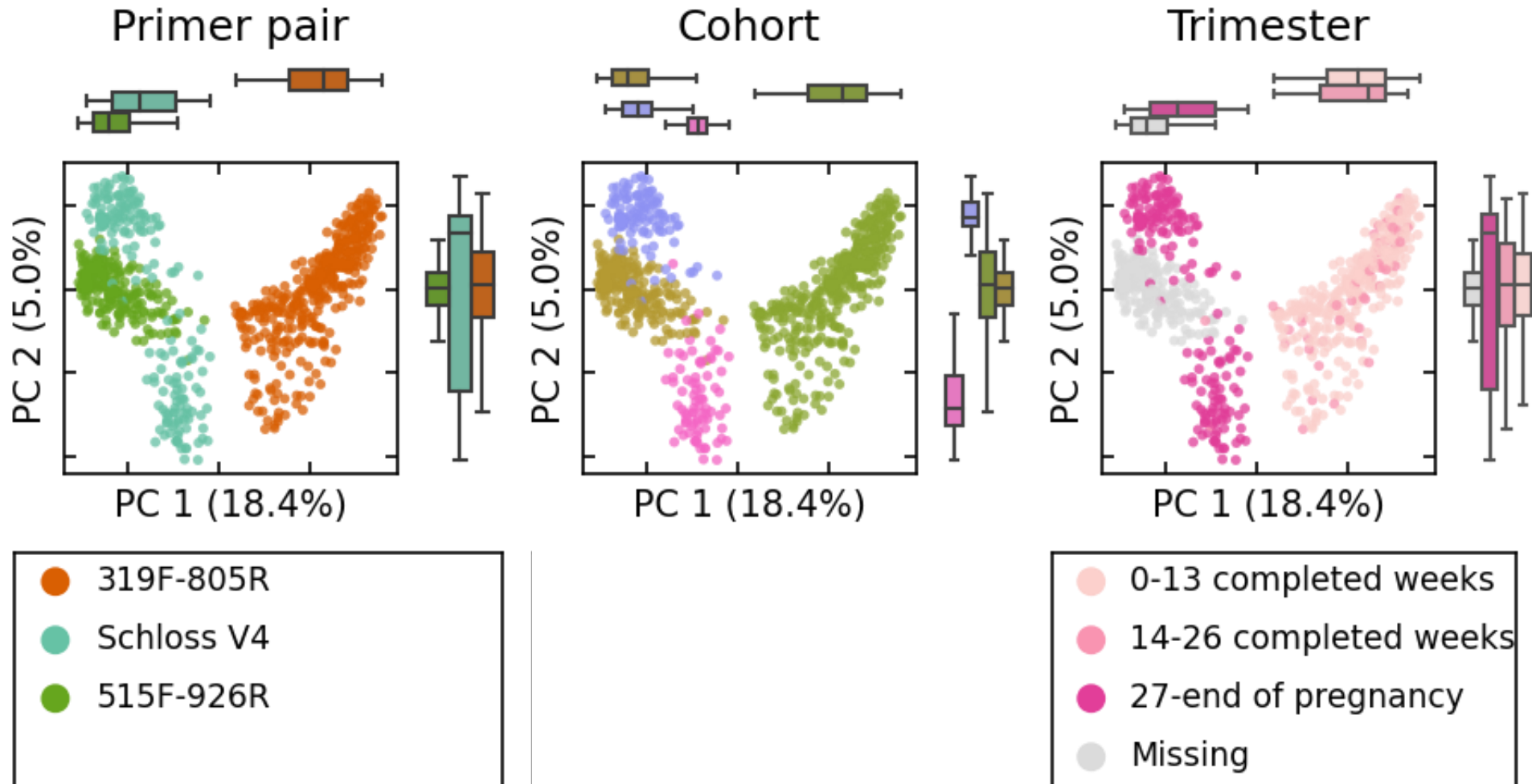
# Primer Pair and Lifestage are Associated with Fecal Bacterial Communities



Justine  
Debelius  
DAC

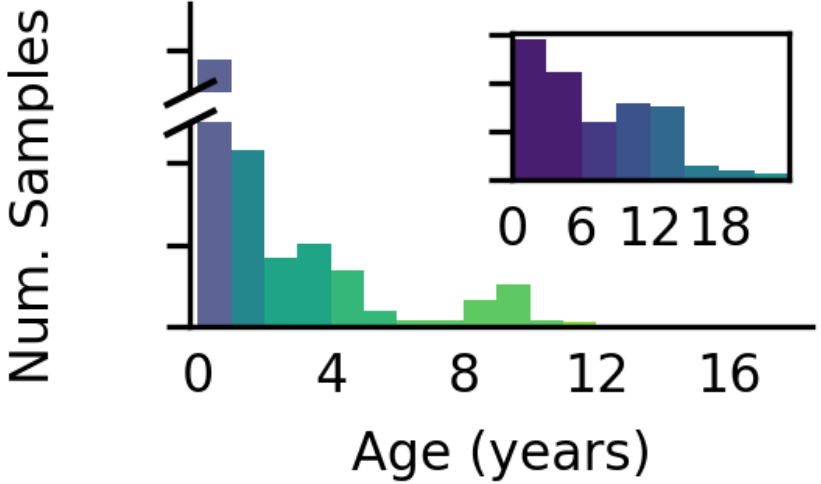
Unweighted UniFrac PCoA of Fecal samples in the Silva 97% OTU table with at least 1,000 sequences

# Primer Pair and Trimester are Associated with Prenatal Fecal Bacterial Communities

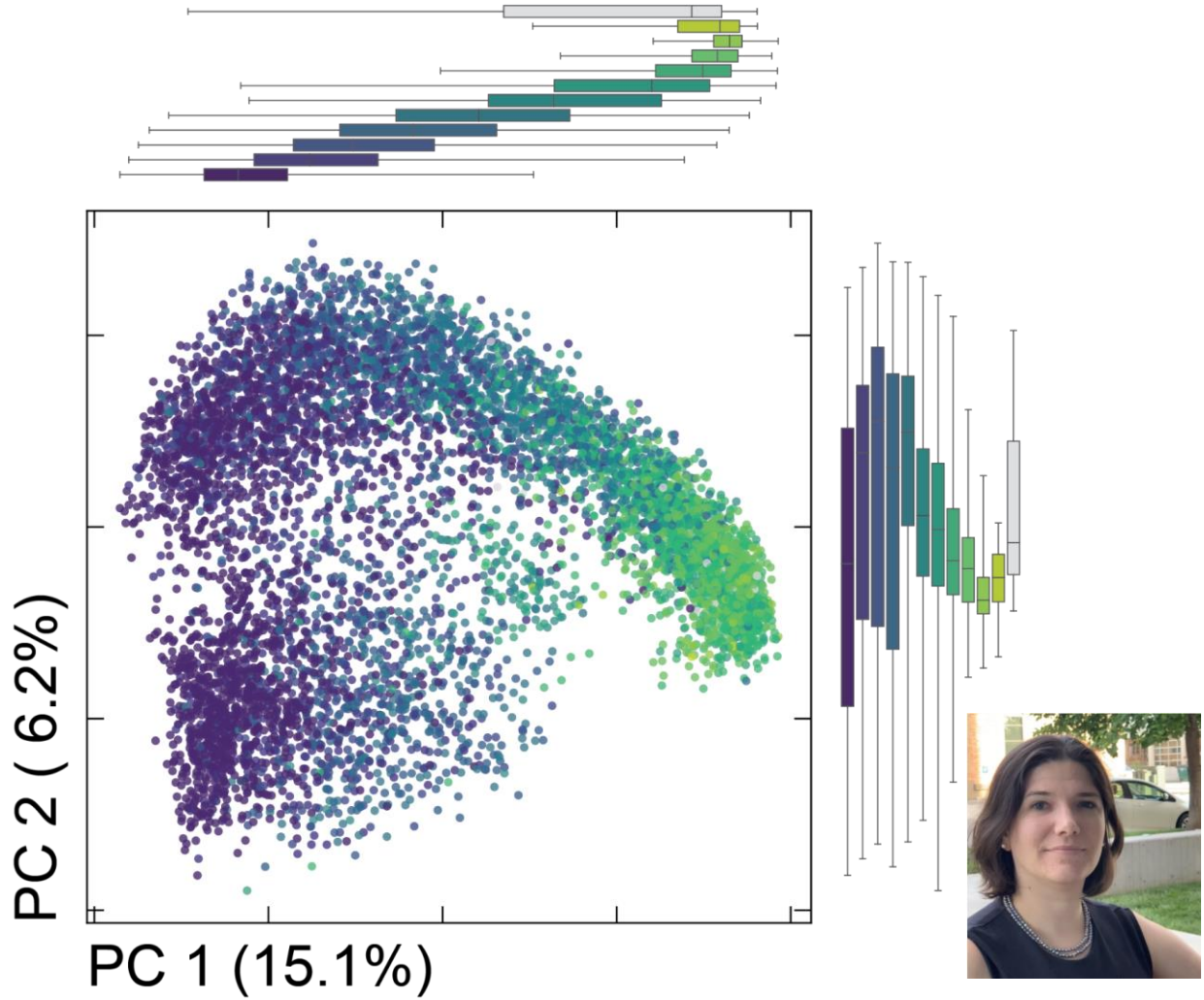


Justine  
Debelius  
DAC

# The Bacterial Composition of Fecal Samples Differs by Child Age

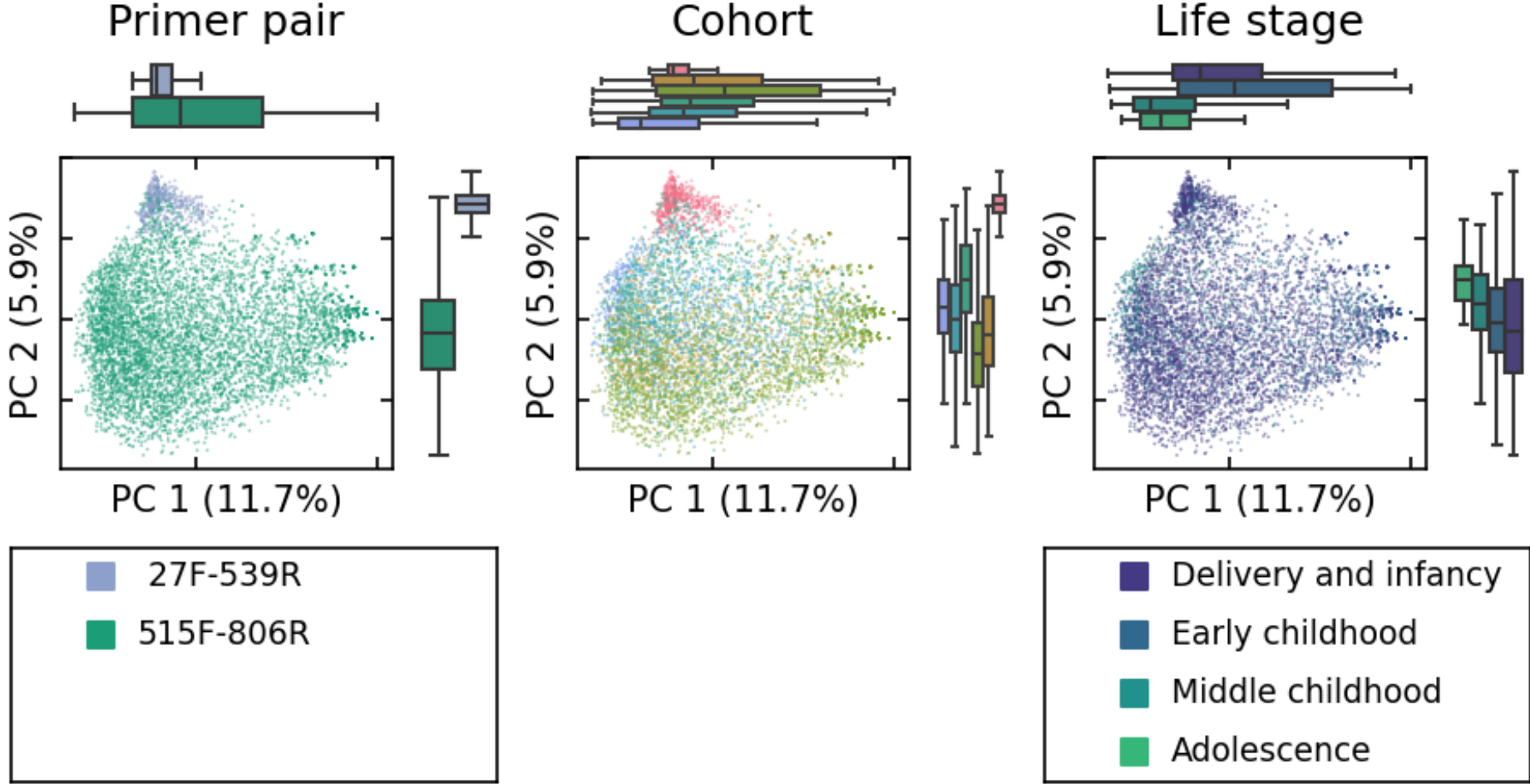


- 0-3 months
- 3-6 months
- 6-9 months
- 9-12 months
- 12-18 months
- 18-24 months
- 24-36 months
- 3-5 years
- 6-10 years
- 10-13 years
- 13-18 years
- missing



Justine Debelius  
DAC

# The Bacterial Composition of Airway Samples Differs by Primer Pair and Lifestage



Justine Debelius  
DAC

Unique child nasal or nasopharyngeal samples in the Silva 97% OTU table with at least 1,000 sequences

# Why study infants?

- Defined diets
  - Especially early in life
- No autonomy regarding diet
- Immune system isn't fully developed
- Gut microbiota isn't fully developed – or, rather, is still in a dynamic state



# Why study infants?

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- Immune system isn't fully developed
- Gut microbiota isn't fully developed – or, rather, is still in a dynamic state



At this point in development, more than at many other points in time across the lifespan, we have the chance to alter the microbiome through diet, and the immune system, and other systems, through the microbiome.



## Child Health Advances *from* Research *with* Mothers



### **Pregnancy Cohorts**

- ARCH
- MARCH

### **Primary Funding Sources**

- Michigan Health Endowment Fund
- NIH ECHO Program



## **ECHO**

Environmental influences  
on Child Health Outcomes



Nigel Paneth



Jean Kerver

# CHARM Microbiome Collaboration

Andrea Cassidy-Bushrow



Kim McKee



Michael Petriello



Sara Santarossa



Sarah Comstock



Rebecca Knickmeyer



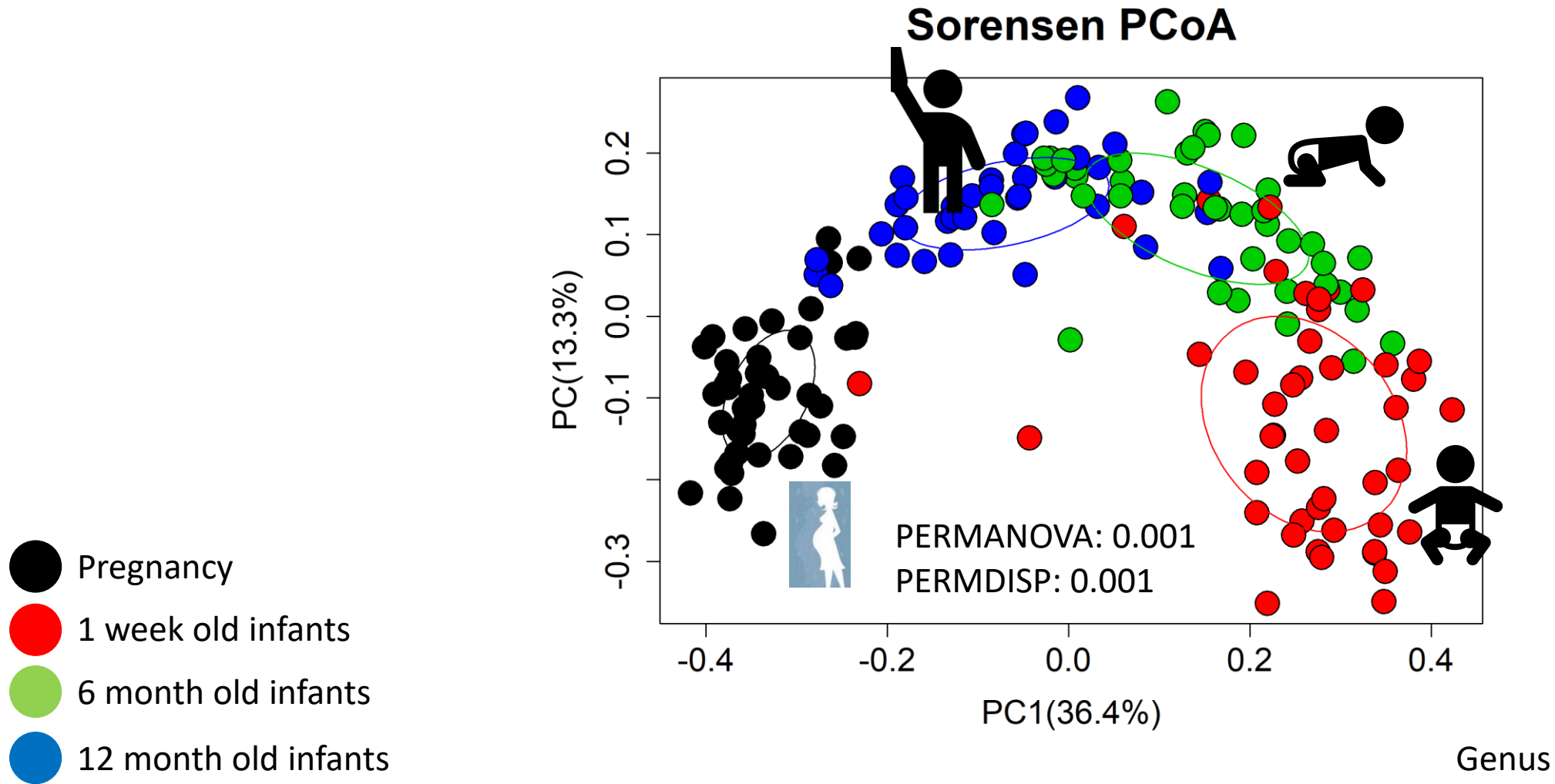
Tengfei Ma



Lixin Zhang

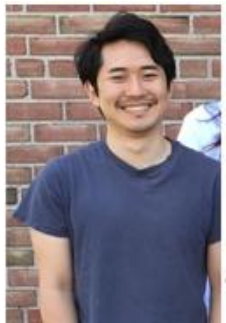
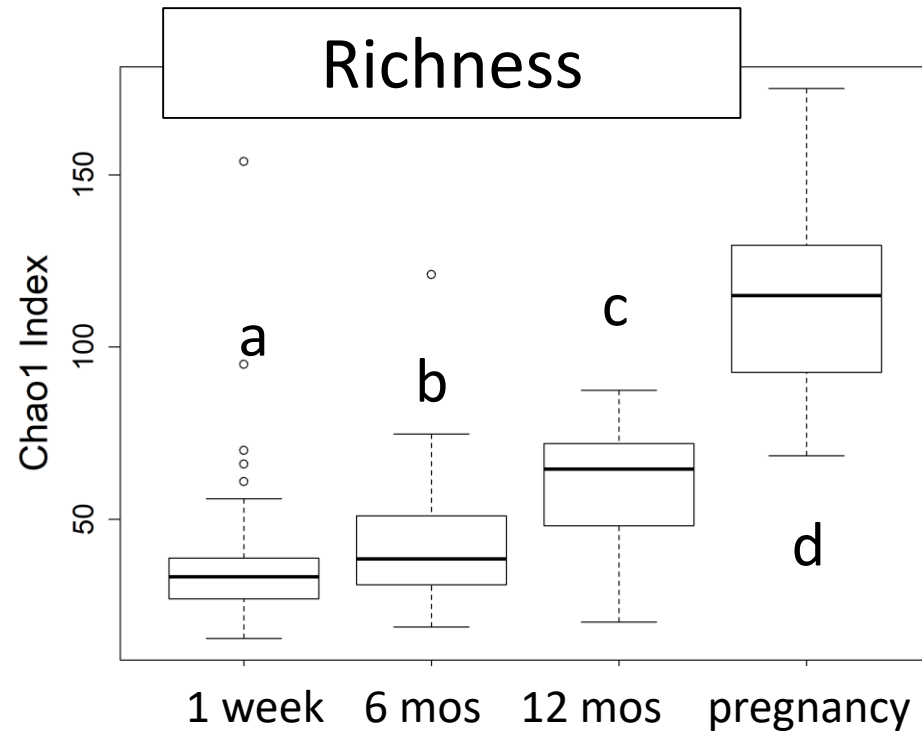


# Members of Fecal Microbial Communities Differ by Time Point Across the Lifespan



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Sugino

# Alpha Diversity is Greatest in Pregnancy Fecal Microbial Communities



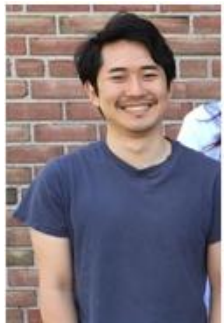
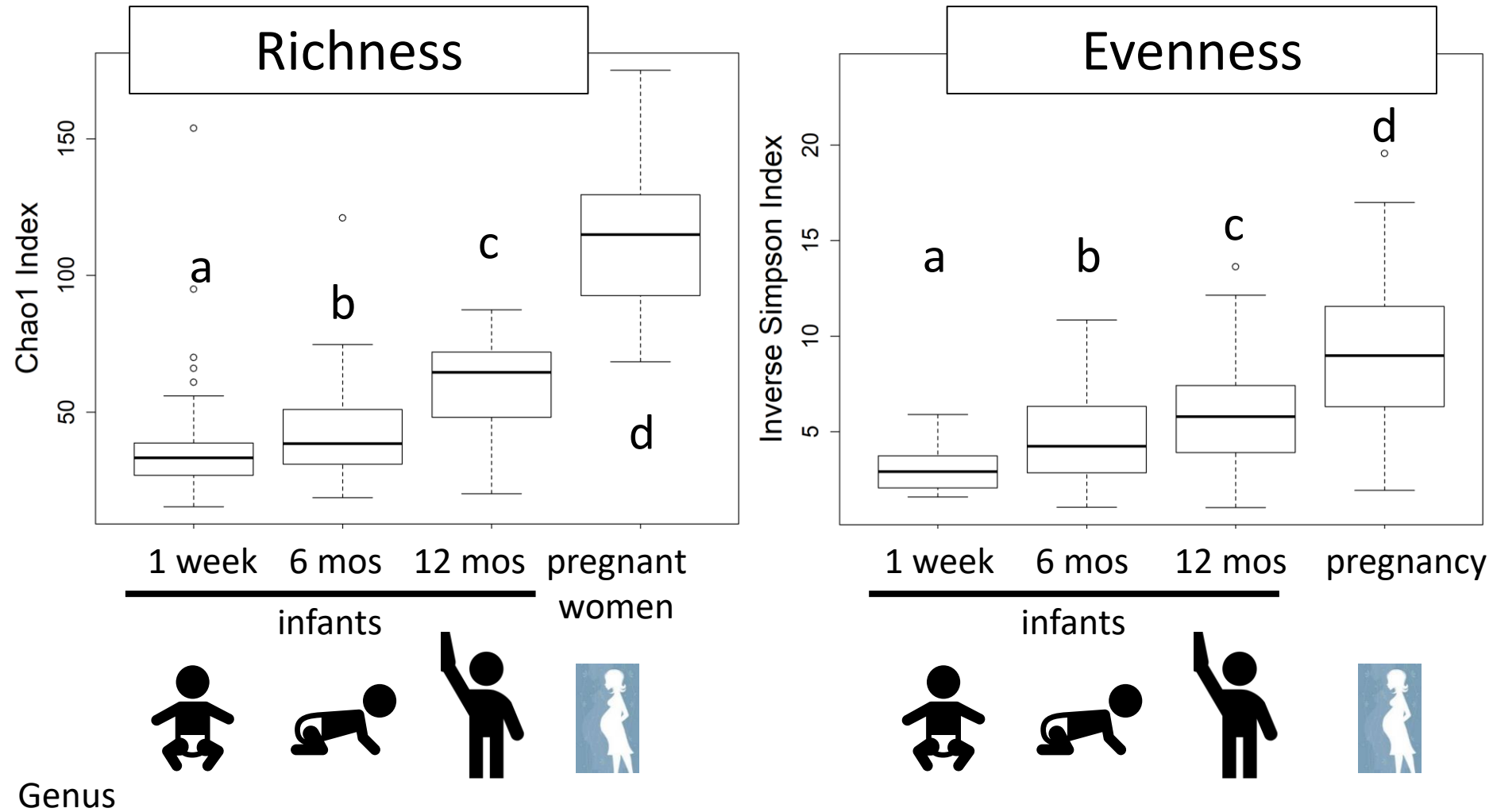
Kameron Sugino

infants



Genus

# Alpha Diversity is Greatest in Pregnancy Fecal Microbial Communities



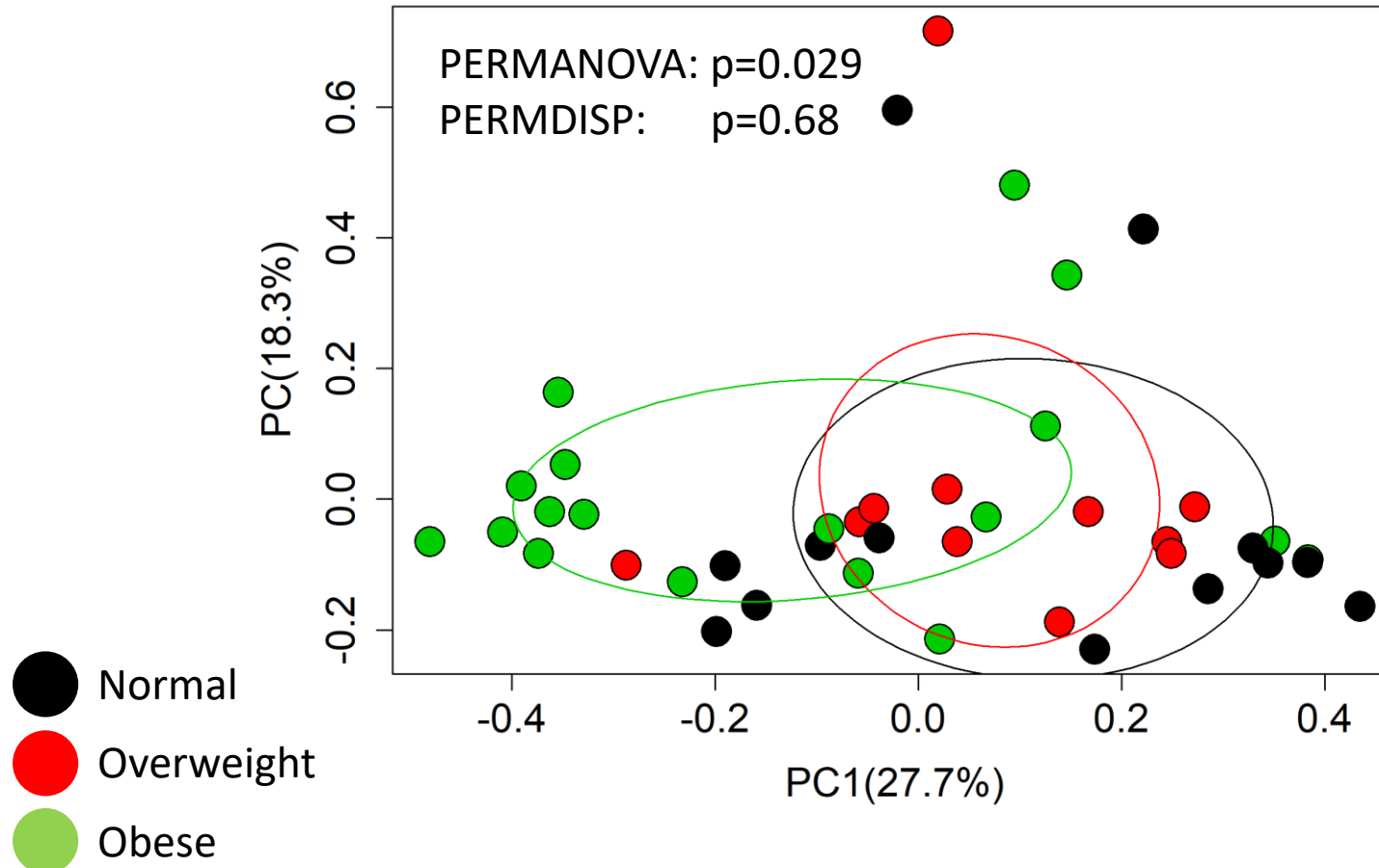
Kameron Sugino

Genus

# The Fecal Microbial Communities of 6 month old Infants Born to Women who were of Normal Weight Prior to becoming Pregnant are Different from those of Infants Born to Women with Pre-Pregnancy Obesity



## Genus: Bray-Curtis PCoA

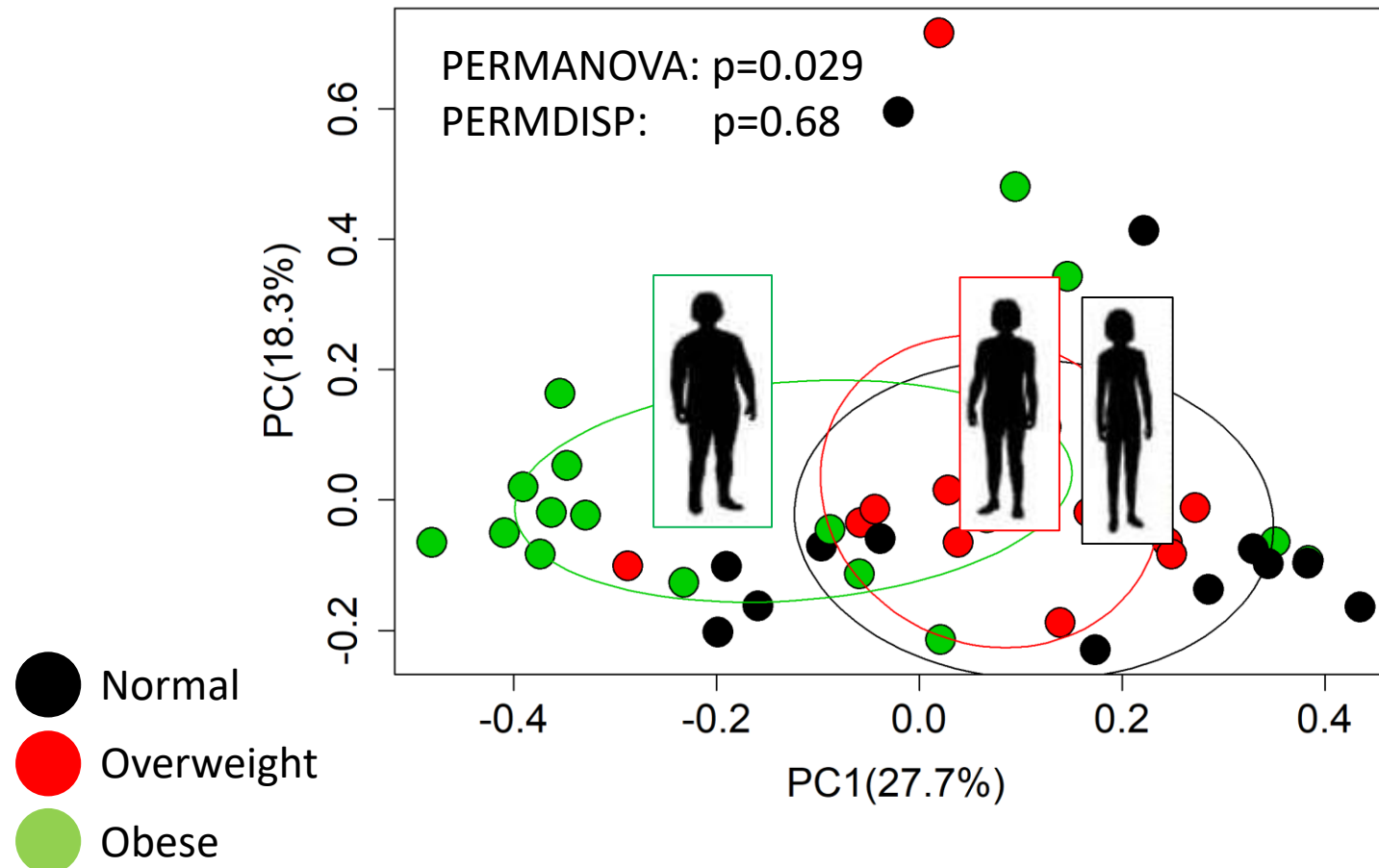


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# The Fecal Microbial Communities of 6 month old Infants Born to Women who were of Normal Weight Prior to becoming Pregnant are Different from those of Infants Born to Women with Pre-Pregnancy Obesity



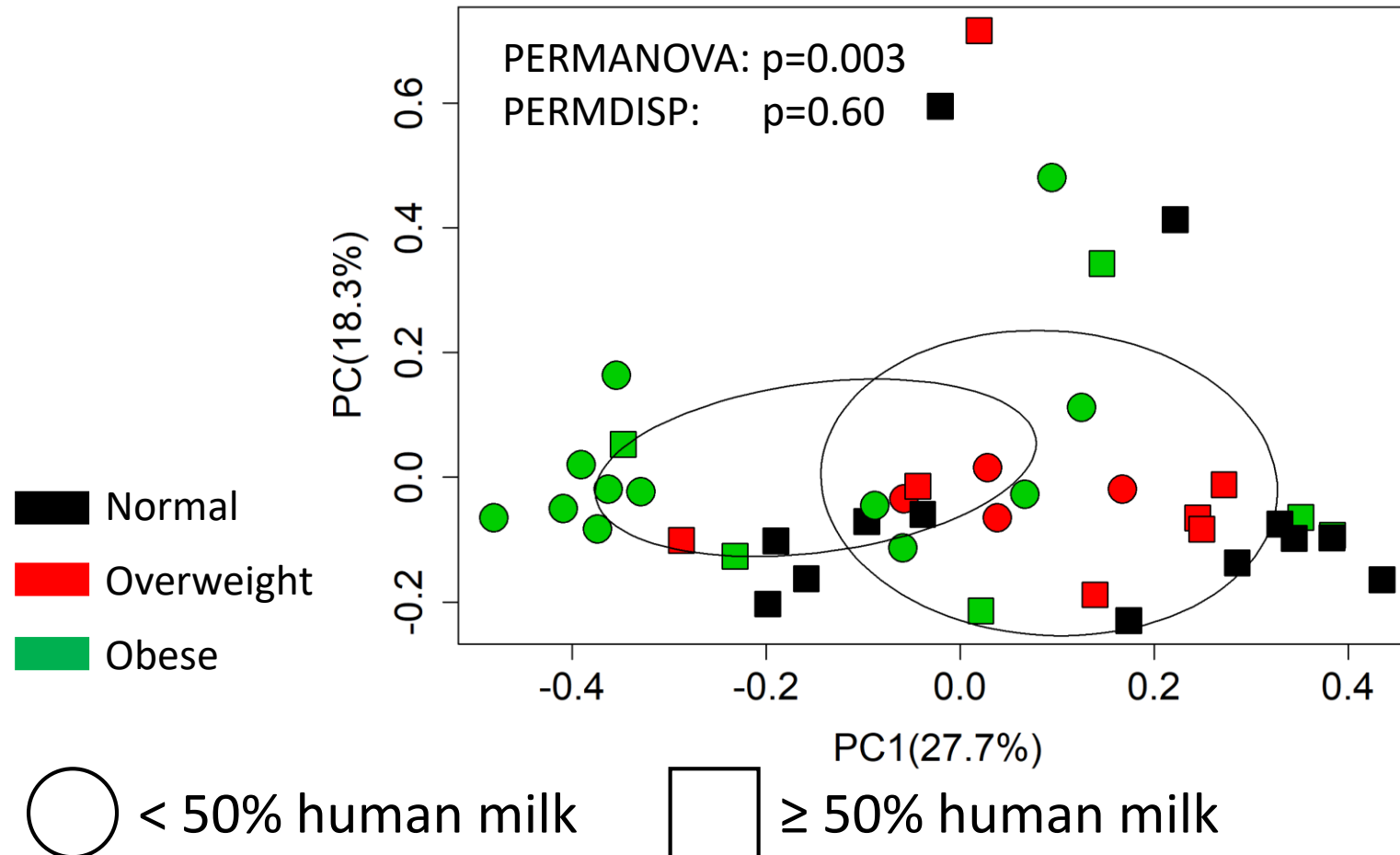
## Genus: Bray-Curtis PCoA



# However, this Association is Significantly Confounded by Human Milk Exposure



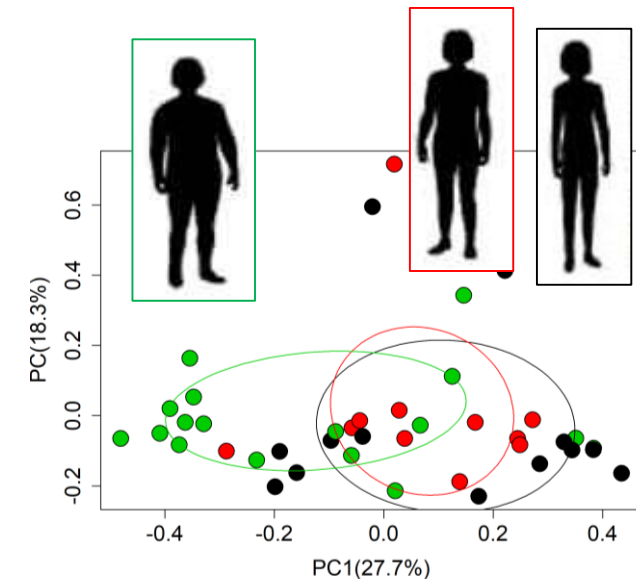
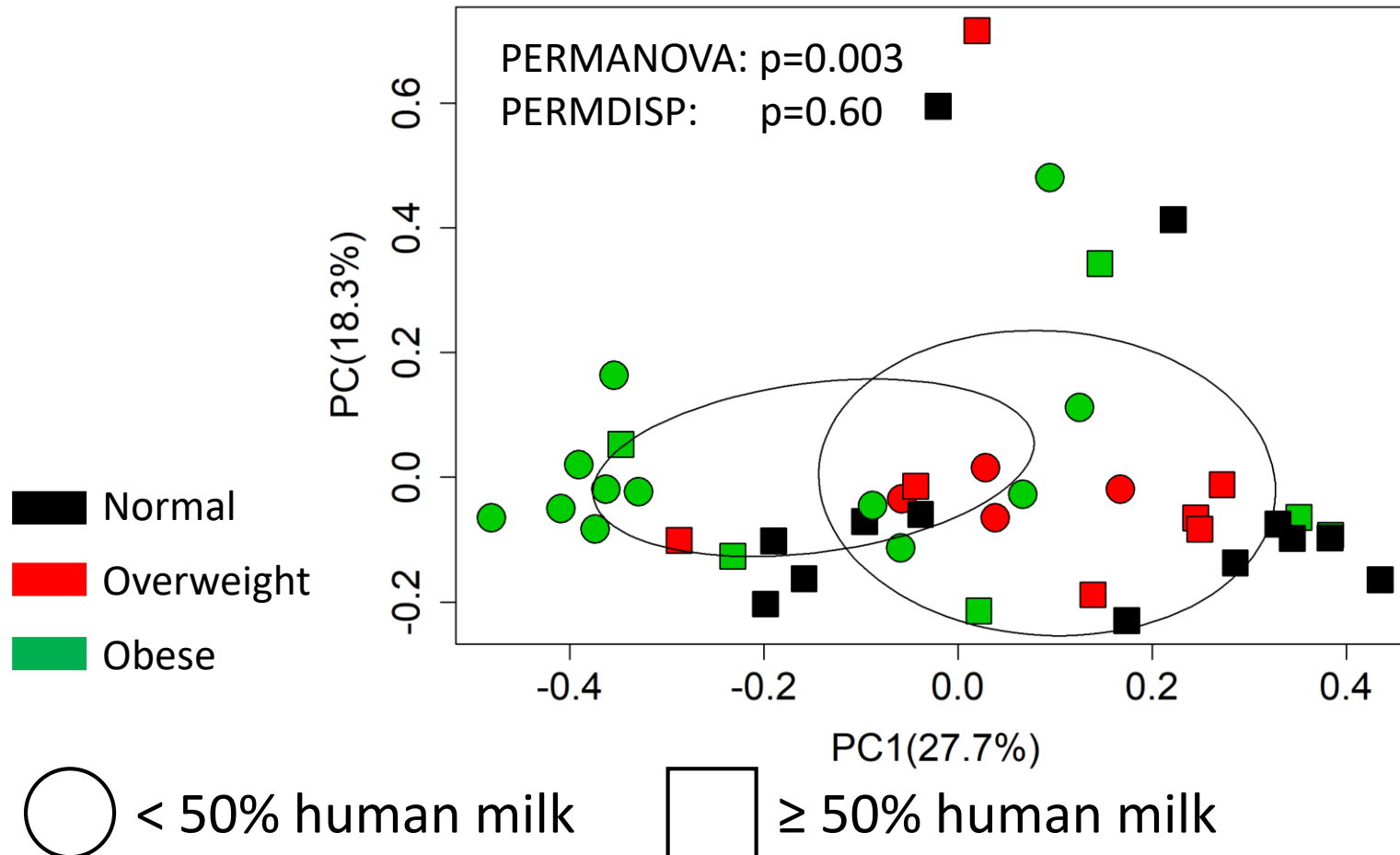
Genus: Bray-Curtis PCoA



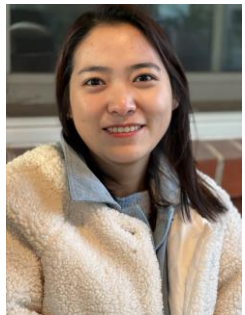
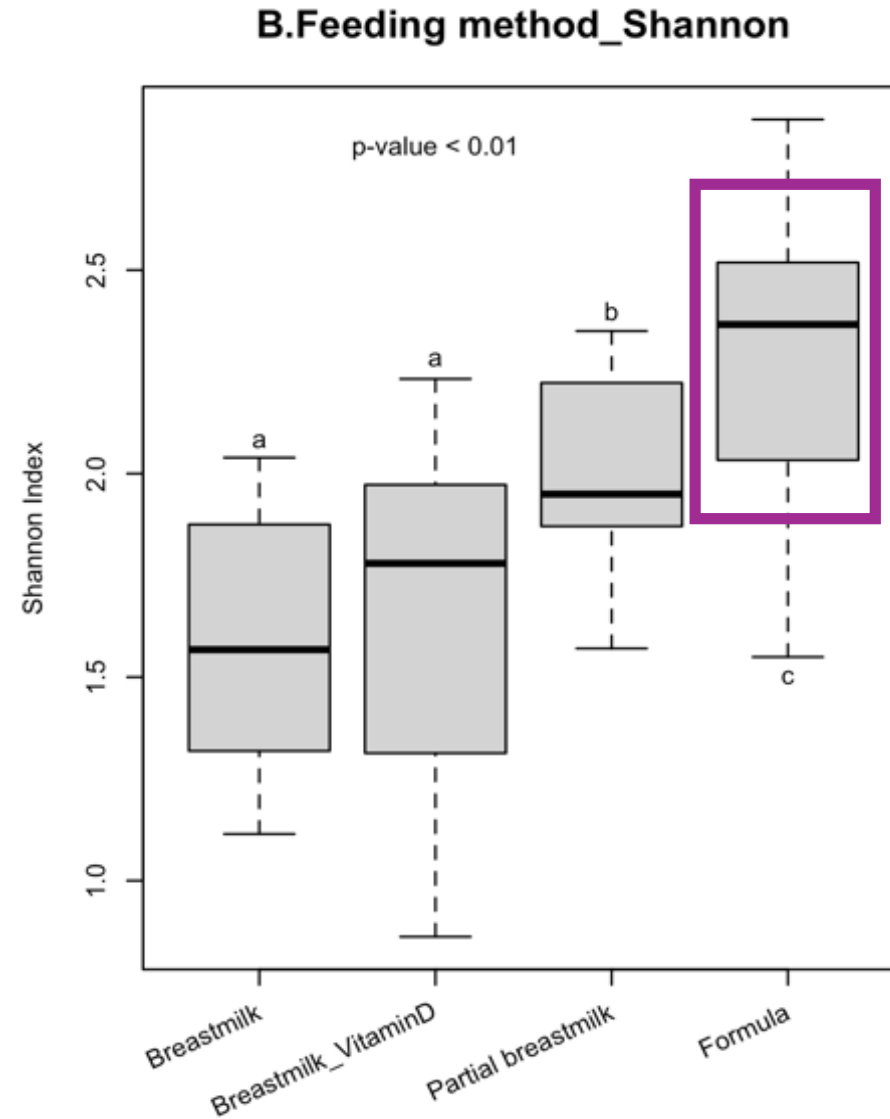
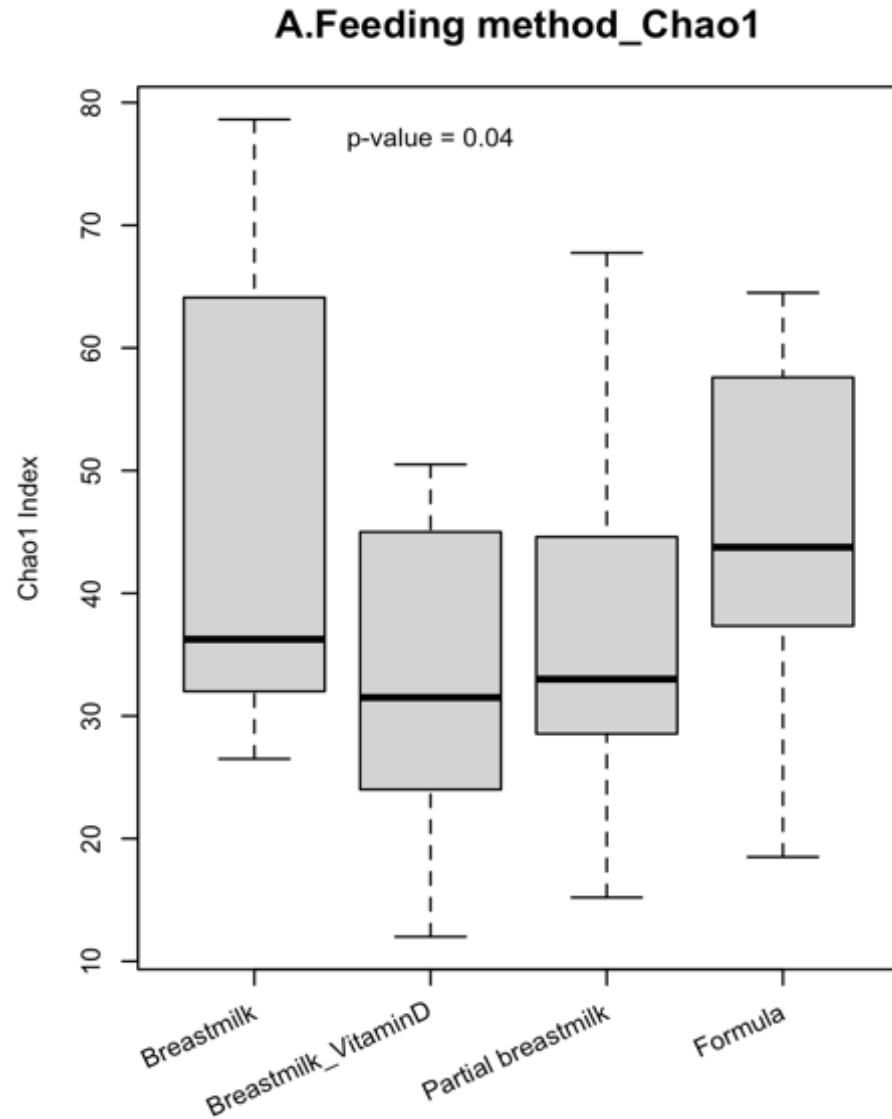
# However, this Association is Significantly Confounded by Human Milk Exposure



Genus: Bray-Curtis PCoA



# 3 Month Old Infants Fed Formula had Greater Shannon Alpha Diversity Compared to Infants Fed any Human Milk in the 24 Hours Prior to Sample Collection

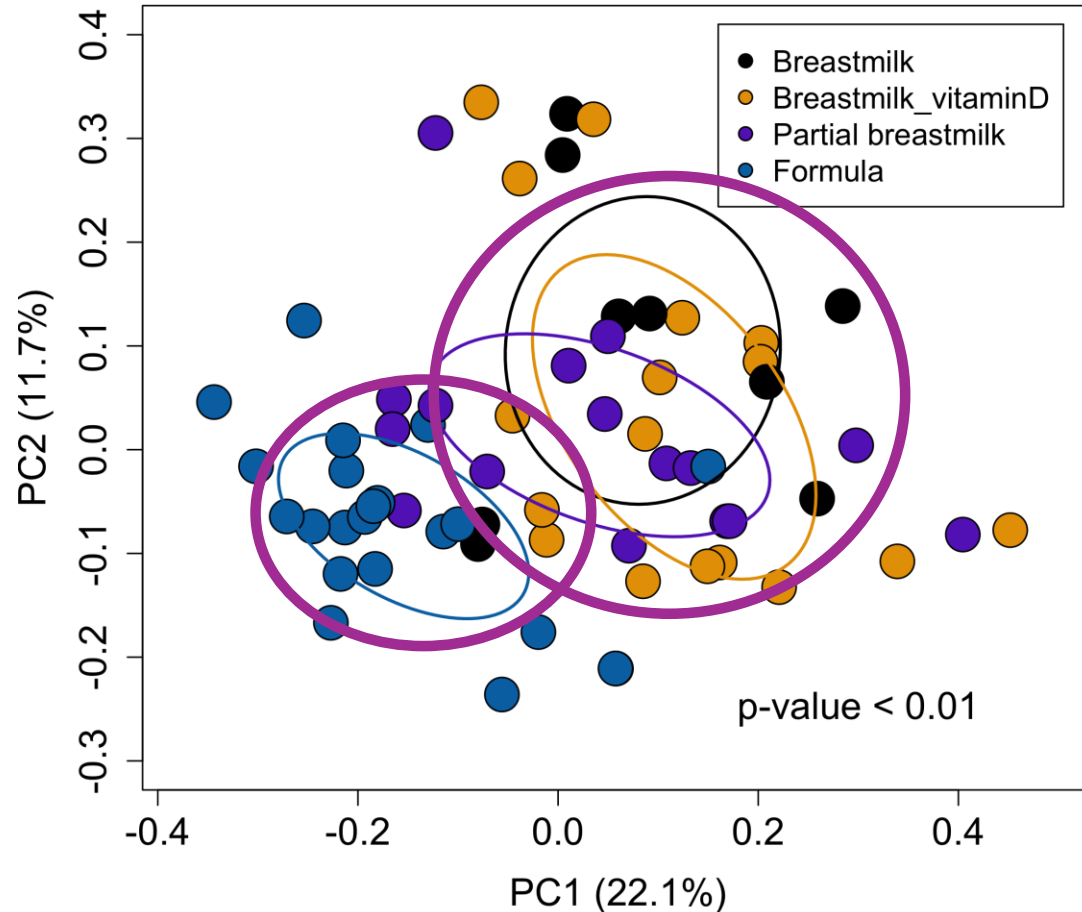


Sihan Bu

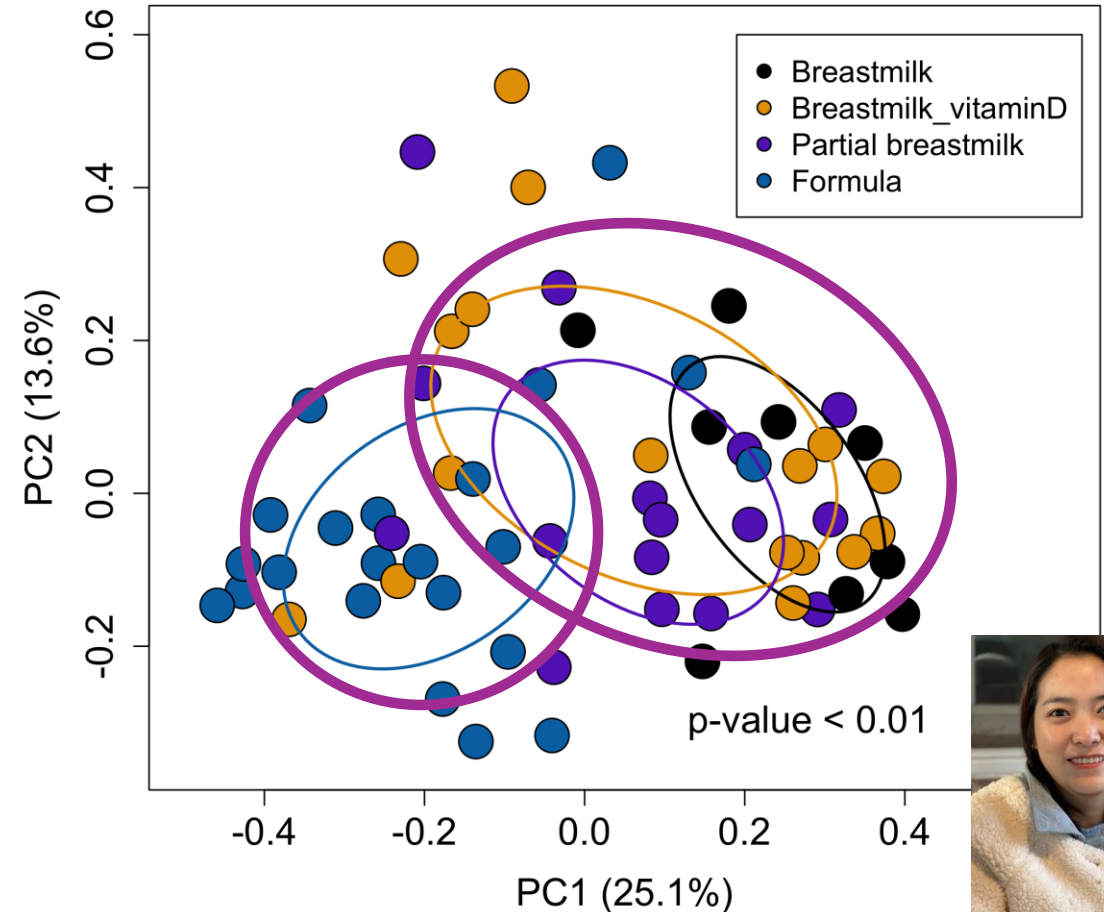
# 3 Month Old Infants Exclusively Fed Formula had Distinct Gut Microbiotas from those Exclusively Fed Human Milk, with Mixed Fed Infants having Microbiotas More Similar to those Infants Exclusively Fed Human Milk



## A. Sorensen

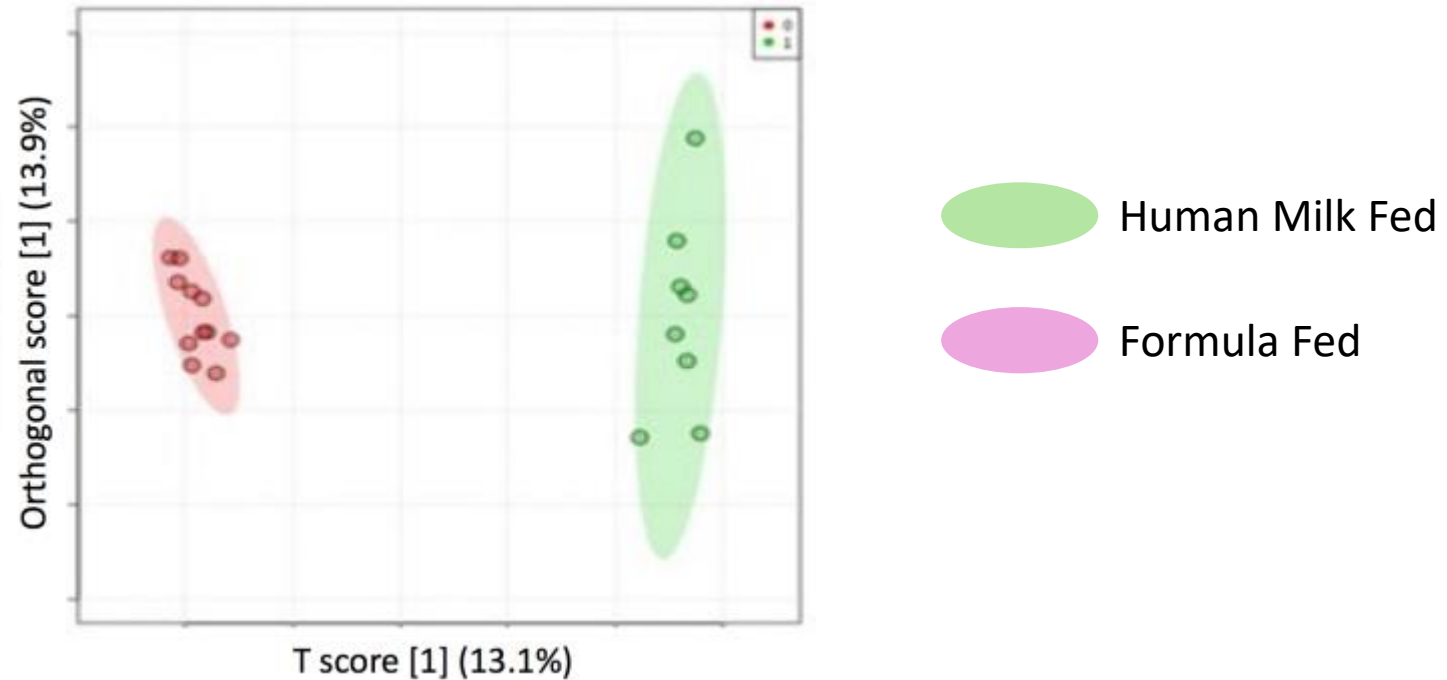


## B. Bray-Curtis



Sihan Bu

# Metabolites in the Stool of 6 Month Old Infants Differ by Diet



**HHEAR** Human Health Exposure  
Analysis Resource

Unpublished, NIH CHEAR lab (Susan Sumner, Susan McRitchie), Dan Rajasinghe (Pestka Lab)  
Leimanis Laurens & Comstock 2020 *Nutrients*, review article



# Infant Stool Samples have Unique Human Milk Oligosaccharide Metabolizing Gene Repertoires

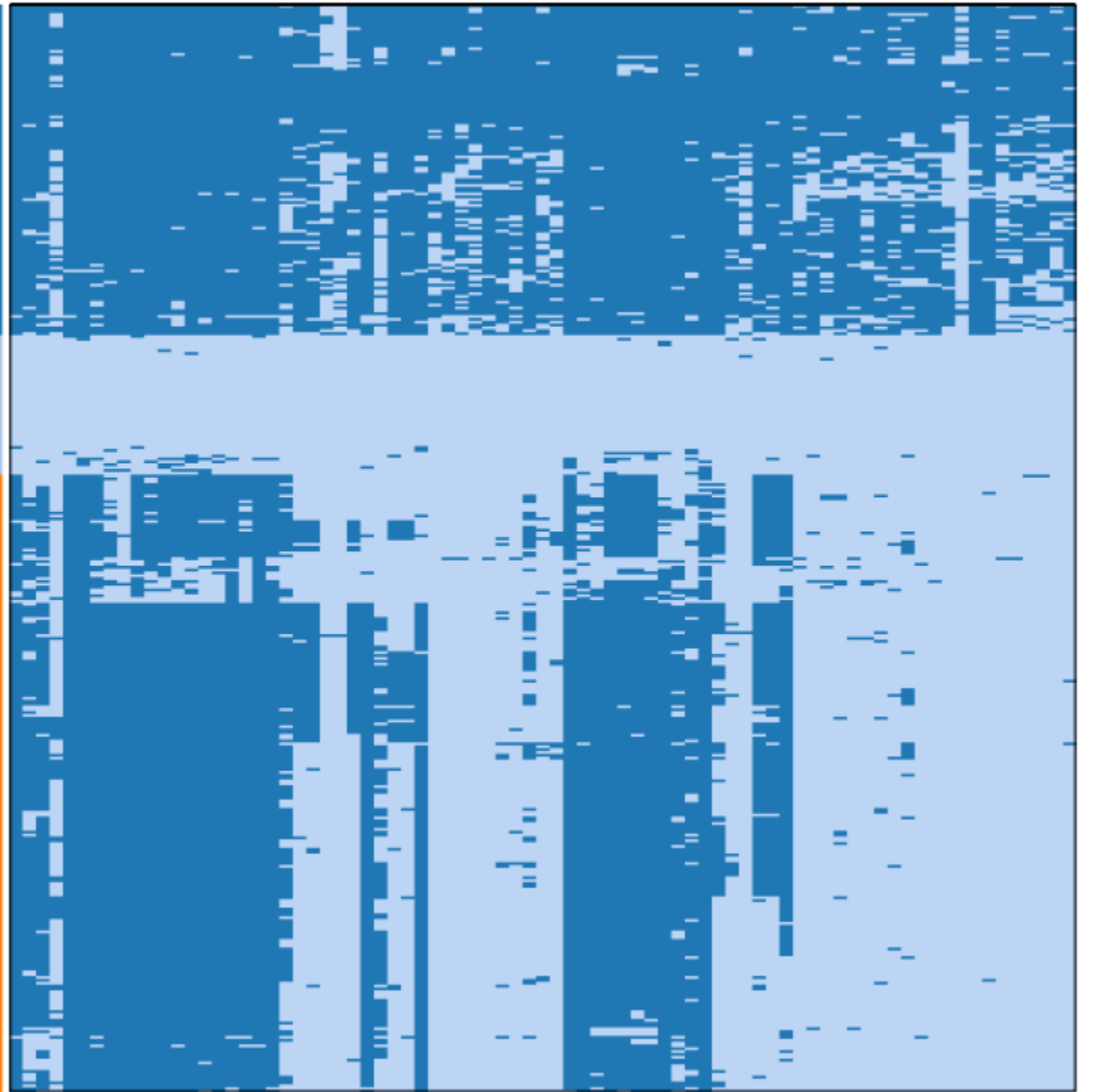


Vanja  
Klepac-Ceraj



Guilherme  
Fahur Bottino

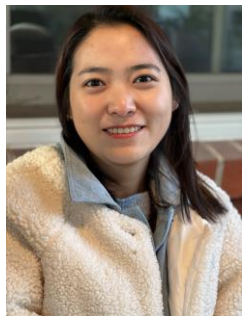
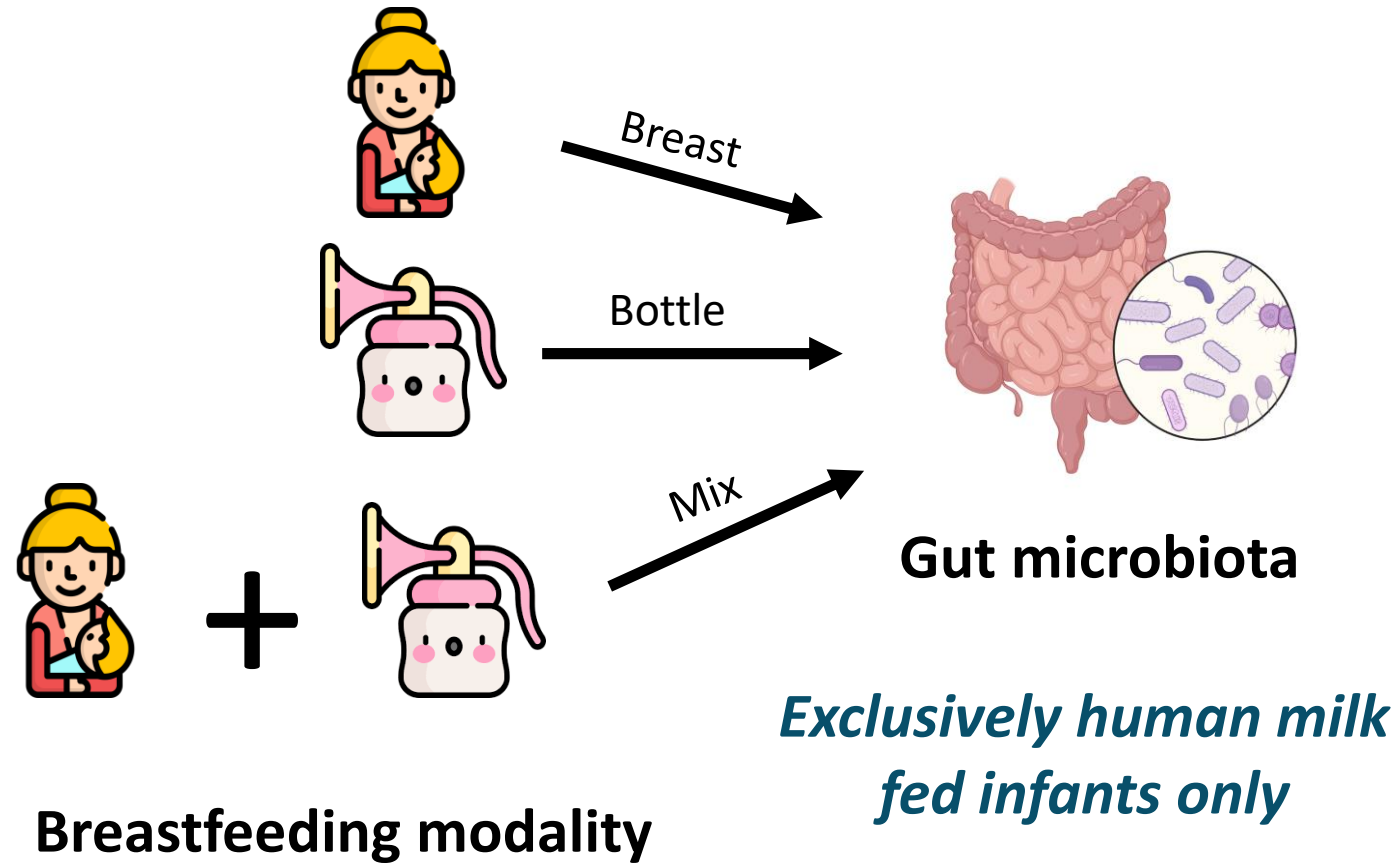
↑  
Infants



HMO Metabolizing Genes →



# Associations Between Breastfeeding Modality and the Infant Gut Microbiota

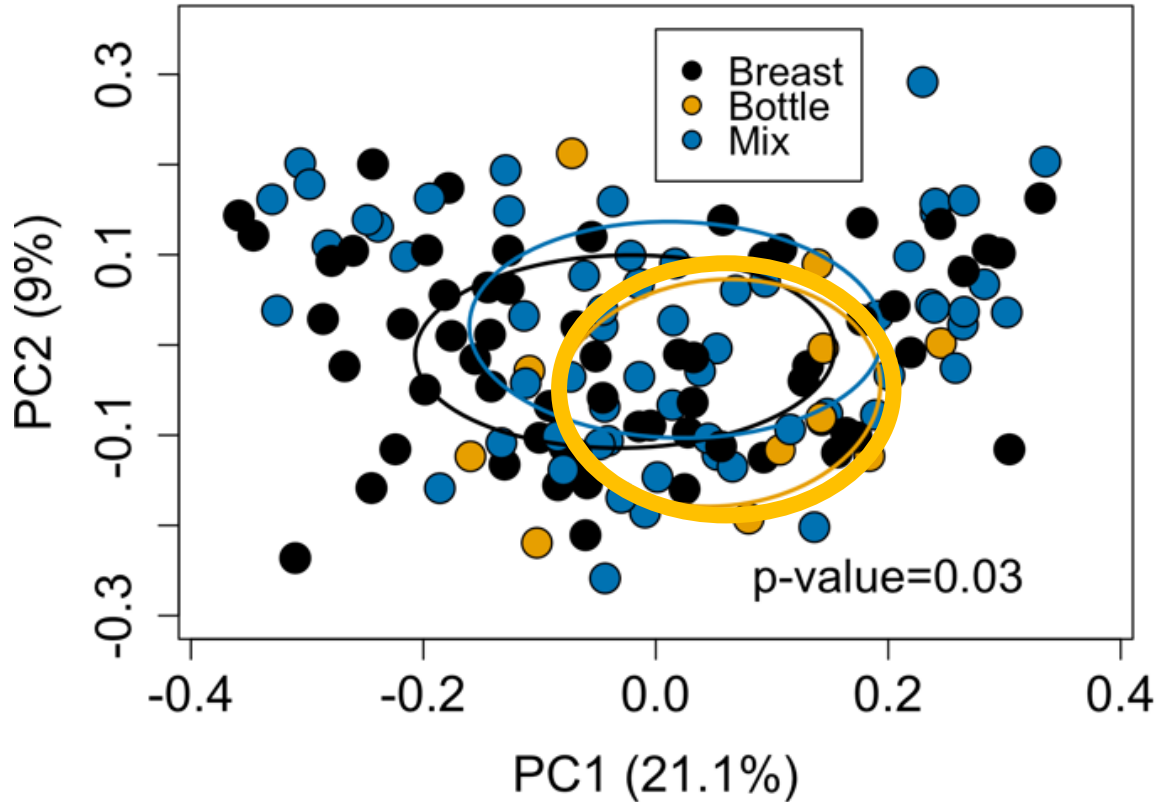


Sihan Bu

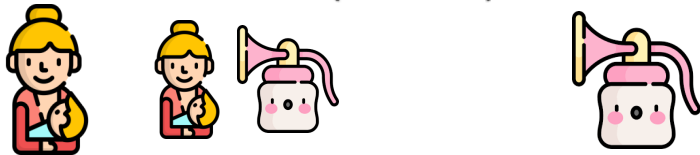
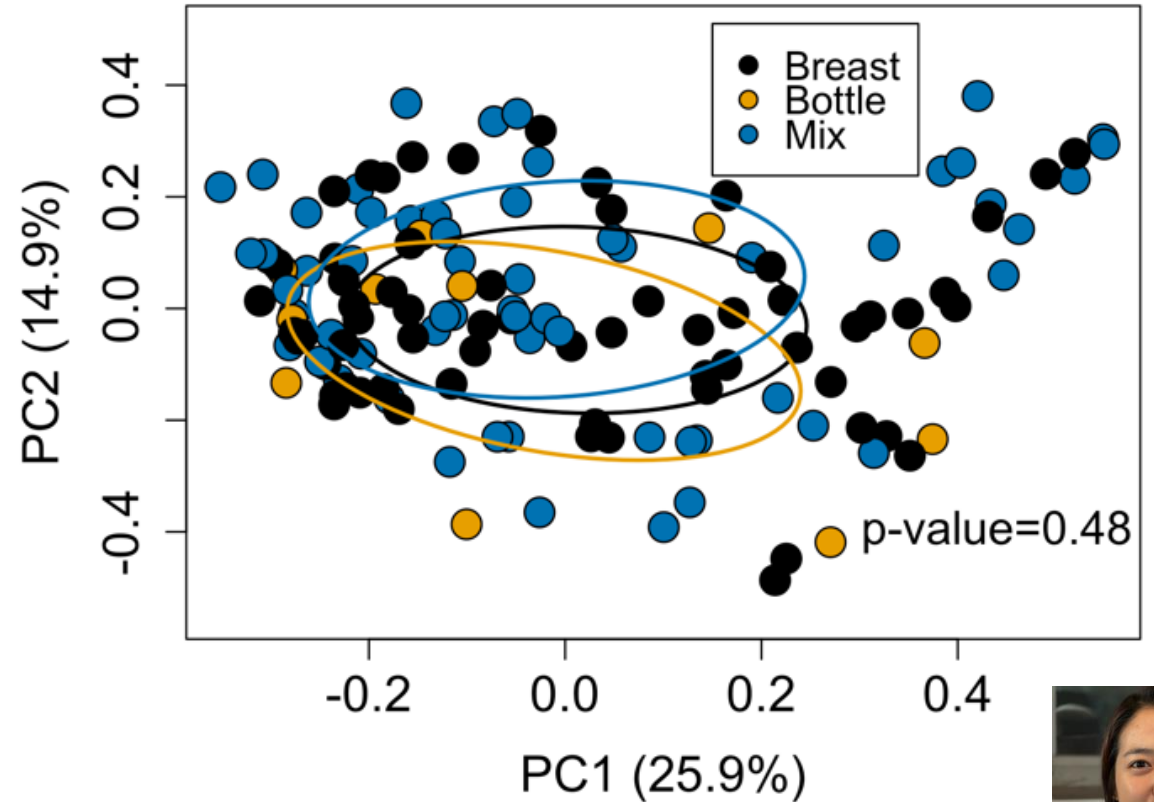
# The Gut Microbiotas of Exclusively human Milk Fed 3 Month Old Infants had Distinct Gut Microbial Community Membership According to Breastfeeding Modality



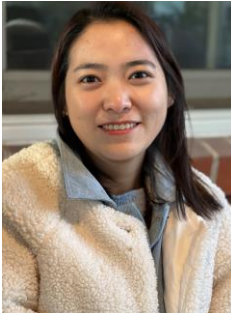
### A. Sorensen



### B. Bray-Curtis



Sihan Bu



# Exposures Contributing to the Longitudinal Development of the Infant Gut Microbiome

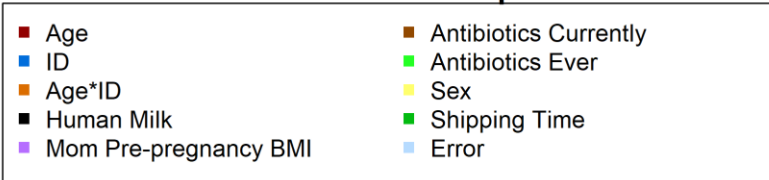
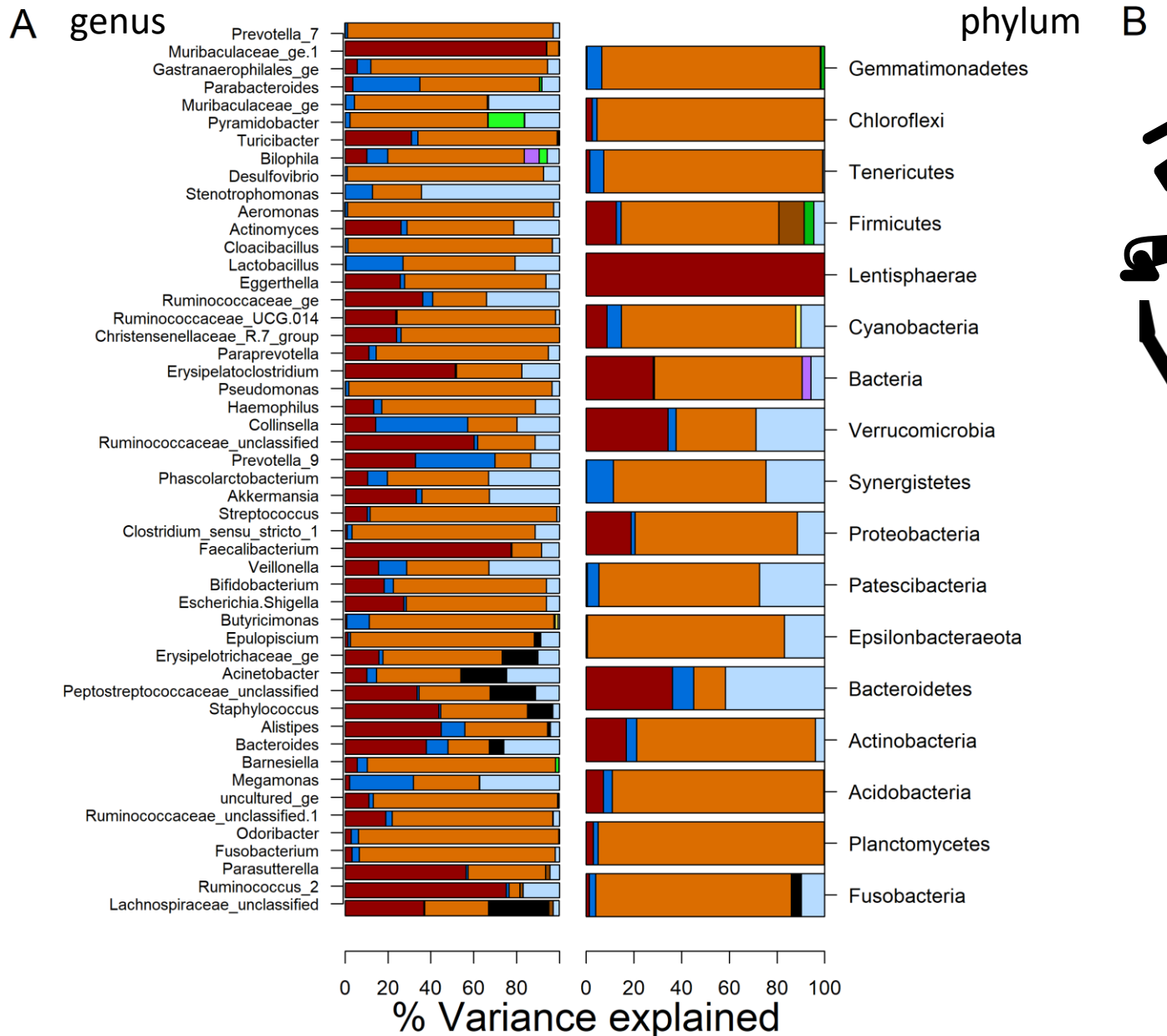


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Sugino



Tengfei Ma

Sugino, Ma 2021 *Microorganisms*



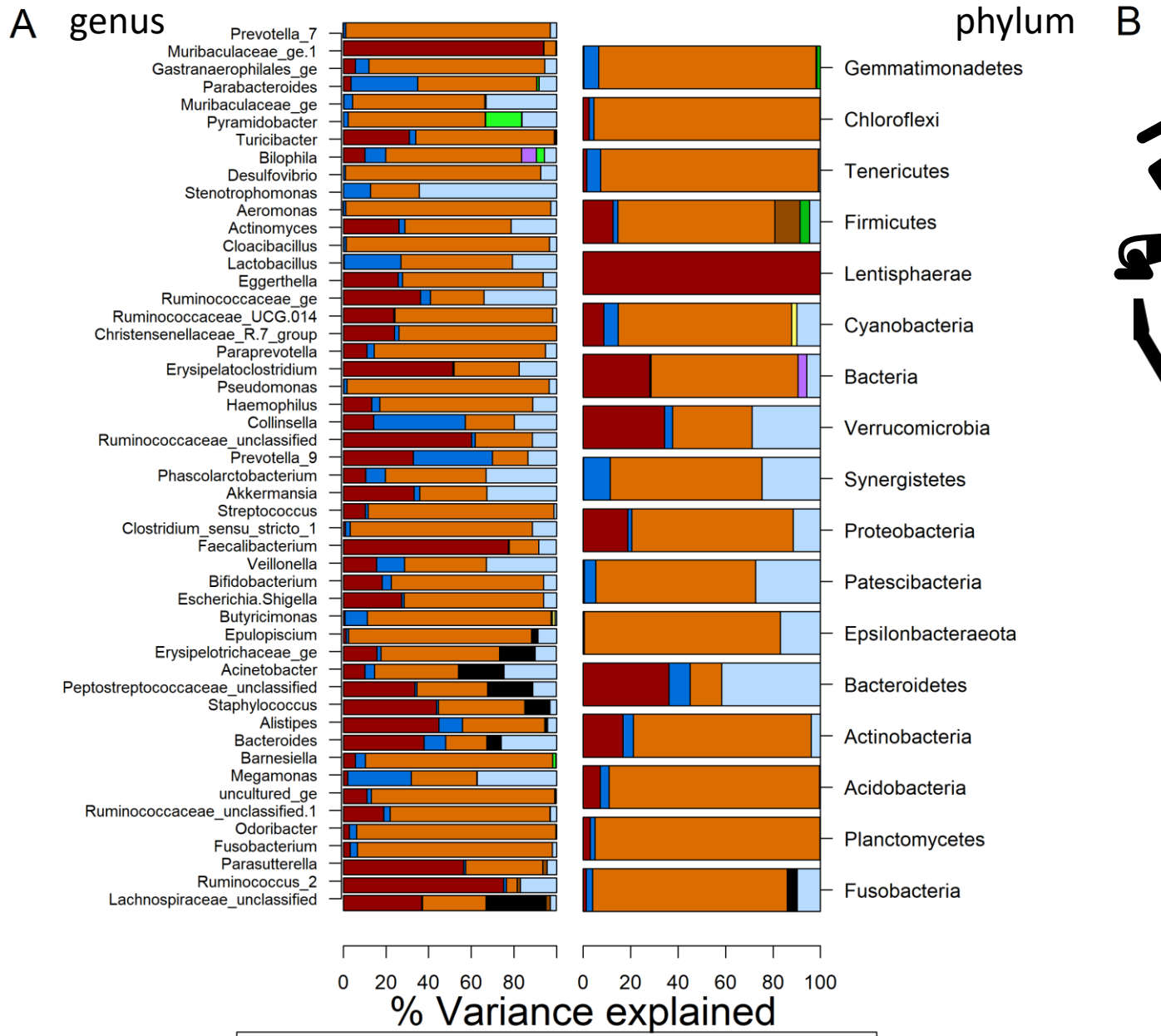
# Exposures Contributing to the Longitudinal Development of the Infant Gut Microbiome



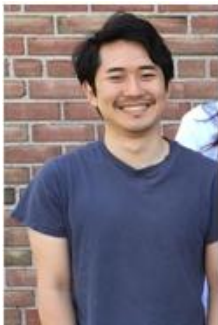
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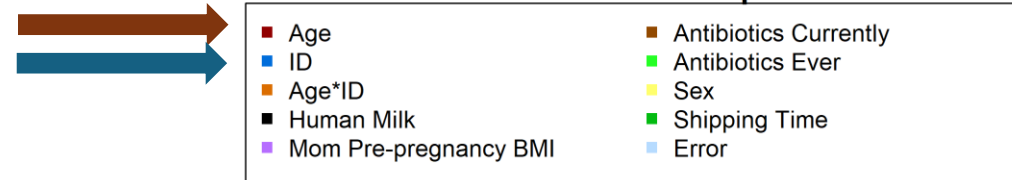
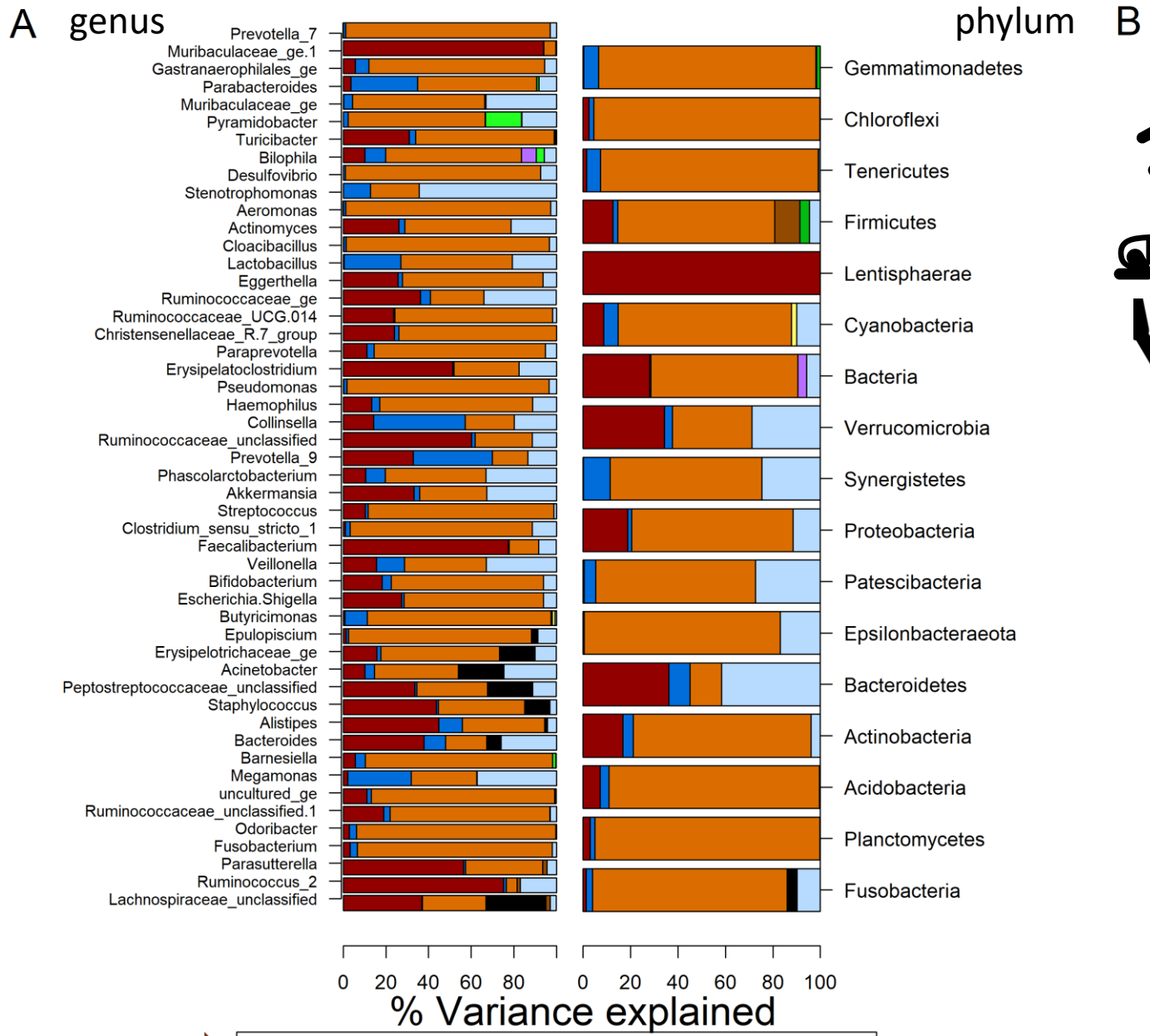
# Exposures Contributing to the Longitudinal Development of the Infant Gut Microbiome



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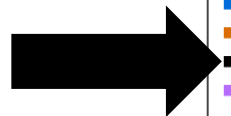
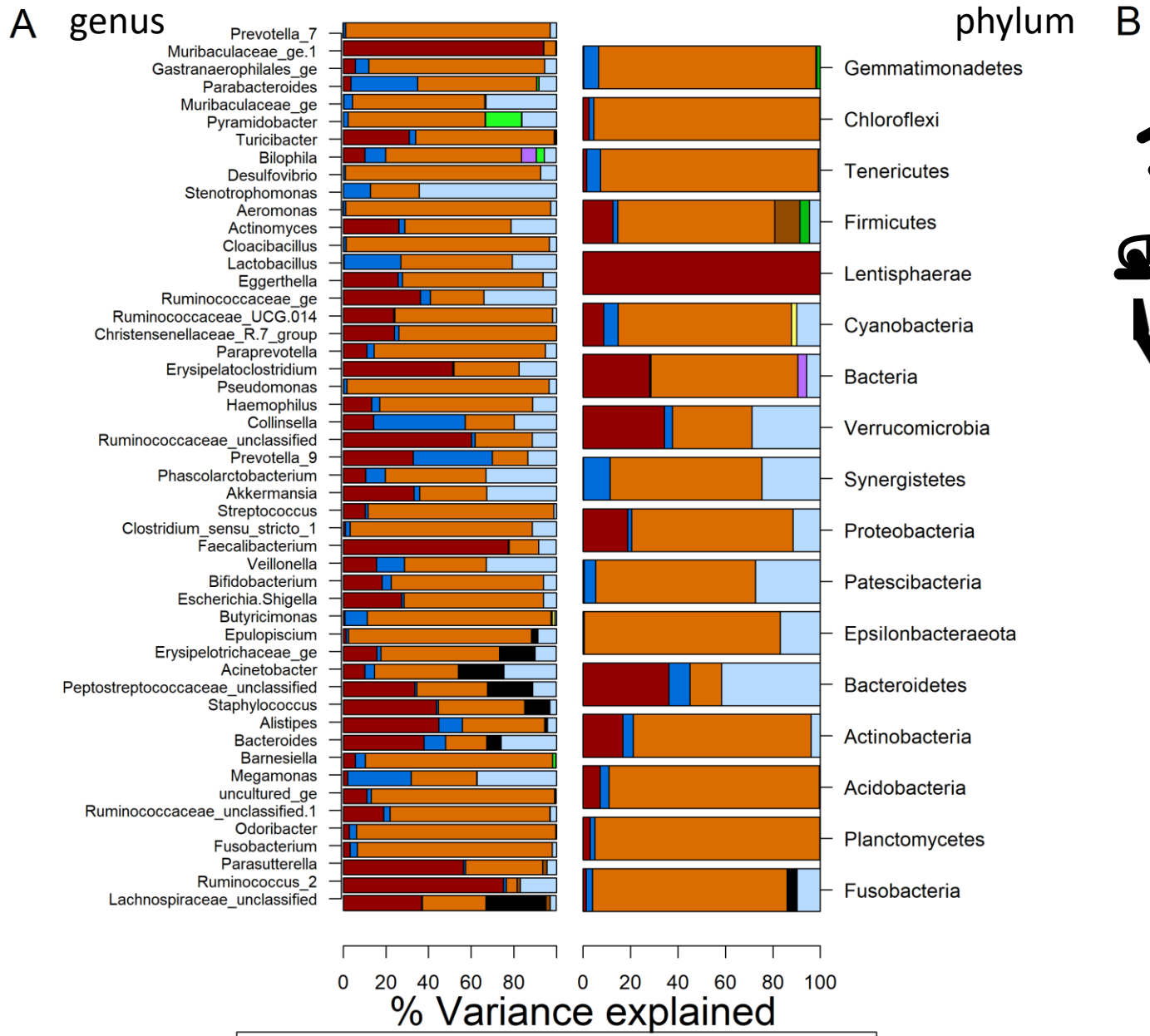
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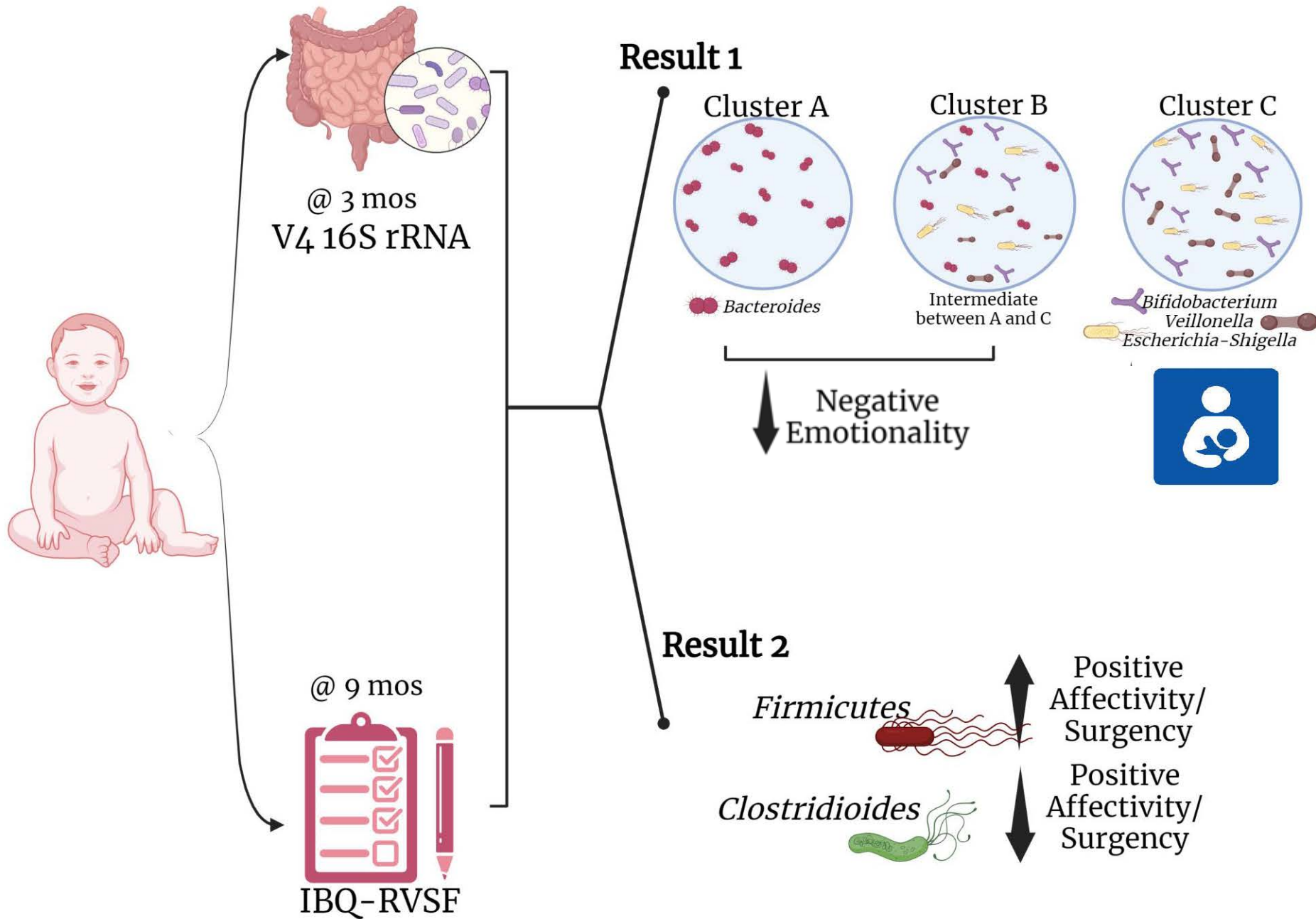


Kameron  
Sugino



Tengfei Ma





Dana Nzerem



Ongoing ECHO-  
Wide Analyses are  
Assessing  
Associations  
between the  
Various  
Microbiotas and  
these Child Health  
Outcomes

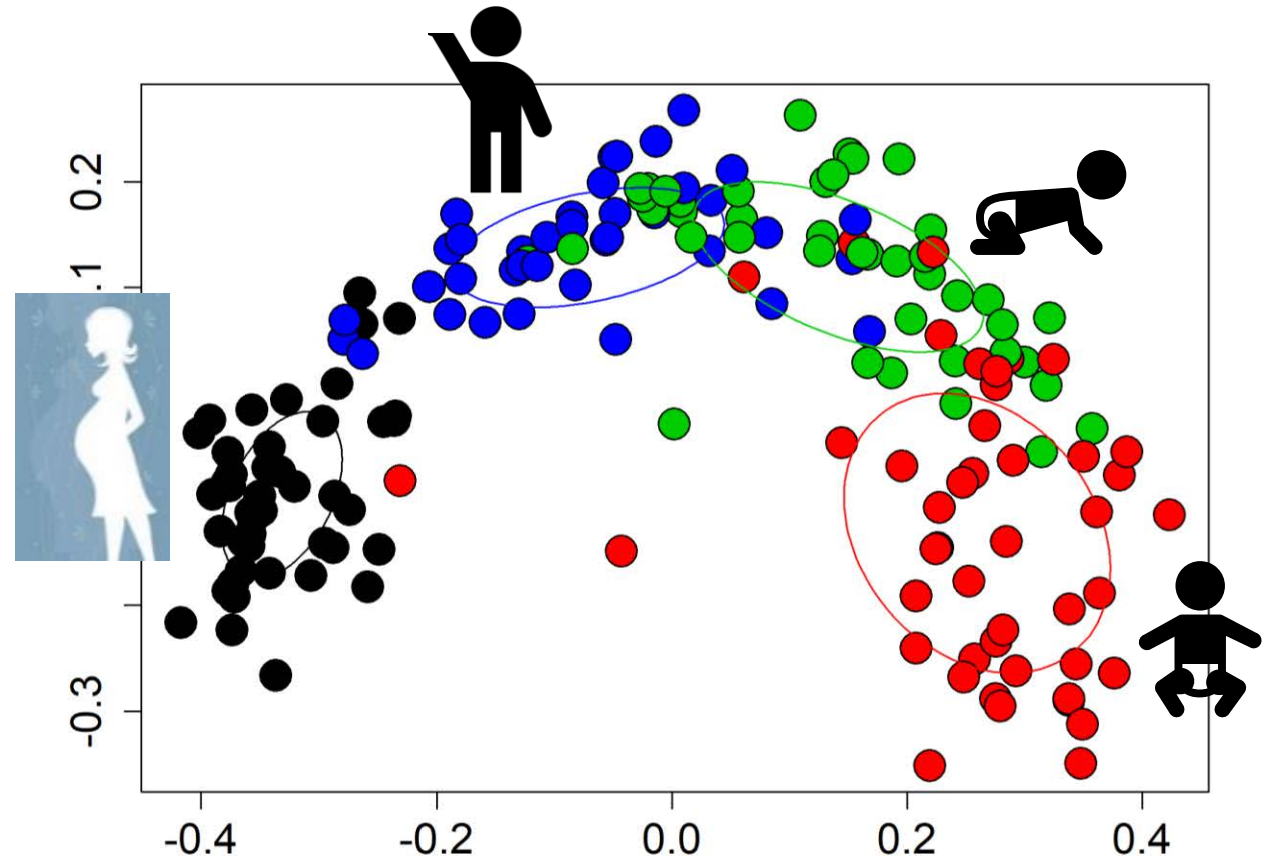
- 
- Allergic Rhinitis
  - Asthma
  - Food Allergy
  - Anxiety and Depression
  
  - Child Development (ASQ)
  - Child Temperament (IBQ)
  - Autism-Related Behaviors
  - Obesity
  - Preterm Birth
  - Neurodevelopment
-

# Summary & Outlook

- Host-associated microbiomes are important modifiable factors playing key roles in human development and health
- ECHO has both extant data and extant samples that can be used to determine which exposures build host-associated microbiomes that ensure appropriate child development
- Further extant samples could also be analyzed using whole metagenome sequencing or for metabolites
- Ongoing efforts ECHO-wide should generate over a dozen manuscripts by the end of 2025



# Thank You!





# ECHO

Environmental influences  
on Child Health Outcomes

**A program supported by the NIH**