Microbe-Aware Precision Medicine Katherine S. Pollard, PhD Gladstone Institutes UCSF Department of Epidemiology/Biostatistics, Institute for Human Genetics, & Institute for Computational Health Sciences Chan Zuckerberg Biohub Investigator

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Personal Path to Studying the Microbiome Math, computer science, and anthropology:

The field of bioinformatics didn't exist when I was in college

Career beginnings:

- Comparing human and chimp DNA

Personal relevance:

Living with two autoimmune diseases

Found the same building blocks are being assembled differently



The Human Microbiome

Microbes in our bodies:

- Contribute 300x more genes than human cells do
- Communicate and exchange molecules with human cells
- Integral to immune system
- Metabolize diet and drugs
- Interact with human genetics to make us who we are

Make up ~5 lbs. of body weight (most of which are gut microbes)

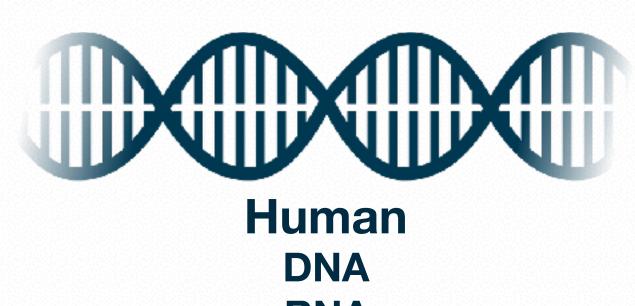


Precision Medicine 1.0

Inflamed

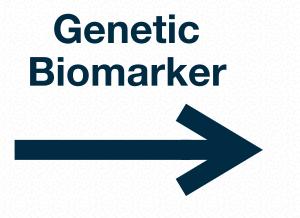
Gut







RNA Protein







Microbiome Clinical Research

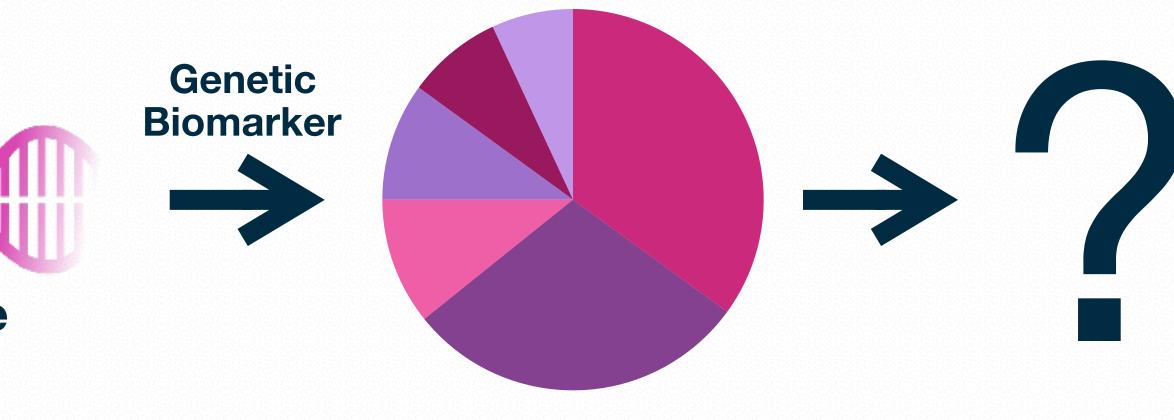
Sequencing

Pooled Microbe DNA RNA Protein

Joint Pain

Inflamed

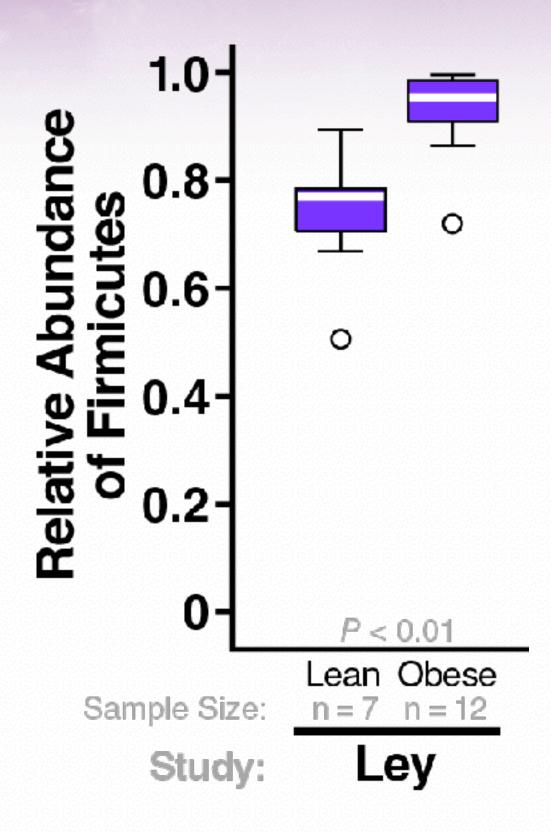
Gut



Percent Sequences from Each Microbe

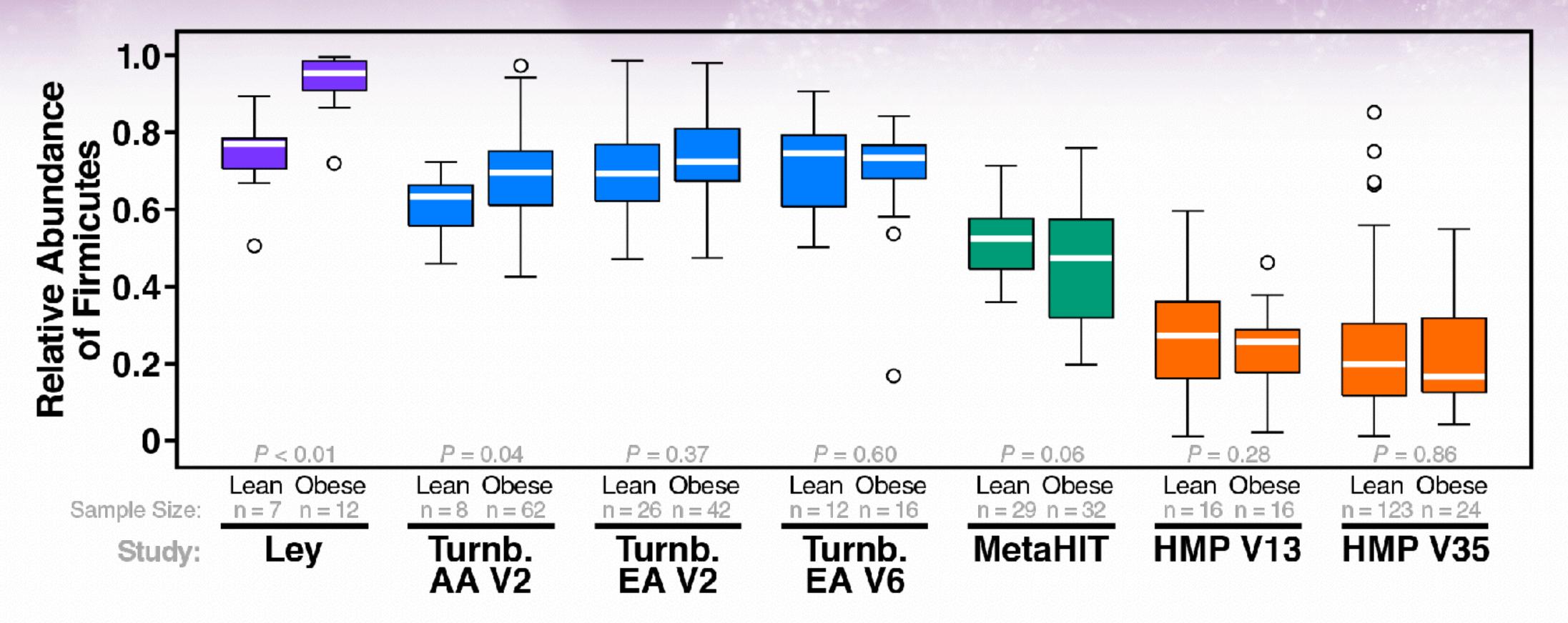


Microbe Abundance Fails as a Disease Biomarker





Microbe Abundance Fails as a Disease Biomarker



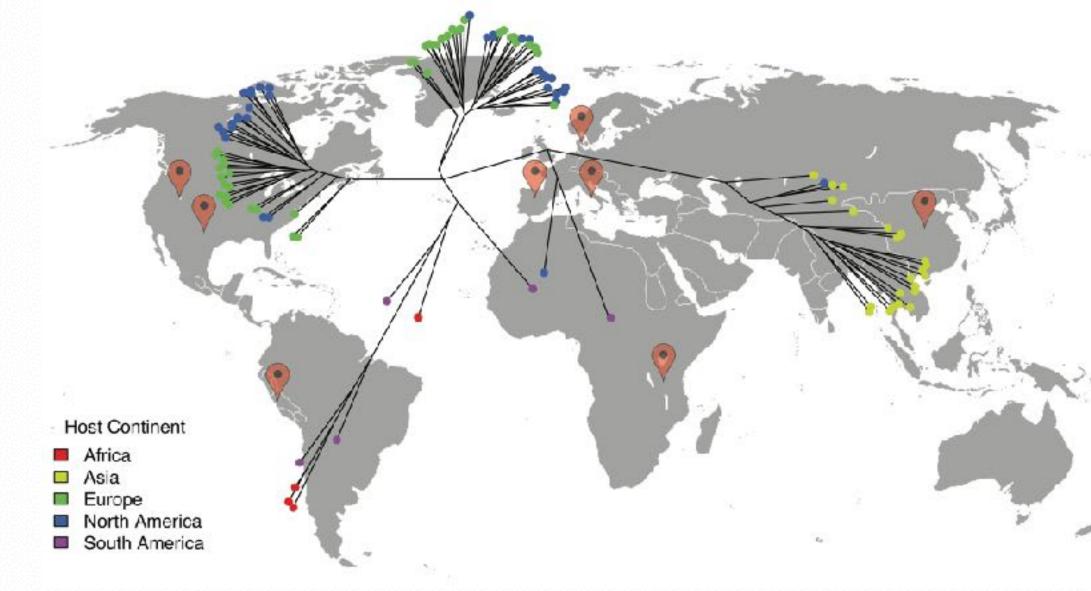
- Much more variation across studies than between lean and obese groups within studies

Inconsistent association between obesity and phylum level composition of gut microbiome



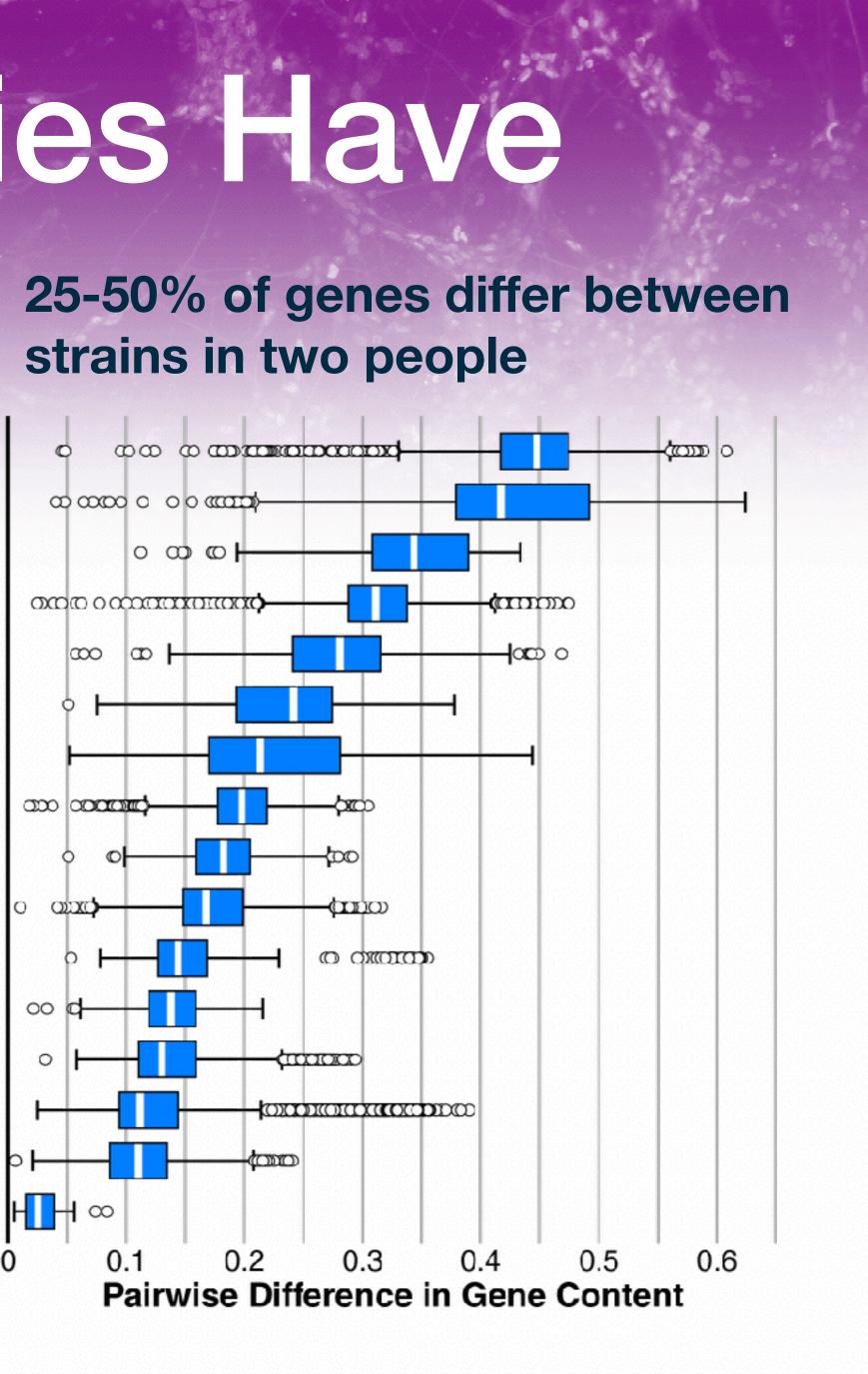
Strains of Same Species Have Different Genes 25-50% of genes differ betwee strains in two people

Stool metagenomes from 2 people Find shared species For each species, compare genes



Data: Healthy individuals from 8 studies, downloaded from SRA Nayfach & Pollard (2015)

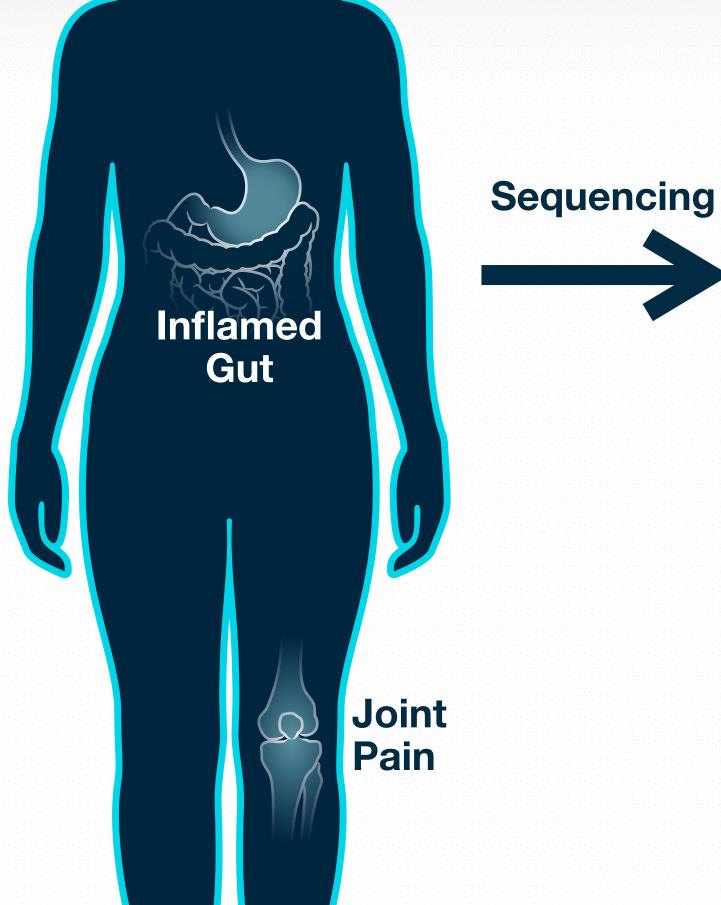
Bacteroides ovatus Bacteroides vulgatus Parabacteroides distasonis Bacteroides uniformis Eubacterium rectale Faecalibacterium prausnitzii Bacteroides plebeius Bacteroides stercoris and account Faecalibacterium prausnitzii Prevotella copri o Faecalibacterium prausnitzii Bacteroides massiliensis 00 0 Faecalibacterium cf. Ruminococcus bromii Alistipes putredinis Replicates H



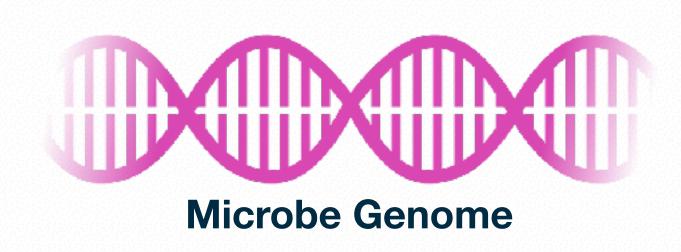
Idea: Study Microbes at the Level of Genetic Mutations, Just Like Human DNA



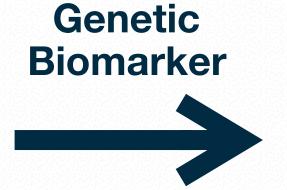
Precision Medicine 2.0







Human DNA RNA Protein



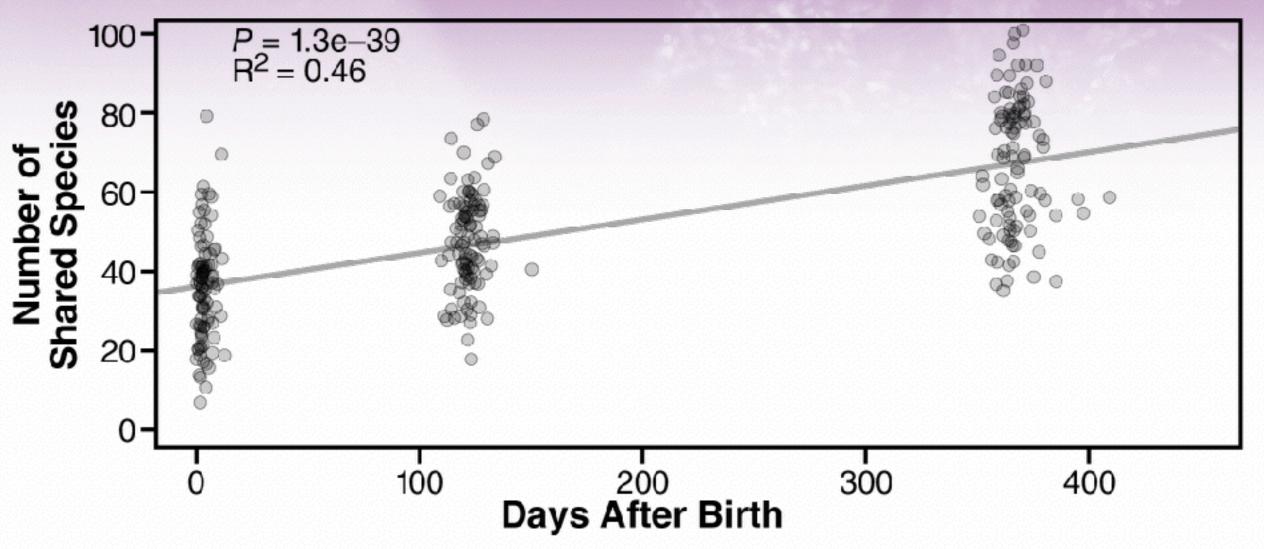




How Can We Use Microbiome Genetic Data?



Study Example: Infant Gut Strains Not From Mom



Data: Backhead et al. (2015)

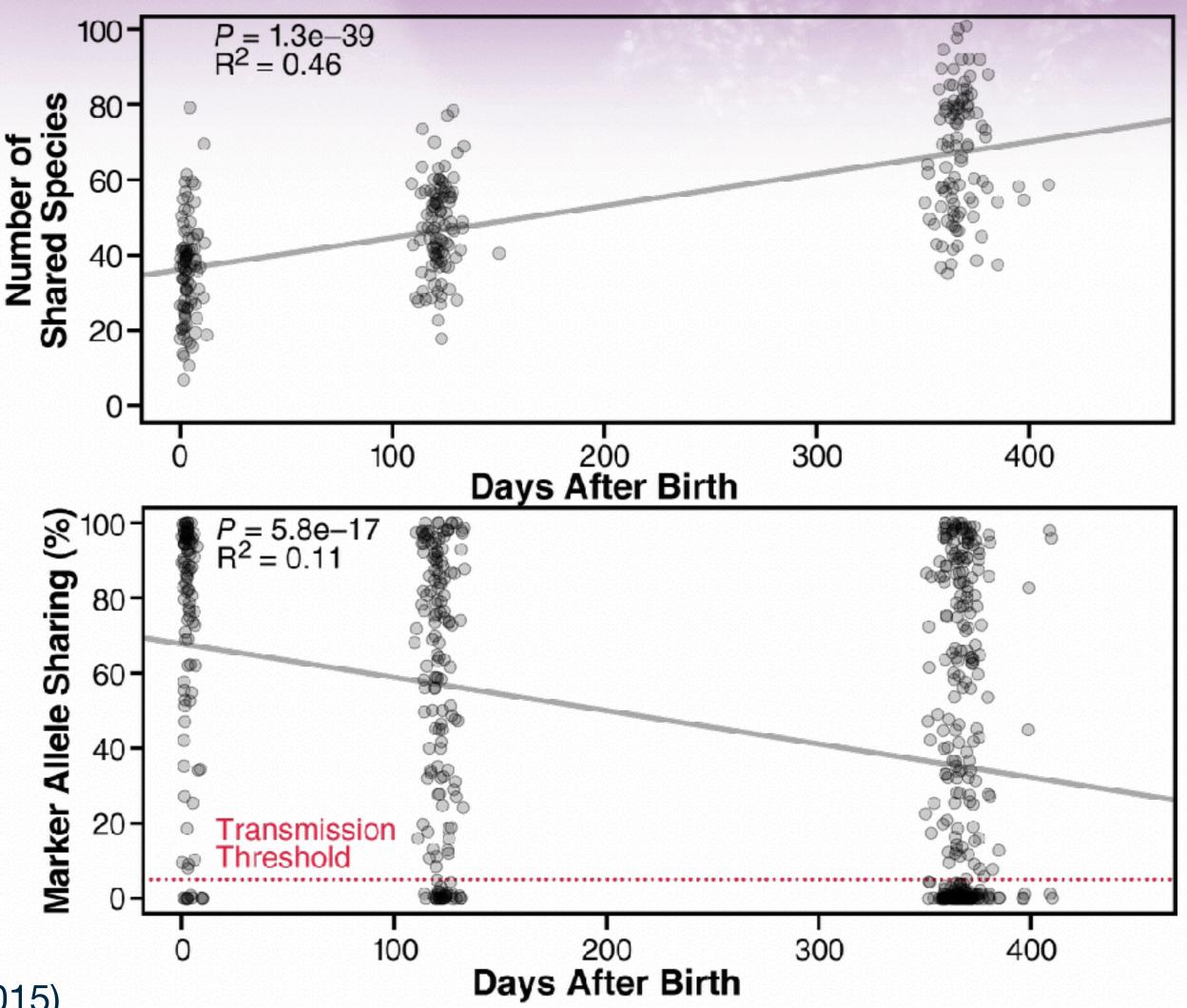
- Species more similar over time
- Same trend with unrelated mothers

Idea: Track strains with "private" mutations in each mom. Are they in her baby?

Nayfach et. al (2016)



Study Example: Infant Gut Strains Not From Mom



Data: Backhead et al. (2015)

 Species more similar over time

• Strains less similar over time

Conclude: Infant likely colonized by sources other than mom

Nayfach et. al (2016)



What Have We Learned?

- Human microbiomes encode cryptic functional variation that is missed unless you investigate individual strains and genes.
- Microbiome diversity is massive compared to what is in current outside North America/Europe.
- Bioinformatics and metagenomics enable individual strains and
- colonize humans and host disease.

databases, especially in natural environments, lab mice, and humans

genes to be tracked. Examples: transmission, antibiotic resistance.

Microbe genetic variation correlates with traits such as ability to



The Future of Microbiome Science & Medicine

- Unlocking biomedical problems that can't be solved by studying human cells alone.
- Genetic testing for human and microbial cells in our bodies.
- Challenges for microbiome precision medicine:
 - Complexity of microbial communities and their evolution
 - Sensitivity for <u>rare</u> microbes/genes: could be important!
 - Microbial "dark matter": what do mutations mean?
 - Processing and learning on terabytes of data
 - Communicating this complexity to patients/consumers/readers



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