

# QMD: A new method to quantify microbial absolute abundance differences between groups

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# Background

## Microbiome

IN NUMBERS

**100 Trillion**

sybiotic microbes live in and on every person and make up the human microbiota

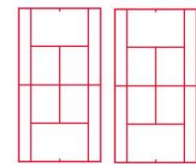
The human body has more microbes than there are stars in the milky way

**95%**

of our microbiota is located in the GI tract

**150:1**

The genes in your microbiome outnumber the genes in our genome by about 150 to one



The surface area of the **GI tract** is the same size as 2 tennis courts

You have **1.3X**

more microbes than human cells

**>10,000**

Number of different microbial species that researchers have identified living in and on the human body

**2kg**

The gut microbiota can weigh up to 2Kg



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The microbiome is more medically accessible and manipulable than the human genome

**90%**

It is thought that of disease can be linked in some way back to the gut and health of the microbiome

**5:1**

**Viruses:Bacteria** in the gut microbiota

**2.5**

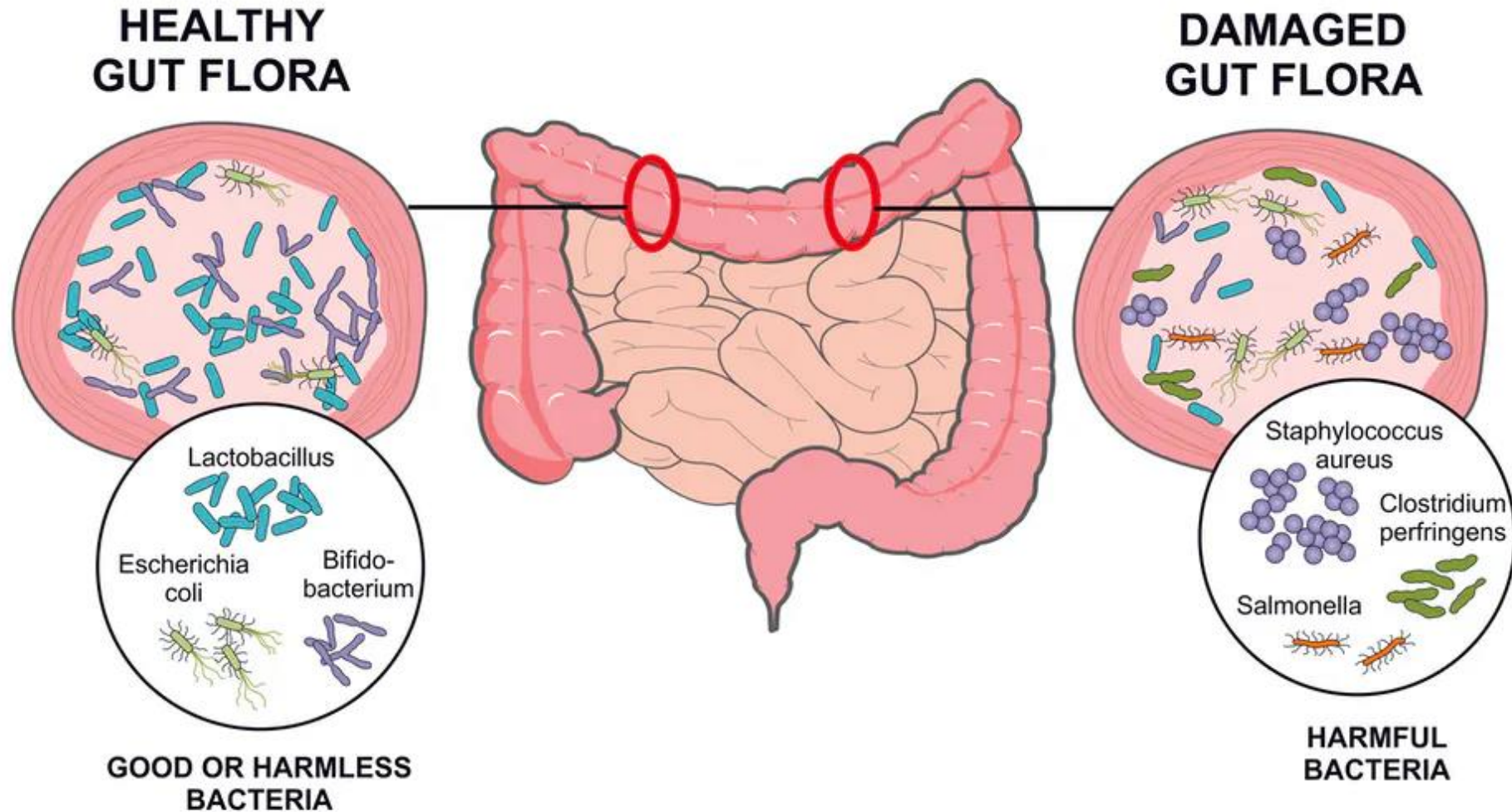
The number of times your body's microbes would circle the earth if positioned end to end



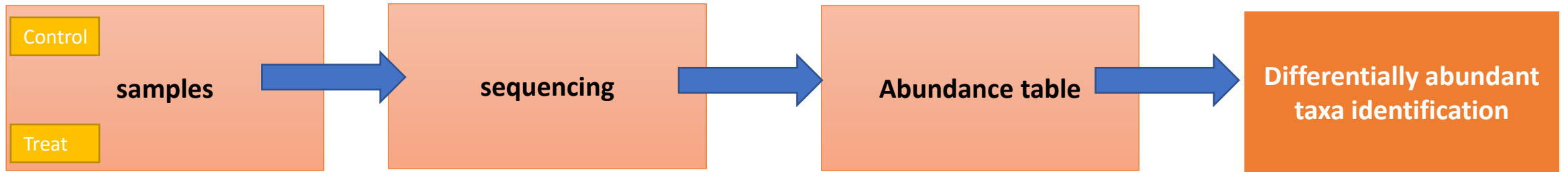
Each individual has a unique gut **microbiota**, as personal as a fingerprint



# Background

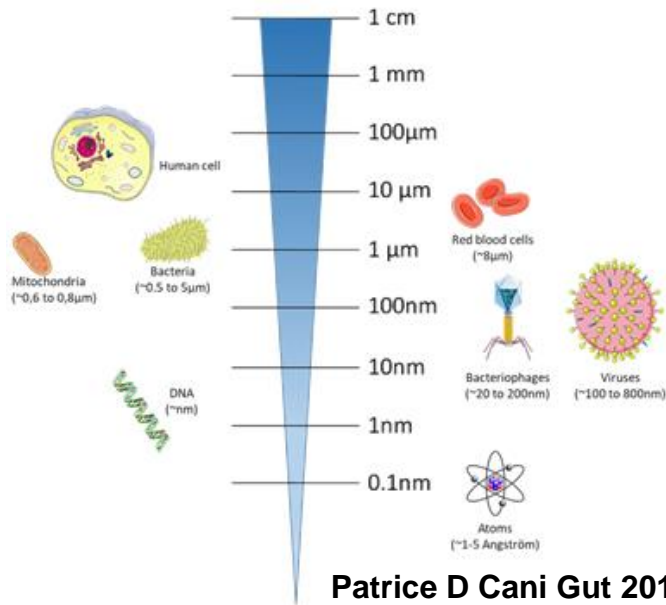


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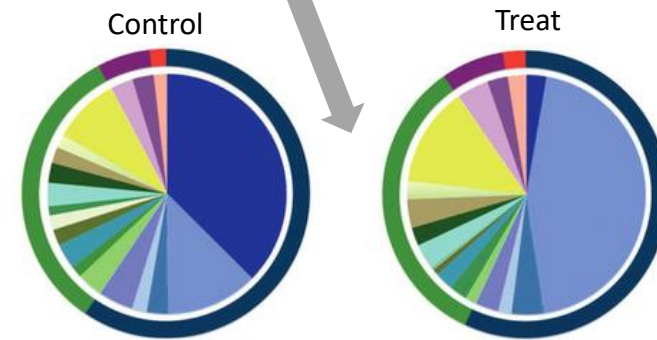


$10^{13}$  « human cells »  
 $10^{14}$  « microbial cells »  
 $10^{12}$  bacteriophages/g of fecal material  
 $10^{11}$  bacteria/g of fecal material

Absolute microbial abundance  
the microbial load per unit sample mass

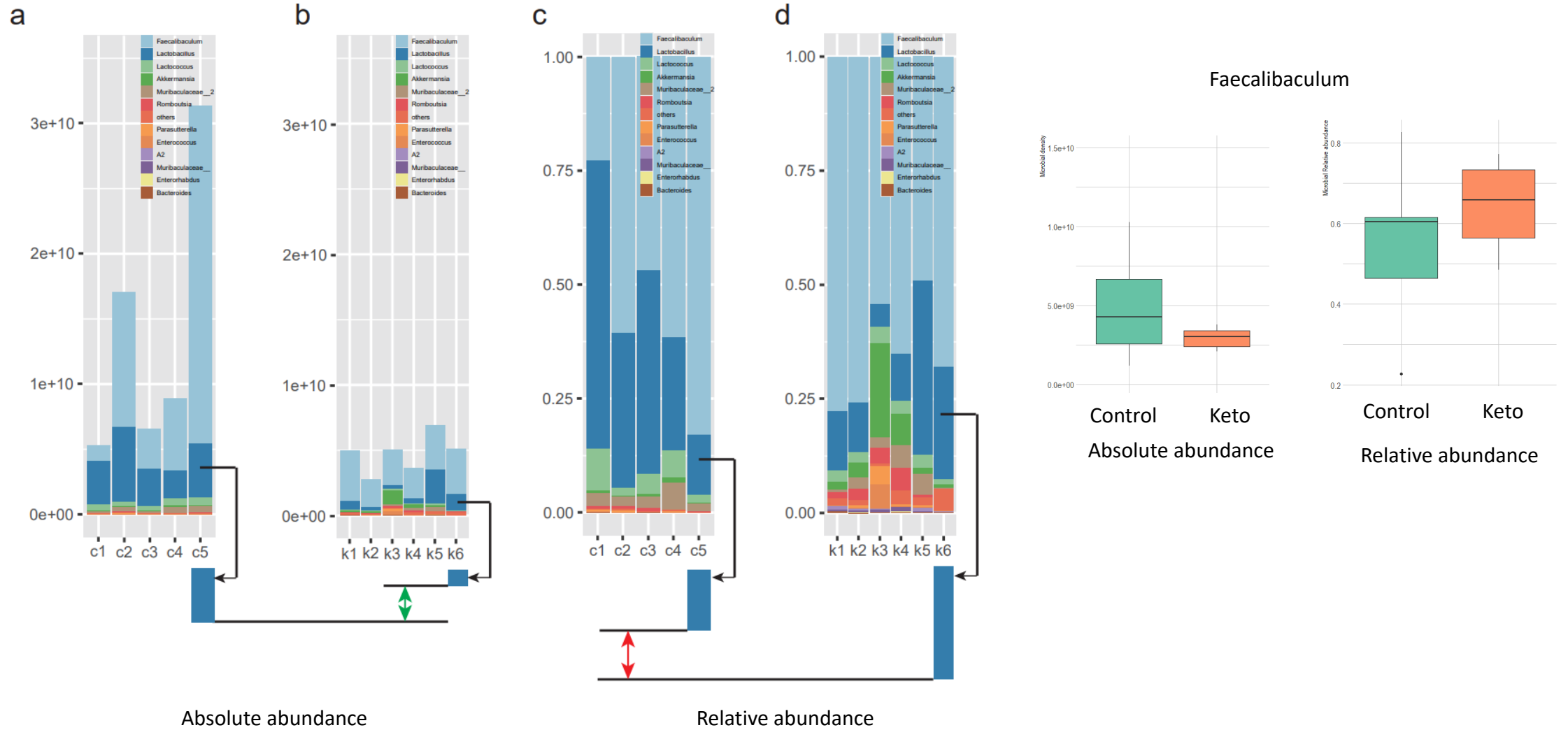


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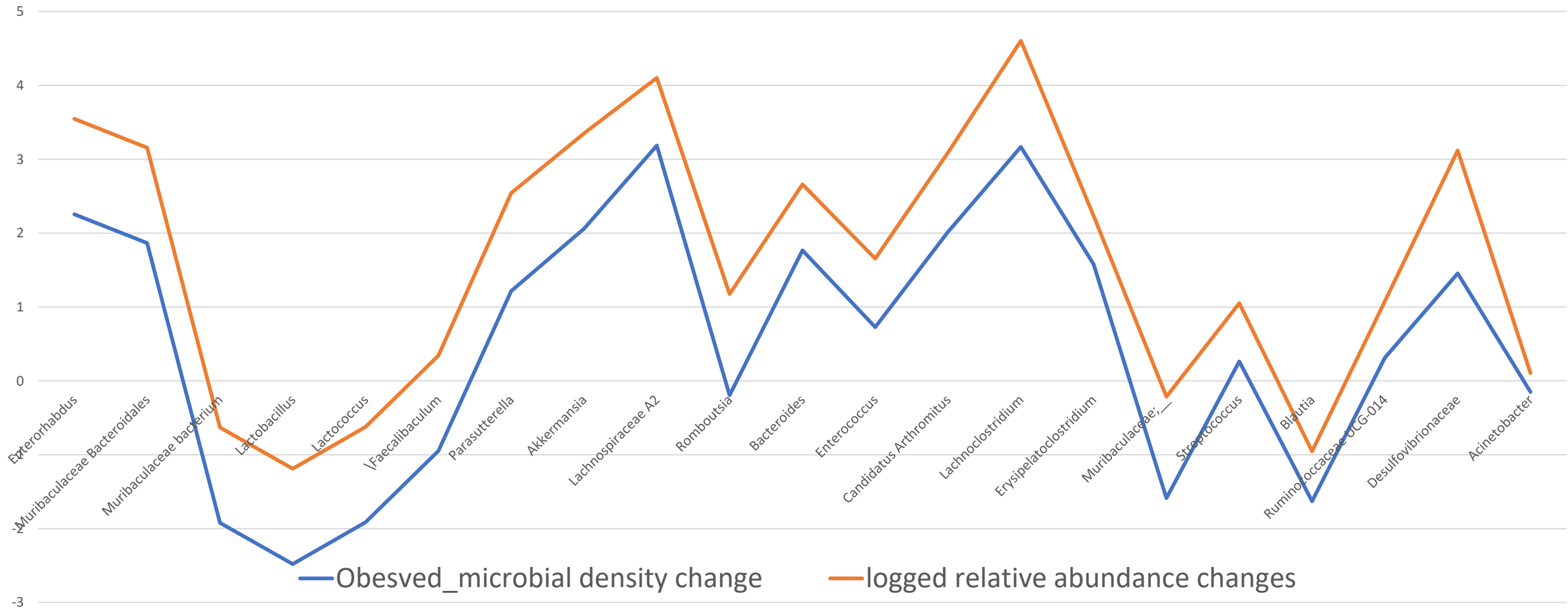


Relative abundance  
compositional data of absolute abundance

# Results

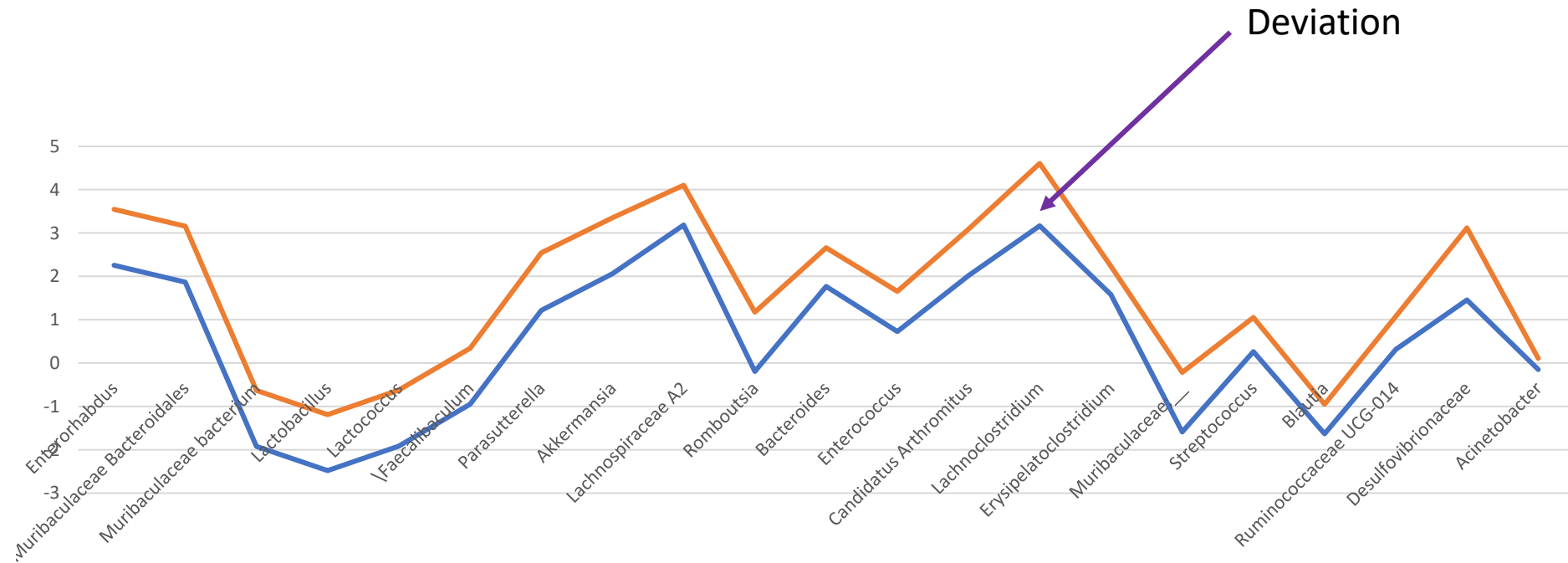


# Results



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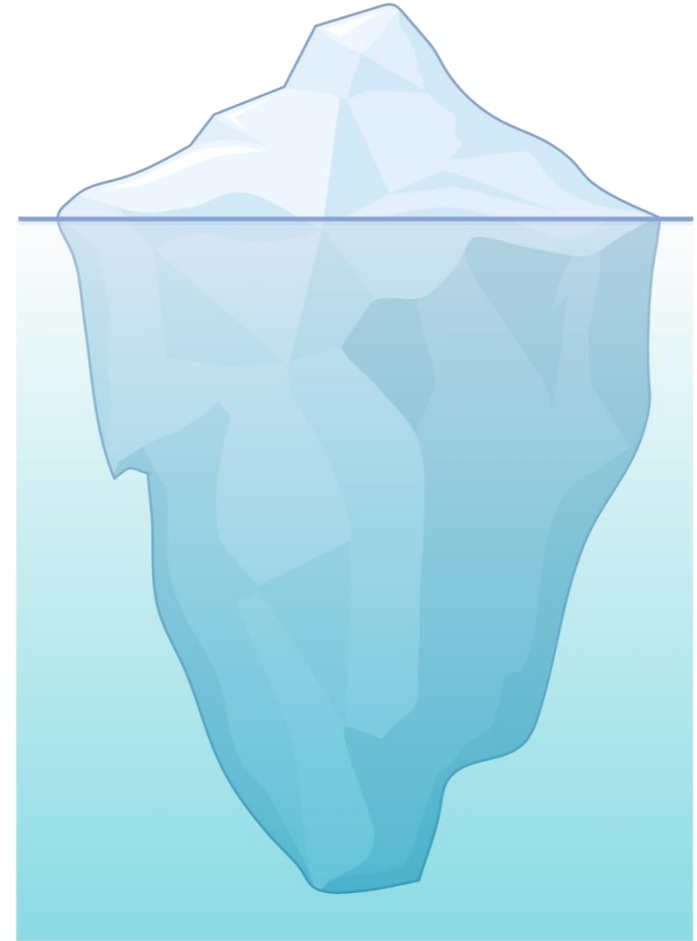
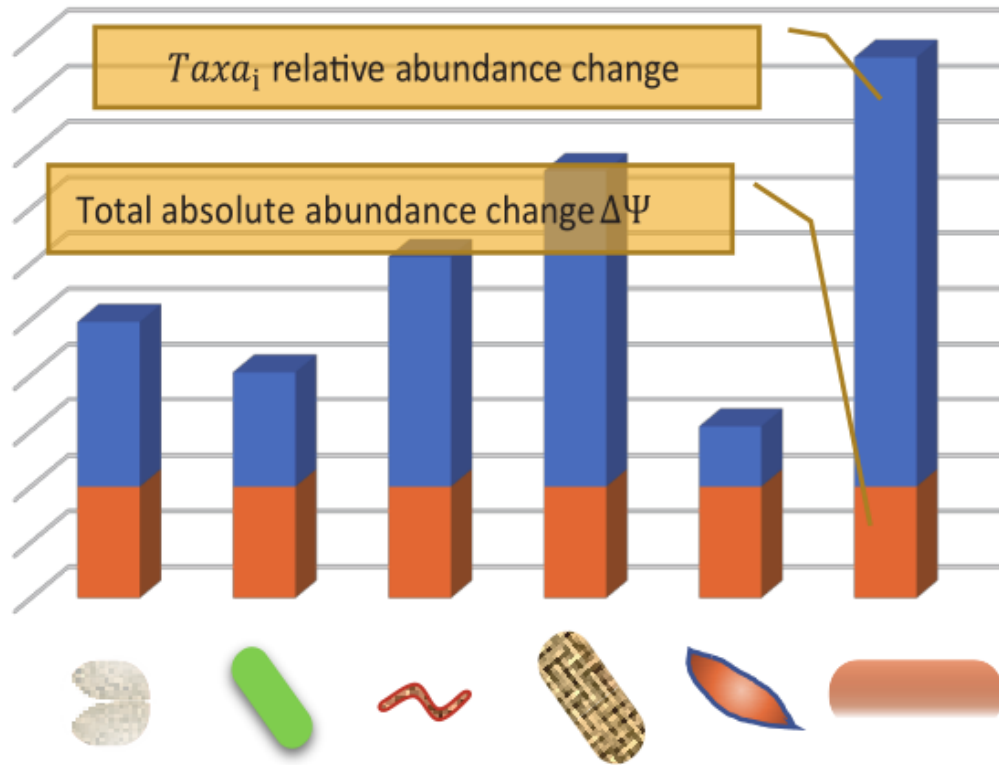
## Core idea on QMD





# Results

Microbial abundance change  $\Delta M_i$  for  $Taxa_i$



## **QMD software acquisition**

# QMD software acquisition

## **QMD software usage**

## **QMD software usage**

The input data in QMD is the relative abundance.

# Summary



**iMeta:** Integrated meta-omics to change the understanding of the biology and environment

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“*iMeta*” is an open-access Wiley partner journal launched by scientists of the Chinese Academy of Sciences. *iMeta* aims to promote metagenomics, microbiome, and bioinformatics research by publishing original research, methods, or protocols, and reviews. The goal is to publish high-quality papers (Top 10%, IF > 15) targeting a broad audience. Unique features include video submission, reproducible analysis, figure polishing, APC waiver, and promotion by social media with 500,000 followers. Three issues were released in [March](#), [June](#), and [September](#) 2022.



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