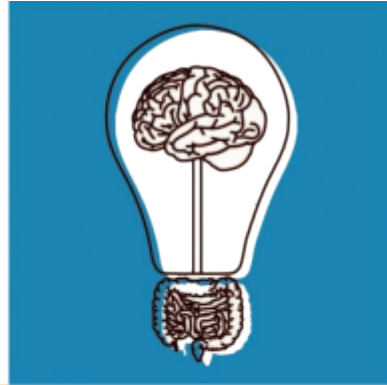
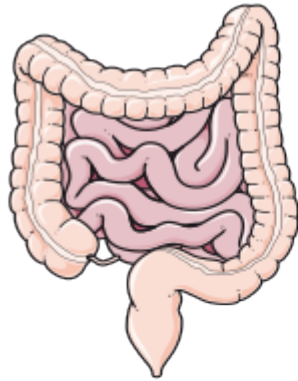
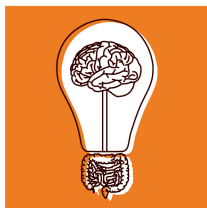


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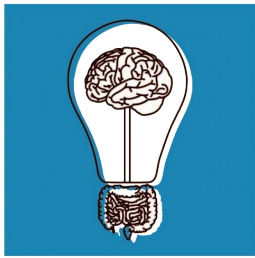
Welcome to Your Microbiome!



Welcome to your **MAGIC / IMAGINE** microbiome report! In this report, you will find an introduction to the human fecal microbiome, a description of your personal microbiome, and some more detailed information about the specific bacteria that were abundant in your sample.



Inflammation, Microbiome & Alimentation  Gastro-Intestinal & Neuropsychiatric Effects



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Introduction

The human gut is home to hundreds of species of microbes, mostly bacteria. In fact, your gut contains as many bacterial cells as there are human cells in your whole body! This microbial community is known as your ‘gut microbiome’.

The gut microbiome has several very important roles to play in keeping us healthy. It helps us to break down and digest the food that we eat, produces vitamins that we require, trains and maintains our immune system, and serves as the first line of defense against infection from bacteria that could do us harm.

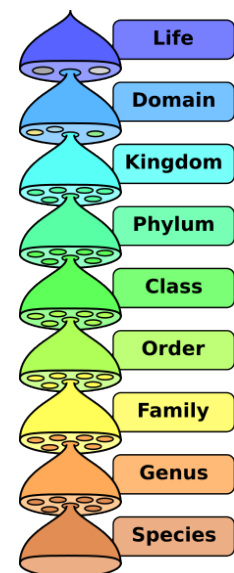
We are still very much at the beginning of understanding all the things the gut microbiome does, how our actions and environment affect it, and how we can use it to keep people healthier and living longer. The **MAGIC** study (a sub-study of the **IMAGINE** project that you are participating in) is an ambitious project that will improve our understanding of how three important variables (genes, diet, and mental health) impact the gut microbiome in people with inflammatory bowel disease (IBD) and irritable bowel syndrome (IBS), and in turn how all four factors together impact the disease course.

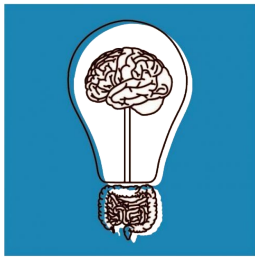
Studying the microbiome

A key component of the **MAGIC** study is generating microbiome profiles for each participant. So, how do we do that?

Bacteria, just like plants and animals, can be classified into closely related groups called **species**. Those species can then be classified into bigger groups called **genera** (singular: genus), and genera can be classified into **families**, and so on up the tree of life.

Each bacterial species has a unique genetic “barcode” that can be used to identify it. To determine the composition of each sample’s microbiome, we extract the DNA from your stool sample and then isolate and sequence these bacterial DNA barcodes. We don’t sequence any human DNA, just the bacterial barcodes. We generate 10,000 to 50,000 barcode sequences per sample. Each sequence is then labeled with





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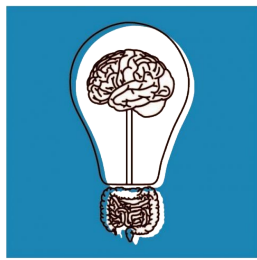
its taxonomic identity (which species, genus, family, etc. it belongs to) and the number of bacteria present in each species is counted.

You can think of the bacteria in your gut like a jar of jelly beans. The barcode tells us what colour each jelly bean is, and the number of times we see that barcode in our sequences tells us how many jelly beans there are of that colour. This allows us to sort the bacteria into species and generate the “taxonomic bar chart” you’ll see in this document.



As there are hundreds of species in a sample, we quickly run out of colours! Therefore, we will use the categories at the genus or family level, and also only display the bacteria that are abundant enough to show up clearly on the chart.

These microbiome profiles are only the beginning. We use the information in them to compare profiles between healthy controls and people with IBD/IBS, and to investigate ways that a person’s microbiome changes with their health status. We also try to identify individual microbes that might be associated with specific illnesses. Understanding these associations between our microbes and our health will lead to new treatments that target the microbiome directly: increasing “good” bacteria and decreasing “bad” bacteria.



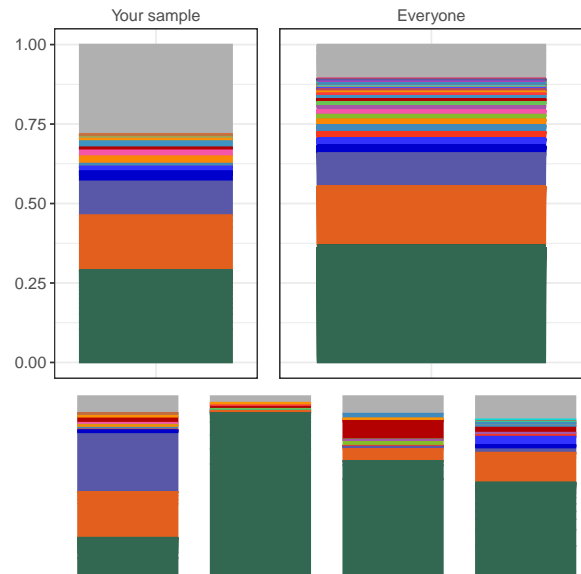
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Your Sample


















This **taxonomic bar chart** shows your personal fecal bacterial community. Bacteria are grouped into **families** based on how closely related they are.

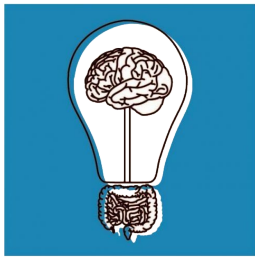
The bar chart is stacked from most abundant bacterial family on the bottom, to least abundant on the top, with very low-abundance bacteria grouped together as "Other". Next to it is a chart showing the average community of all the people who participated in the study, and across the bottom are four anonymous individuals chosen to show the range of variation in this study. As you can see, it's quite wide!

Below are the names of the most common bacterial families found in this study.

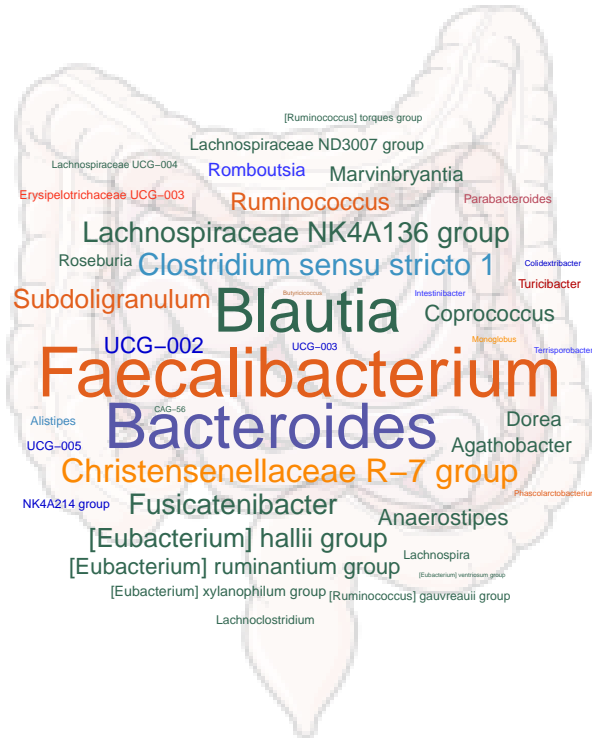


Family

 Lachnospiraceae	 Rikenellaceae	 Tannerellaceae
 Ruminococcaceae	 Christensenellaceae	 o_Clostridia UCG-014
 Bacteroidaceae	 [Eubacterium] coprostanoligenes group	 Butyricicoccaceae
 Oscillospiraceae	 Erysipelotrichaceae	 Acidaminococcaceae
 Peptostreptococcaceae	 Clostridiaceae	 Other
 Erysipelatoclostridiaceae	 Monoglobaceae	



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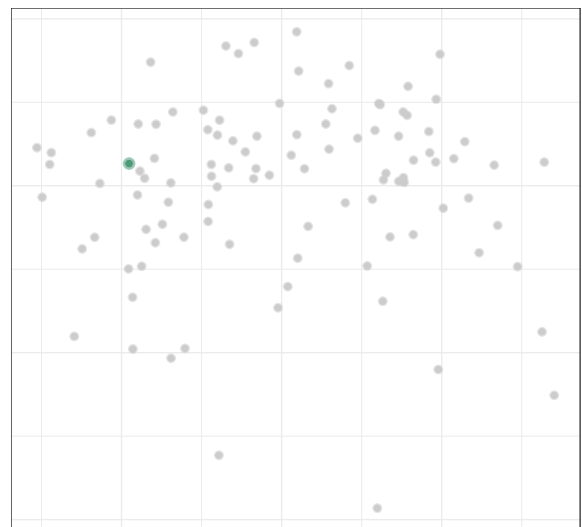


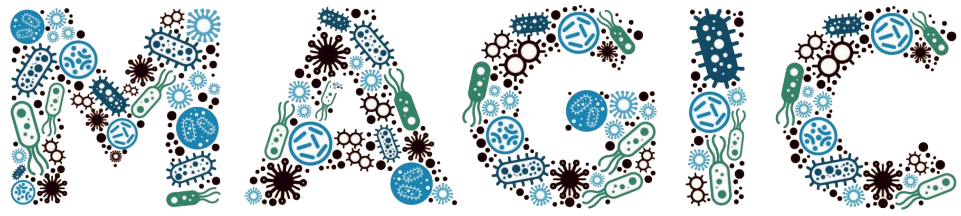
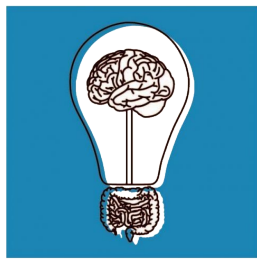
← More Detail

This word cloud shows your personal bacterial community at a finer level of detail. Within each family, bacteria can be subdivided into several **genera** (singular, **genus**). The size of each word represents the relative abundance of that genus, and the colour shows which family that genus comes from.

You Are Here →

There are nearly 4,000 people participating in this study so far! We have graphed everyone together based on how similar or different their gut microbiomes were. In the next graph, points that are closer together are more similar to each other, and points that are farther apart are more different. Your sample is shown in green. Remember that your position in this graph doesn't say anything about how healthy your gut microbiome is. As we've seen above, there is a wide range of normal variation in the human gut.





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Your Bacterial Families

Everyone's microbiome is different. In your microbiome, the four most abundant bacterial families were *Lachnospiraceae*, *Ruminococcaceae*, *Bacteroidaceae*, and *Oscillospiraceae*. Here is a little bit of information about what functions these four families perform in the gut.

Lachnospiraceae

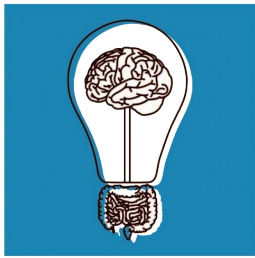
This family of bacteria is found in the gut and plays an important role in the breakdown of complex carbohydrates. Lachnospiraceae are known for their ability to ferment a variety of dietary fibers, producing short-chain fatty acids (SCFAs) such as butyrate, propionate, and acetate. These SCFAs provide an energy source for the body, improve gut health, and have anti-inflammatory properties. Research has also linked Lachnospiraceae to improved metabolic health and a reduced risk of obesity.

Ruminococcaceae

Ruminococcaceae are involved in the fermentation of dietary fiber and the production of SCFAs. These bacteria also play a role in regulating the immune system and maintaining gut health. Research has shown that reduced levels of Ruminococcaceae in the gut are associated with inflammatory bowel diseases such as Crohn's disease and ulcerative colitis.

Bacteroidaceae

Bacteroidaceae is a family of bacteria found in the gut that are involved in the breakdown of complex carbohydrates, such as dietary fibers and resistant starches. These bacteria produce enzymes that can break down plant-based foods, making the nutrients more accessible to the body. Bacteroidaceae also play a role in regulating the immune system and maintaining gut health, and their presence has been associated with a reduced risk of inflammatory bowel diseases.



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Oscillospiraceae

Members of the Oscillospiraceae family of bacteria have been linked to improved glucose metabolism and may have a role in regulating blood sugar levels. These bacteria are involved in the breakdown of complex carbohydrates and the production of SCFAs such as butyrate, which have been shown to improve gut health and protect against inflammation.