The background of the slide features a close-up photograph of a dense, sprawling colony of small, green and blue fluorescent bacteria or algae growing on a dark, textured surface. The organisms form intricate, branching patterns of glowing green and blue against the black background.

# Introduction to biological data

MSB 2023

# Overview & class objectives

## **Objectives:**

- Discuss the two main types of biological research
- What is sampling design and sampling bias?
- What is experimental design?
- Where can you find biological datasets?

Note: Here we'll only cover biological data usable for statistical analysis

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**#2212 165**



# Types of biological research

## Descriptive / correlative research

Descriptive research aims to accurately describe a population/ phenomenon.

*What is the viral diversity associated to the panda gut microbiota?*

Correlational research investigates relationships between variables without manipulating any of them.

*What is the association between pet ownership and allergic disease development in children?*

**Answer *what, where, when and how* but not *why*.**

# Types of biological research

## Descriptive / correlative research

- Descriptive research aims to accurately describe a population/ phenomenon.

*What is the viral diversity associated to the panda gut microbiota?*

- Correlational research investigates relationships between variables without manipulating any of them.

*What is the association between pet ownership and allergic disease development in children?*

→ Use sampling design

## Experimental research

- Experiments are used to study causal relationships.

You manipulate one or more independent variable and measure their effect on one or more dependent variables.

*What is the effect of Caffeine intake on adult cognitive performances?*

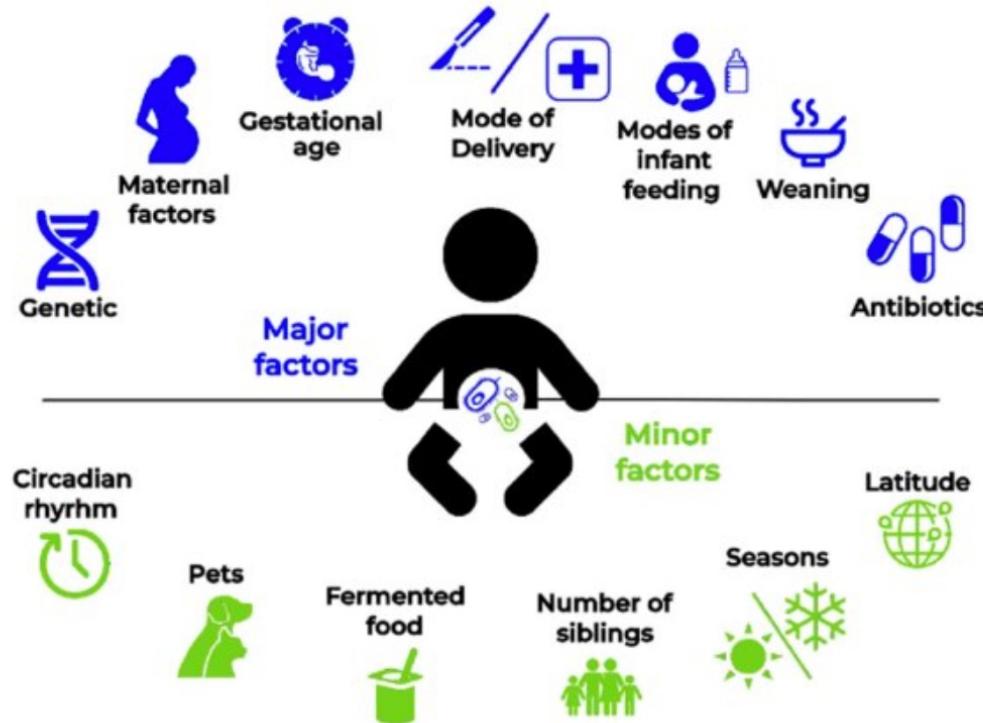
→ Uses experimental design

## Sampling design

---



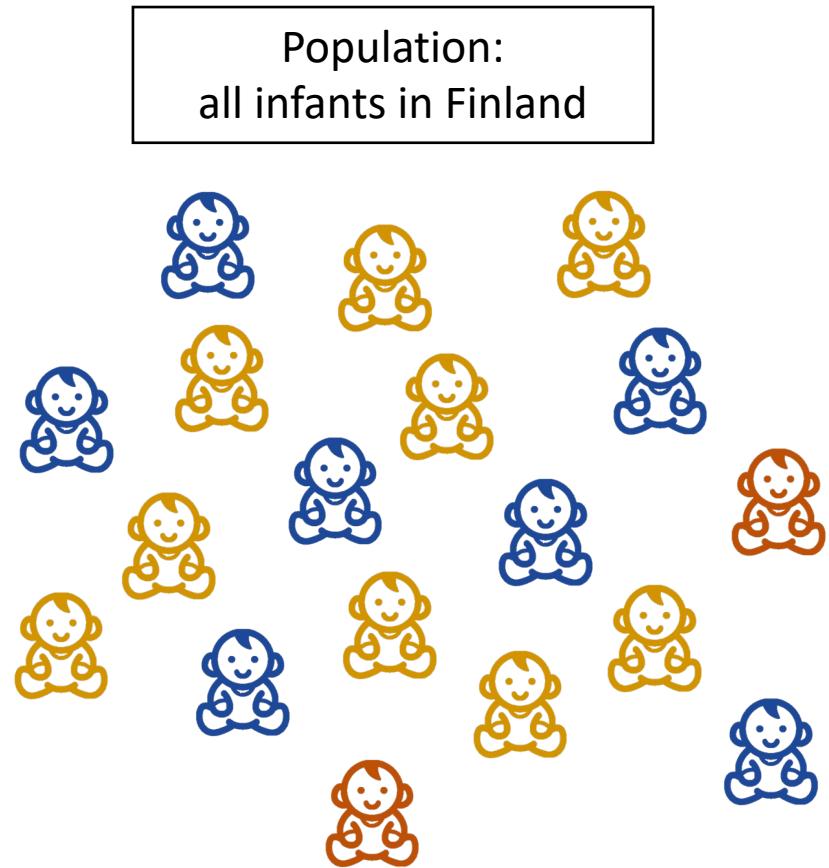
# The HELMi birth cohort



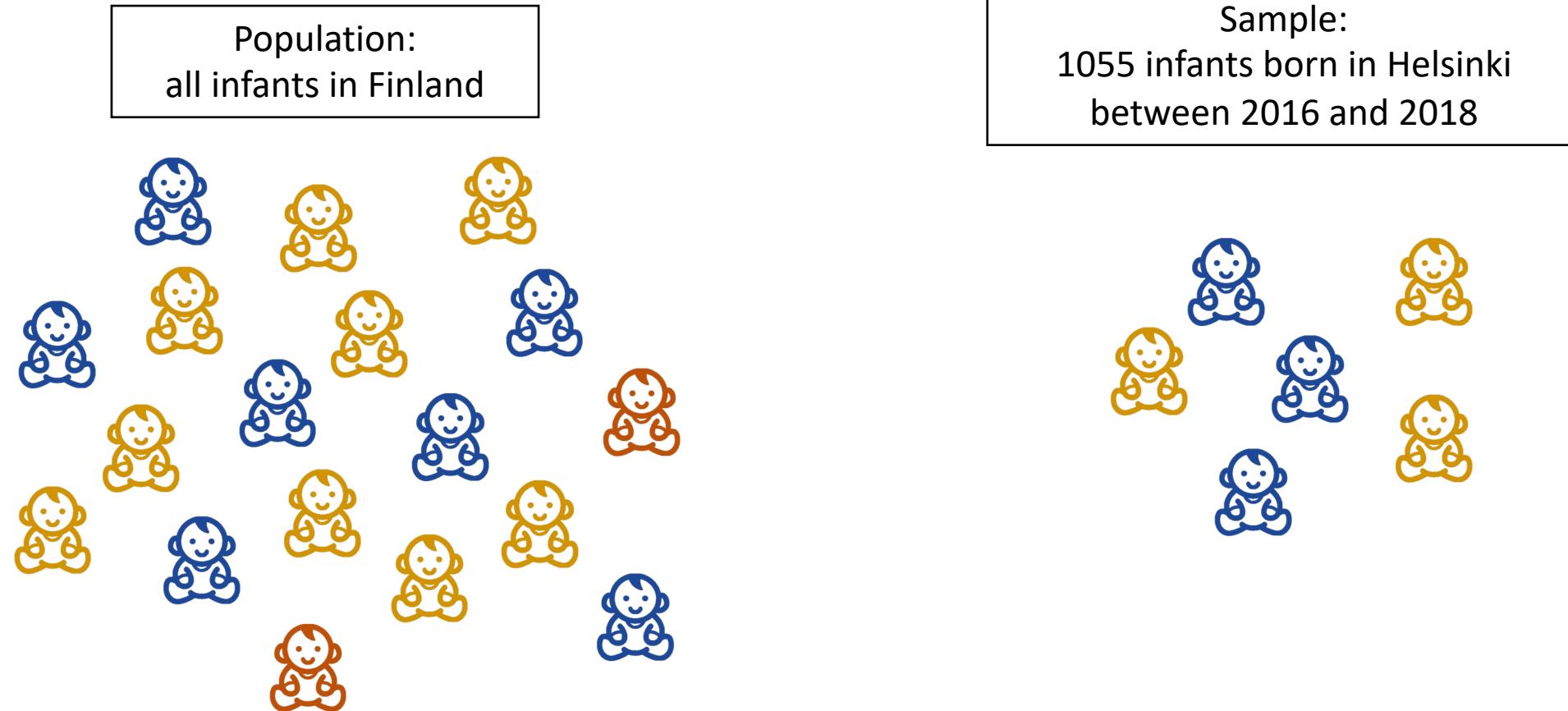
HELMi (Health and Early Life Microbiota) is a **prospective general population birth cohort**, set up to identify environmental, lifestyle and genetic factors that modify the intestinal microbiota development in the first years of life and their relation to child health and well-being

<https://bmjopen.bmj.com/content/9/6/e028500>

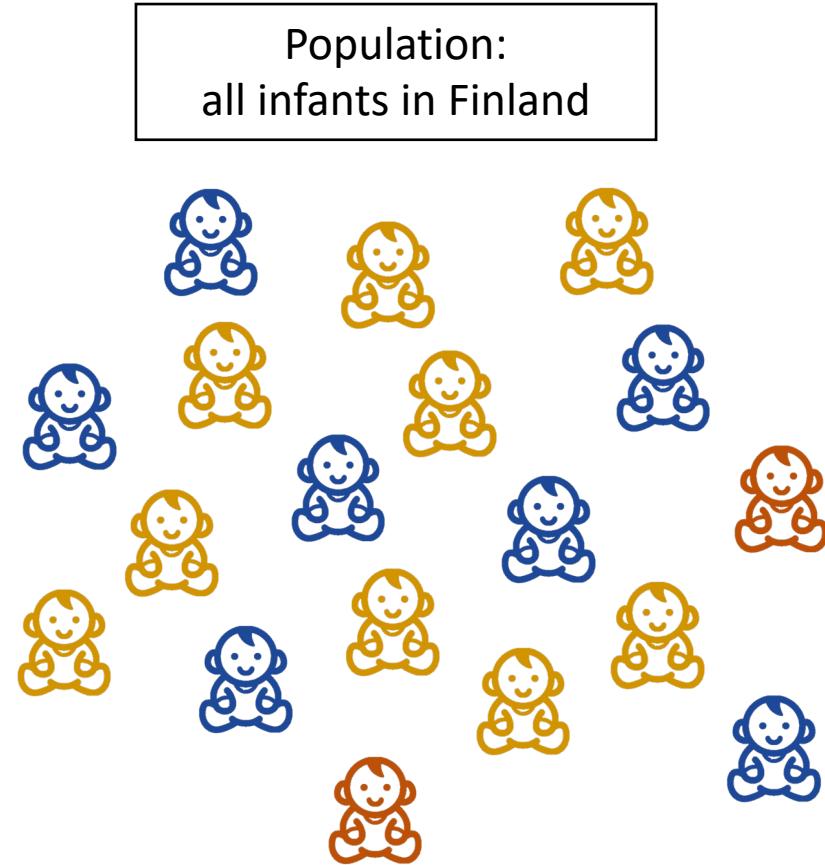
# Population vs sample



# Population vs sample



# Representative or biased sampling

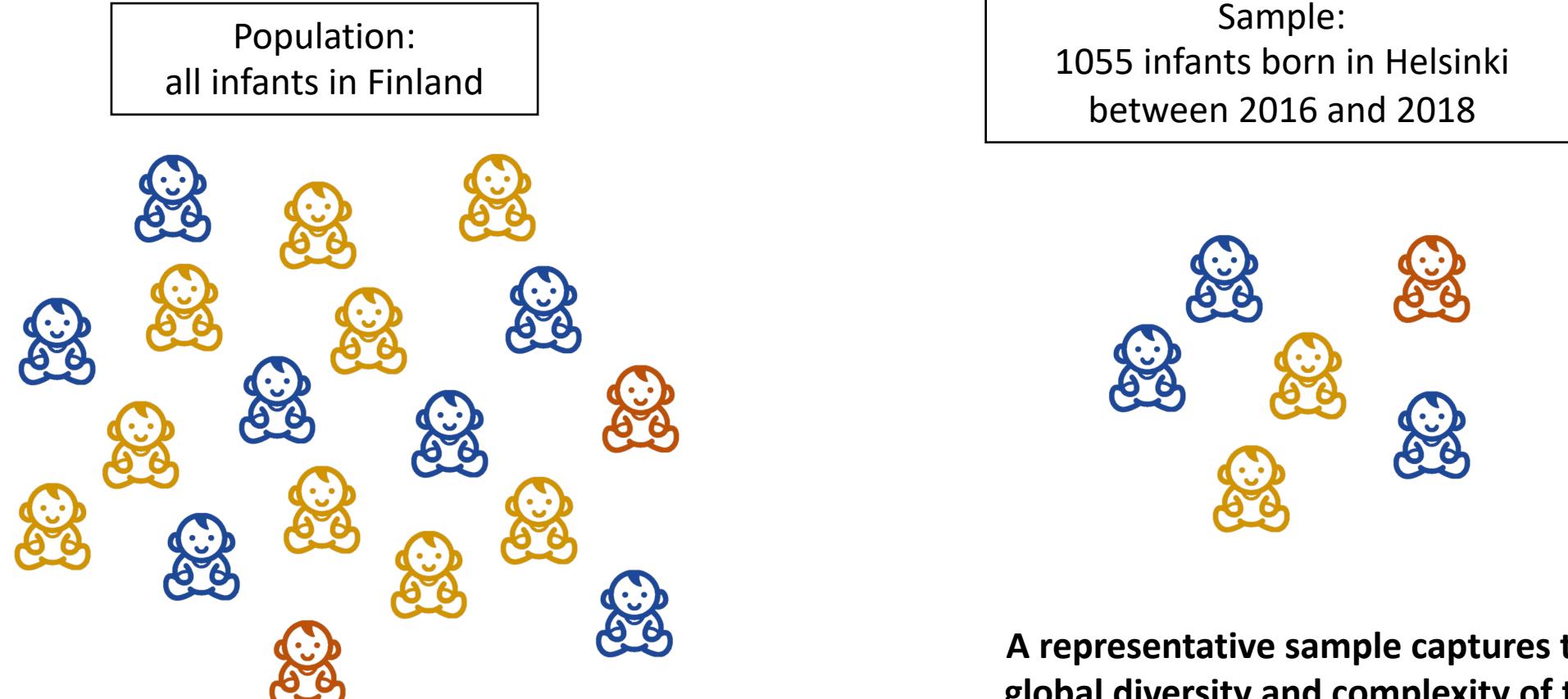


Sample:  
1055 infants born in Helsinki  
between 2016 and 2018

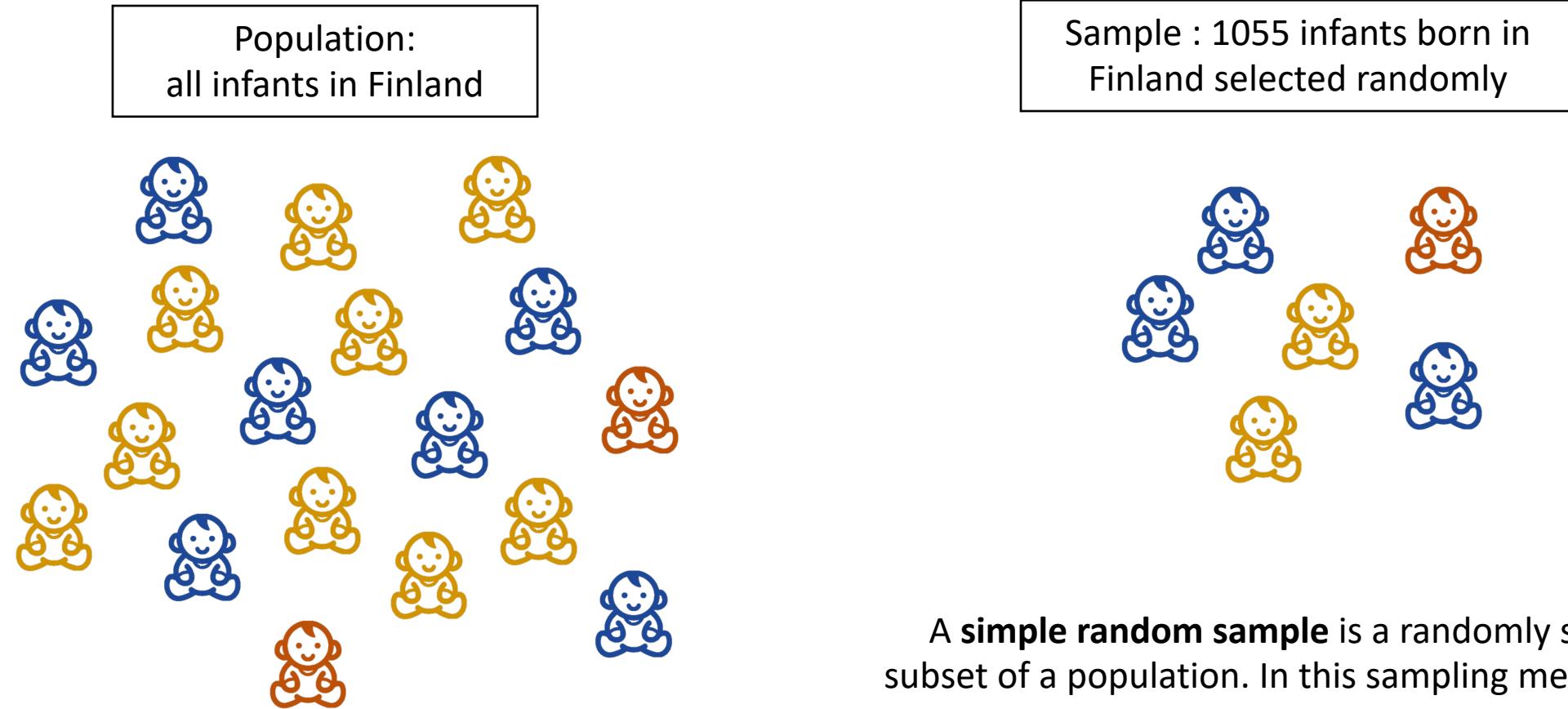


**Biased sampling occurs when one or more parts of the population are favored over others**

# Representative or biased sampling

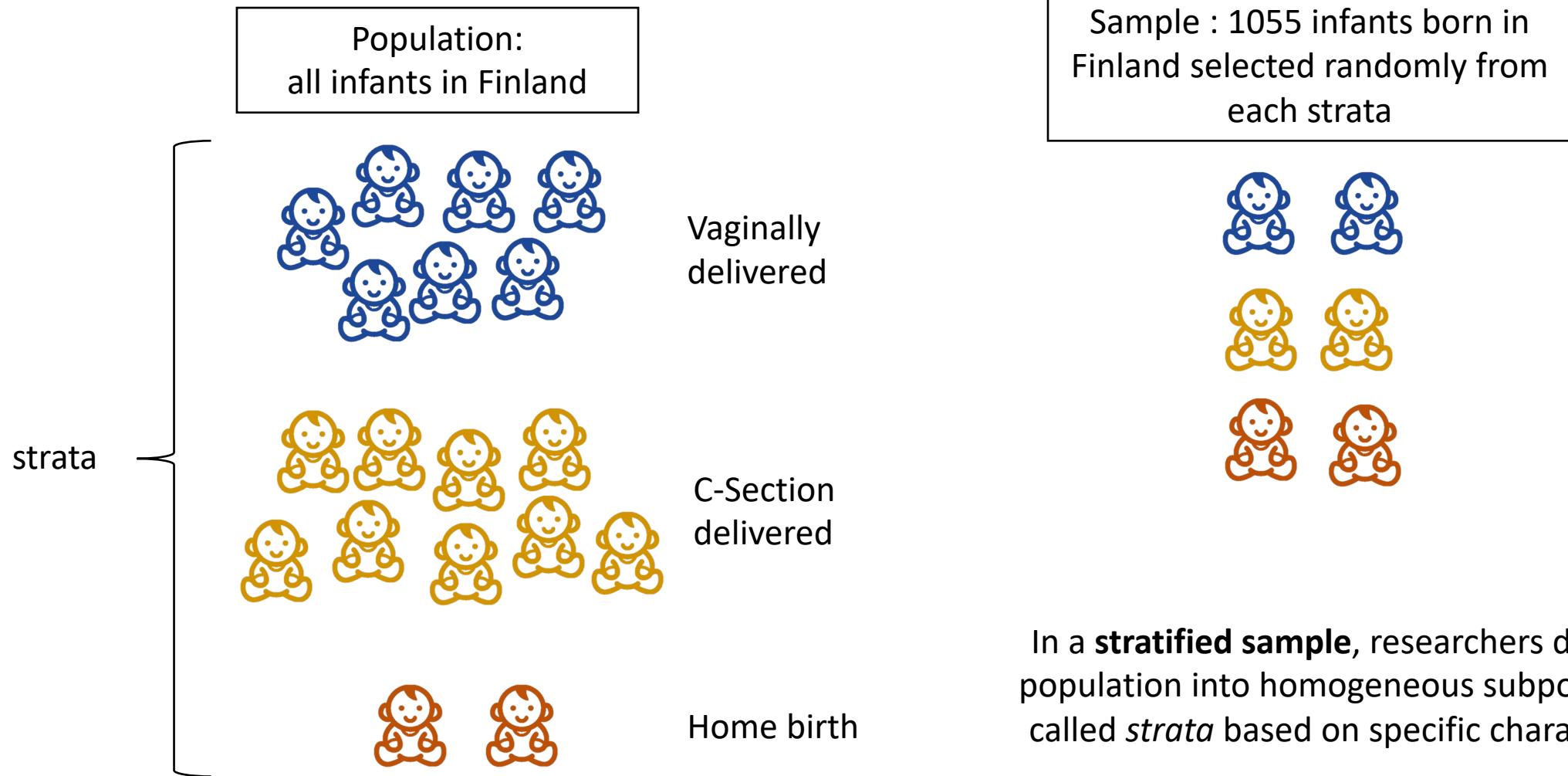


# Types of sampling: simple random sampling

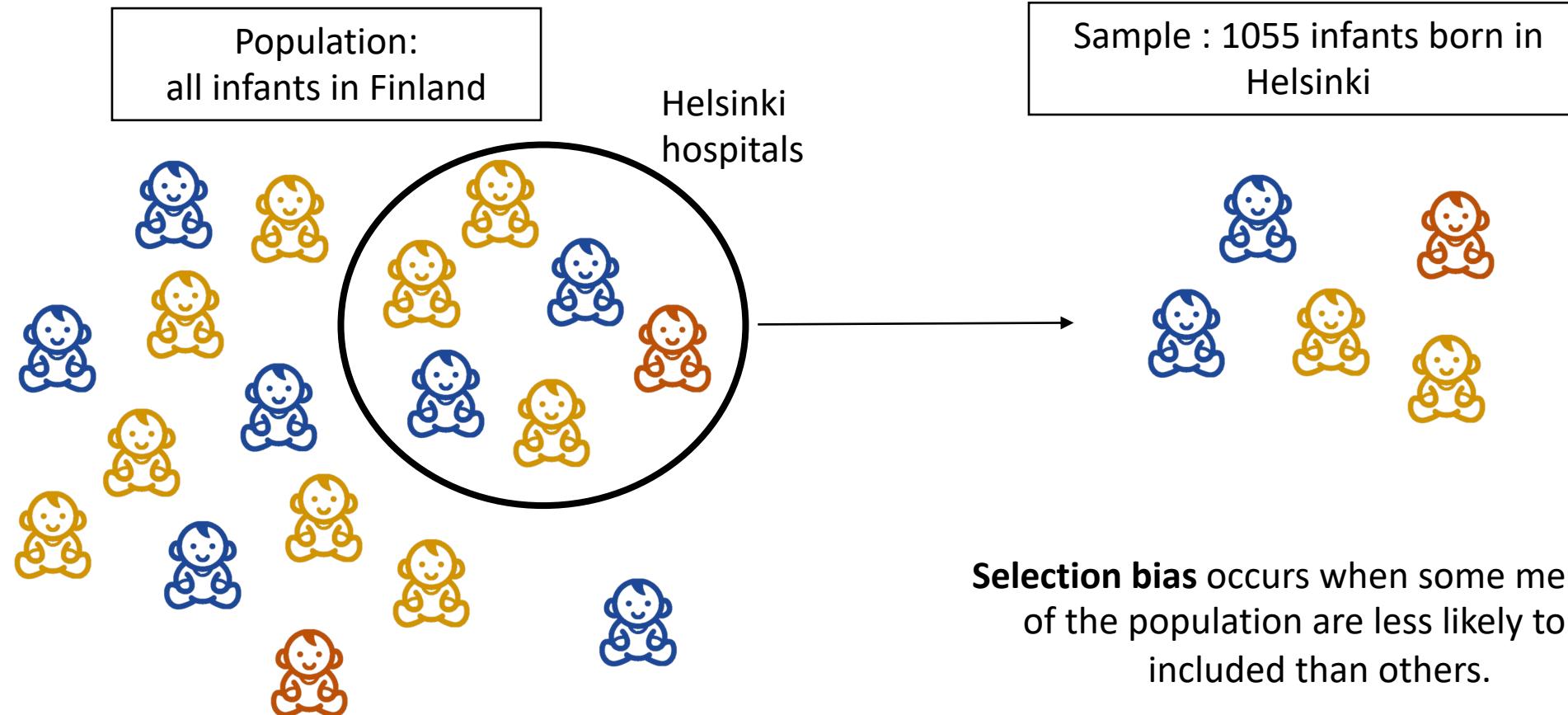


A **simple random sample** is a randomly selected subset of a population. In this sampling method, each member of the population has an exactly equal chance of being selected.

# Types of sampling: stratified sampling



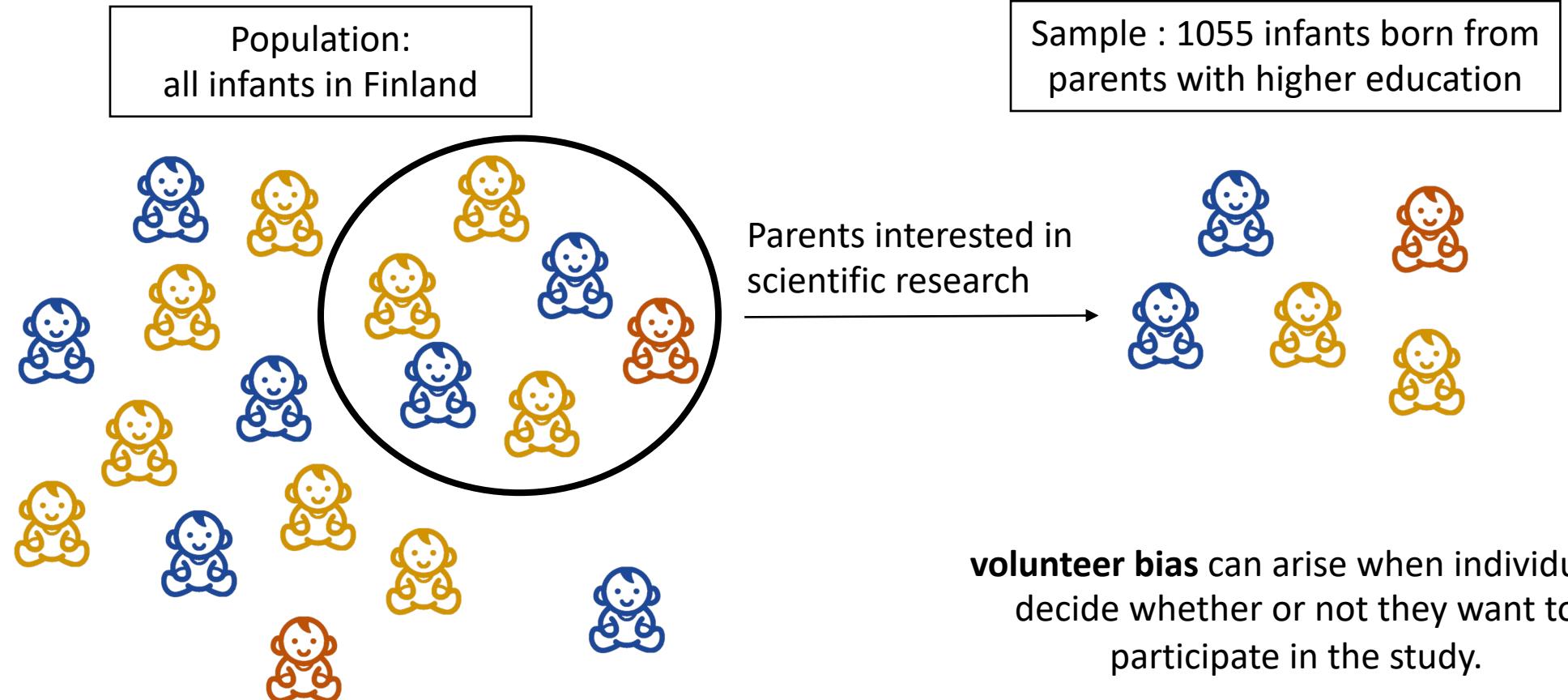
# Bias in sampling: selection bias



**Selection bias** occurs when some members of the population are less likely to be included than others.

As a result, the sample is not representative of your population.

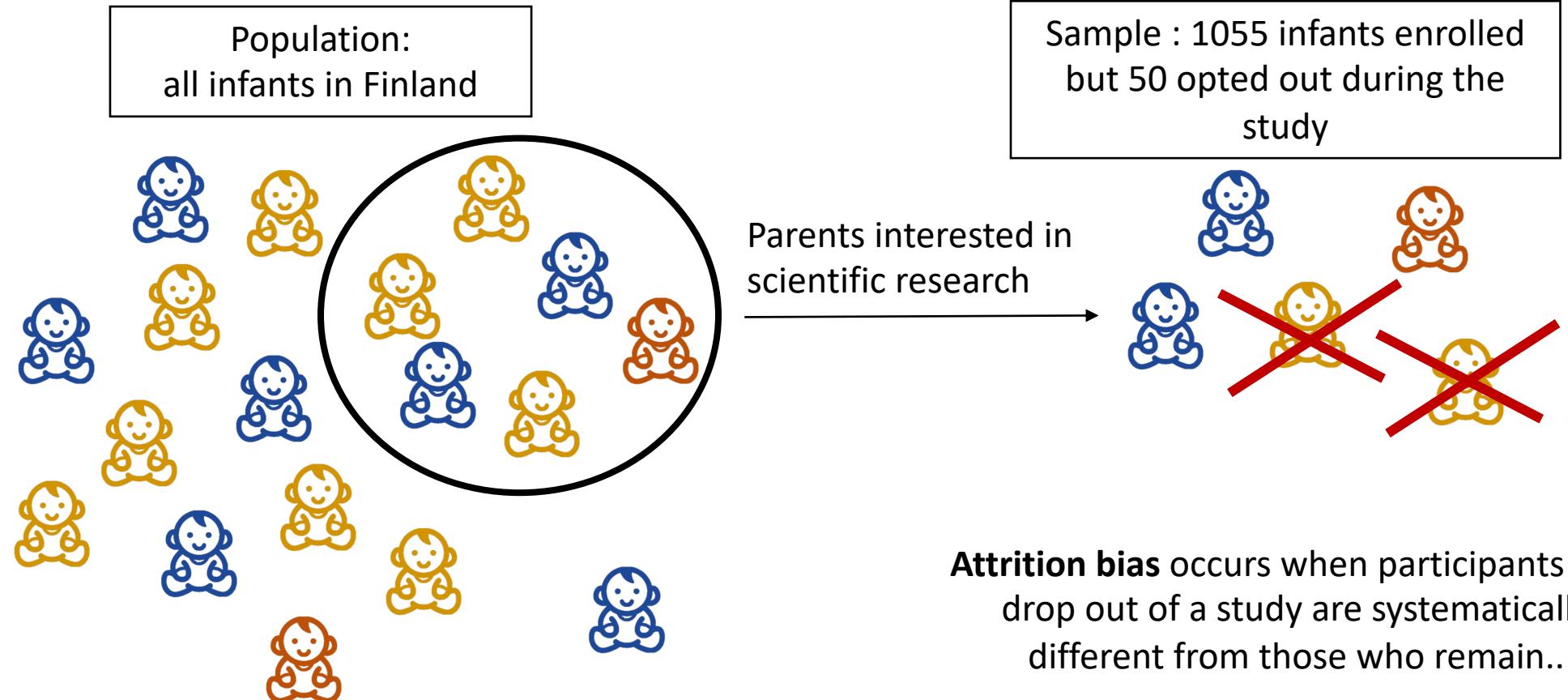
# Bias in sampling: Volunteer bias



**volunteer bias** can arise when individuals decide whether or not they want to participate in the study.

Participants may differ from those who don't—for example, in terms of motivation.

# Bias in sampling: Attrition bias



# Let's Recap!

- Descriptive research tries to describe a biological phenomenon or population through sample collection
- Different sampling design methods can be used to try to obtain a representative sample
- However, different types of biases can arise and limit the generalizability of your finding.



# Let's recap!

Join at

**slido.com**

**#2212 165**

## Characterization of the Gut Microbiota in the Red Panda (*Ailurus fulgens*)

**Fanli Kong<sup>1</sup>\*, Jiangchao Zhao<sup>2</sup>\*, Shushu Han<sup>1</sup>, Bo Zeng<sup>1</sup>, Jiandong Yang<sup>3</sup>, Xiaohui Si<sup>3</sup>, Benqing Yang<sup>4</sup>, Mingyao Yang<sup>1</sup>, Huailiang Xu<sup>3\*</sup>, Ying Li<sup>1\*</sup>**

**1** Institute of Animal Genetics and Breeding, Sichuan Agricultural University, Chengdu, Sichuan, China, **2** Department of Pediatrics and Communicable Disease, University of Michigan, Ann Arbor, Michigan, United States of America, **3** Sichuan Agricultural University, College of Animal Science and Technology, Ya'an, Sichuan, China, **4** Sichuan Fengtongzhai National Nature Reserve, Baoxing, Sichuan, China

### Abstract

The red panda is the only living species of the genus *Ailurus*. Like giant pandas, red pandas are also highly specialized to feed mainly on highly fibrous bamboo. Although several studies have focused on the gut microbiota in the giant panda, little is known about the gut microbiota of the red panda. In this study, we characterized the fecal microbiota from both wild ( $n=16$ ) and captive ( $n=6$ ) red pandas using a pyrosequencing based approach targeting the V1-V3 hypervariable regions of the 16S rRNA gene. Distinct bacterial communities were observed between the two groups based on both membership and structure. Wild red pandas maintained significantly higher community diversity, richness and evenness than captive red pandas, the communities of which were skewed and dominated by taxa associated with Firmicutes. Phylogenetic analysis of the top 50 OTUs revealed that 10 of them were related to known cellulose degraders. To the best of our knowledge, this is the first study of the gut microbiota of the red panda. Our data suggest that, similar to the giant panda, the gut microbiota in the red panda might also play important roles in the digestion of bamboo.

What type of sampling design was used here?

- Random sampling design
- Stratified sampling design

### Sample collection

Fecal samples were collected from captive and wild red pandas, and immediately put into a liquid nitrogen container and stored at  $-80^{\circ}\text{C}$ . Sixteen fecal samples of wild animals were collected from Fengtongzhai National Nature Reserve (Baoxing, Sichuan Province, China) with the help of experienced trackers. Six samples from captive red pandas were obtained from Bifengxia Ecological Zoo (Ya'an, Sichuan Province, China).



- Large scale citizen science project
- Adults send fecal samples and receive a personalized report for free
- In 2017: 15,096 samples from 11,336 participants

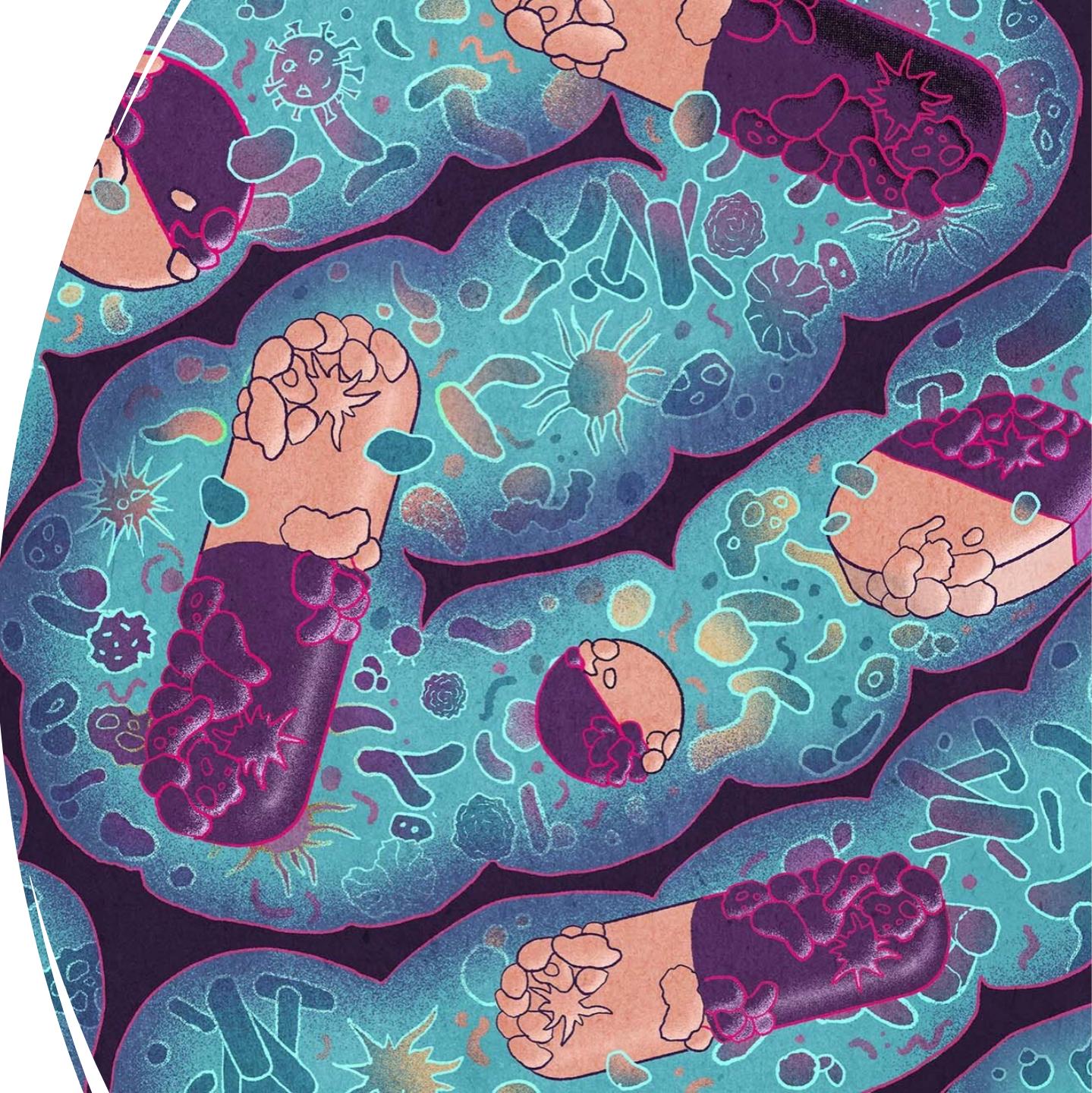
## Cohort characteristics.

AGP participants primarily reside in the United States ( $n = 7,860$ ). However, interest in the AGP rapidly expanded beyond the United States to the United Kingdom ( $n = 2,518$ ) and Australia ( $n = 321$ ), with 42 other countries or territories also represented (Fig. 1A; see also Table S1 in the supplemental material). Participants in the United States inhabit urban ( $n = 7,317$ ), rural ( $n = 29$ ), and mixed ( $n = 98$ ) communities (2010 U.S. Census data based on participant ZIP codes) and span greater ranges of age, race, and ethnicity than other large-scale microbiome projects (2–6).

What type of sampling bias is probably limiting the generalization of the American gut project?

- Selection bias
- Volunteer bias
- Attrition bias

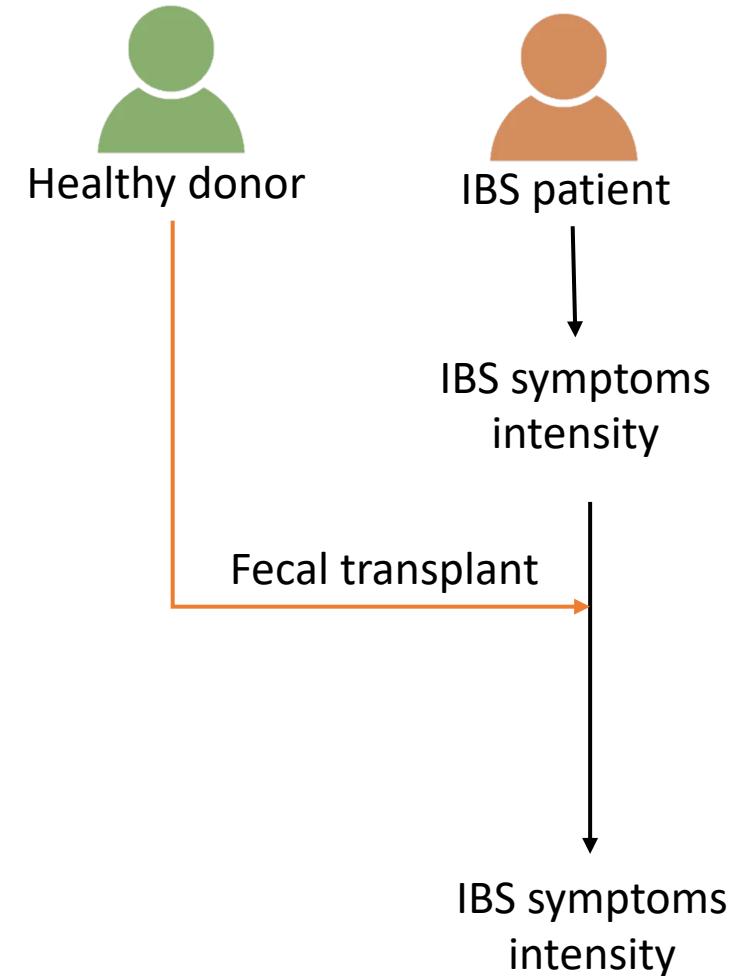
## **Experimental design**



# FMT for IBS study

IBS is a common functional gastrointestinal disorder which impairs patients' quality of life.

- Current treatments do not relieve symptoms for all patients
- FMT has been proposed as a potential treatment for IBS patients



# FMT for IBS study

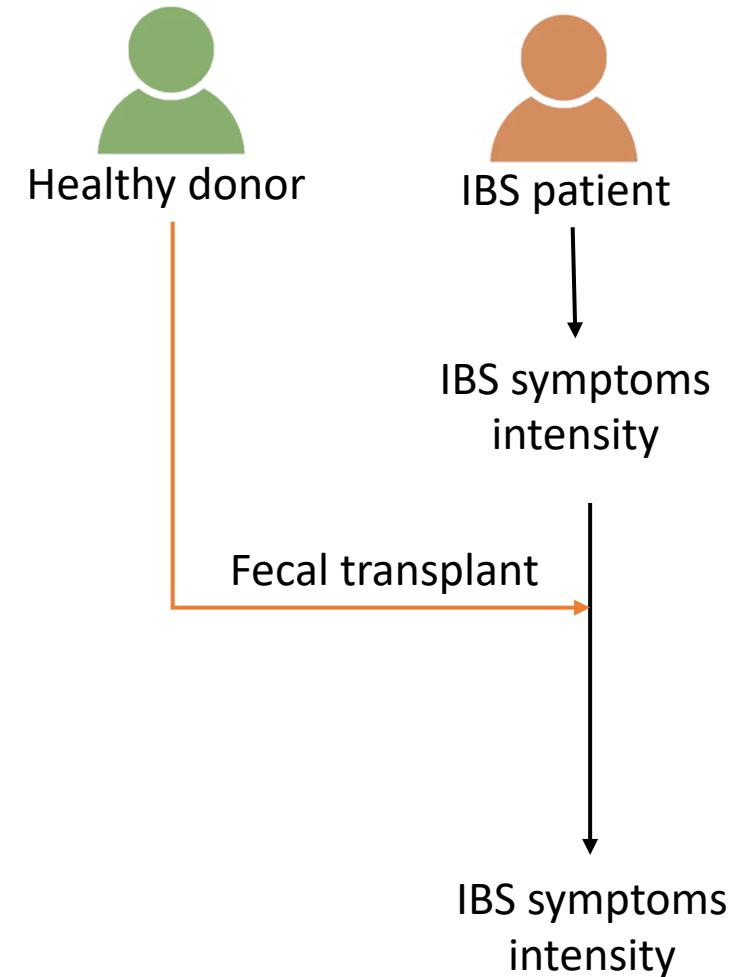
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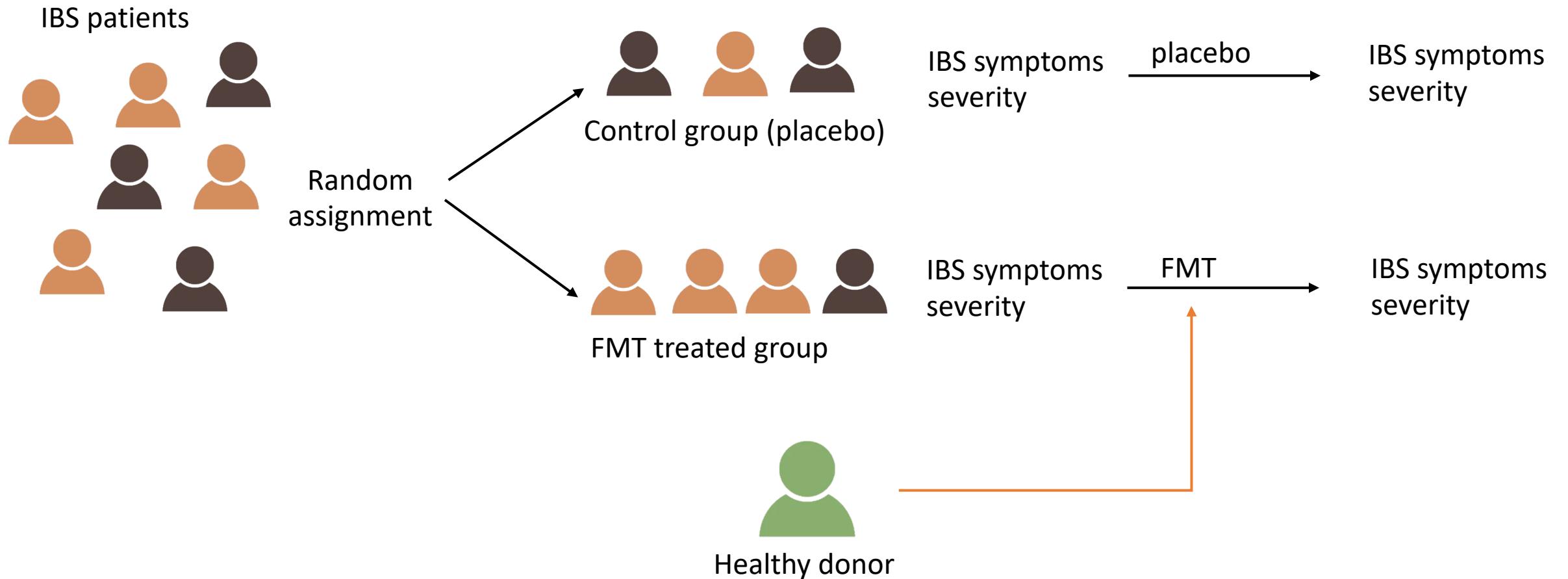
**Independent variable:** receiving FMT

**Dependent variable:** IBS symptoms severity

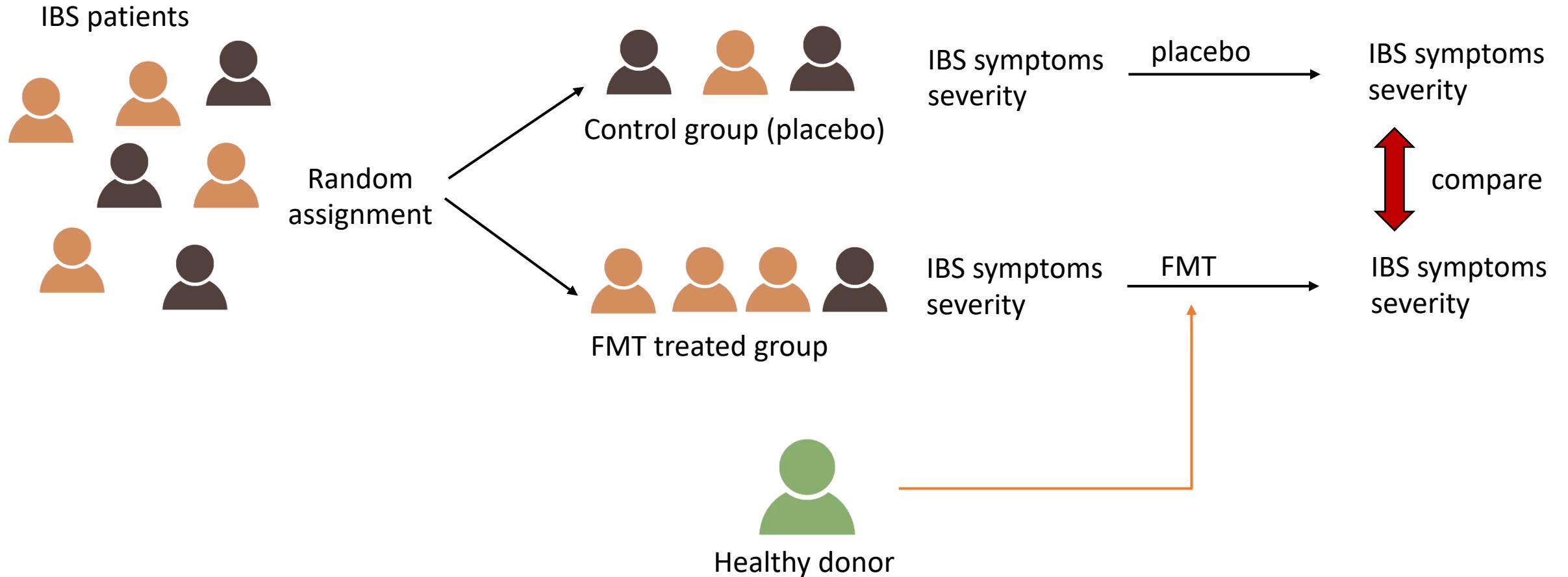
**Null Hypothesis:** receiving FMT is not associated with a change IBS symptoms severity



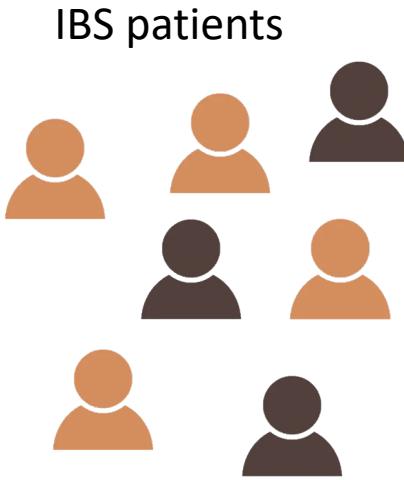
# Randomized design



# Randomized design

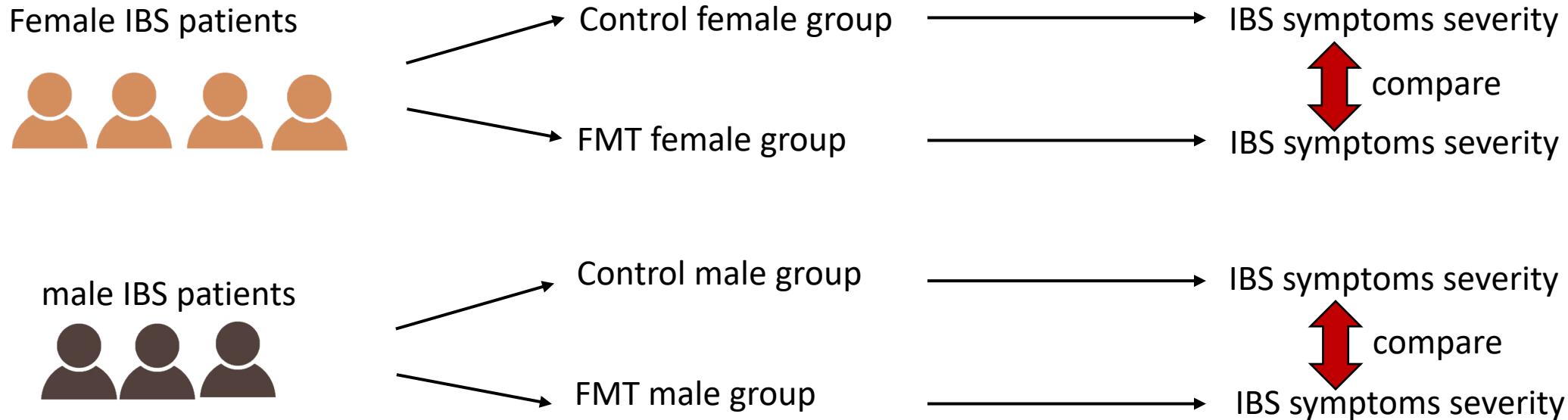


# Randomized block design



We expect from the literature  
that sex has an effect on the  
severity of IBS symptoms

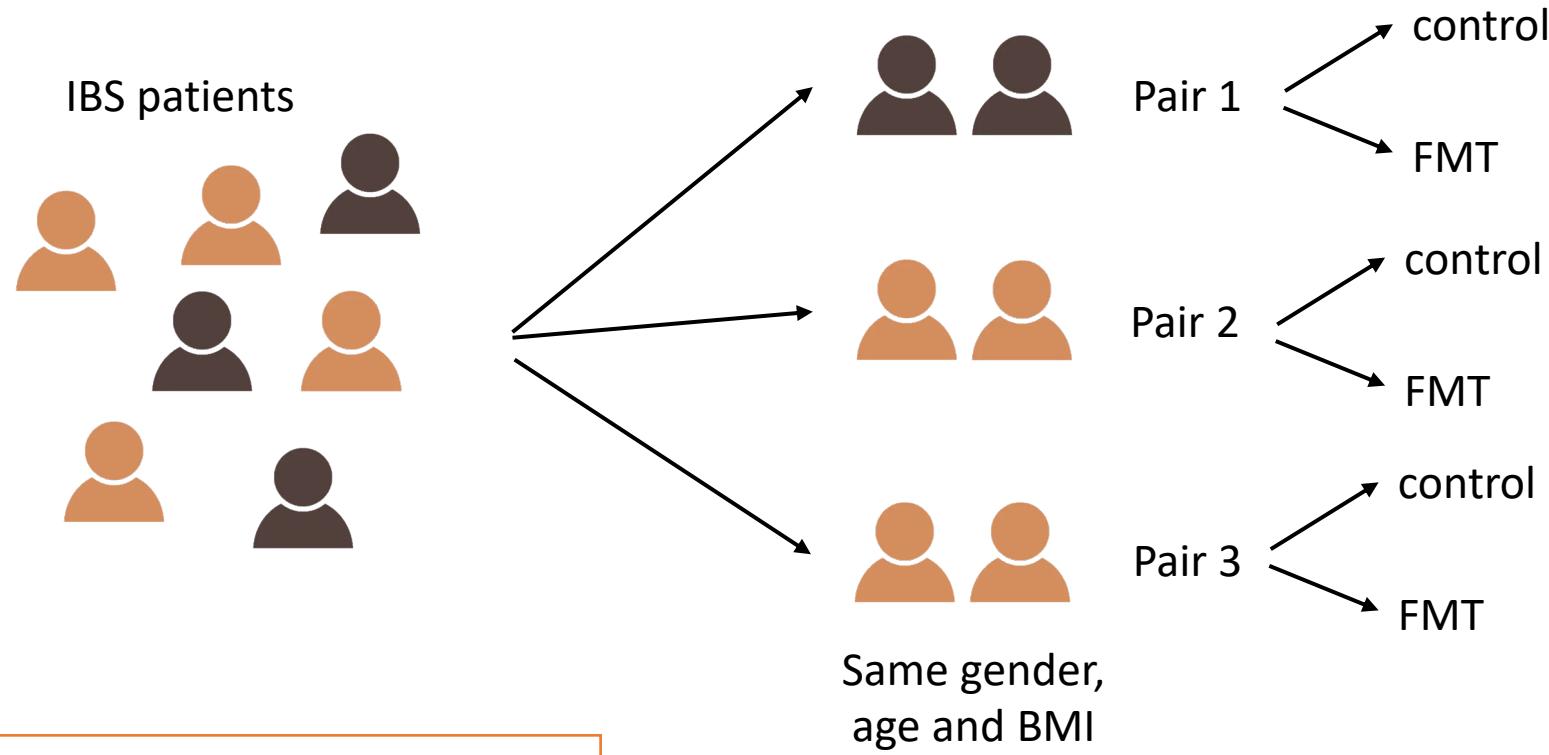
# Randomized block design



We expect from the literature  
that **sex** has an effect on the  
severity of IBS symptoms

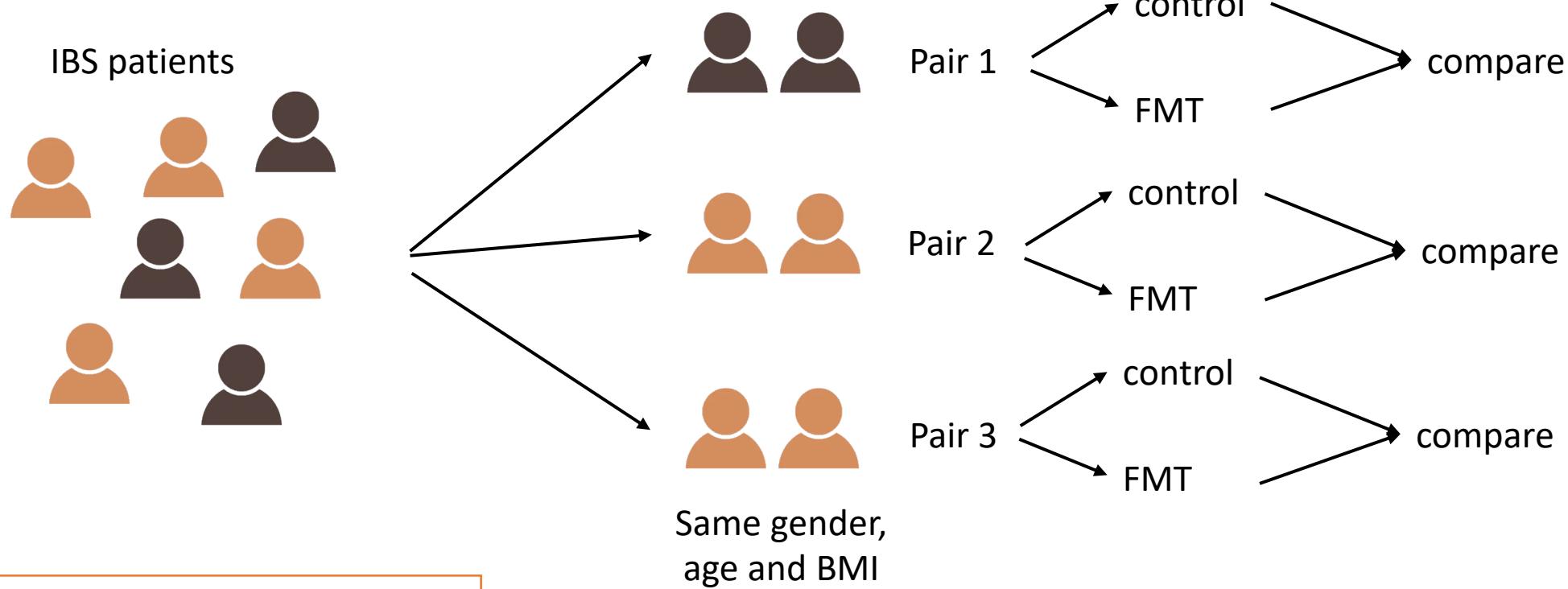
Sex : blocking variable

# Match paired design



We expect from the literature  
that **sex, age and BMI** has an  
effect on the severity of IBS  
symptoms

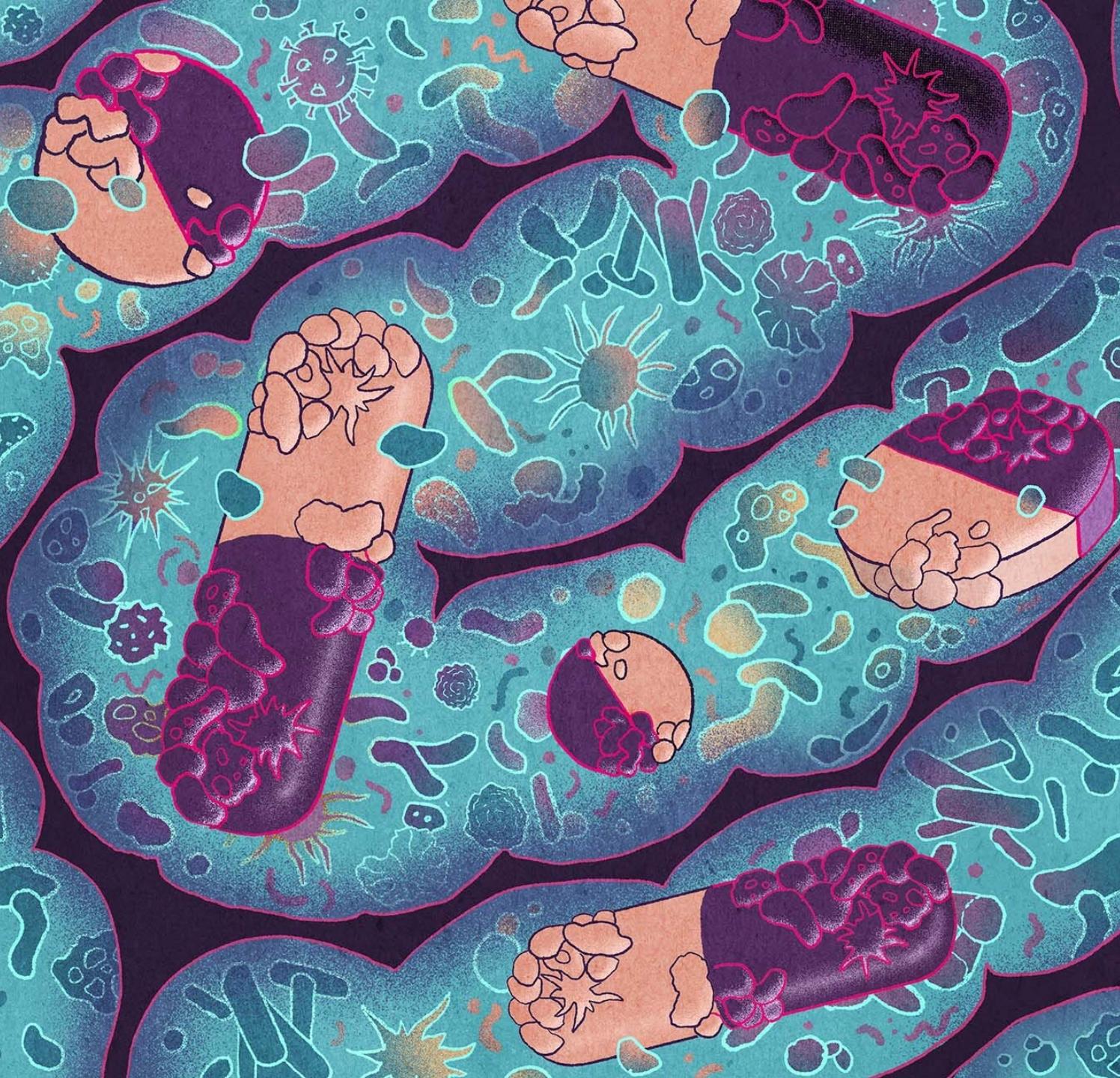
# Match paired design



We expect from the literature  
that **gender, age and BMI** has  
an effect on the severity of IBS  
symptoms

# Let's Recap!

- Experimental research attempts to infer a causation through experimental design
- Experimental design needs to control for potential confounding effects.



# Recap experimental design

**Efficacy of antibiotic treatment in patients with chronic low back pain and Modic changes (the AIM study): double blind, randomised, placebo controlled, multicentre trial**

*BMJ* 2019 ;367 doi: <https://doi.org/10.1136/bmj.l5654> (Published 16 October 2019)

Cite this as: *BMJ* 2019;367:l5654

## Abstract

**Objective** To assess the efficacy of three months of antibiotic treatment compared with placebo in patients with chronic low back pain, previous disc herniation, and vertebral endplate changes (Modic changes).

**Setting** Hospital outpatient clinics at six hospitals in Norway.

**Participants** 180 patients with chronic low back pain, previous disc herniation, and type 1 (n=118) or type 2 (n=62) Modic changes enrolled from June 2015 to September 2017.

**Interventions** Patients were randomised to three months of oral treatment with either 750 mg amoxicillin or placebo three times daily. The allocation sequence was concealed by using a computer generated number on the prescription.

**Main outcome measures** The primary outcome was the Roland-Morris Disability Questionnaire (RMDQ) score (range 0-24) at one year follow-up in the intention to treat population. The minimal clinically important between group difference in mean RMDQ score was predefined as 4.

What type of Experimental design are we talking about here?

- Random design
- Randomized block design
- Match paired design



Industrial Crops and Products

Volume 175, January 2022, 114244

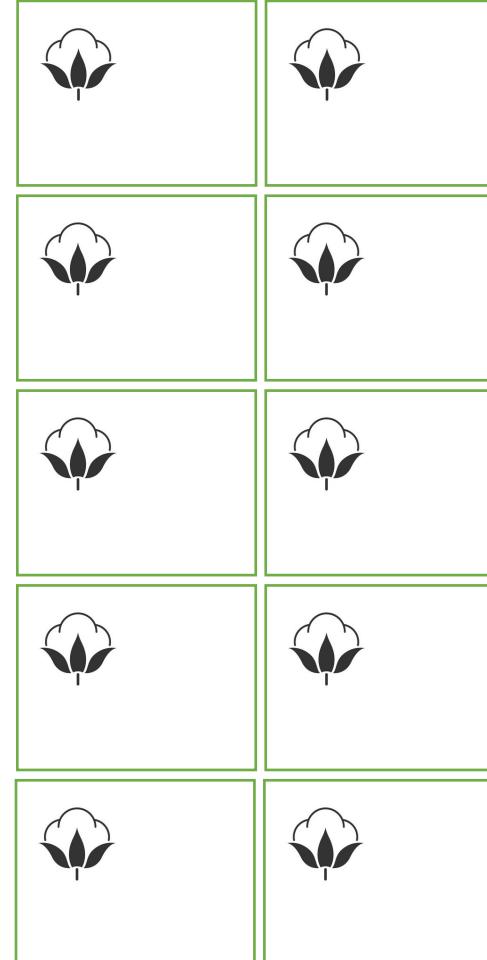


## Irrigation with ionized brackish water affects cotton yield and water use efficiency

Kai Wei, Jihong Zhang, Quanjiu Wang , Yi Guo, Weiyi Mu

### Highlights

- Ionized technology is an ecologically-safe and simple for brackish water treatment.
- Field experiments tested cotton responses to irrigation ionized brackish water and irrigation amount.
- Ionized treatment decreased soil salt accumulation and improved water use efficiency.
- Future work will focus on understanding the mechanisms that affect seed cotton yield and water use efficiency through the ionized treatment.





Industrial Crops and Products

Volume 175, January 2022, 114244

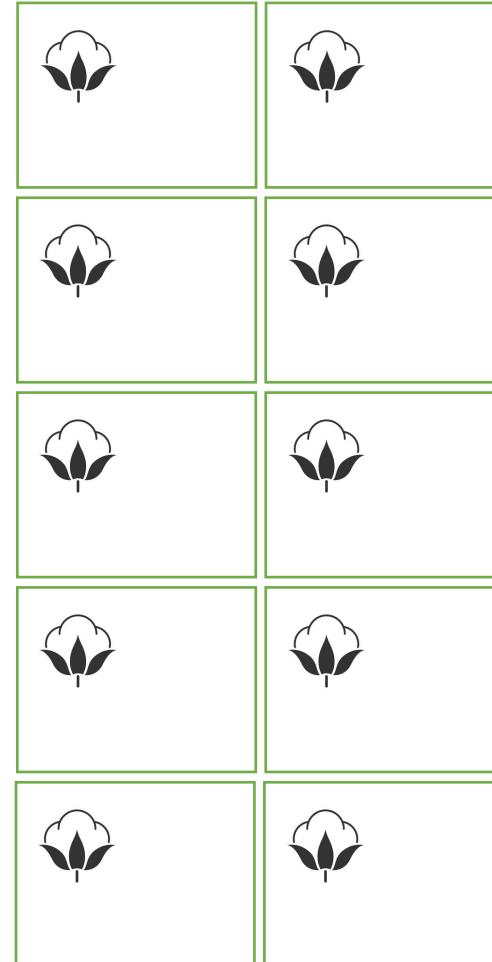


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Randomly assigned:

Non ionized   
Or ionized water

Five irrigation treatments  
to mimic a water deficit:

- W1:   
W2:   
W3:   
W4:   
W5:



Industrial Crops and Products

Volume 175, January 2022, 114244

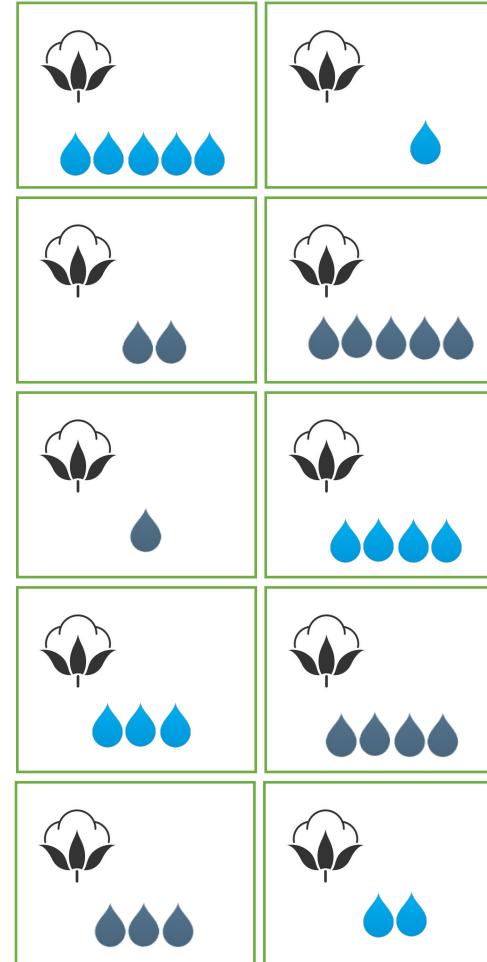


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Randomly assigned:

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Five irrigation treatments to mimic a water deficit:

W1:

W2:

W3:

W4:

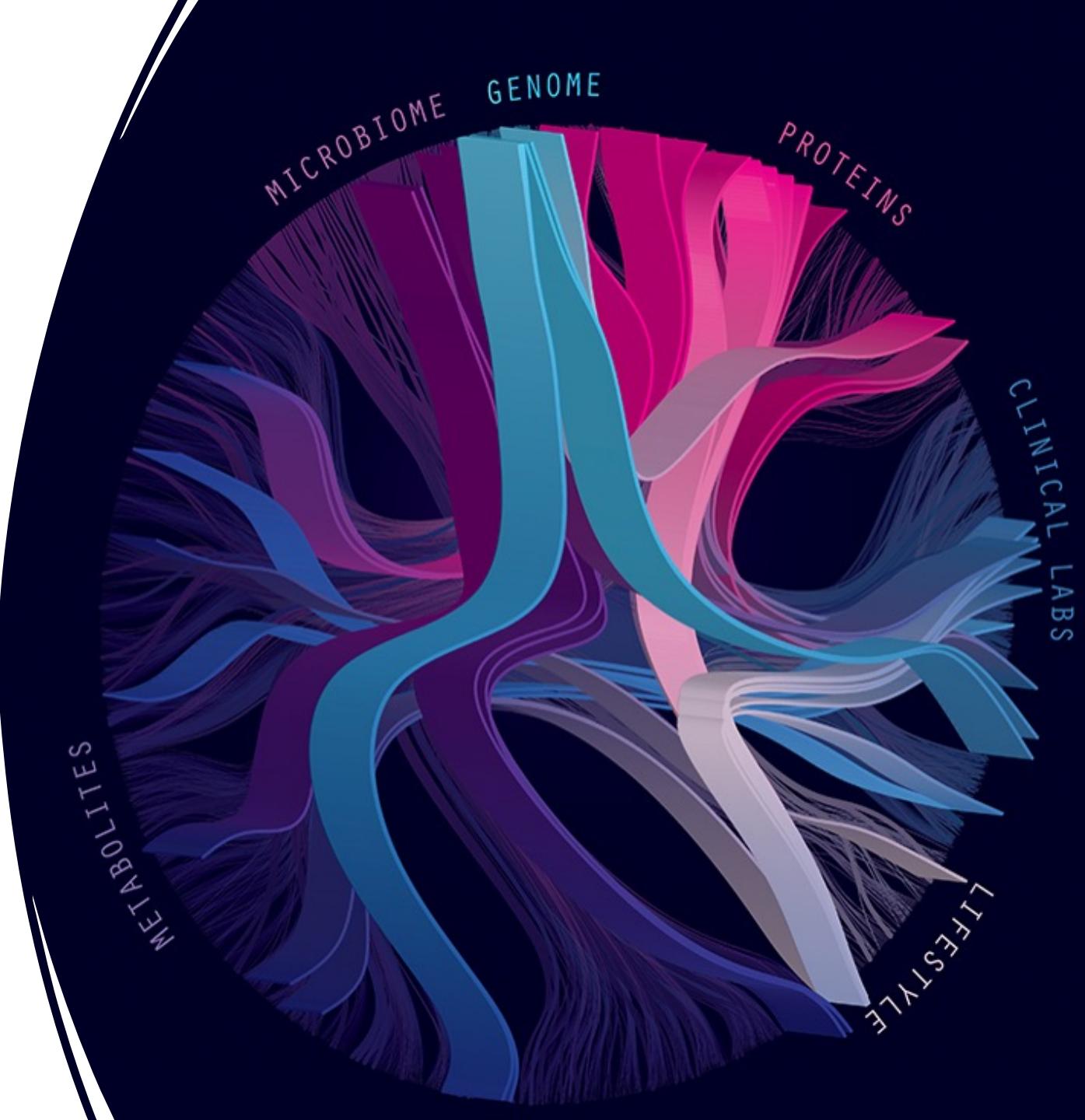
W5:

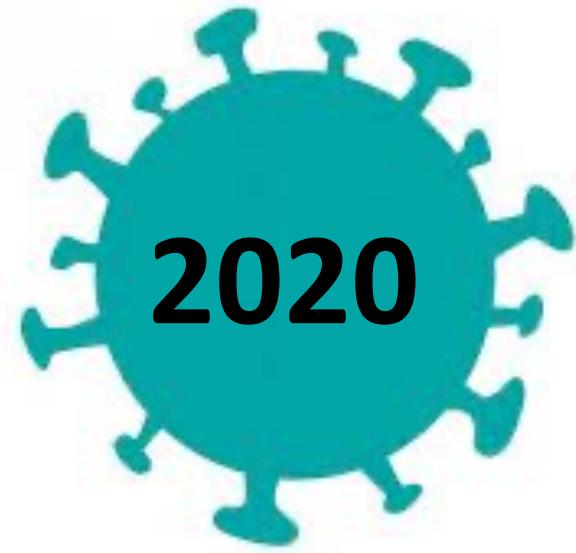
What type of Experimental design are we talking about here?

- Random design
- Randomized block design
- Match paired design

## Biological data and where to find them

---





**How did scientists share their information about  
COVID-19 internationally?**



**Search**[Advanced search](#)

## **PDBe-KB COVID-19 Data Portal**

Protein Data Bank in Europe - Knowledge Base



### Aggregate information about :

- COVID protein functions
- Structural data for the viral protein

# PDBe-KB ➤ Spike glycoprotein

[What's new?](#)

## Representative structures for UniProt P0DTC2

PDB chains with highest data quality, coverage and best resolution

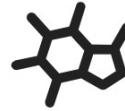
[Click to view in 3D](#)

Gene: S

**Organism:** Severe acute respiratory syndrome coronavirus 2 (2019-nCoV)**Uniprot:** P0DTC2 [go to UniProt **Biological function:** May down-regulate host tetherin (BST2) by lysosomal degradation, thereby counteracting its antiviral activity [go to UniProt 

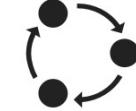
461

Structures



48

Ligands



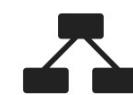
14

Interactions



1

Functional annotations



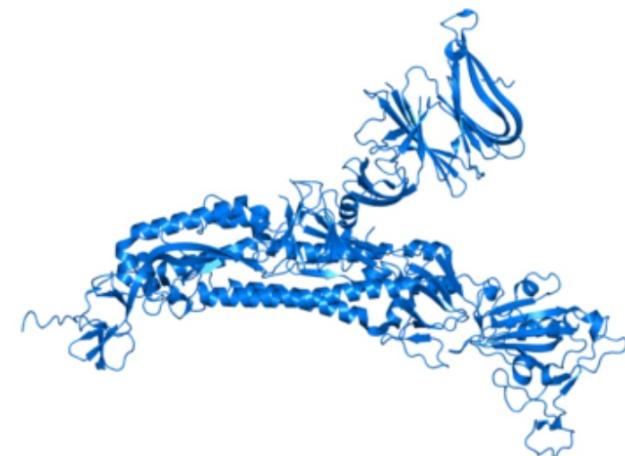
34

Similar proteins



3389

Publications

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What is the  
difference  
between primary  
and secondary  
database ?



# Primary

## NCBI Genome database (GenBank)



### Genome

This resource organizes information on genomes including sequences, maps, chromosomes, assemblies, and annotations.

#### Using Genome

[Help](#)

[Browse by Organism](#) UPDATED

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[PASC \(Pairwise Sequence Comparison\)](#)

#### External Resources

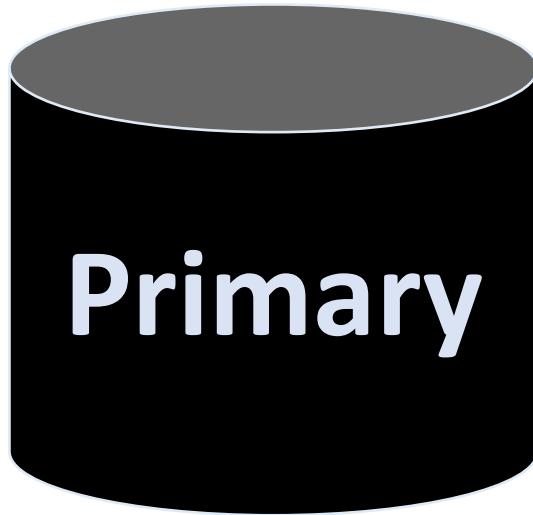
[GOLD - Genomes Online Database](#)

[Bacteria Genomes at Sanger](#)

[Ensembl](#)

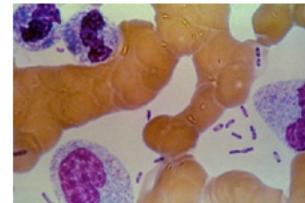
- Experimental data are submitted directly by researchers

# NCBI Genome database (GenBank)



- Experimental data are submitted directly by researchers
- Archival database with a large amount of redundancy

[Organism Overview](#) ; [Genome Assembly and Annotation report \[606\]](#) ; [Genome Tree report \[499\]](#) ; [Plasmid Annotation Report \[143\]](#) ID: 153



## ***Yersinia pestis***

Causative agent of plague

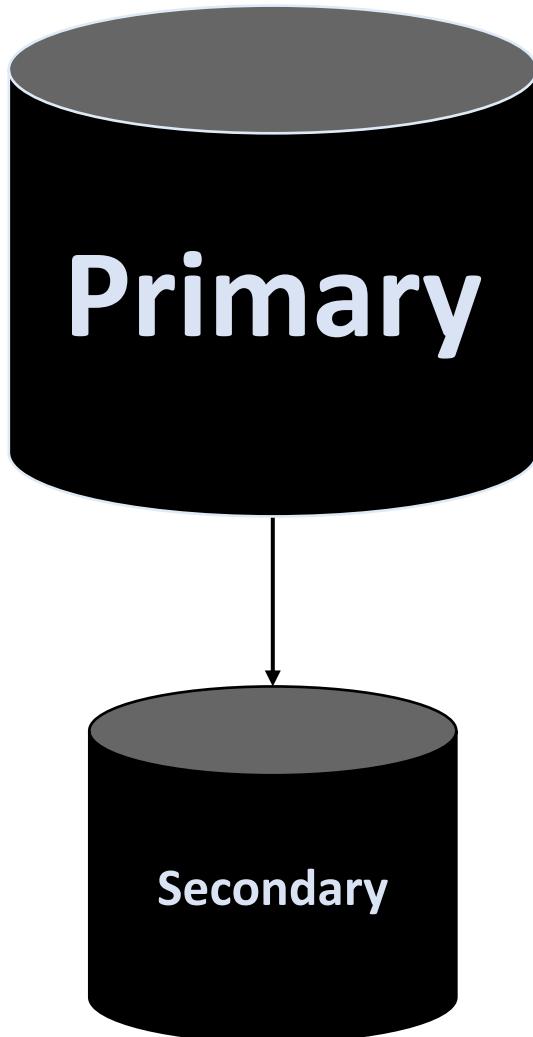
**Lineage:** [Bacteria\[31558\]](#); [Proteobacteria\[10185\]](#); [Gammaproteobacteria\[3786\]](#); [Enterobacteriales\[690\]](#); [Yersiniaceae\[68\]](#); [Yersinia\[22\]](#); [Yersinia pseudotuberculosis complex\[4\]](#); [Yersinia pestis\[1\]](#)

***Yersinia*.** This genus consists of 11 species, 3 of which are human pathogens. Specific virulence factors are encoded within pathogenicity islands (PAIs) that are required for the invasive phenotype associated with *Yersinia* infections. These PAIs may be carried on extrachromosomal plasmids or on the chromosome. One key virulence plasmid [More...](#)

### **Summary**

**Sequence data:** genome assemblies: 606;

**Statistics:** median total length (Mb): 4.59631  
median protein count: 3882  
median GC%: 47.6



# EMBL-EBI Protein Family database (Pfam)



## Pfam 34.0 (March 2021, 19179 entries)

The Pfam database is a large collection of protein families, each represented by **multiple sequence alignments** and **hidden Markov models (HMMs)**. [More...](#)

### QUICK LINKS

[SEQUENCE SEARCH](#)

[VIEW A PFAM ENTRY](#)

[VIEW A CLAN](#)

[VIEW A SEQUENCE](#)

[VIEW A STRUCTURE](#)

[KEYWORD SEARCH](#)

[JUMP TO](#)

### YOU CAN FIND DATA IN PFAM IN VARIOUS WAYS...

Analyze your protein sequence for Pfam matches

View Pfam annotation and alignments

See groups of related entries

Look at the domain organisation of a protein sequence

Find the domains on a PDB structure

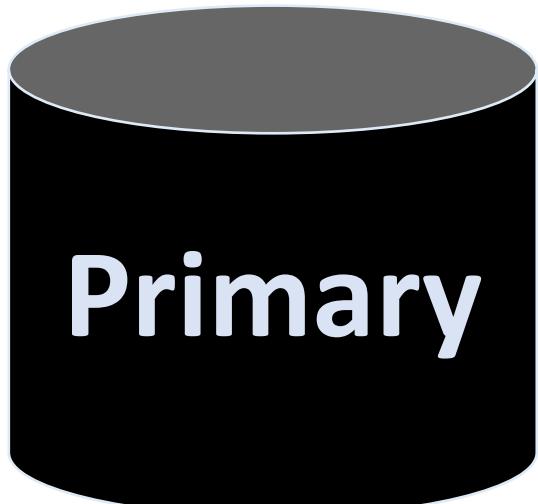
Query Pfam by keywords

enter any accession or ID [Go](#) [Example](#)

Enter any type of accession or ID to jump to the page for a Pfam entry or clan, UniProt sequence, PDB structure, etc.

Or view the [help](#) pages for more information

- Data derived from analyzing entries in primary databases
- Curated database with reduced redundancy



# Saccharomyces Genome Database (SGD)

The SGD homepage features a header with the SGD logo, "Saccharomyces GENOME DATABASE", a "MENU" button, and a search bar containing "search: actin, kinase, glucose". Below the header is a slide show of fluorescence microscopy images showing green foci and red nuclear pore complexes. A caption below the images reads: "Hsf1p-target genes (green) coalesce into foci after heat shock (nuclear pore complex, red). Image courtesy of S. Chowdhary and A. Kainth, Gross Lab, LSU Health Sciences Center." A series of small circular navigation dots is located below the images.

## About SGD

The *Saccharomyces* Genome Database (SGD) provides comprehensive integrated biological information for the budding yeast *Saccharomyces cerevisiae* along with search and analysis tools to explore these data, enabling the discovery of functional relationships between sequence and gene products in fungi and higher organisms.

- Subset of a primary database
- Specifically built for the specific needs of a community

[Explore SGD](#)



The background features a dark, abstract design composed of numerous thin, curved lines in shades of purple, blue, and red, creating a sense of depth and motion. Overlaid on this background are several text labels in a sans-serif font, which are partially cut off at the edges: 'MICROBES' at the top left, 'PROTEINS' at the top right, 'LIFECYCLES' at the bottom right, 'METABOLISM' at the bottom left, and 'DATA' in the center.

Looking at  
data  
availability  
statements



## Sources of gut microbiota variation in a large longitudinal Finnish infant cohort



### Data sharing statement

Sequencing data are accessible in ENA along with limited metadata (Study ID: PRJEB55243 <https://www.ebi.ac.uk/ena/browser/view/PRJEB55243>). Additional data can be obtained from the corresponding author upon reasonable request.

[Roosa Jokela<sup>a</sup>](#), [Alise J. Ponsero<sup>a</sup>](#), [Evgenia Dikareva<sup>a</sup>](#), [Xiaodong Wei<sup>a</sup>](#), [Kaija-Leena Kolho<sup>b c</sup>](#),  
[Katri Korpela<sup>a</sup>](#), [Willem M. de Vos<sup>a d</sup>](#), [Anne Salonen<sup>a</sup>](#)  

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The screenshot shows the ENA homepage with a teal header. The header includes the ENA logo (a green DNA double helix), the text "European Nucleotide Archive", and navigation links for "Home", "Submit", "Search", "Rulespace", "About", and "Support". To the right of the main content area, there are three small boxes labeled "Enter Examples", "PRJE Examples", and a question mark icon.

#### Project: PRJEB55243

The Health and Early-Life Microbiota (HELMi) is a birth cohort study of 1055 healthy Finnish children who are currently followed from birth until 4 to 5 years of age. The HELMi infant-parents 16S rRNA data set is derived from stool samples from infants collected from 3 weeks of age to 2 years, and their parents' (pregnant mother and father or other partner) stool samples collected in the weeks around delivery. Infant stool samples were collected at 3, 6 weeks and 3, 6, 9, 12, 18 and 24 months of age. The samples were collected by the parents at home and samples were stored at home at -20°C until being brought to the lab in frozen form. Upon receipt the samples were immediately stored at -80°C until processing. Fecal DNA was generated by repeated beat beating method and the 16S rRNA gene hypervariable V3-V4 region was amplified and sequenced using Illumina MiSeq or HiSeq sequencing technology. The study protocols have been approved by the ethical committee of The Hospital District of Helsinki and Uusimaa (263/13/03/2015) and are performed in accordance with the principles of the Helsinki Declaration. The guardians have provided an informed, written consent. participation is voluntary and the participants can withdraw from the study at any point. The study does not include any invasive procedures for infants.



### Sources of gut microbiota variation in a large longitudinal Finnish infant cohort



Roosa Jokela<sup>a</sup>, Alise J. Ponsero<sup>a</sup>, Evgenia Dikareva<sup>a</sup>, Xiaodong Wei<sup>a</sup>, Kaija-Leena Kolho<sup>b c</sup>,  
Katri Korpela<sup>a</sup>, Willem M. de Vos<sup>a d</sup>, Anne Salonen<sup>a</sup>  

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**Note: you are entitled to contact the corresponding author of any paper and ask to receive the original dataset used in a study.**

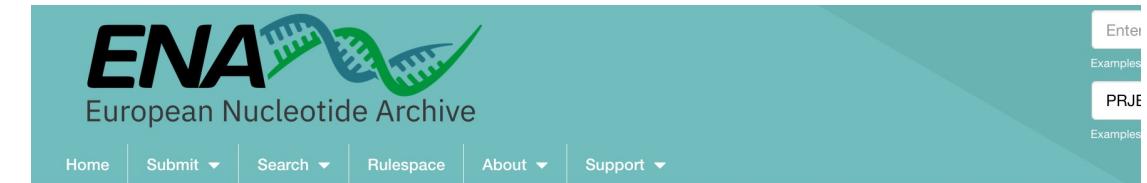
**Include in the email :**

- who you are
- why you want to reuse the dataset
- what part of the dataset you need

**But do not ask for sensitive data!**

### Data sharing statement

Sequencing data are accessible in ENA along with limited metadata (Study ID: PRJEB55243 <https://www.ebi.ac.uk/ena/browser/view/PRJEB55243>). Additional data can be obtained from the corresponding author upon reasonable request.



The screenshot shows the ENA homepage. The main title 'ENA' is displayed with a green DNA double helix graphic. Below it is the subtitle 'European Nucleotide Archive'. A horizontal menu bar contains links for 'Home', 'Submit', 'Search', 'Rulespace', 'About', and 'Support'. To the right of the main content area, there are three small rectangular boxes: the top one is labeled 'Enter Examples', the middle one is labeled 'PRJE Examples', and the bottom one has a question mark icon.

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# Modular Control of Human Movement During Running: An Open Access Data Set

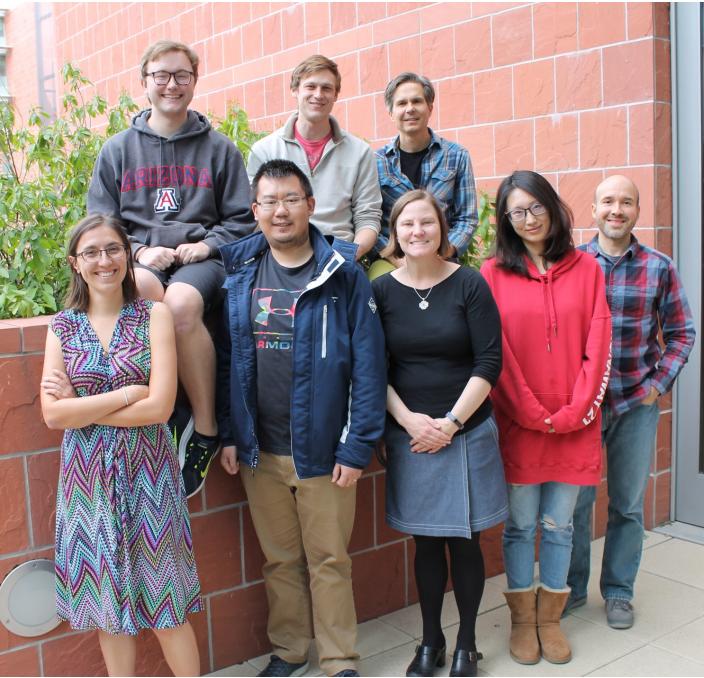
Alessandro Santuz<sup>1,2\*</sup>Antonis Ekizos<sup>1,2</sup>Lars Janshen<sup>1</sup>Falk Mersmann<sup>1,2</sup>Sebastian Bohm<sup>1,2</sup>Vasilios Baltzopoulos<sup>3</sup>Adamantios Arampatzis<sup>1,2\*</sup><sup>1</sup> Department of Training and Movement Sciences, Humboldt-Universität zu Berlin, Berlin, Germany<sup>2</sup> Berlin School of Movement Science, Humboldt-Universität zu Berlin, Berlin, Germany<sup>3</sup> Research Institute for Sport and Exercise Sciences, Liverpool John Moores University, Liverpool, United Kingdom

propulsion, early swing, and late swing. We foresee many possible applications of our data that we can summarize in three key points. First, it can be a prime source for broadening the representation of human motor control due to the big sample size. Second, it could serve as a benchmark for scientists from multiple disciplines such as musculoskeletal modeling, robotics, clinical neuroscience, sport science, etc. Third, the data set could be used both to train students or to support established scientists in the perfection of current muscle synergies extraction methods. All the data is available at Zenodo ([doi: 10.5281/zenodo.1254380](https://doi.org/10.5281/zenodo.1254380)).

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- It is an URL
- It is an identifier for the Zenodo website
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