

# *my.microbes* Study Information

## Package

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Thank you very much for your interest in *my.microbes*. The associated scientific study has the goal to lay a foundation for an improved understanding of microbial gut communities that live within us.

This document is split into the following sections:

1. Information section with details about the study
2. A detailed overview of costs associated with the study and how you can contribute
3. Informed consent section, which you will have to sign if you decide to join the study
4. Appendices: sample questionnaire, which you will have to fill online; information about sample collection procedure; a diagram showing the details of our sample and data handling procedures; a glimpse into the analysis results

Please study all sections carefully and do not hesitate to contact us if you have any questions. Since this is an expensive study requiring high quality data, we kindly ask the participants to help covering some of the associated costs through a contribution of at least 500 EUR (see the financing section starting on page 12). Larger contributions or even donations to assist with the financing of this research are welcome. Note that a donation is tax-deductible in most countries.

If you are willing to provide your stool sample, please understand that you will also have to provide a minimal set of personal information, which includes age, gender, body mass index (or weight and height), current area of residence, and smoking habits. This minimal information will, however, **not** reveal your identity. We assure you that your identity will be handled strictly confidential, and will be protected according to generally accepted principles of information security. The data analysts will not know your identity. However, you can also opt to let the analysts (and only them) have access to it to be able to contact you regarding unexpected scientific findings or feedback.

Together with the anonymised sequence data derived from your sample, this information will be utilized as part of the study while analyzing your microbiome, and may now and in the future be used in scientific publications

and in follow-up research, as well as shared anonymously with other study participants. If you want to monitor some aspects of the study, we could assist in providing you with information on your own sample. In this case, you have to specify whether you want to use the opportunity to share information with other participants.

You should understand that it is very unlikely that your results will have any immediate personal relevance, leading either to potential therapies or cures. At the moment, we are primarily trying to understand the basics of the interactions between our microbes and ourselves. Note however, that with the growth of our participant database and our knowledge about the subject, we are hoping to find relevant correlations between the microbial compositions and the health status in the future. We point already now microbial compositions that might be associated with some diseases according to some recent scientific studies.

If you are not willing to make any of your information public, despite it being anonymised, note that you CANNOT join the study. We are open to discussion about the issue, so please feel free to contact us with your questions or concerns.

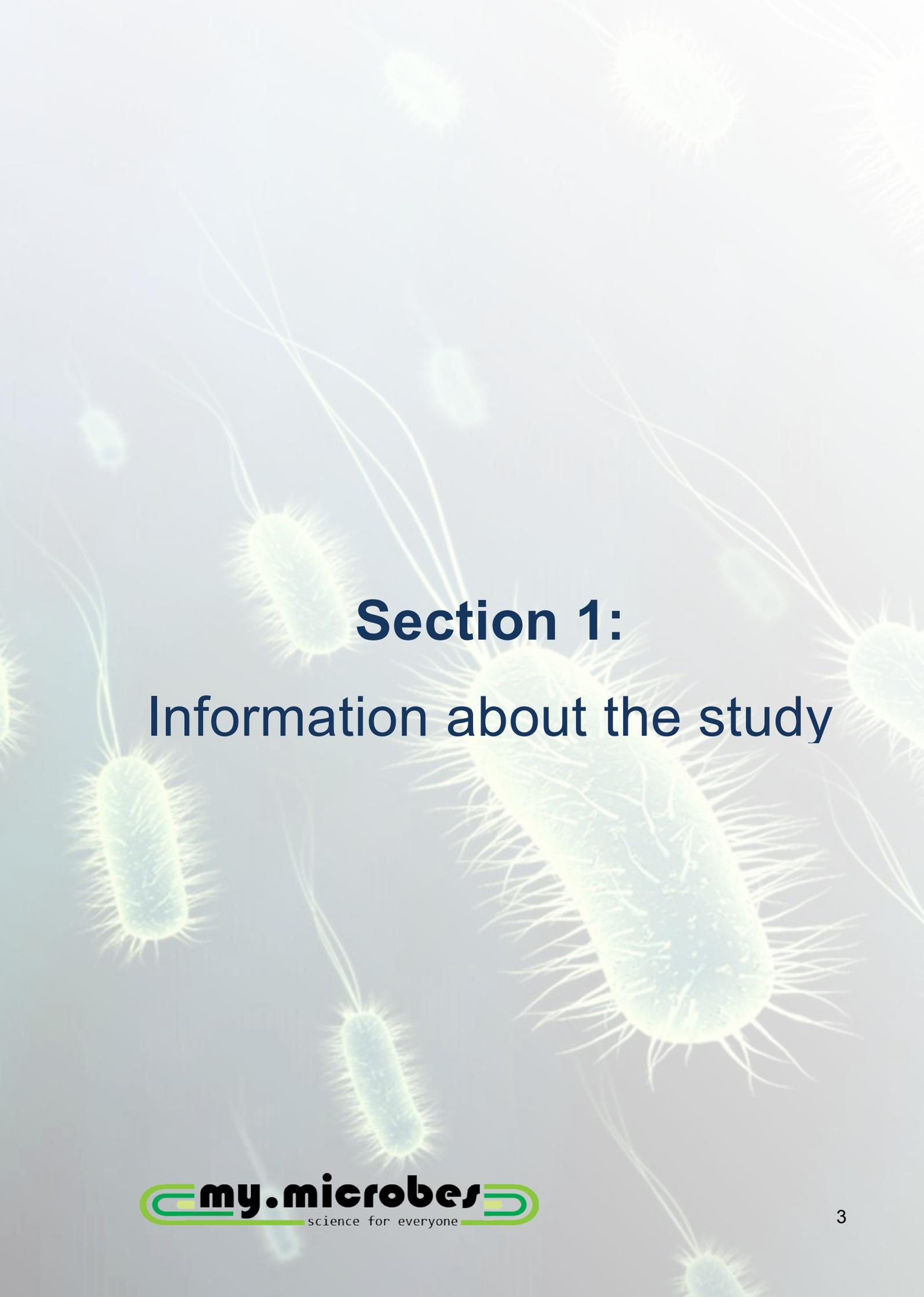
We hope you are as enthusiastic as we are about exploring the ecosystems within us and that you will decide to donate your sample in agreement with the terms described below.

If you have decided, after carefully checking all the information, to join the study, please sign the informed consent section and send it to our mailing address, written below. When we receive the signed consent form, we will send you a sampling kit and your personal participant ID, which will be used throughout the study.

Sincerely yours,  
*my.microbes* team

**Our mailing address:**

*My.microbes study*  
**EMBL**  
Meyerhofstr. 1  
69126 Heidelberg  
Germany



# Section 1:

## Information about the study

## Human microbiome research

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The human microbiome – that is, the assemblage of microorganisms that live inside and on the surface of our bodies – is estimated to outnumber our own cells by a factor of ten. It aggregates over a hundred times more genes as there are in the human genome. Scientists from all over the world have started to collect, decipher, and analyze human gut microbial samples. These microorganisms are known to perform useful functions, such as fermenting food material, producing vitamins, preventing growth of pathogens, etc. Moreover, scientific studies have indicated associations of the microbiome with immune disorders and metabolic diseases, such as inflammatory bowel disease, obesity and diabetes. Even links to neurological disorders have been suggested and there is also evidence that individuals can be classified into one of several gut types, which have recently been coined “enterotypes”. Taken together, studying the human microbiome is at the cutting edge and thus a very active field of research. Spurred by these achievements, we initiated *my.microbes* – a scientific study that aims at better understanding of our microbes based on a large cohort of at least 5,000 people. Using reliable data and statistics, we will tackle basic questions such as:

- **Which are the microorganisms that compose our microbiomes and what do they do?**
- **How variable are microbiomes between different individuals and geographic locations?**
- **Which microbes are inherited and which are picked up from the environment?**
- **Does a human being carry individual microbial strains and do we keep them over lifetime?**
- **Do all humans carry pathogens and when do they become dangerous?**
- **How can profiling our microbiomes become medically or nutritionally relevant in the future?**

Analyzing the composition and function of gut microbial samples will eventually contribute to an improved understanding of the balance between humans and their microorganisms, and its importance in health and disease.

## How does it work and why should I participate in *my.microbes*?

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The technology used to decode genetic material (DNA sequencing) and interpreting the information contained in the vast amount of data generated during this process has greatly advanced over the last decade. This approach is crucial to help answering the questions mentioned above. However, **the costs of DNA sequencing and data analysis still remain a major roadblock** for further advances. **But**, if we want to define what a “normal” state of the microbiome is and successfully detect deviations from it, **larger cohort sizes are the only key to success**. Thus, our primary goal is to ramp up the number and diversity of microbiome samples that will be analyzed in a global context to successfully address these questions.

With the initial goal of analyzing up to 5,000 samples from individuals with diverse backgrounds (nationality, age, disease groups, etc.), we will extract information (encoded in DNA) directly from a non-invasively collected stool sample. In case you want to donate a sample, we will ask for some data about your personal background (recorded by a questionnaire). Linking these data will provide us with a basis for analyzing your sample in the context of all other participants and prior knowledge. Thus, by participating in this project, your valuable contribution will help pushing forward the boundaries of current knowledge. Furthermore, you will be able to learn more about your own gut microbiome, if you wish (see next sub-section).

The Principal Investigator of the study is Peer Bork, PhD, who is a Senior Scientist and Joint Head of the Structural and Computational Biology unit at the European Molecular Biology Laboratory (EMBL). The study is conducted by researchers at EMBL with help of the French National Institute for Agricultural Research (INRA); the project has also links to specialized physicians. Thus, you can rest assured that a highly experienced team will process your sample with access to state-of-the-art laboratory, computational, and DNA sequencing resources.

## What can I learn about my own microbiome and other participants?

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It is important to note that human microbiome research is still in its infancy and assessing its practical potential is a long process that is currently in exploratory phase. The results obtained by analyzing your sample may help detecting deviations of your gut microbiome from the population average or even indicate potential associations to certain diseases, but they are preliminary in nature and currently do not have proven health relevance. Thus, we urge you to participate in this scientific study to help advance science and not for medical/diagnostic purposes or as replacement of medical advice by a physician,

both of which we cannot provide. **This study does not purport to produce medical information or to provide medical or health-related advice to participants.**

If you agree to these conditions, we can (optionally) extract, as a token of our appreciation, from our global database some data about your own gut microbiome. Due to this transparency, you directly monitor how your contribution was used. To give a brief overview (for details, please see Appendix IV), we will provide information on: (i) basic DNA sequencing statistics, (ii) deviations of your gut microbiota from the population average, (iii) your enterotype (i.e. which of the three microbial community types you harbor), (iv) general (i.e not personalized) overview of how your sample contributed to our analyses of antibiotic resistance potentials of gut microbiota in different populations, and optionally (v) other microbiota-related properties, such as associations with a growing number of actionable diseases (such as colorectal cancer, type 1 diabetes, type 2 diabetes, and inflammatory bowel diseases) whereby we only reveal details if such association is found to be statistically significant. Even though these properties are inferred from statistically solid information on the forefront of current scientific knowledge, it is important to understand that they are not yet backed by prospective clinical trials. In addition, the genetic imprint of your gut microbiome will be placed in the context of those from all other participants, where the more similar two samples are, the closer they will appear in this network.

Furthermore, **if you agree to share your data, we intend to enable you in the future to connect to other participants that are also willing to share information**, to learn more about their digestive diseases and clinical data, for example. We will also facilitate anonymous contact between participants who opt for allowing other participants to contact them. You will then be able to share experiences, remedies, and health/diet tips in your own responsibility. Your personal information will always be anonymous, unless you decide to share it with someone else.



# Section 2: Financing

# *my.microbes* study participation: financing and procedure

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This section gives an overview of the overall costs associated with the *my.microbes* scientific study and the financing needed. The overall cost of the study will be in the region of EUR 15 million. The expenses required with sample testing are significant, and exceed EUR 2,500 per sample. This is driven by the following:

- Staffing and technology. The study requires significant highly skilled scientists as well as the use of robotic, computer and sequencing equipment plus associated infrastructure and overheads
- Sample analysis. This is performed through collaboration between EMBL and biobyte solutions GmbH ([www.biobyte.de](http://www.biobyte.de)) whereby biobyte is taking on the routine work and some non-scientific aspects of this study. Note that biobyte solutions GmbH is an EMBL-affiliated company in which EMBL holds a minority stake, and its participation will be on an at cost-basis.

Since our resources are limited, we need to find financing of EUR 4 million to top up the funds which we have already secured. We would welcome financial contributions towards the costs of the study, where sums over EUR 500 would provide us with the security of funding we need to make the study viable and ensure the quality of open access published analysis.

## The procedure:

If you decide to join the study,

- 1) You need to confirm your interest and provide your address (by email or by visiting a dedicated web page: <http://my.microbes.eu/join>) to obtain your personal study **participant ID**.
- 2) You will then receive detailed instructions by email including a quotation from our logistics partner indicating the shipping costs, which are based on the address you provided in step 1.

3) You can then transfer your desired contribution to the overall costs (EUR 500 or more, plus the shipping costs, the exact amount of the latter depends on the address you provided). You will have to make sure that you include your participant ID in the transfer purpose field (which will allow us to link the payment to you) and the keyword OUR in the keyword field (which will make sure the full amount you transfer will reach our account). Please see the example below:

<b>Account holder:</b>	European Molecular Biology Laboratory
<b>Bank name:</b>	Commerzbank AG
<b>IBAN:</b>	DE41 6728 0051 0465
<b>SWIFT/BIC:</b>	COBADEFFXXX
<b>Transfer purpose:</b>	<i>COST CENTRE 17202 MY.MICROBES PARTICIPANT_ID</i>
<b>Keyword:</b>	OUR

## Analysis steps and costs per sample

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**Sample sequencing depth ( $\pm 30\%$ , giga base pairs)** 5 Gbp

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**Sample collection and processing (INRA or EMBL)**

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- Sample collection kit, shipped to participant's address (EMBL)
  - DNA extraction (INRA or EMBL)
  - Shipping of DNA to sequencing center (only in case of INRA)
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**Data processing and analysis (EMBL/biobyte solutions)**

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- DNA library preparation (EMBL)
  - DNA sequencing (EMBL)
  - Data storage (EMBL)
  - Cluster CPU cost (EMBL)
  - Microbes DNA screening (biobyte solutions)
  - Data cleanup / preliminary processing (biobyte solutions)
  - Maintenance and update of results (biobyte solutions)
  - Visualization (biobyte solutions)
  - Participant relations (biobyte solutions)
  - Various scientific analyses by specialized personnel (EMBL)
- 

**Current total analysis costs (full cost calculation)** 2662 €

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## Shipping of collected samples to Germany or France

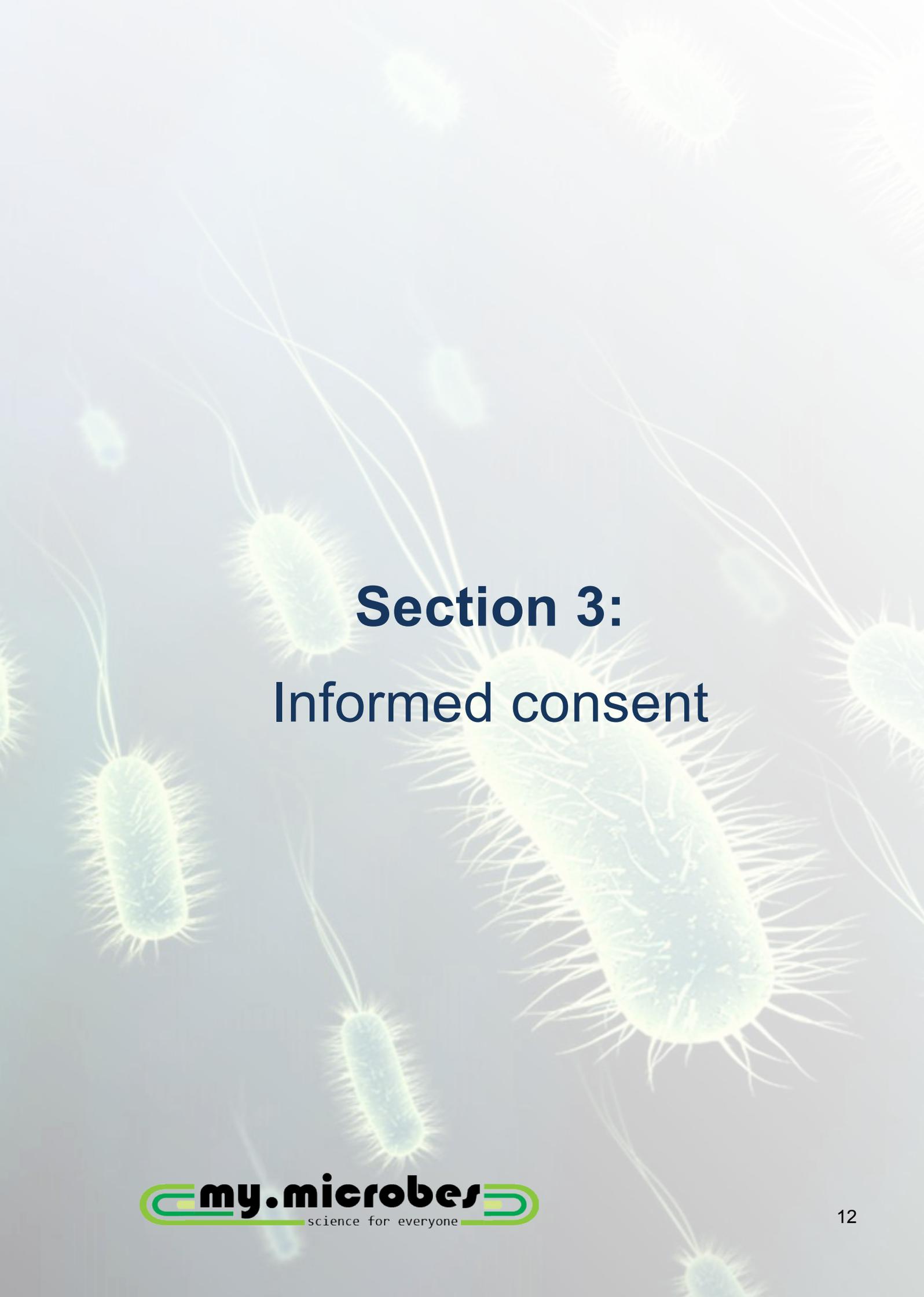
The success of the whole analysis critically depends on the amount of time between the stool sample collection and the initial DNA extraction, which takes place in Paris, France or Heidelberg, Germany. To make sure your sample reaches us in proper condition, it has to be kept at very low temperatures during transit. Therefore, the shipping costs listed are significantly higher than what you would expect for a normal package. You can organize the shipping yourself, but we can also arrange the shipping for you. In any case, **we have to ask you to take over the shipping costs**, in addition to your financial contribution.

### Notes:

- Approximate prices listed for a single sample are for one shipment. If you find other people interested in participation, shipping costs can be shared between up to 50 samples per shipment, which would significantly lower the total cost per person.
- The initial processing of the samples occurs either in Paris, France or Heidelberg, Germany. If you live nearby, or have a possibility of visiting Paris or Heidelberg, sampling can be arranged in both cities and sample transport would not cost anything. Note that for non-Europeans, a few days in Paris or Heidelberg for sample donation can be cheaper than shipping the samples!
- We can arrange the shipping for you and the final costs will be determined individually once you have decided to join the study. The shipping costs vary even within countries depending on the exact address.

Locations	Single sample	Bulk shipping*	Company
Within France	100 €	10 €	Cryoglobe
Within Germany	200-260 €	20-26 €	World Courier
Within Europe	230-350 €	23-35 €	World Courier
USA and World Wide	650-1550 €	65-155 €	World Courier

**\*Bulk shipping:** calculated on the basis of shipping 10 samples, however up to 50 can be sent in one shipment. It implies that if you find one other person to join the study, your own shipping costs will be cut in half already.



# Section 3: Informed consent

# Informed Consent to Participate in Microbiome Research

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Participant : \_\_\_\_\_  
(Last Name, First Name)

I have read the information about the study *my.microbes* and herewith consent to participate in this research project based on following terms:

The study, its methods of collecting the sample, and the methods of analyzing the data have been approved by the Ethics Committee of the European Molecular Biology Laboratory (EMBL). The study will be conducted in Germany where EMBL has its headquarter (to reduce costs, some samples might have to be sent to Paris for initial processing and subsequent delivery to EMBL). This is a limited study currently aimed at recruiting 5000 participants. EMBL may stop recruiting when this limit is reached.

I am an adult and willing to contribute my microbiome data to this study. Participation in this study is voluntary. To support the financing of this important research, I will contribute **at least EUR 500**. My contribution supports the scientific research and helps offset part of the study costs, the rest of which is covered by the involved institutions and scientists.

I guarantee that I will provide **my own fecal sample** (and not a 3<sup>rd</sup> party's). I will collect the sample and preserve it according to the instructions received from EMBL until collected by the shipping company. I am aware that I face minimal risks or inconvenience while participating in this study.

- In case of a security breach, personally identifying information, my microbiome data and answers to the questionnaire may be stolen. But although EMBL cannot provide a 100%-guarantee that my personal information will be safe, I have been informed that strong security measures will be employed to minimize the risk of a security breach.
- I acknowledge that EMBL does not provide compensation or treatment in the event of an injury resulting from participating in this study and that, to the extent permitted by law, any liability in that respect is excluded.

I understand that EMBL will perform a screening procedure to estimate the amount of microbial DNA in my sample and will not process the sample further for inclusion in the study if the microbial DNA content is not enough to perform the sequencing and/or analysis. I have been informed that in such an event I can either get my contribution refunded or opt to send newly collected fecal samples

by paying the extra shipping costs. I agree that EMBL is not responsible for results obtained from samples that were mishandled during collection, storage at home, or transportation to them.

I confirm that participating in this study is permitted in my country of residence, and notably that providing fecal sample does not violate the laws of export of biological material in my country of residence, especially related to fundamental research.

By providing my fecal sample, I transfer the property on it to EMBL, which will use it for research, particularly for the study *my.microbes*. EMBL may also use the material for other research related to the subject of this study. In any event, my personal information will be protected. EMBL will use my sample in an efficient manner as part of the study. All samples will be stored deep-frozen for a maximum of 10 years at EMBL or on its behalf in the French National Institute for Agricultural Research (INRA) in Paris.

I further agree to provide **Minimal Required Information** about me that will **not reveal my identity**. These are: year of birth, gender, height, weight, smoking status, dietary habits, country of birth, nationality, ethnicity and current location. This information will be used while analyzing my microbiome and may be used, now and in the future, in scientific publications and follow-on research. I agree to make this Minimal Required Information publicly available without revealing my identity.

I may optionally provide additional personal information, including disease status. If I provide this information, it will be used while analyzing my microbiome and may be used, now and in the future, in scientific publications and follow-on research. My identity, however, will always remain anonymous and confidential. I guarantee that **I will not falsify any information I provide to EMBL**.

I also agree to make my microbiome data publicly available along with the Minimal Required Information. I understand that the fecal sample may contain some of my own DNA and that in some cases (e.g., bloody stool, inflammation in the intestine) there might be a significant amount of my own DNA in the sample. Although EMBL will try to remove these DNA sequences to the best of its ability using all currently publicly-available human reference genomes and state of the art technology, I understand that it is possible for traces of my own DNA to remain in the publicly available microbiome data.

I further understand that it is currently not possible to identify me from my microbiome data, but there is a risk that technological developments in the future may make this possible. In such an event, I understand that I have the choice to ask EMBL to not make my microbiome data public anymore.

Any and all intellectual property rights derived from research made using my microbiome data belong to EMBL. Intellectual property rights shall include, but not be limited to, discoveries, know-how, inventions, copyrights, trademark, trademark applications, patent applications, patents, together with any divisions, continuations, continuations-in-part, reissues or extensions thereof and any future national or foreign patents or patent applications which may issue therefrom.

I have been informed that at any time I can withdraw my participation in the study and ask for the disposal of my fecal sample and that in case of such withdrawal, my microbiome data will not be used in the study. However, I accept that my contributions generally cannot be refunded. EMBL may decide, at its sole discretion, to end my participation in this study at any time. In such event, I may ask EMBL to refund my contribution.

## Optional access to a subset of data related to my own microbiota

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If I participate in this study, I can opt to receive partial access to the data generated by the study. As a token of appreciation, EMBL will provide an identifier code, so that I can see some aspects of the study related to my own microbiota that illustrate what my contribution was used for. I can also choose to have the raw sequence data of my sample delivered to me. Within the framework of the study, EMBL will use best efforts to elucidate the **composition and gene repertoire of participants' microbiomes** and infer some information that might become useful in the future, such as which enterotype a sample belongs to, or whether a sample contains a subset of microbiota that has in external scientific studies been associated with a particular disease. However, my participation in this study is **for research and educational purposes only** and I will not receive any official medical advice. The results of the study need to be independently validated before they can have therapeutic value. **I have understood that this study does not intend to produce medical information or to provide medical or health-related advice to participants.**

Very little is currently known about our microbiota, but the knowledge is constantly expanding, so that the results of my microbiome analysis may have medical relevance in the future. However, I understand that only a trained physician familiar with my medical history may then be able to interpret the report and assess any medical relevance. I acknowledge that the my.microbes team, comprising basic researchers, is not qualified to provide me with any interpretation of the results in relation to health or disease. I have also been informed that similarities of my microbiome to disease-specific microbiomes do **not** mean that I am predisposed to such disease. EMBL is not liable for any misinterpretation of the study results.

## Privacy and Security

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I am aware of the fact that for participating in this study sensitive personal information about me will be collected, stored and used. The use of my data will be in accordance with applicable laws and is based on my consent.

1. I agree that in the course of this study personal information about me will be collected (electronically and/or on paper) and stored on electronic data processing media at the EMBL headquarter. My data will be stored in pseudonymised (encrypted) form. EMBL will use a double blind encryption scheme. My name and contact information will be kept strictly confidential. If results from studying my microbiome will be published, my identity will not be revealed.
2. My microbiome will be analyzed by scientists who will be unaware of my identity unless I explicitly specify that the analysts are allowed to know it. Prior to analyzing my microbiome, the scientists will remove any information that can identify me (such as name or address, but also any currently identifiable human DNA). In some instances, also some of the Minimal Required Information will be removed if it may reveal my identity. I understand that it is currently not possible to identify me from my microbiome data, but there is a risk that technological developments in the future may make this possible.
3. Personal and/or genetic information will not be shared with my employer or insurance companies, nor will it be used in any way other than mentioned in this document.
4. I can voluntarily share my data and opt to be contacted by others (e.g., participants with similar health conditions or similar microbiome communities). All communication will be anonymous unless I personally share contact information with other participants.
5. Envisioned communication between participants of the study is out of their own interest and initiative. EMBL will facilitate this communication so that I and other participants can share experience and useful tips. Any information in such communication is the opinion of the individual sending the message and not the opinion of the study organizers. Additionally, any such communication shall **NOT** be considered as medical advice.
6. I agree that EMBL may use my personal data for further scientific research and that EMBL may contact me if after this study further scientific questions arise. For research and publication purposes my pseudonymised or anonymised data may be shared with other scientific institutions.
7. I agree that the personal data I provided in order to participate in the study will be stored for a maximum of 10 years at EMBL after the end of the study. After this period my data shall be deleted, except data I chose to communicate to other participants as indicated in Nr. 4 and 5 above. Even in this case, my rights of data access, correction and deletion remain unaffected.
8. I have been informed that at any time I can withdraw my consent to participate in the study and to the use of my data. After a withdrawal, my microbiome data will not be used in the study.

## Contact information

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If you have any questions or concerns about this study, please do not hesitate to contact us at [contact@my.microbes.eu](mailto:contact@my.microbes.eu).

## Signature

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I have read this document and the study information and understand them completely. I agree to the above conditions of participation in the study and volunteer to participate in the study. I also confirm that I have received all required permissions and clearances relevant to participation in this study.

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First and Last Name of Participant

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Place, Date  
Participant

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Signature of the



# Appendix 1: Questionnaire

You will have to fill the following questionnaire if you decide to join the study. This is just an example to give you an idea about the information we require. The actual questionnaire will be provided via a secure online form.

## Essential information (required)

*Answering the questions in this section is mandatory and this data will be used anonymously in our network.*

1. What is your birth year ?  
Date: (YYYY)
2. What is your Height ?  
Your height in centimeters :    cm or in feet-inch :    '    "
3. What is your Weight ?  
Your weight in kilograms:    kg or in pound :    lb
4. What is your gender ?  
 Male     Female
5. Are you a smoker ? If no, are you an ex-smoker ? (select one)  
 Yes     No     Ex-smoker
6. What is your usual diet? (select one)  
 Omnivorous     Vegetarian     Vegan     Other  
If you selected 'other' please describe here (e.g. diabetics):
7. What is your country of birth ?
8. What is your nationality ?
9. What is your ethnicity ?
10. What is your country of residence ?
11. In case we identify microbiota subsets that have been linked to diseases in external studies (but are not yet backed by prospective clinical trials), do you wish to have access to this information? If you select 'No', this information will not be accessible to you, but will still be available to the data analysis team in anonymized form. Please note that you may be obliged to disclose such information about disease markers or disease associations vis-à-vis insurance companies (e.g., before concluding new insurance contracts) or other institutions in the future.  
 Yes     No
12. In case we make a potentially interesting finding during the analysis of your sample, do you consent to be contacted by our data analysis team? This will make your email address available to the scientists

performing the analysis, and will allow them to ask you direct questions. All the scientists involved will have signed a **Non-disclosure Agreement** protecting your personal information.

Yes       No

## Digestive diseases information (required)

Have you been diagnosed with a digestive disease?  Yes  No

If **yes**, please indicate your disease(s) from this following list (Multiple choice is possible):

- 1) Barrett's Esophagus
- 2) Celiac Disease
- 3) Digestive Cancer:
  - a) Colorectal
  - b) Stomach
  - c) Esophageal Cancer
  - d) Pancreatic
  - e) Liver and Biliary
- 4) Diverticular Disease
- 5) Duodenal Ulcer
- 6) Dyspepsia
- 7) Gastric Ulcer
- 8) Gastroesophageal Reflux Disease
- 9) Hepatitis
- 10) *H. Pylori* infection
- 11) Inflammatory Bowel Disease
- 12) Crohn's Disease
- 13) Ulcerative colitis
- 14) Irritable Bowel Syndrome
- 15) Lactose Intolerance
- 16) Liver Disease
- 17) Pancreatitis
- 18) Others diseases ? (free text):

## Voluntary clinical information (optional)

Please answer the following questions only if you are completely sure. The more questions you answer the more fine-grained will be our analysis of your sample.

- 1) What is your sagittal diameter ?  
Your diameter in centimeters (integer):      cm or in inch:      "
- 2) What is your blood type ? (select one)  
 A+  A-  B+  B-  O+  O-  AB+  AB-
- 3) Have you taken antibiotics in the last 2 months ?  Yes  No
- 4) Can you indicate your mode of birth ? (select one)
  - a. How ?  Cesarean section  Vaginal
  - b. Where ?  Hospital/Clinic  Home
- 5) Can you indicate if you were breastfed during your infancy ?  
 Yes  No  
If **yes**, can you indicate how long ? (select one)



## **my.microbes experience sharing**

*Sharing your metadata within our network will increase the scope of my.microbes study.*

Do you want to receive your personalised results (free of charge) to be able to monitor some study aspects and learn more about you own microbiota ?

Yes  No

If **yes**, then please specify whether you are willing to share personal infos to connect with others:

1. Do you want to anonymously share your **digestive disease information** in *my.microbes* network ?  
 Yes  No
2. Do you want to anonymously share your **voluntary information** in *my.microbes* network ?  
 Yes  No
3. Do you want to be contacted by others who have similar microbial profiles?  
 Yes  No

If you want to share additional information or if you have a special request, please fill the box below:

SAMPLE  
Do not fill



# Appendix 2: Sample collection procedure

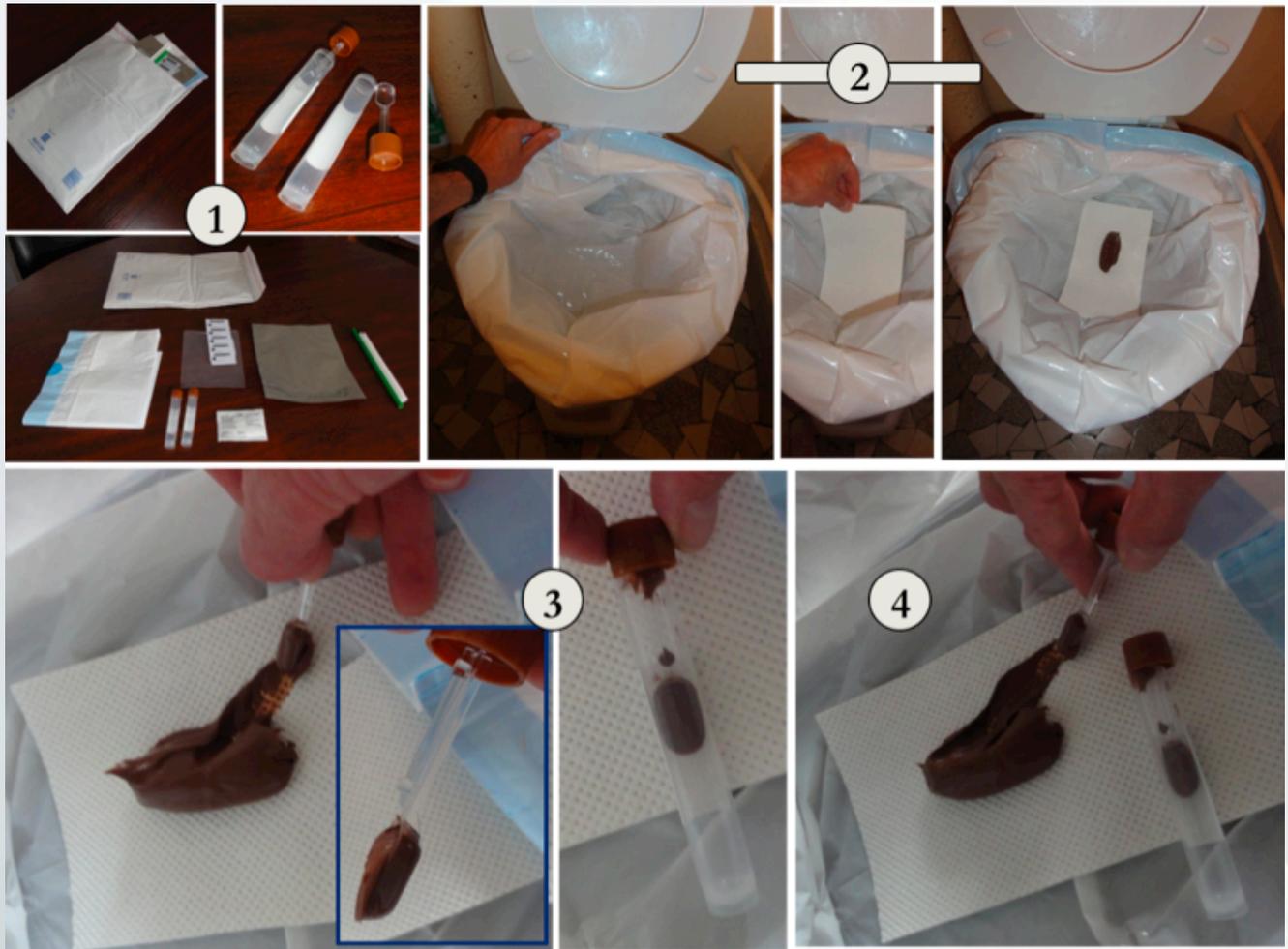
## Self-collection of fecal sample for laboratory analysis

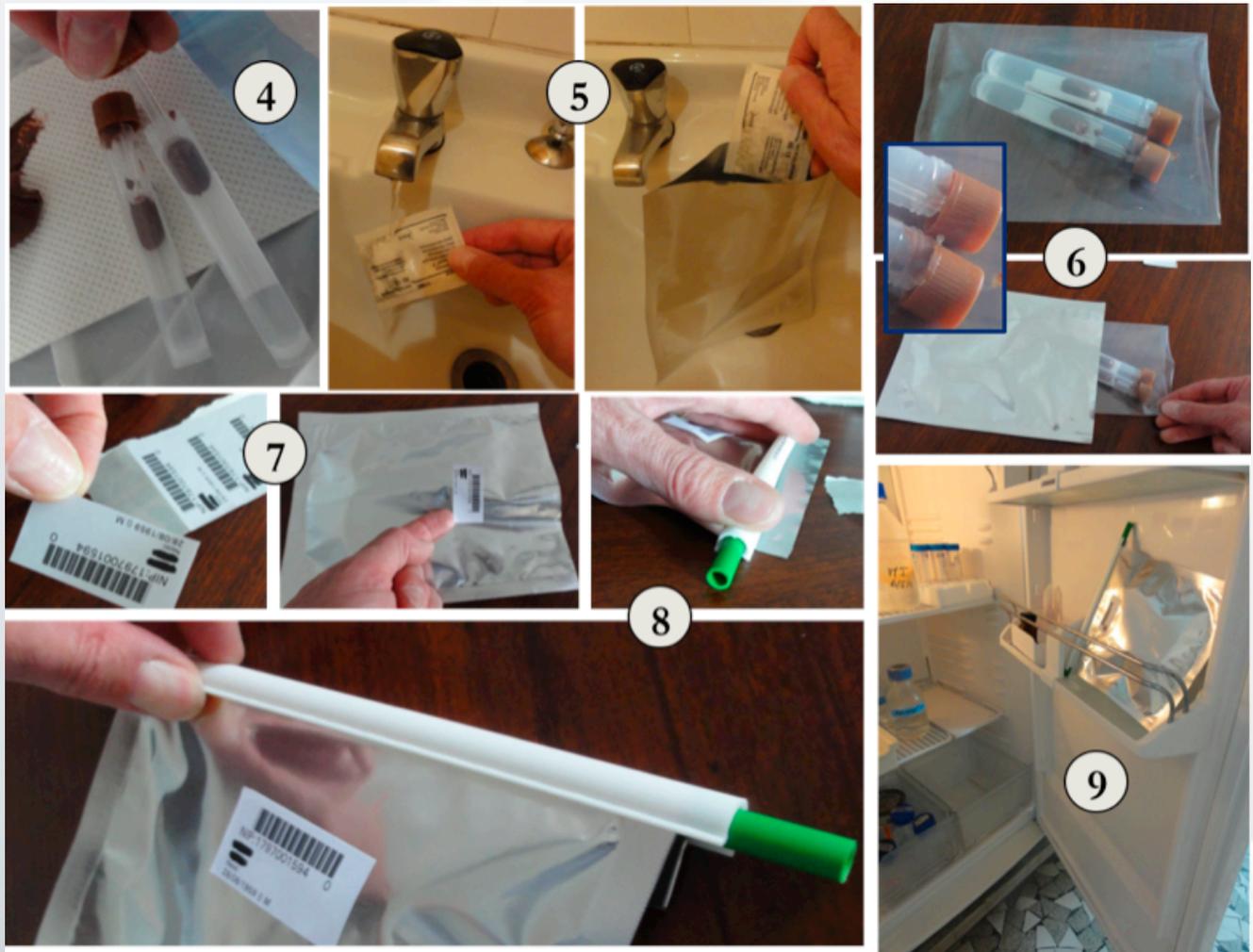
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Please follow the steps using the pictures as a reference (numbers correspond to numbers in the pictures):

1. Use the complete kit that you received by mail. It contains:
  - i. A plastic lining to cover the toilet
  - ii. A tissue lining to put inside the plastic lining
  - iii. Two plastic tubes with a spoon attached to the lid
  - iv. A small transparent plastic bag
  - v. A series of labels
  - vi. A large opaque plastic bag
  - vii. A small sachet of catalyst
  - viii. A clipping system to close the large opaque plastic bag
2. Place the plastic lining over the toilet bowl. (Note: it is better if you urinate before fecal sample collection). Then place the tissue lining inside the plastic lining.
3. After defecation, fill up a first spoon with feces. Do not overfill; insert spoon in its tube and **DO NOT CLOSE** the tube.
4. Repeat as for 3 with the second spoon.
5. Wet the sachet of catalyst for a few seconds under a small flow of water, and insert the sachet in the opaque plastic bag.
6. Insert the two plastic tubes (NOT CLOSED) into the small transparent plastic bag, and insert the small plastic bag with the tubes into the large opaque plastic bag.
7. Take one label and place it on the opaque plastic bag (add information as prescribed).
8. Use the clipping system to close the opaque plastic bag tightly. The best way is to place the green tube underneath and the white clip above, and to press hard starting at one end.
9. Place the opaque plastic bag with tubes and catalyst in your fridge or freezer (-20 to 8 °C).

Then follow the instructions for your sample to be picked up and delivered to the laboratory.





10. As shown here, you may flush the remaining feces in the toilet and dispose of the plastic lining as regular garbage.



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# Appendix 3:

## Sample and data handling



# Appendix 4:

An example of a subset of results that  
will be made accessible

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## DNA sequencing statistics

The following table gives an overview of basic statistics of the DNA sequence which was extracted from your sample.

Raw DNA amount:		15,346,005,086 bases (15.35 Gb) which is <b>206.9%</b> above average
High quality DNA:		12,604,063,163 bases (12.60 Gb) which is <b>152.1%</b> above average
Human DNA contamination:		0.175082%, which is <b>very low</b>

## Highlights of detected deviations in your sample

### Microbial genera/species with highest deviation from population average

The following microbial genera/species are present in high abundance in your sample, compared to our current participant population (921 samples).

[Detailed information and disclaimers](#)

Genus	Deviation
<i>Eubacterium</i>	<b>+88.14%</b>
<i>Sutterella</i>	<b>+45.61%</b>
<i>Capnocytophaga</i>	<b>17.57%</b>

Species	Deviation
<i>Eubacterium siraeum</i>	<b>+92.32%</b>
<i>Eubacterium eligens</i>	<b>+30.71%</b>
<i>Bacteroides dorei</i>	<b>+3.48%</b>

## Enterotyping analysis

Your enterotype is "ET 1" with a classification confidence of **91.5%**.

**Enterotype 1** is enriched in the bacterial genus *Bacteroides* and is also referred to as the *Bacteroides* enterotype. *Bacteroides* is one of the most abundant groups in the human gut. It is present at a detectable level in almost all humans, but it is found in significantly elevated levels in this enterotype.

Recent research has suggested that *Bacteroides* enterotype may be linked to long-term protein and animal fat diet.

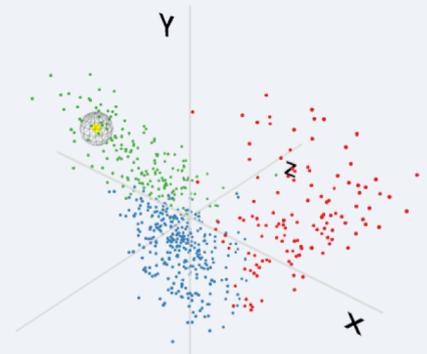
**29.5%** of our participants belong to this enterotype.

**Legend**

- Enterotype 1
- Enterotype 2
- Enterotype 3

**Help**

Click and move the mouse to rotate the view. Zoom in and out using mouse wheel. Your sample is represented with a larger yellow dot.



## Other microbiota-related properties

### Subset of microbiota that has been associated with individual diseases

Based on the analysis of your gut microbiota composition, we have detected the presence of the following possible disease markers.

**Disclaimer:** These associations have been shown only in limited cohorts, and have not been validated through independent large-scale clinical trials.

[Detailed information and disclaimers](#)

Disease	Association
<i>Colon cancer</i>	<b>increased compared to average population risk</b>
<i>Diabetes type 2</i>	<b>within average population risk</b>
<i>Crohn's disease</i>	<b>within average population risk</b>

**Legend**

**Distance to population average**

**CLOSE** **DISTANT**

Colors only represent the deviation from population averages, and are NOT directly related to your health status. Click the help icon in each table for detailed information.

## Overview of a subset of analyses and expected results

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### 1. DNA sequencing statistics

We expect to sequence ca. **5 gigabases of DNA, or 5,000 million bases** (for comparison, the entire human genome is encoded in about 3.3 gigabases) although the actual amount of DNA sequence varies for each sample so that we will give you some statistics about the particular sample. Note, that there is an expected low fraction of sequences originating from the human genome that is removed prior to further analysis.

### 2. Microbial composition analysis

We calculate a breakdown of the amounts of the microorganisms that are detected in a gut microbial sample and summarize them at two levels of taxonomic resolution, species and genus. Results for the highest deviations from the population average are highlighted (all in comparison with >1000 other individuals). An example figure showing detailed microbial composition on a genus level can be seen on page 34.

### 3. Functional analysis

We carry out basic functional analyses to determine what functions your microorganisms are capable of. For example, some microbes that reside in our guts can produce vitamins that we cannot produce ourselves. Our analyses extract indications of how abundant such functions are in each gut microbial sample.

### 4. Antibiotic resistance potential

The antibiotic resistance potential is calculated for each gut microbial sample and put into context of both the whole study population and also the participant's country of residency. Even though we cannot provide individual results for each participant (due to ethical concerns as nobody can correctly interpret these results yet), a general overview of the results and the information of how each sample contributed will be available.

### 5. Enterotype analysis

Gut microbial samples can be classified into one of several major gut microbial types called "enterotypes" based on the microbial composition of a sample. We determine which of these enterotypes each sample belongs to and place it in a global network where the most similar samples will be closest in distance.

### 6. Analysis of disease-associated microbiota

In external studies on diseased vs. healthy individuals, certain microbiota have been found to differ in specific disease states. We screen for this subset that may be indicative for a certain actionable disease (e.g. colorectal cancer, type 2 diabetes, or inflammatory bowel diseases). Note that these associations have been shown only in limited cohorts, so there is no proof yet that these trends hold in the total human population. In case of an association, which may imply an increased risk, a

collaborating physician specialized in this particular disease will be notified. He/she will evaluate the data (anonymously) and provide direct feedback as a comment in our results database. If needed, he/she will recommend further consultations with a local doctor or specialist. Note that this part of the analysis is optional, has to be specifically agreed upon in the questionnaire, and is not intended as medical advice, just as a reporting of the status of sample's microbiota with respect to the respective studies.

## 7. **Global context analysis and science for everyone**

We place all results in the context of previously collected data. Thus, it is possible to determine how similar each gut microbial community is to those from any other sample. Participants that agree to share their data will be able in the near future to obtain more information about other participants without knowing their identity, for example, about their digestive diseases and clinical data. Your participation may thus lead to discoveries that go beyond the actual scope of this study.

### **An example detailed overview of microbial composition at the genus level**

(The Y-axis is the % of the total microbiota in your sample, the grey boxes indicate the distribution of the respective genus in >1000 samples from our database and red dots indicate an unusual abundance compared to the >1000 other samples)

## Microbiota composition analysis

These graphs show how your personal gut microbiota compare to the averages of our current sampled population. In your sample, a total of **79.5%** of all assembled sequences were successfully mapped to a microbial genus, and a total of **71.1%** were mapped to a microbial species. The raw data can be downloaded in plain text, tab-delimited format: [genera mapping data](#) or [species mapping data](#).

### Graph display options

Select the desired display parameters below and click the 'Display chart' button. For detailed explanation of each parameter, simply hover your mouse over the control. Similarly, detailed information about any point in the chart will be shown when you hover the cursor over it.

Display    from  sorted by  [Display chart](#)

