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Gut metagenome associations with extensive digital health data in a volunteer-based Estonian microbiome cohort

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## Outline

#### PART I Estonian Microbiome cohort

### PART II Lessons learned and ongoing work

#### PART III

#### Microbiome studies in the Estonian Biobank

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# Estonian Biobank



OMICS profiling	Sample size
Whole genome sequencing	3,000
Whole exome sequencing	2,500
Genome-wide genotyping arrays	200,000
Microbiome (Metagenomics)	2,509
Genome-wide methylation arrays	821
Genome-wide expression arrays	1,100
mRNA sequencing	600
Total RNA sequencing	50
Metabolomics (NMR)	10,840

## Initiation of the Estonian Microbiome Cohort (EstMB) in 2017



10000

5000

5000

Estonian population by age 01.01.2020

## Electronic health records allow to track individual health trajectories

- Health Insurance Invoices;
- Prescriptions;
- Estonian Cancer Registry;
- Estonian Causes of Death Registry;
- Estonian Cancer Screening Registry;
- Population Registry;
- e-Health;
- The North Estonia Medical Centre;
- Tartu University Hospital





ARTICLE Mttps://doi.org/10.1038/s41467-022-28464-9 OPEN Gut metagenome associations with extensive digital health data in a volunteer-based Estonian microbiome cohort

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Diversity of the gut microbiome is associated with more than 100 factors representing lifestyle, health, medical procedures and drug usage



B Pearson correlation with microbial alpha-diversities; \* FDR<0.05

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# Not only recent antibiotic usage, but long-term and history of antibiotic usage is associated with the gut microbiome



**Removed recent users** (within the last 6 months)

Summarized the amount of prescriptions over the **last 10** years



### Long-term antibiotic usage contributes to "common dysbiosis" and adjusting for it helps to identify disease-specific signals



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# Antibiotics usage history can influence the results of microbiome-based diagnostic tools



Elastic net models to predict a disease (10 data splits)

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#### The long-term usage of antibiotics is reflected in the microbiome composition

What about other drugs and their long-term effect?



#### **Antidepressant usage shows similar "accumulation" effects**



#### Antibiotics usage shifts the microbiome composition

What will happen next, does it lead to higher risk for some diseases?



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### **Microbiome studies in Estonian Biobank**

#### Estonian Microbiome project

MB samples:

- Oral microbiome data
- Longitudinal data (2<sup>nd</sup> time-point MB sample collection)

Study focuses:

- Microbiome assembled genomes (MAGs)- new strains, genetic variations etc.
- MB-drug interactions
- Association with Incident diseases

#### CLINICAL cohorts

- Gut-health related diseases (colorectal cancer, IBD)
  - MB biomarkers
- Metabolic diseases (T2D)
  - drug-MB interactions
- Microbiome and women's health (PCOS, infertility)

#### **Microbiome and antidepressants usage**



#### Improving early (personalized) CRC screening



Same probes used for occult blood tests in CRC screening programs can be also used for microbiome anaysis





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- Anu Reigo
- Steven Smith
- **Prof Andres Metspalu** ۲

Web: https://genomics.ut.ee/et/teadus/





**EMBO** 

Euroopa Lii

Euroopa

Regionaalarengu Fond

Eest

**Mobilitas** 

ESF programm



#### **ESTONIAN MICROBIOME PROJECT EstMB**



Lennart Meri (President of Estonia, 1992-2001)



